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چهاردهمین گنجره بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Abstracts for Oral Presentations

آدرس دبیرخانه:

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چهاردهمین گنگره بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Title: Significant reduction of essential trace elements of iron, selenium and zinc in patients with Coronavirus disease

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Abstract

Nowadays, the vital role of mineral elements in all biological activities, especially enzyme reactions, has been well clarified, so that some of these elements in very small amounts give additional power to cellular activities. The outbreak of the corona virus disease made it clear the necessity and importance of administration of zinc supplement along with anti-inflammatory drugs in the prescriptions of infected patients. Plenty of the research works were conducted on the role of these elements during the spread of the global and deadly corona virus, and a review of recent researches and data obtained from meta-analysis shows that among the 5 essential elements for humans, which include magnesium, copper, iron, zinc and Selenium, the last three elements have had a significant decrease in most patients with coronavirus, compared to healthy people. Even the trend of reducing these elements has been associated with the severity of the disease. However, they have not seen any significant difference between the amount of two elements copper and magnesium in severe and non-severe disease and in survivors and those who died due to this disease compared to healthy people. In this session, the importance of each of these elements will be discussed in order to clarify the necessity of prescribing these elements in affected people.

Keywords: Trace elements, Fe, Se, Zn, Coronavirus disease

Visceral and Cutaneous Larva Migrans

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Abstract

Human visceral and cutaneous larva migrans (CLM and VLM) are caused by a group of nematode zoonoses. The most common causative agents of human CLM are the helminths of gastrointestinal tract of carnivores including: *Ancylostoma caninum*, *Ancylostoma braziliense*, *Ancylostoma tubaeforme* and *Uncinaria stenocephala* and nematodes of the small intestine of ruminants and camelids including: *Bunostomum phlebotomum* in cattle and *B. trigonocephalum* in sheep and goat. Many of these agents are prevalent in carnivores and ruminants in Iran. So, the potential of the disease is present and prevalent in Iran. Their larvae causing cutaneous larva migrans or creeping eruption lesions while penetrating into the skin of human. However, due to misdiagnosis it is rarely reported in Iran. Similarly, human intestinal hookworms (*Ancylostoma ceylanicum*, *Ancylostoma duodenale*, and *Necator americanus*) penetrate the skin and cause a localized pruritic, erythematous, popular rash that resembles a cutaneous eruption. CLM is distinct from the cutaneous manifestations of *Strongyloides stercoralis* infection called larva currens. The latter shows rapid movement in the skin. Other non-larval cutaneous migrations, including loiasis, scabies, or larva with dermal penetration, are also excluded from CLM. The prevalence of cutaneous larva migrans (CLM) certainly depends on factors including the presence of infected dogs or cats and contact with soil. In some studies, conducted in people who had constant contact with the ground and wet sand, 58.2% showed signs of infection. Usually CLM is diagnosed by clinical manifestations. Biopsy is not recommended. Optical coherence tomography (OCT), which is potentially able to visualize structures in the skin with an 8 micro m resolution has been used for diagnosis. Inventing new microscopes which is able to observe under skin could be useful for diagnosis. Visceral larva migrans (VLM) results from the migration of specific helminth larvae into various human viscera. Eyes and central nervous system may also be infected. The disease is caused mainly by *Toxocara* species including *T. canis* and *T. cati*, but human VLM due to other helminthic agents has also been reported. Ingestion of *Toxocara* spp. embryonated eggs, raw and uncooked meat, liver and giblets are common rout of infection to VLM. The prevalence of *Toxocara* in Iran is different [(Soil contamination: 3.9-78.0%), (Canis familiaris: 18.0-31.0%), (Felis catus: 22.6-43.4%)]. Iranian people have different prevalence rates of *Toxocara* antibodies (9.8-37.7%). Diagnosis of the disease is based on clinical and paraclinical tests. Using laboratory tests especially application of recombinant antigens is promising for human diagnosis. Keeping pets in home without awareness of their zoonotic parasites is a potential source of human infection which should be considered well.

Comparison of peripheral blood cell morphology in ICU and non-ICU patients with Covid-19: A descriptive cross-sectional study

کوشر حسینی © (P),^۱ فخرالدین صبا
اعلوم پزشکی کرمانشاه

نوع پذیرش: oral | کد مقاله: G-03614

Abstract: *Background:* This descriptive-analytical study investigated the peripheral blood morphologic changes in Covid-19 patients. The purpose of this study was to demonstrate the abnormal blood cells morphological changes of COVID-19 patients to predict any specific abnormalities that could help in the prognosis and initial diagnosis. *Materials and Methods:* A total of 150 Covid-19 patients admitted to the Golestan Hospital, Kermanshah University of medical sciences, including 96 ICU patients and 50 non-ICU patients and 50 controls were recruited in this study through simple random sampling method. All cases were men and had no hematological malignancies and thalassemia. Blood cell Morphology has been studied on samples of blood taken from 200 samples by the hematologist. *Results:* Count of Leukocytes and neutrophil were significantly higher in patients with covid-19. However, red blood cells, hemoglobin, hematocrit, and lymphocytes in patient group were significantly lower. Comparison between ICU and non-ICU patients demonstrated, lymphopenia (P0.01), microcytosis (P0.05), macrocytosis (P0.05), bite cell (p0.01), schistocyte cells (p0.01), and polychromasia (p0.01) in ICU patients. Also, there was no significant difference thrombocytopenia, giant platelets, neutrophilia and rouleux formation and toxic granulation between patients in ICU and non-ICU. *Conclusion:* In summary, the blood film of patients with COVID-19 showed various morphological changes. Hence, blood cell morphological abnormalities can be used for identifying infection of COVID-19 and predictor for the disease severity. **Keywords**

Evaluating Aprepitant single-dose plus granisetron and dexamethasone in children receiving highly emetogenic chemotherapy for the prevention of chemotherapy-induced nausea and vomiting: A triple-blinded randomized clinical trial

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نوع پذیرش: oral | کد مقاله: G-58492

Abstract: Background: This study was performed to evaluate the degree of 3-day chemotherapy-induced nausea and vomiting (CINV) in children with cancer who received highly emetogenic chemotherapy (HEC) to ascertain the efficacy of aprepitant single-dose on day L 1 plus granisetron and dexamethasone (DEX). Materials and Methods: This clinical trial study was conducted on 120 patients in the age range of 5 to 18 years old who received chemotherapy. Patients were divided into two groups; Group A received aprepitant at 125 mg/kg on day 1 orally, followed by 80 mg/kg daily on days 2 and 3 and Group B received a single dose of aprepitant 125 mg/kg on day 1 orally and placebo on days 2 and 3. All groups received granisetron 3 mg/m² on day 1 and DEX on days 1 to 3. The primary and secondary endpoints were to evaluate the proportion of patients with acute, delayed and overall CINV within each group. Results: There were no significant differences between the two groups for vomiting, nausea or the use of rescue therapy. The number of patients without vomiting on day 1 was similar in both groups (96.5% vs. 98.3%, respectively; $p = 0.848$). Conclusion: According to the results of this study, a single dose of aprepitant 125 mg/kg was as effective as administering three doses of aprepitant on 3 days. Therefore, the use of a single dose of aprepitant in combination with other standard treatment regimens to prevent CINV in children who received HEC was safe and efficacious and can be beneficial. **Keywords:**



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Aprepitant, Dexamethasone, Granisetron, Nausea Vomiting Clinical Trials:
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Effect of supplementation with ferrous sulfate or ferrous gluconate on prophylaxis of iron deficiency in toddlers 6-24 months old: Randomized clinical trial

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نوع پذیرش: oral | کد مقاله: G-13576

Abstract: *Background:* Iron Deficiency Anemia (IDA) is one of the most common anemias, especially in children 4 to 23 months. Therefore, prophylaxis is necessary to improve iron status as well as reduce ID and ID in Toddlers. The aim of this study was to compare the efficacy of daily supplementation with ferrous gluconate (FG) and ferrous sulfate (FS) on iron status in toddlers. *Methods:* A total of 120 healthy toddlers were divided randomly into 2 groups at the Amir-Kabir Hospital, Arak, Iran and received FS and FG from March 2020 to December 2020. Iron status were evaluated at baseline and after 6 months of supplementation. The statistical significance of the differences in iron status between FS and FG groups was calculated using Student's t test and the Pearson's χ^2 test for qualitative variables. SPSS software (version 16, Chicago, IL) was used for statistical analysis. *Results:* Comparison of iron status of FS and FG groups toddlers at baseline and after 6 months of supplementation showed that there was a significant difference in Hb (10.46 vs 12.45, $p=0.001$), and ferritin level (28.08 vs 59.63, $p=0.001$). *Conclusion:* Although prophylaxis with FG led to a higher Hb and ferritin levels, our study recommended that both FG and FS supplements were effective for prophylactic use in the prevention of IDA. However, FG was more effective than FS because FG group that received FG supplementation indicated a higher Hb and ferritin levels in comparison to the FS group that received FS supplementation. *Keywords:* Ferrous Sulfate, Ferrous Gluconate, Iron deficiencies, Prophylaxis clinical trial code; IRCT20190902044674N1

RHD genotyping of Rh-negative among blood donors in Sistan and Baluchestan Province of Iran

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نوع پذیرش: oral | کد مقاله: G-06145

Abstract: Background: Antigen D is a group of Rh blood group antigens that are involved in hemolysis due to blood transfusion and hemolytic diseases of infants. The deletion of the RHD gene by the hybrid Rhesus box mechanism causes the Rh-negative phenotype. The presence of this hybrid marker is used to confirm the deletion of the RHD gene and to determine zygosity. Clinical applications of rhesus box hybrid determination include resolving inconsistencies in Rh group genotyping, zygosity determination in Rh-positive fathers, and RHD determination of Rh-negative fetuses. The aim of this study was to investigate the genetic background of RhD-negative phenotype in blood donors in Sistan and Baluchestan province. Materials and Methods: The molecular analysis of the hybrid Rhesus box was performed on the 200 Rh-negative samples using (PCR-SSP) and (PCR-RFLP). The existence of different exons of the RHD gene was investigated using Real-Time PCR. Results: Of the 200 Rh-negative blood samples, 198 samples were homozygous and lacked the RHD gene (99%), while two samples were heterozygous and had the RHD allele (1%). Heterozygous samples had RHD*01N.73 allele and the RHD*01N.18 allele. Conclusions: The results showed that RHD gene deletion is the most common genetic mechanism of the Rh-negative phenotype in Sistan and Baluchestan province of Iran. **Keywords:** Hybrid Rhesus box, deletion of the RHD gene, Rh- negative phenotype.

Evaluation of Factors Related to the incidence of Thalassemia in Family Members of Thalassemia Major Patients

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نوع پذیرش: oral | کد مقاله: G-93401

Abstract: *Background:* Beta-thalassemia is one of the complex diseases that cause many social and economic problems for the patient and his family. This study aimed to the evaluation of factors influencing the rebirth of thalassemia (intermedia or major) in family members of thalassemia major patients in Sistan and Baluchestan province. *Materials and Methods:* This study is a descriptive-analytical study performed on all families of thalassemia major patients who experienced an incidence of thalassemia in their members. Data was collected through direct interviews and review of patients' files. The results were analyzed using SPSS software version 17. *Results:* In this study, statistical evaluations showed that the incidence of thalassemia in family members of thalassemia major patients whose mothers are housewives was 100% and in families that had no premarital counseling was 91.7%. There was a significant relationship between variables related to mothers' awareness of thalassemia, including their place of residence and Sistani and Baluchestani ethnics, and the incidence of thalassemia in family members of thalassemia major patients (in both cases, P-value = 0.05); However, there was no significant relationship between other variables related to mothers' awareness such as age groups and maternal education with the incidence of thalassemia in family members of thalassemia major patients (P-Value = 0.98 and P-Value = 0.22, respectively). *Conclusion:* Informing and educating before marriage for high-risk families with thalassemia children, as well as financial support for low-income families can inform parents, prevent the incidence of thalassemia, and improve the quality of life of these patients. **Keywords**

Investigation of the prevalence of bacterial contamination of platelet pheresis in Bushehr transfusion organization in 2022

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نوع پذیرش: oral | کد مقاله: G-29304

Abstract: Background: Due to the importance of blood and blood products and microbial infections transmitted through blood, bacterial infection caused by pheresis platelets is one of the important cases in blood transfusion medicine. Despite the progress made, microbial infection caused by platelets is still very dangerous. Therefore, a study was conducted Investigation of the prevalence of bacterial contamination of platelet pheresis in Bushehr transfusion organization in 2022. Materials and Methods: In a cross-sectional study, 81 platelet pheresis samples were randomly collected at different times. And sampling was done from the cord of the accessory bag and 1 cc of platelet pheresis were cultured in Thioglycolate medium and placed in an incubator at 37 degrees Celsius for one week and checked for turbidity and if turbidity is observed in the medium We will culture blood agar and put it in aerobic jar, anaerobic jar and CO2 jar conditions for 48 hours. Results No signs of microbial contamination were observed in the 81 cases investigated in Thioglycolate environment, and the cultures of all samples were reported as negative. Conclusion: Considering the importance of bacterial contamination in the platelet product, It is particularly important to perform a screening test in blood transfusion centers and medical centers before injecting it into the patient. Keywords: Blood donor, Blood transition, platelet pheresis

Evaluation of Platelet Activation in Different Methods of PRP Isolation

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نوع پذیرش: oral | کد مقاله: G-65473

Abstract: *Background:* Platelet rich plasma (PRP) therapy has been one of the hottest topics in regenerative medicine concerning the treatment of various diseases. Exogenous platelet activation and degranulation of growth factors during platelets isolation are the main challenges in clinical applications of PRP therapy. Hence, the present study aimed to compare the platelet activation during PRP preparation in different methods. *Materials and Methods:* Blood is collected from healthy volunteers and divided in three different groups: gel tube containing ACD-A, gel tube containing sodium citrate, tube without gel containing ACD-A and tube without gel containing sodium citrate. Data regarding platelet count, platelet distribution width (PDW), mean platelet volume (MPV), Platelet-Large Cell Ratio (P-LCR) and Plateletcrit (PCT) were analyzed by automated hematology analyzer. Moreover, the concentration of platelet-derived growth factor-BB (PDGF-BB) was measured by ELISA in different groups. *Results:* The results showed that there was a significant difference in platelet capture efficiency (1.9-fold to 3-fold increase in platelet concentration). The highest platelet capture efficiency was obtained with ACD-A without gel tube. Also, the secretion of PDGF-BB in gel containing sodium citrate group was significantly higher than other groups (P0.05). *Conclusion:* Based on these results, the highest platelet recovery and



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growth factors obtained in ACD-A without gel tube. There are positive correlations between increased of MPV and PDW and the growth factor with activation platelets during PRP preparation. **Keywords?**

آدرس دبیرخانه:

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Prevalence of Iron deficiency anemia in patients undergoing cardiac surgery

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نوع پذیرش: oral | کد مقاله: G-61873

Abstract: *Background:* Anemia is prevalent in patients undergoing cardiac surgery. Iron deficiency is the commonest cause of anaemia in the cardiac surgery patients. preoperative anemia is an important risk factor for perioperative transfusion requirements, which is associated with morbidity and mortality. thus, preoperative anemia correction is an important factor in improving the condition of these patients. The aim of this study was to evaluate the prevalence of iron deficiency anemia in candidate patients for cardiac surgery. *Material and Methods:* In a cross-sectional study, in Shahid Rajaei cardiovascular, medical, and research center, Tehran during one year period (November 2018 to September 2019), 165 patients who were candidates for cardiac surgery entered our study. for diagnosis preoperative anemia, the laboratory test (Complete blood count) were performed. (Anemia is defined as hemoglobin (Hb) levels 12 gr/dl in women and 13gr/dl in men, according to the World Health Organization (WHO) and the frequency of anemic patients before surgery was evaluated. Additional laboratory tests such as Complete blood count (CBC), serum iron level, serum ferritin level, Total iron binding capacity, Reticulocyte count, Bun, Cr and CRP level to diagnosis iron deficiency anemia from other types anemia were performed. Chi-square, Mann Whitney, t-test and SPSS22 software were used to statistical analyzes the data. *Result:* Of the total 165 patients who were candidates for cardiac surgery, 52.1% (n=86) were anemic and 47.9% (n=79) were non-anemic. of the 86 anemic patients, 75.6% (n=65) had iron deficiency anemia, 15.1% (n=13) had chronic anemia disease and 9.3% (n=8) had other anemias. Regarding the association to the types of anemia and gender can be said that of all patients with iron deficiency anemia 60% (n=42) were women and 24.7% (n=23) were men P value (0.05). In patients with chronic diseases anemia, 11.8% (n=11) were male and 2.9% (n=2) were female (p value 0.05). The prevalence of iron deficiency anemia in female anemic patients was significantly higher compared to male anemic patients (P value 0.05). *Conclusion:* Based on the results, preoperative anemia in patients undergoing cardiac surgery in Shahid Rajaei Heart Hospital has a significant frequency and the main causes of iron deficiency anemia can be mentioned. As a result, by diagnosing and correcting anemia before cardiac surgery, the complications of anemia during and after surgery and ectopic transfusion can be reduced. **Keywords?**

AML-derived extracellular vesicles negatively regulate stem cell pool size: a step toward bone marrow failure

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نوع پذیرش: oral | کد مقاله: G-20678

Abstract: *Background:* Long-term repopulating hematopoietic stem cells (LTR-HSCs) have been previously shown to reside in close proximity to osteoblasts, where they take shelter in the bone marrow (BM) microenvironment against cytotoxic and apoptotic stimuli. Nevertheless, the function of the HSC niche is believed to undergo an adaptive evolutionary modification during leukemogenesis. Recent studies have demonstrated that leukemic clones can impact BM homing through extracellular vesicle (EV) secretion. However, the exact mechanism driving BM conversion is still unclear. In the present study, the human osteoblast cell line (MG-63) were subjected to various concentration of sera-derived EVs of patients with acute myeloid leukemia (AML) and healthy volunteers to assess if they are associated strongly enough to alter the expression pattern of cross-talk molecules involved in niche interactions. *Materials and Methods:* To gain a brief insight into the EVs secretion criteria, first, we conducted a comparative analysis of sera-derived EVs by dynamic light scattering (DLS), transmission electron microscopy (TEM), and Bradford assay. After incubating MG-63 cell lines with the increasing concentrations of the EVs, Trypan-blue and microculture tetrazolium test (MTT) assays were used to evaluate the cell survival, logarithmic growth, and metabolic activity. Finally, the expression levels of OPN, ANGPT-1, and JAG-1 transcripts were evaluated through qRT-PCR technique. *Results:* Here, we report that AML-derived EVs can affect the viability, cell growth and metabolic activity of the human osteoblasts cell line (MG-63) compared to those receiving healthy-derived EVs. We also found that leukemic EVs tend to induce overexpression of OPN but reduce the expression of ANGPT-1 and JAG-1 genes in the osteoblast transcriptome, which may provide a potential context imposing selective suppression of HSC pool size. *Conclusion:* These findings extend the general concept of a novel mechanism in which leukemic EVs would make it possible to create a specialized pre-metastatic microenvironment in the interest of tumor expansion, allowing leukemic clones to overcome their HSCs counterparts. *Keywords:* acute myeloid leukemia, osteoblast, extracellular vesicles, hematopoiesis, cell adhesion molecule

Inhibition of c.Myc in chronic myeloid leukemia intensifies the anti-leukemic effects of HDAC inhibitor

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نوع پذیرش: oral | کد مقاله: G-78634

Abstract: *Purpose:* Promising efficacy of Histone deacetylase (HDAC) inhibitors which was proved by the results of preclinical studies, has led to evaluate the potential of this agents in various clinical studies. Recently, some studies have reported the anti-leukemic effects of HDAC inhibitors in chronic myeloid leukemia (CML) and declared that this epigenetic regulator can be considered as a therapeutic option in this hematological malignancy. However, it has been reported that the efficacy of this drugs can be diminish by some mechanisms of resistance. Over expression of the c.Myc, one of the most important promoters of cell cycle progression is one of the most studied mechanisms of such resistance. In this study, to determine the effects of c.Myc inhibition on the efficacy of HDAC inhibitors in CML, we evaluated the efficacy of a well-known HDAC inhibitor, panobinostat, in the presence of a small molecule inhibitor 10058-F4 in CML-derived K562 cells. *Material and methods:* The human Bcr-Abl positive K562 cells were cultured with different concentration of panobinostat and 10058-F4 either as in a single or combined modality. Cell survival and proliferation was investigated using trypan blue and MTT assay at different time intervals. Moreover, the effects of panobinostat along with 10058-F4 on cell cycle distribution and apoptosis were assessed using flow cytometric analysis and AnnexinV/PI staining. Then, quantitative real time PCR (qRT-PCR) was implied to explore the exact molecular mechanisms of interaction between panobinostat and 10058-F4. *Results:* Based on the results of Trypan blue staining and the MTT assay both viability and metabolic activity of K562 cells were reduced more vigorously in the combinatorial modality in comparison to single agents of panobinostat and 10058-F4. The results of flow-cytometric analysis demonstrated that this combination exerted its anti-leukemic effects mainly through the induction of apoptosis which this was further confirmed by the results of molecular assay, where we found a significant alteration in the expression of apoptosis-related genes in favor of apoptosis induction. Moreover, the results of PI staining showed that this apoptosis was mainly associated with a G1 cell cycle arrest. *Conclusion:* Taken together, our findings suggest that 10058-F4 could increase the efficacy of panobinostat in CML derived K562 cell and we can increase the efficacy of HDAC inhibitors by c-Myc inhibition. However, this claim should be further confirmed by more preclinical and clinical studies. *Keywords?*

Anti CD19-PAMAM G4-PEG nano-complex as a potential targeted delivery system against leukemia

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نوع پذیرش: oral | کد مقاله: G-74280

Abstract: *Background:* In recent decades, cancer has been dramatically leading to high amounts of death all over the world, and leukemia is one of the progressing cancers which should stop somehow. To stop its health-threatening incidence, nanoparticle-based targeting drug delivery systems are crucially needed. As a result, the polyethylene glycol (P) modified and anti-CD19 antibody (Ab) decorated polyamidoamine (PAMAM G4: P) dendritic nano-complex was developed for effective delivery of sodium butyrate drug (D) to Reh6 leukemia cells in this research work. *Materials and Methods:* After the synthesis of nano-complex, several analytical devices such as FT-IR, TGA, DLS, Zeta potential analyzer, and TEM was applied to the qualification and quantification of syntheses and conjugations. Nanometric size (less than 50 nm in diameter), -4.2 mV surface charge, high drug loading efficiency (14.42%), and appropriate controlled drug release (less than 50% within first 8 hours at pH 7.4) profile at different pHs were observed for Ab-P-P-D nano-complex. *Results:* In the biomedical phase, the MTT assay was demonstrated 13.04% cell viability at 800 nM after 24 hours of treatment. IC50 was obtained for 100 nM concentration. The Bcl2 and caspase9 genes were indicated less than half and more than 15 folds of expressions at post-treatment time, respectively. The cell cycle arrest was drastically depicted more than 15 folds of cell Reh6 suppression in comparison to control. Moreover, the leukemia cells treated with Ab-P-P-D have demonstrated 42.39% apoptosis which was potentially several folds more than control. These data have verified the potency of nanocarrier as an effective drug delivery system. *Conclusion:* The results of present study have verified the potency of nanocarrier as an effective drug delivery system. **Keywords:** Dendritic nanoparticle, Polyethylene glycol, Anti-CD19 antibody, Sodium butyrate, Targeted drug delivery, Leukemia

Relationship between HbA2 level on hematological parameters in patients with thalassemia and Sickle cell disease in Bushehr, Iran

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نوع پذیرش: oral | کد مقاله: G-35961

Abstract: Background: Hemoglobin A2 ($\alpha_2\delta_2$), which accounts for less than 3% of total hemoglobin (Hb) in adults, is assumed to have little physiological importance due to its low amount. Microcytosis and elevated Hb A2 levels are signs of beta-thalassemia trait (BTT). Hb A2 levels were higher not only in those with BTT, but also in those with Hb S and Hb C, and the α -Thal genotype had an effect on Hb A2 levels. This study aims to investigate the levels of Hb A2 and their influence on several hematological parameters in patients with SCD and Thalassemia. Materials and methods: This cross-sectional descriptive-analytical study included patients with SCD and thalassemia referred to Mehr Bushehr Laboratory for hematological tests and hemoglobin electrophoresis. Hemoglobin A2 levels were assessed using Sebia capillary electrophoresis, and hematological parameters were determined using xn-1000 Sysmex. The analyses were carried out using SPSS version 22. Statistical differences were considered significant at a 0.05 significance level, and all data were reported as the mean \pm standard error of mean (SEM). Results: seventy-eight patients were included in our study, comprising 45 patients with beta-thalassemia and 32 patients with SCD with mean age of 25.5 ± 2.59 and 27.31 ± 2.45 years respectively. There were 17 (53.1%) females and 15 (46.9%) males in the SCD group, and 31 (68.9%) females and 14 (31.1%) males in the beta-thalassemia group. In the SCD group the mean Hb A2 concentration was 2.86 ± 0.15 and had a positive correlation with RBC (0.31), RDW (0.04), Hb (0.293) and an inverse correlation with MCV (-0.11), MCH (-0.16) and in beta-thalassemia group mean Hb A2 concentration was 4.96 ± 0.09 and had a positive correlation with RBC (0.65) and an inverse correlation with MCV (-0.27), MCH (-0.24), Hb (-0.09) and RDW (-0.013). Conclusion: In our investigation, Hb A2 and RBC had a direct correlation in both groups, as well as an inverse relationship with MCV and MCH. Hb and RDW had a direct correlation with HbA2 in the SCD group but showed an inverse correlation in the beta-thalassemia group. **Keywords:** thalassemia, Sickle cell disease, hematological parameters, Bushehr.

Changes in hematological and inflammatory parameters in covid 19

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نوع پذیرش: oral | کد مقاله: G-29861

Abstract: Background: The Covid-19 epidemic in 2019 caused a global emergency that is quickly evolving and altering, placing stress on the global health systems. Various characteristics in this disease, including hematological, biochemical, and radiographic data, are described in new research. Our research's goal is to find prognostic variables that may be used while making decisions on how to treat COVID-19-infected individuals. Materials and Methods: Over the course of the investigation, 260 people were examined and tested for covid-19. Then, in these statistics, absolute lymphocyte count, absolute neutrophil count, R test and CRP test were determined at the time of entering the hospital and their relationship with the results of receiving Covid was determined. Results: In this study, 127 patients (45%) were female and 153 patients (54%) were male. The population's age distribution was 61/9 years. The oldest person was 99 years old, while the youngest was one years old. We examined the impacts of ESR, CRP, neutrophils, and lymphocytes in different patients. 182 of the investigated individuals (69.2%) had positive CRP readings, while 81 individuals (30.8%) had negative ones. ESR increased in 203 people (77.2%) and decreased in 60 people (22.8%). Then, we were faced with the examination of neutrophils, the rate of change of which was relatively low in our statistical population, so that 23 equal people (8.2%) had neutropenia and 81 equal people (28.9%) were associated with an increase in neutrophils or neutrophilia, but the results of 176 The equivalent number (69.2%) was normal. The amount of lymphocytes was a next component we looked into, and we observed a significant decrease in it. These were the outcomes: 142 normal instances or (50.7%), 132 persons or (47.1%) with lymphopenia, and only (2.1%) or 6 more individuals, reported lymphocytosis. Conclusion: The findings also indicated that COVID-19 indicators such as lymphocyte percentages, neutrophils, CRP, and



چهاردهمین گنگره بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



ESR might be employed and Clinicians. Inflammatory and lymphopenia tests were found to be diagnostic markers with good sensitivity in patients, and researchers can use our findings to create multivariable prognostic models that could ultimately facilitate decision-making and improve patient crucial outcomes. **Keywords**

آدرس دبیرخانه:

تهران، خیابان کارگر شمالی، رویروی مرکز قلب تهران،
کوچه دانش ثانی، بعد از تقاطع صالحی، پلاک ۱۵، واحد ۲

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Connection between changes in haematological and inflammatory parameters with the consequences of covid 19 virus infection

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نوع پذیرش: oral | کد مقاله: G-94531

Abstract: Background: Connection between changes in haematological and inflammatory parameters with the consequences of covid 19 virus infection Introduction: Corona virus disease 2019 (COVID-19) an infectious disease caused by the SARS-cov-2 virus that causes acute respiratory syndrome. In some patients, the infection with covid 19 has been associated with various consequences such as hospitalization in the ICU, the need for a ventilator, and the death rate. In this study, we seek to investigate the relationship between haematological and inflammatory parameters with the mentioned outcomes. Method and material: In this research we examined 280 patients with covid 19 who were hospitalized. Then in these patients, we determined absolute lymphocyte count, absolute neutrophil count, ESR test, and CRP test upon entering the hospital and examined their relationship with the consequences of covid infection. Result: 280 patients tested for covid 19 throughout the institution during the study period. In this research 153 (54/6 %) patients were male and 127 (45/4%) were female. The average age of people was 61/9 years. No signification relation was found between ESR and CRP with the above outcomes, although ESR was higher in patients hospitalized in ICU and the duration of hospitalization was morethan 5 days compared to the opposite group. Also, patients hospitalized in ICU and deceased people had a higher amount of neutrophils. Conclusion: Although lymphopenia was found as a diagnostic marker with good sensitivity in patients, a high count of neutrophils can act as a prognostic parameter and its higher values indicate a more inflammatory state and a bad prognosis of the disease. **Keywords:** covid 19, ESR, CRP, Hospitalize. ICU

The Impact of EGCG and RG108 on SOCS1 Promoter DNA Methylation and Expression in U937 Leukemia Cells

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نوع پذیرش: oral | کد مقاله: G-12870

Abstract: *Background:* The available evidence has increasingly demonstrated that a combination of genetic and epigenetic factors, such as DNA methylation, could be considered as causing leukemia. Epigenetic changes and methylation of the suppressor of the cytokine signaling 1 promoter (SOCS1) CpG region silence SOCS1 expression in cancer. In the current study, we evaluated the impact of epigallocatechin gallate (EGCG) and RG108 on SOCS1 promoter methylation and expression in U937 cells. *Materials and Methods:* In the current study, U937 leukemic cells were treated with EGCG and RG108 for 12, 24, 48, and 72 h and SOCS1 promoter methylation and its expression were measured by methylationspecific PCR (MSP) and quantitative real-time PCR, respectively. *Results:* The outcomes indicated that the SOCS1 promoter is methylated in U937 cells, and treatment of these cells with either EGCG or RG108 reduced its methylation. Moreover, we observed that SOCS1 expression was significantly upregulated in a time-dependent manner by both EGCG and RG108 in U937 cells compared with control cells. In the RG108-treated group at 12, 24, 48, and 72 h, SOCS1 expression was upregulated by 1, 4.2, 16.6, and 32.6 -fold respectively, and in the EGCG-treated group, by 0.5, 3.2, 10.8, and 22.3 -fold, respectively. *Conclusion:* Treatment with either EGCG or RG108 reduced SOCS1 promoter methylation and increased SOCS1 expression in U937 cells in a time-dependent manner, which may play a role in leukemia therapy. **Keywords:** DNA Methylation, EGCG, Leukemia, RG108, SOCS1.

The effect of nanoparticles containing antioxidant enzymes on some quantitative, qualitative indicators of Red Blood Cells

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نوع پذیرش: oral | کد مقاله: G-89763

Abstract: زمینه و هدف: بر اساس آمارهای سازمان انتقال خون ایران، عوارض نگهداری کیسه های خون سبب تحمیل هزینه های بسیاری به سازمان انتقال خون می شود و بسیاری از این آسیبها به گلبولهای قرمز به دلیل بروز استرس اکسیداتیو است. لذا به نظر می رسد با اضافه کردن آنزیم های آنتی اکسیدان سوپر اکسید دیسموتاز و کاتالاز به نانوپارتیکل Aib-PLGA، با کاهش استرس اکسیداتیو در کیسه های خون بتوان گامی در راستای بهبود کیفیت کیسه های خون و در پی آن بهبود سلامت بیماران و همچنین کاهش هزینه های عوارض ناشی از تزریق خون برداشت. مواد و روشها: برای ساخت نانوپارتیکل از روش الکترو اسپری استفاده شد. ۲۰ کنستانتره گلبول قرمز فشرده گرفته شد. نانوپارتیکل ها وارد کیسه های تست شد و از تاریخ اهدا به مدت ۳۵ روز (۵ هفته) در شرایط استاندارد نگهداری شد. در روزهای ۱، ۷، ۱۴، ۲۱، ۲۸ و ۳۵ از کیسه ها نمونه گیری شد و با گروه کنترل مقایسه شد. آزمایشات بر روی نمونه های گرفته شده انجام شد. یافته ها: تغییرات مرفولوژیک در گروه تست در مقایسه با گروه کنترل کمتر بود. تست های پروفایل همولیز کمی (گلبول قرمز، هموگلوبین، همتوکریت، پتاسیم و آهن) تغییرات معنی داری در گروه های کنترل و تست در هفته های متوالی نشان داد ($p < 0.05$) جز پتاسیم و آهن. پارامترهای استرس اکسیداتیو (گلوکاتایون پراکسیداز، گلوکاتایون ردوکتاز، گلوکز ۶ فسفات دهیدروژناز، بالانس پروکسیدانت آنتی اکسیدانت و مالون دی آلدید) تغییرات معنی داری را در روزهای هدف نشان داد ($p < 0.05$). نتیجه گیری: به نظر می رسد استفاده از نانوپارتیکل های آنتی اکسیدانی علاوه بر بهبود کیفیت گلبول های قرمز ذخیره شده با کاهش استرس اکسیداتیو می تواند از عوارض بعد از انتقال خون جلوگیری کند. کلمات کلیدی

Evaluation of the Xpert MTB/RIF test accuracy for diagnosis of pulmonary tuberculosis in Mazandaran province

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نوع پذیرش: oral | کد مقاله: G-60718

Abstract: *Bakground:* Mycobacterium tuberculosis (MTB) is a causative agent of tuberculosis (TB) which remains as an endemic disease in the North regions of Iran. The sputum smear examination and the culture method were the primary and gold standard methods for TB diagnosis, respectively. Recently, the Xpert MTB/RIF assay (Xpert), was introduced for rapid diagnosis of TB. The aim of this study was to evaluate the performance of the Xpert assay for diagnosis of TB in Mazandaran province. *Methods:* The pulmonary TB suspected cases which referred to Tuberculosis Reference laboratory, Gorgan, Iran, between March 2018 to February 2019 were included to this study. The specimens were decontaminated by Petroff's method then examined using smear microscopy and cultured into Lowenstein-Jensen (LJ) media. The Xpert analysis was performed according to the manufacturer's instructions. Sensitivity and specificity of smear microscopy and Xpert were calculated using a culture method as reference standard. *Results:* Of 42 presumptive TB cases, 31 (73.8%) had culture proven TB. Compared to the culture method, sensitivity and specificity of Xpert was 93.5% (29/31) and 100% (11/11), respectively. Sensitivity and specificity for smear microscopy was 83.9% (26/31) and 100% (11/11), respectively. *Conclusion:* Our findings showed the excellent sensitivity and specificity for the TB detection using Xpert method. In comparison with the culture as a reference standard, the Xpert assay reported two false-negative results, which were smear-negative, too. This could be attributed to low bacillary load in the specimens because the detection limit of the Xpert assay is higher than the culture method. Showing the high sensitivity for Xpert, the smear microscopy could be replaced with Xpert for rapid detection MTB in sputum specimens. *Keywords:* Mycobacterium tuberculosis, Xpert MTB/RIF, Lowenstein-Jensen, Smear microscopy, Tuberculosis

Evaluation of ErbB and ErbB3 expression in HT-29 cell line in presence of *E. coli* Nissle 1917 (EcN) as a novel probiotics

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نوع پذیرش: oral | کد مقاله: G-58961

Abstract: *Background:* Intestinal microbiota is widely considered to be one of the most important components of maintaining homeostasis balance. Looking ahead, it has been shown that probiotic bacteria play an important role in modulating the immune system and exhibiting anti-cancer properties. Regulation of ErbB signaling plays an important role in colon cancer. In our study, we examine the potential of anti-cancer activity of probiotic bacteria against colon cancer by targeting members of the ErbB family. *Materials and Methods:* In the present study, the HT-29 cell line was used. After cell proliferation to a certain extent, 200,000 cells were transferred to the 6 well plates for 24 hours to increase the confluence to 85-80%, then, the cell line was treated in the presence of a certain amount of bacteria at MOI: 10 and MOI:100 for 24h. In order to evaluate the expression of ErbB2 and ErbB3 genes in the presence of the probiotic strain (*E. coli* Nissle1917), RNA was extracted according to the manufacturer's kit instructions. Then, after cDNA synthesis, we examined the expression of genes using specific primers. It should be noted that GAPDH and B-actin were used as reference genes in this study. *Results:* Expression of ErbB2 and ErbB3 genes in the presence of both bacterial concentrations of MOI: 10 and MOI: 100 showed a decrease in expression compared to the control group (group without bacterial treatment), this reduction in expression at MOI: 10 was significance while decrease in gene expression at higher concentrations (MOI: 100) was not statistically significant. On the other hand, expression of the ErbB2 gene compared to the control group showed a more severe decrease than ErbB3. *Conclusion:* It seems that the study of expression changes in these genes can be one of the therapeutic or diagnostic targets in colon cancer studies. There are two important *Keywords?*

Evaluation of the effect of leech saliva on infectious opened wound healing with *Pseudomonas aeruginosa* in rat

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Background: wound infection control and improvement of wound healing process are important issues in wound management. Leech saliva has antimicrobial and anti-inflammatory properties that can improve the wound healing process.

Methods & materials: This study was conducted on 60 male rats (15 animals in 4 groups). Skin wounds with diameter of 1cm were made on the dorsal region of rats and infected with a suspension containing 10^6 CFU/ml of *Pseudomonas aeruginosa*. Then the groups separately were treated with euserin ointment, nitrofurazone 0/2% ointment and 5% leech saliva ointment (95gr euserin and 5gr leech saliva). The control group didn't receive any therapy. The treatment of the groups was renewed every 48h for 21 days. Then, 5 rats from each group were euthanized on days 7, 14, 21 and sterile samples were taken from them for microbial and histopathological investigations.

Result: after 21 days, epithelialization, reduction of fibroblast concentration, collagen formation and reduction of inflammation in leech saliva group were better than euserin and control groups and had a significant difference with them ($P < 0/05$) and didn't have a significant difference with nitrofurazone group ($P > 0/05$). Angiogenesis was observed more in leech saliva group and had a significant difference with nitrofurazone group, whereas didn't have a significant difference with control and euserin groups. In leech saliva group, a significant decrease in bacterial population was observed compared to control and euserin groups, whereas leech saliva group didn't have a significant difference with nitrofurazone group.

Conclusion: The study results showed that leech saliva has anti-microbial and anti-inflammatory properties and accelerates epithelialization. Therefore leech saliva can be a suitable alternative to common antibiotics and can be used to control and infectious wound healing with *Pseudomonas aeruginosa*.

Keywords: *Pseudomonas aeruginosa*, Infectious wound healing, Leech saliva

An Outbreak of Food-borne Botulism: a case series

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نوع پذیرش: oral | کد مقاله: G-93705

Abstract: Background: Food-borne botulism is one of the potentially fatal forms of food poisoning, usually caused by ingestion of home-canned vegetables, fruits, dairy and fish products. The aim of this study was to report an outbreak of botulism due to homemade Doogh, a traditional beverage made from milk, in Hamadan, Iran. Case Presentation: During an outbreak from 3rd to 10th October, 2022, 21 patients were referred to the hospital because of food poisoning. All patients had a history of consumption of Doogh. After careful physical examination, all of them were hospitalized. Botulism was Confirmed in all patients except for the first patient. It was confirmed by obtaining botulism toxin in the gastric juice of patients and remains of Doogh. The first patient was a 35-year-old woman who admitted after 12 hours of drinking due to respiratory distress. Twenty subsequent patients were diagnosed as botulism with the following symptoms: diplopia (95.23%), nausea and vomiting (85.71%), blurred vision (80.95%), and dizziness (61.90%). All of the 21 patients received botulinum antitoxin and symptoms improved during their hospitalization. Conclusions: Immediate diagnosis based on a careful history and physical examination is essential for the management of botulism. People should be notified about proper food handling and preparation of traditional homemade foods. **Keywords:** Botulism; Clostridium Botulinum; Outbreak

Distribution of Non-Tuberculosis Mycobacteria Strains from Suspected Tuberculosis Patients By molecular method

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نوع پذیرش: oral | کد مقاله: G-53879

Abstract: *Background:* The genus Mycobacterium contains more than 150 species. Non-tuberculosis mycobacteria (NTM) often cause extrapulmonary and pulmonary disease. Mycobacteria detection at species level is necessary and provides useful information on epidemiology and facilitates successful treatment of patients. This retrospective study aimed to determine the incidence of the NTM isolates and Mycobacterium tuberculosis (Mtb) in clinical specimens collected from Iranian patients during 2019–2022, by PCR–restriction fragment length polymorphism analysis (PRA) of the hsp65 gene. *Material&Methods:* A cross-sectional study was implemented on 478 Acid-Fast isolates, were obtained from Lowenstein-Jenson media which belonged to different individuals who referred to laboratory during years 2019-2022. After biochemical differential tests, DNA extracted and PCR-RFLP on hsp65 gene performed by using of 2 pairs primer for Neasted PCR and restriction enzymes (BstEII and HaeIII) for digesting of PCR products. Obtained patterns were investigated in Mycobacterium identification site. *Result:* Of 478 Mycobacterium isolates, 328 (68.6. %) cases showed MTBC pattern with resulted bands after digested by Enzymes. 150 (31.4%) isolates belonged to NTM groups, , the most commonly identified organism was Mycobacterium simiae (38.6%), followed by Mycobacterium kansasii (20.1%), Mycobacterium gordonae (21.9%), Mycobacterium fortuitum (5.1%), Mycobacterium intracellulare (5.1%), Mycobacterium flavescens (3.4%), Mycobacterium chelonae (3.4%) and Mycobacterium fortuitum (2.4%). *Conclusion:* This prevalence of NTM infections underlines the need for serious enforcement of infection control strategies such as PCR-RFLP assay which focuses on the analysis of hsp65 gene in order to rapid identification of Mycobacterial organisms which is required for appropriate treatment and reduction in drug resistances. PRA method, in comparison with classical methods, is rapid, useful and sensitive for the phylogenetic analysis and species detection of mycobacterial strains. Mycobacterium simiae is the most common cause of infection by NTM in patients with non-HIV and HIV which demonstrated a high outbreak and diversity of NTM strains in our laboratory. *Keywords:* Non-tuberculosis mycobacteria, Heat shock protein 65 , PCR–RFLP

Phenotypic and genotypic characterization of extended-spectrum beta-lactamase associated antibiotic resistance, biofilm formation and genetic diversity of *Escherichia coli* strains recovered from urinary tract infections

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نوع پذیرش: oral | کد مقاله: G-08319

Abstract: *Background:* This study used phenotypic and molecular techniques to examine the antimicrobial susceptibility pattern and the presence of extended-spectrum beta-lactamases (ESBLs) in uropathogenic *Escherichia coli* (UPEC) strains isolated from patients with catheter-associated urinary tract infections (CAUTI) and community-acquired urinary tract infections (UTIs). Additionally, the potential of isolates to produce biofilms as well as their clonal diversity, were also investigated. *Methods:* A cross-sectional study was accomplished on a collection of non-duplicate UPEC isolates obtained from CAUTIs from May 2021 to September 2021. Antimicrobial resistance and phenotypic screening tests for ESBL production were done according to the latest CLSI guidelines. Also, the presence of ESBL genes were determined using PCR assays. In 96-well microtiter plates, biofilm production was evaluated. Finally, ERIC-PCR was used to investigate the clonal diversity of the isolates. *Results:* A total of 76 confirmed UPEC isolates were obtained from patients admitted to a teaching hospital in Shiraz, Iran. The double disk synergy test (DDST) revealed that 65% of UPEC isolates were positive for ESBL production. The most resistance rates seen in ESBL-positive strains were against nalidixic acid and cotrimoxazole. The majority of non-ESBL producing isolates were susceptible to ceftriaxone. The frequency of ESBL genes of blaCTX-M, blaTEM and blaSHV were 78.9%, 30.3% and 9.2% respectively. Forty-two isolates (55.3 %) were positive for biofilm formation. ERIC-PCR divided ESBL isolates to nine clusters named A-I. *Conclusion:* The high prevalence of blaCTX-M in conjunction with biofilm production among the isolates poses a high pathogenic capacity of UPEC strains. Molecular genotyping indicated that the UPEC strains belonged to diverse clones. **Keywords?**

Synthesis of copper nanoparticles using microorganisms and their inhibitory effect on *Escherichia coli* PTCC 1330, *Staphylococcus aureus* PTCC 1112

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نوع پذیرش: oral | کد مقاله: G-71935

Abstract: *Background:* Synthesis of metal nanoparticles (NPs) using microorganisms is an important strategy that can be replaced by chemical and physical approaches. Due to the fact that nanoparticles are used as industrial catalysts in chemistry and medicine, they have received attention in recent decades. Microorganisms inherently have the ability to reduce metals through their special metabolic pathways. Considering the antibacterial activity that copper nanoparticles have, they can be a suitable alternative to antibiotics. *Materials and Methods:* The supernatant of each of the microorganisms (*Fusarium oxysporum* PTCC 5115, *Saccharomyces cerevisiae* PTCC 5269, *Lactobacillus fermentum* PTCC 1638, *Lactobacillus acidophilus* PTCC 1643) was placed in the incubator shaker. After 24 h, $\text{CuSO}_4 \cdot 5\text{H}_2\text{O}$ was added to the microbial cell culture to a final concentration of 1 mM. The reaction mixture was incubated for 24 h to 48 h on a rotatory shaker at 150 rpm at 22 °C. During the incubation period, the solution color change from blue to dark green (which is indicative of the reduction of CuSO_4 to CuNPs) was monitored. Using the spectrophotometric method, the use of XRD, FTIR, electron microscope devices and the use of the Atomic Absorption Assay method, the copper nanoparticles produced by the four desired microorganisms were identified and measured, and their inhibitory effect on *Escherichia coli* PTCC 1330 and *Staphylococcus aureus* PTCC 1112 was confirmed by disc diffusion and MIC (minimum growth inhibition concentration) methods. *Results:* The X-ray diffraction and scanning electron microscope analysis of synthesized CuNPs revealed spherical-shaped nanoparticles with an average size of 22.3 nm ranged between 11 and 33 nm. The results obtained by microdilution tests were in agreement with the disc diffusion tests, where the antibacterial activity of synthesized CuNPs was higher against the gram-negative bacteria than the gram positive. The CuONPs synthesized by all bacteria showed an MIC against the Gram-negative bacteria from 3.12 to 25 $\mu\text{g}/\text{mL}$, against Gram-positive bacteria from 12.5 to 25 $\mu\text{g}/\text{mL}$. In *Staphylococcus aureus* bacteria, the highest MIC was related to copper nanoparticles of *Lactobacillus acidophilus*, and in



چهاردهمین گنگره بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Escherichia coli, the highest MIC was related to copper nanoparticles obtained from Saccharomyces cerevisiae. **Conclusion:** The results showed that copper nanoparticles have antibacterial activity and can be a suitable alternative to antibiotics. Of course, more research is needed in this field. **Keywords:** copper nanoparticles, Escherichia coli, Staphylococcus aureus.

Loop-Mediated Isothermal Amplification test for rapid identification of clinically-relevant *Nocardia* strains isolated from BAL samples

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نوع پذیرش: oral | کد مقاله: G-87140

Abstract: *Background:* *Nocardia* species are gram-positive and acid-fast bacteria. They are widely distributed in the environment and cause severe infections in humans. Nocardiosis is not easily identifiable, due to the lack of pathognomonic clinical signs. The present study design to develop and evaluate simple and quick method based on a loop-mediated isothermal amplification (LAMP) assay for detection of *Nocardia* spp, strains isolated from Bronchoalveolar lavage (BAL) samples. *Methods:* In this cross-sectional study, during one year from August 2021 to August 2022, a total of 357 Bronchoalveolar lavage (BAL) samples were collected from Shariati and Ayatollah Rohani hospitals affiliated to Tehran and Babol University of Medical Sciences, in the north of Iran, respectively. Polymerase chain reaction (PCR) and partially acid-fast staining were used to test all samples. The optimal LAMP reaction condition was at 65°C for 45 min, with the recognition limit as 1 pg DNA/tube and 100 CFU/reaction. In addition to calcein and manganous ions, agarose gel electrophoresis was used to visualize the amplified LAMP products. *Results:* Out of 357 BAL samples, 0 (0.0%), 4 (1.1%), 9 (2.5%) and 10 (2.8%) *Nocardia* strains were identified by direct staining of partial acid fast, microbiological culture-based, PCR and LAMP methods, respectively. *Conclusion:* We have developed a new LAMP technique for the recognition of *Nocardia* which is fast, very precise, simple, and low-cost. According to our knowledge, this is the first report of the LAMP method being used to detect *Nocardia* species in BAL samples. *Keywords?*

Prevalence and antimicrobial resistance of *Shigella* species isolated from diarrheal patients in Ahvaz, southwest Iran

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نوع پذیرش: oral | کد مقاله: G-26709

Abstract: *Background:* Shigellosis is a significant global human health problem, and *Shigella* is in charge of almost 165 million cases of this disease annually, of whom 163 million cases are in developing countries and 1.5 million cases are in developed countries. The main aims of the current survey were to identify *Shigella* spp. isolated from diarrheal patients by conventional biochemical tests, determine the antimicrobial susceptibility profiles by disk diffusion method, and detect the ipaH gene using the PCR assay. *Materials and Methods:* The bacterial isolates were identified as *Shigella* spp. By microbiological tests and were serogrouped by the slide agglutination test. Antimicrobial susceptibility testing was performed using the disk diffusion method. PCR was performed to detect the ipaH gene. *Results:* The *Shigella* strains were isolated from 522 patients with various diarrhea, including bloody diarrhea (3%), mucoid plus bloody diarrhea (1.9%), mucoid diarrhea (3.2%), and watery diarrhea (3.2%). Overall, 69 (13.2%) isolates were positive for *Shigella* spp., of which 34 (49.3%) serotypes were identified as *Shigella flexneri*, 22 (31.9%) serotypes were identified as *Shigella sonnei*, 9 (13%) serotypes were identified as *Shigella boydii*, and 4 (5.8%) serotypes were identified as *Shigella dysenteriae*. Antibiotic susceptibility tests revealed that the highest resistance percentage was related to ampicillin (82%) and trimethoprim-sulfamethoxazole (77%), and ciprofloxacin and ceftriaxone were the best antibiotics against *Shigella* isolates. *Conclusion:* We concluded that *Shigella* spp. can be considered as an etiological agent of diarrhea in southwest Iran. Since the drug resistance pattern of *Shigella* differs geographically and over time within a country, continuous and regular surveillance program is necessary. *Keywords:* *Shigella*, diarrhea, resistance, Iran

Detection of *Tropheryma whipplei* in valves specimens of patients with culture-negative endocarditis using Real-time PCR methods in Iran

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نوع پذیرش: oral | کد مقاله: G-03517

Abstract: Background: Blood culture-negative endocarditis (BCNE), that is, endocarditis in which blood cultures using usual laboratory methods remain sterile, may account for 2.5% to 70% of all cases of endocarditis, depending on countries. Recently, *Tropheryma whipplei* has been recognized as one of the causative agents of BCNE. However, there is no information about the role of this bacterium in BCNE cases in Iran. The aim of the current study was to investigate the prevalence of *Tropheryma whipplei* in heart valve specimens in Iran. Materials and Methods: In this study, 168 BCNE patients were included in the study during 2016-2020 at the Tehran Heart Center. The Paraffin-embedded heart valve tissue specimens of these patients were collected and the genomic DNA was extracted from them. Then, these samples were tested for detection of *Tropheryma whipplei* using the Real-time PCR method. Results: The 10 (5.95%) positive samples were identified for *Tropheryma whipplei* in this study. Conclusion: This study is the first report of *Tropheryma whipplei* in endocarditis cases in Iran. It is suggested that this bacterium be considered in BCNE cases in Iran by clinicians. **Keywords:** Infectious endocarditis, negative culture, *Tropheryma*, Molecular Detection

Tubrona: Tuberculosis and COVID-19 Co-infection; a single center analysis from Mashhad, Iran

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نوع پذیرش: oral | کد مقاله: G-23960

Abstract: *Background:* The Coronavirus disease (COVID-19) pandemic has affected millions of people all over the world. Tuberculosis (TB) is also continuing every year with high mortality. There is limited evidence of the interaction between severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) infection and pulmonary tuberculosis. The aim of the present study was to determine MTB/SARS-CoV-2 co-infection (Tubrona) prevalence and its mortality. *Materials and Methods:* From June 2020 to February 2022, 402 respiratory clinical samples from tuberculosis suspected cases were referred to the TB Reference Laboratory of Mashhad University of Medical Sciences. All samples were assessed for the presence of Mycobacterium tuberculosis (MTB) via Ziehl-Neelsen and fluorescent staining techniques besides conventional PCR for 16SrRNA and IS6110. Additionally, the presence of SARS-CoV-2 was detected utilizing a one-step RT-PCR kit. Also, Drug susceptibility testing was performed for isoniazid, rifampin, and ethambutol on MTB positive samples. Chi-square and T-test were used to examine the relationship between variables (significance level=P-value 0.05). *Results:* Out of 402 examined specimens, MTB and SARS-CoV-2 infections were detected from 209 and 78 samples, respectively. The co-infection with MTB/SARS-CoV-2 was detected in 35 samples; particularly, the MTB/SARS-CoV-2 co-infection was higher among omicron variants compared to previous SARS-CoV-2 variants. In addition, our findings suggested that the MTB/SARS-CoV-2 risk of mortality was higher than pulmonary TB or COVID-19. Our study revealed that the frequency of MTB/SARS-CoV-2 was relatively low. *Conclusion:* The results showed that the mortality rate in patients with co-infection was approximately 2 times more than mortality in people who had only tuberculosis. Further investigation is required to define if COVID-19 may reactivate or worsen active TB disease. *Keywords?*

High frequency of enterotoxigenic *Bacteroides fragilis* and *Enterococcus faecalis* in the paraffin-embedded tissues of Iranian colorectal cancer patients

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نوع پذیرش: oral | کد مقاله: G-01293

Abstract: *Background:* The association between specific bacteria and colorectal cancer (CRC) has been proposed. Only a few studies have, however, investigated this relationship directly in colorectal tissue with conflicting results. So, we aimed to quantitate *Streptococcus gallolyticus*, *Fusobacterium* spp, *Enterococcus faecalis* and enterotoxigenic *Bacteroides fragilis* (ETBF) in formalin-fixed and paraffin-embedded (FFPE) colorectal tissue samples of Iranian CRC patients and healthy controls. *Materials and Methods:* A total of 80 FFPE colorectal tissue samples of CRC patients (n=40) and healthy controls (n=40) were investigated for the presence and copy number of above bacterial species using quantitative PCR. Relative quantification was determined using $\Delta\Delta CT$ method and expressed as relative fold difference compared to reference gene. *Results:* Relative abundance and copy number of *E. faecalis* and ETBF were significantly higher in CRC samples compared to control group. *E. faecalis* was more prevalent than ETBF in tumor samples. Frequency of ETBF and *E. faecalis* in late stages (III/IV) of cancer was significantly higher than early stages (I/II). We did not detect a significant difference in abundance of *S. gallolyticus* and *Fusobacterium* spp between two groups. *Conclusion:* Our study revealed the higher concentration of *E. faecalis* and ETBF in FFPE samples of CRC patients than controls. However, additional investigations on fecal and fresh colorectal cancer tissue samples are required to substantiate this correlation. **Keywords:** *Bacteroides fragilis*, Colorectal cancer, *Enterococcus faecalis*, *Fusobacterium* spp, *Streptococcus gallolyticus*.

High Level Sero-Prevalence against *Leptospira interrogans* among Wild Foxes, Jackals and Stray Dogs in the North Khorasan Province, Iran

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نوع پذیرش: oral | کد مقاله: G-47906

Abstract: *Background:* Leptospirosis is an important neglected zoonotic disease that affects people and animals in humid, tropical, and subtropical regions. Wild canines carry the pathogen and may contaminate natural sources and can act as a direct or indirect source of human infection. The study was designed to understand the Sero-Prevalence of leptospirosis among domestic and wild canines in Bojnurd county, northeast Iran. *Materials and Methods:* A total of 77 serum samples, comprising 29 sera from asymptomatic wild canines (foxes (n=25) and jackals (n=4)) and 48 sera from asymptomatic stray dogs, were investigated. The infecting serovars were identified and antibody titers were measured by standard microscopic agglutination test (MAT) using serial serum dilutions. *Results:* Among all serum samples, 44.1% reacted positively to one *Leptospira interrogans* serovars. The rate of positive reactions was higher in stray dogs than in wild canines (55.2% and 37.5%, P=0.159). A positive reaction with L. i. Pomona, L. i. Australis, and L. i. Tarasovi was detected only among jackals and foxes. Among the stray dogs, the highest number of positive sera were found for L. i. Grippotyphosa (61.1%) and L. i. Canicola (50%). The highest titer detected was for L. i. canicola (1:1600) in two stray dogs and against L. i. Icterohaemorrhagiae and L. i. Pomona (1:800) in a single jackal. *Conclusion:* The study revealed that leptospirosis seems endemic among wild canines in the North Khorasan Province of Iran. Detailed monitoring of canines is necessary for better understanding the epidemiology of infection in our and other Iranian regions. **Keywords?**

Mycobacterium tuberculosis genotypes in an ethnically diverse area with millions of pilgrims and thousands of immigrants

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نوع پذیرش: oral | کد مقاله: G-03985

Abstract: *Background:* Immigration is considered as a risk factor of tuberculosis (TB). Qom province receives millions of pilgrims and significant numbers of immigrants each year. Most of the immigrants to Qom, arrive from neighboring TB-endemic countries. This study aimed to identify the current circulating M. tuberculosis genotypes in Qom province using 24-locus MIRU-VNTR genotyping. *Materials and methods:* Eighty six M. tuberculosis isolates were collected during 2018–2022 from patients referring to Qom TB reference laboratory. The DNA of isolates was extracted then 24 loci MIRU-VNTR genotyping was done using the web tools available on MIRU-VNTRplus. *Results:* About half (47.7%) of the studied isolates belong to Afghan immigrants. Out of 86 isolates, 39 (45.3%) were of Delhi/CAS genotype, 24 (27.9%) of NEW-1, 6 (7%) of LAM, 6 (7%) of Beijing, 2 (2.3%) of UgandaII, 2 (2.3%) of EAI, 1 of S (1.2%) and 6 (7%) isolates had no corresponding profiles with MIRUVNTRplus data. *Conclusion:* The resemblance of Afghan and Iranian genotypes provides evidence that immigrants actually partake in the circulation of M. Tuberculosis. This study provided essential information about the circulating M. tuberculosis genotypes, their geographical distribution, the relationship of TB risk factors with these genotypes and the impact of the presence of immigrants on the situation of TB in Qom province. *Keywords?*

Investigation of the potential presence of *Porphyromonas gingivalis* in esophageal squamous cell carcinoma (ESCC) Paraffin-Embedded Tissue Samples

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نوع پذیرش: oral | کد مقاله: G-59137

Abstract: *Background:* Esophageal cancer is the eighth most common cancer and the sixth leading cause of cancer death worldwide. Evidence suggest that there is a link between bacterial infection and malignancy. There are few studies on the prevalence of *Porphyromonas gingivalis* in esophageal squamous cell carcinoma (ESCC), so this study aimed to investigate the possible presence of this bacterium in ESCC tissue samples. *Materials and Methods:* In this study, 34 samples of esophageal squamous cell carcinoma were collected to evaluate the potential presence of *Porphyromonas gingivalis*. After extracting the DNA, the polymerase chain reaction (PCR) technique was used to molecularly detect the presence of the bacterium. *Results:* The age range of the study population was 26 to 90 years with a mean age of 63 years. A majority of the tissue samples come from stage I cancer (73.5%). Based on the molecular analysis, no *P. gingivalis* was detected in any of the biopsy specimens. *Conclusions:* *P. gingivalis* infection and ESCC were not correlated based on the current in this study. Likely, the use of fresh samples, more accurate diagnostic methods, geographic differences, as well as larger sample sizes, all contribute to the differences in results between related researches, which can be clarified through performing large-scale studies. **Keywords:** *Porphyromonas gingivalis*, esophageal squamous cell carcinoma, Polymerase chain reaction.

Identification of ISAbal, tet (39), tetX and AbaR antibiotic resistance islands in Acinetobacter baumannii strains isolated from children

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نوع پذیرش: oral | کد مقاله: G-73859

Abstract: Background?? Methods: A total of 74 A. baumannii isolates were recovered from patients at one of the children's hospital in Tehran, Iran. Species identification was performed by appropriate biochemical tests and PCR amplification of the blaOXA-51-like and rpoB genes. Antibiotic susceptibility profile was determined by Kirby-Bauer disk diffusion as described by the clinical and laboratory standards institute (CLSI). The antibiotic disks used in this study were: meropenem, imipenem, piperacillin/tazobactam, amikacin, ciprofloxacin, levofloxacin, gentamicin, ceftazidime, cefepime, ceftriaxone, cefotaxime, trimethoprim, sulfamethoxazole, tobramycin, ampicillin-sulbactam, doxycycline, tetracycline, and minocycline. Also, minimum inhibitory concentration (MIC) of colistin was determined by broth microdilution test. The presence of ISAbal, tet(39), tetX and AbaR antibiotic resistance islands was measured by polymerase chain reaction (PCR). Results: Among the 74 isolates of A. baumannii, 50 samples belonged to males (67.6%) and 24 samples belonged to females (32.4%). 62.2% of children were less than one year old and 8.1% of patients were over 10 years old. The highest rate of isolation of A. baumannii was related to children hospitalized in the intensive care unit (70.27%). All isolates were semi-sensitive to colistin. The highest resistance of A. baumannii isolates against carbapenems including meropenem and imipenem was observed. On the other hand, resistance to ceftriaxone, amikacin, cotrimoxazole, piperacillin/tazobactam and ciprofloxacin was over 80%. Resistance to at least one antibiotic from three or more antibiotic classes was considered as MDR and resistance to at least one antibiotic from all drug classes except one or two antibiotics (colistin or tigecycline) was considered as XDR. Thus, in this study, there were 68 (91.89%) MDR isolates and 55 (74.32%) XDR isolates. The frequency of ISAbal, AbaRs and tetA (39) in A. baumannii isolates was 94.6%, 91.9% and 2.7% respectively, while tetX gene was not found in any of the isolates. Conclusions: The high prevalence rates of ISAbal and AbaRs among A. baumannii isolates can explain the rapid dissemination of antibiotic resistance. Therefore, finding such genes that can affect antibiotic resistance should be given more attention. **Keywords?**

Molecular Detection and Serotyping of Streptococcus pneumoniae in Children with Suspected Meningitis in Northeast Iran

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نوع پذیرش: oral | کد مقاله: G-23159

Abstract: *Background:* To date, more than 90 Streptococcus pneumoniae (S. pneumoniae) capsular serotypes are known. The prevalence of these serotypes varies according to the geographical area and the regional vaccination program. Due to the lack of regular vaccination programs for S. pneumoniae in developing countries, serotyping of the prevalent isolates is useful in selecting the correct vaccine. The present study aimed to evaluate common serotypes of pneumococcal meningitis in Bojnurd, Iran. *Materials and Methods:* All cerebrospinal fluid (CSF) samples suspected for bacterial meningitis were analyzed. The samples were collected during 2014-2018 in the Laboratory of Imam Reza Hospital (Bojnurd, Iran). Due to the high rate of false-negative cultures, polymerase chain reaction (PCR) was used for the detection of *lytA* and *psaA* genes of S. pneumoniae. In addition, the modified Marimon's PCR method was used for serotyping the bacteria. The data were analyzed using Pearson's Chi-square test. *Results:* Out of the 901 CSF samples, 106 cases tested positive for S. pneumoniae using the PCR method, while only 92 cases tested positive using the conventional methods. Based on the Marimon's PCR method, serotypes 23F, 19F, 19A, 1, 14, and serogroup 6A/B were the most common types. Serogroups 18C, 15A/F, 15B/C, 9A/V, 7A/F, 11A/D/F, and 22A/F were also detected in isolates. Note that 2.8% of the samples were non-typable (NT). *Conclusion:* The results showed that only 13 serotypes were responsible for all meningitis cases. Pneumococcal capsular vaccine-13 (PCV-13) is the preferred choice against common serotypes of S. pneumoniae in northeast Iran. *Keywords:* Streptococcus pneumoniae, Serogroup, Vaccines, Meningitis

Evaluation of *Helicobacter pylori* colonization, Non Tuberculosis Mycobacterial strains and detection of biliary Tuberculosis in gallbladder diseases

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نوع پذیرش: oral | کد مقاله: G-25670

Abstract: *Background:* Bile in healthy people is sterile and free of any bacteria, and the presence of microorganisms in human bile can be a sign of a clinical problem. Therefore, postoperative infection and its prevention are one of the concerns of surgeons. *Helicobacter pylori* is one of the most common chronic bacterial infections in the gastrointestinal tract. Today, chronic biliary disorders such as chronic cholecystitis and cholecystitis are widespread worldwide. Mycobacteria are pervasive microorganisms and are recognized as the most important environmental opportunists. Nowadays, reports about biliary tuberculosis and non-mycobacterial tuberculosis are presented. Therefore, identification and differentiation of Mycobacterium species are essential, and molecular methods are useful tools for the diagnosis of biliary infections. The aim of the present study was to evaluate the presence and type of species isolated from bile specimens, considering the importance and risk factors of HP, NTM, and MTB. *Methods:* This descriptive-research study was conducted in Imam Reza Hospital in Tabriz during one year, from August 1399-1401 with the informed consent of all patients. The statistical population of patients referred to Imam Reza Hospital who have surgery for gall bladder diseases was sampled completely randomly during different months, and the number of samples is 100. Following the removal of the gallbladder by a qualified medical professional using an appropriate technique, such as laparoscopy or surgery, samples were immediately sent to the lab. The CTAB method was used for DNA extraction. After PCR, it was sent for sequencing with the help of two 16S rRNA genes and ureC. *Results:* In this study, the ureC gene was used to diagnose *Helicobacter pylori*, and 19 (34.55%) ureC positive cases were reported. 16S rRNA was used to identify Mycobacterium strains, and 36 samples (65.45%) were reported to have Mycobacterium tuberculosis and NTM. *Conclusion:* More research on the pathogenicity and pathophysiological effects of these bacteria will help explain the involvement of bacteria in gallstone formation. If the factors involved in the formation of stones by these bacteria and the type of stones are investigated more closely, more recent data may be obtained in this field, taking into account the potential role of bacteria as effective factors in the formation of gallstones. In conclusion, the findings of this investigation showed that DNA



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from non-tuberculosis mycobacteria and Helicobacter were detected in the bile and tissue of individuals with gallbladder illnesses. **Keywords:** Helicobacter pylori, Mycobacterium tuberculosis, Gallstones, Nontuberculous Mycobacteria

Survey of bacteremia in suspicious Covid-19 pediatric by BACTEC during SARS-COV-2 pandemic in Mofid children hospital in 2020-2022

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نوع پذیرش: oral | کد مقاله: G-59084

Abstract: *Background:* Sepsis is a complex and important disorder can cause by invasive pathogen such as bacteria and is potentially fatal. On the other hand, the frequency of multidrug resistance bacteria has grown significantly in recent years whole of the world. With the recent pandemic of covid-19 children are in hazard of a bacterial co-infection when they are suspected of a COVID-19 that it is a would makes the situation worse. This study aimed to survey the prevalence of Gram-negative bacteria in children suspected of COVID-19 *Material and Method:* Blood culture of children with clinical suspicion to COVID-19 were done by BACTEC during two years of COVID-19 pandemic in the clinical lab of pediatric health institute. The BACTEC bottles had been characterized by selective cultures and biochemical tests as standard routine after the device's alarm. *Results:* According to the results, 421 hospitalized children suspected of COVID-19 infection were surveyed. 60.5% and 39.5% of them were boys and girls, respectively. 51.8% of the patients were under three years old and 48% percent were older than three years old. COVID-19 positive confirmed in 24% of patients by Real- Time PCR. The most common clinical presentation was in order: fever, shortness of breath, and cough. The most frequent isolated bacteria were: Pseudomonas spp. (21.6%), Klebsiella spp. (20.7%). Most cases of COVID-19 were seen in patients with Klebsiella spp. followed by and Pseudomonas spp. *Conclusion:* Bacteremia could be a life threatening, increasing the length of hospital stay, and death. Moreover, co-infection with COVID-19 can lead to complications and worsen the prognosis. Thus, the investigation of the resistant patterns of bacteria, molecular studies. *Keywords:* Sepsis, COVID-19, bacteremia, Gram-negative

The study of the effect of bacteriophage in combination with doxycycline against methicillin-resistant *Staphylococcus aureus*

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نوع پذیرش: oral | کد مقاله: G-04162

Abstract: *Background:* Methicillin-resistant *Staphylococcus aureus* (MRSA) is a significant threat to human health. MRSA, a supple bacterium that adopts a variety of antibiotic resistance mechanisms, is the cause of multiple life-threatening conditions. As a treatment strategy against MRSA infections phage therapy has the potential of becoming alternative remedy. The aim of this study was bacteriophage isolation against MRSA isolates and the study of the effect of the phage in combination with doxycycline against MRSA. *Methods:* MRSA strains were isolated from hospitalized bed-sore patients and confirmed as MRSA by PCR assay for *mecA* gene. The phage was isolated from Imam Khomeini hospital sewage. The spot test and the double layer agar (DLA) techniques were used for validation of phage presence. Pure plaques were amplified for further characterization. DLA method was also used for host range determination. The morphology of the phage was observed using transmission electron microscopy (TEM). Thermal and pH stability of the isolated phage was determined by incubation of phage suspension at various temperatures (-20, 4, 25, 37, 60, and 80°C) and pH ranges (2, 4, 7, 10, and 12) for 1 hour. Minimum inhibitory concentration (MIC) of doxycycline, and the combination of phage-doxycycline was measured by broth microdilution method, referring to the Clinical and Laboratory Standards Institute (CLSI) for MRSA. The bacteriophage-antibiotic interaction was evaluated by checkerboard assay in the 96-well plate. *Results:* Spherical morphology of bacteriophage with a lipid membrane around capsomere was identified by TEM and the phage was classified into the Cystoviridae family. The optimal temperature of phage activity was observed at 37°C. The phage was sensitive to higher temperature (60°C). Moreover, full inactivation was observed at 80°C. The phage completely lysed at pH 12 however, was stable between pH ranges 2-10. The pure phage was significantly effective against clinical MRSA isolates (80%). The MIC of doxycycline was 64 µg/ml, in contrast, the MIC of doxycycline in combination with phage was reduced by 4 folds. *Conclusion:* The isolated bacteriophage had a specific lytic activity against MRSA. A single



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administration of phage exhibited efficacy in bacterial clearance. The combination of doxycycline and bacteriophage can be a promising candidate for combating MRSA infections.

Keywords: Bacteriophage, Methicillin-resistant Staphylococcus aureus, Doxycycline, Phage-antibiotic combination

Bacillus parabiotic modulates TLR3 and ACE2 gene expressions in RAW264.4 cells induced by viral mimetic Poly I:C

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Background:

Toll-like receptor-3 (TLR3) induces a double-stranded RNA (dsRNA)-mediated inflammatory signal in the cells of the innate immune system. Angiotensin-converting enzyme 2 (ACE2) has been established as the functional host receptor for severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) and induced through TLR3 signals. Simultaneously, the interaction between TLR3, ACE2 and SARS-CoV-2 increases the secretion of soluble ACE2 in the blood and leading to the release of a massive quantity of cytokines (cytokine storm). Here we investigated application of *Bacillus* parabiotics for possible modulation TLR3 and ACE2 gene expressions in RAW264.4 cells under induction of viral infection mimicker Poly I: C.

Method: The murine macrophage cell line RAW264.7 maintained in Dulbecco's modified Eagle medium containing 10% (v/v) FCS. RAW264.7 cells (1×10^5 cells /well) were plated in fresh medium in 6 well plates overnight. Inactivated *Bacillus* probiotic (parabiotic) was obtained by autoclaving bacterial cell pellets (121 °C, 15min). RAW264.7 cells were exposed to spore parabiotic *Bacillus* sp. 1630F (1×10^6 CFU/mL) for 3 hrs. The poly I:C (10 µg/mL) were added to wells and kept for further for 3 hrs. Cell lines only treated by poly I:C were used as inflammatory control. Total RNA was isolated using the Yekta kit (Tehran, Iran) in accordance with the manufacturer's instructions. DNase treated RNA was transcribed into complementary DNA (cDNA) using cDNA synthesis Kit (Invitrogen, Carlsbad, USA) following the manufacturer's instructions. qRT-PCR was performed against some putative TLR3 and ACE2 genes (Applied Biosystems Co, California, USA). The Act1 (beta-actin) gene was used as the internal control, and gene expressions were calculated using the formula $2^{-\Delta\Delta CT}$ while all primer pairs displayed similar amplification efficiency.

Result: We assessed the immunomodulating capacity of heat killed b.1630F on RAW264.7 cell line by examining its effect on expression of ACE2 and TLR3. The result shown that treatment with Poly:IC induced the expression of TLR3 and ACE2. However the expression of TLR3 and ACE2 gene was decreased 126- and 8.5 folds in the presence of parabiotic strain.

Discussion: Our *Bacillus* parabiotic cells showed anti-inflammatory effects on RAW264.4 cells by modulating TLR3 signaling pathway and ACE2 receptor following the inflammation induction by PolyI:C. Therefore, *Bacillus* parabiotic maybe through intra-nasal administration can possibly prevent and even reduce inflammation-related diseases such as SARS-CoV-2.

Keywords: Parabiotic, *Bacillus*, Inflammation, TLR3, ACE2

Assesment of Toxin Profiles and Antibiotic-resistance Patterns of Clostridiom difficile Strains Isolated from Hospitalized Patients with Diarrhea in Imam khomeyni Hospital in Sarab, Iran

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نوع پذیرش: oral | کد مقاله: G-35496

Abstract: *Background:* The lower susceptibility to medications used to treat Clostridiom difficile infection (CDI) has led to a major rise in current concerns about CDI. The severity and prognosis of the disease are related to the toxins that C. difficile strains produce. In this study, C. difficile prevalence, its toxin-producing genes, and patterns of antibiotic resistance to antibiotics were examined in diarrheal samples from hospitalized patients at the Imam Khomeini Hospital in Sarab, Iran. *Materials and Methods:* A total of 115 diarrheal samples from patients who were hospitalized to various wards of the Imam Khomeini Hospital in Sarab between February 2020 and September 2022 were gathered for this investigation. Using a PCR method and culture on specialized culture media (CCFA), C. difficile isolates were identified. The presence of toxin-encoding genes (tcdA and tcdB) and binary toxin genes (cdtA and cdtB) was analyzed by PCR method. The agar dilution method was used to assess if the isolates were resistant to the medications metronidazole, vancomycin, and clindamycin. *Results:* 12 (10.43 percent) C. difficile isolates were discovered from 115 diarrheal samples taken from hospitalized patients. All C. difficile isolates tested positive for the toxin-producing genes tcdA and tcdB by PCR, and four (33.33 percent) and five (41.66 percent) isolates, respectively, tested positive for the binary toxin genes cdtA and cdtB. Three isolates (25 percent), two (16.66 percent), and two (16.66 percent) of the isolates tested positive for resistance to metronidazole, vancomycin, and clindamycin, respectively. All of the isolates also tested positive for resistance to rifampicin. *Conclusion:* Clinical laboratories should frequently carry out C. difficile diagnostic testing on diarrheal specimens of hospitalized patients, according to studies showing that toxic C. difficile with a tcdA+/tcdB+ phenotype is a prominent cause of nosocomial diarrhea in Imam Khomeini Hospital in Sarab. It is important to take C. difficile resistance to conventional antibiotic therapy as a signal to avoid unreasonable antibiotic administration. *Keywords:* Antibiotic resistance; Clostridiom difficile; TcdA; TcdB

Discovery of a New Antimicrobial Peptide, Dendrocin-ZM1, Derived from *Zataria multiflora* Boiss

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نوع پذیرش: oral | کد مقاله: G-14895

Abstract: *Background:* Today, resistance of microorganisms to antibiotics has become a major challenge. To overcome this problem, development of new drugs, besides research on their antibacterial activity, is essential. Among chemical components, antimicrobial peptides (AMPs) exhibit antibacterial activity and can be selected as suitable antimicrobial candidates. In this study, a novel antimicrobial peptide was isolated from *Zataria multiflora* Boiss (ZM). The AMPs produced by this plant have not been described previously. *Materials and Methods:* In this study, a novel AMP was purified by ammonium sulfate precipitation and reversed-phase HPLC and finally identified by sequence analysis using Edman degradation. The *in silico* method was used to examine the physicochemical properties of novel AMP. In this study, the antimicrobial activity of this peptide was examined against four reference strains (gram-positive and gram-negative) and one clinical vancomycin-resistant *Staphylococcus aureus* strain. Moreover, to examine cytotoxicity and hemolytic activity, a HEK-293 cell line and human red blood cells (RBCs) were used, respectively. *Results:* Peptide sequence analysis revealed a fragment of 33 amino acid residues as TTLRLNTLAYKVAWLNVKAFWAA GRA LKKVGR with a molecular weight of 3716.48 Da and this novel antimicrobial Evaluation of the physicochemical properties of dendrocin-ZM1, as an AMP, indicated a net charge of positive 7 and a hydrophobicity percentage of 54%. This peptide had an amphipathic alpha helical conformation. It exhibited broad-spectrum antibacterial activities against the tested strains at minimum inhibitory concentrations (MICs) of 4–16 µg/mL. Besides, this peptide showed negligible hemolysis and cytotoxicity in the MIC range. It also exhibited heat stability at temperatures of 20 to 80 °C and was active in a broad pH range (from 6.0 to 10.0). *Conclusion:* The present study indicates that dendrocin-ZM1 may be considered as a new antimicrobial agent with therapeutic potential against major human bacterial pathogen. *Keywords:* Antimicrobial peptide, *Zataria multiflora*, Cytotoxicity, physicochemical properties, dendrocin-ZM1

Isolation, molecular identification and of antibiotic susceptibility pattern of bacteria causing paranasal sinus infections in children with malignancy with fever without specific focus, in Arak in 1401

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نوع پذیرش: oral | کد مقاله: G-51426

Abstract: *Background:* Children with malignancies are at risk of a wide range of infections, where fever is the main indicator of infection. Sinusitis is the most important type of infection in these patients. Bacterial infections is the major cause of sinusitis, and fungal infections are in the next category. Therefore, the purpose of this study is to investigate the bacterial species causing sinusitis in children with malignancy with fever of unknown origin and determine their antibiotic susceptibility pattern. *Methods:* 90 samples of sinusitis secretions from children aged 5 to 15 years with malignancy were collected from the hospitals of Arak city. For the isolation and initial identification of the isolates, culture was carried out in selected and specific culture media. Different phenotypic and biochemical tests were used for diagnosis of isolates. By using molecular methods including PCR and determination of 16SrRNA gene, the isolates were identified up to the species limit. the isolates were tested for antibiotic sensitivity according to CLSI 2021 guidelines. *Results:* 36 isolates (40%), including 4 isolates of Nocardia (11.12%), 4 isolates of E. coli (11.12%), 3 isolates of Klebsiella pneumoniae (8.33%), 5 isolates of Pseudomonas aeruginosa (13.88%), 3 isolates of S. baumannii (8.33%), 4 isolates of Staphylococcus aureus (11.12%), 3 isolates of Staphylococcus epidermidis (8.33%), 5 isolates of Streptococcus agalactiae (13.88%), 2 isolates of Streptococcus pneumoniae (5.55%) and 3 isolates of Enterococcus faecium (8.33%) were isolated. The isolates were most sensitive to the antibiotics imipenem and trimethoprim-sulfamethoxazole and showed the least sensitivity to erythromycin, ciprofloxacin and clarithromycin. *Conclusion:* The results show that sinusitis can be the cause of fever of unknown origin in cancer patients, and it is recommended to use a combination of molecular and phenotypic methods for accurate identification of isolates, as well as to perform antibiotic sensitivity tests to select the correct treatment and reduce antibiotic resistance. *Keywords?*

Etiological agents of urinary tract infection in diabetic patients

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Background: The evidence indicated that diabetes mellitus (DM) increased the risk of asymptomatic bacteriuria and urinary tract infections (UTIs). Because of the frequency and severity of UTIs in these patients, prompt diagnosis and early therapy are warranted. This study was designed to detect the bacterial species responsible for UTI in diabetic patients.

Materials and Methods: In the current cross-sectional study, 70 culture-positive diabetic patients with UTIs were enrolled. Urine samples were collected. Phenotypic methods and bacterial culture were used to investigate the growth of common bacteria in these samples.

Results: The most common bacteria isolated in these patients were *Escherichia coli* (68.5%), *Klebsiella pneumonia* (25.7%), *Enterococcus faecalis* (11.14%), *Proteus mirabilis* (10%) and *Citrobacter Sp.* (7.4%). Also, ESBL producers were identified in 12 isolates consisting of 8 *E. coli* and 4 *Klebsiella*.

Conclusion: This study showed that the most predominant bacterial agents causing UTIs in diabetic patients were *Escherichia coli*, followed by *Klebsiella pneumonia*. Considering that UTIs are more common in these patients and detection of the ESBL-producing isolates in them, the importance of proper screening programs and health care policies becomes more apparent.

Keywords: *Escherichia coli*, *Klebsiella pneumonia*, ESBL producer, UTIs, Diabetes Mellitus

In vitro evaluation of the inhibitory effect of prodigiosin pigment from *Serratia marcescens* on *Leishmania major*

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نوع پذیرش: Poster | کد مقاله: G-95612

Abstract: *Background and Aim:* Prodigiosin pigment is a red redox compound that is metabolically active and has therapeutic effects on eukaryotic and prokaryotic cells. The opportunistic gram-negative pathogen *Serratia marcescens* produces the prodigiosin pigment. *Leishmania major* is a protozoan that causes cutaneous leishmaniasis and is transmitted by mosquito bites. The main treatment for this infection is the use of 5-valent compounds of anti moan and amphotericin B, which scientists are looking for new ways to treat due to the observed side effects and drug resistance. This study aimed to investigate the effect of prodigiosin pigment extracted from *Serratia marcescens* on *Leishmania major* and also the effect of prodigiosin toxicity on the PC12 cell line. *Material and Methods:* For this purpose, *Serratia marcescens* RTCC 2281 strain was purchased from Razi Vaccine and Serum Research Institute and Prodigiosin pigment was extracted from this bacterium with the help of Ethyl acetate. The relative purity of the pigment was confirmed by thin-layer chromatography, spectrometry UV-Vis and FTIR. We examined its effect on different concentrations against *Leishmania major* and PC12 cell lines. *Results:* Prodigiosin pigment at concentrations of 10000 µg/ml in 24 and concentrations of 10000 and 5000 µg/ml in 48 hours respectively 97%, 98.68%, and 97.29% inhibited parasites. its IC50 level in 48 hours was 62.41 µg/ml and CC50 of this pigment was obtained on the cell line 842.4 µg/ml. All experimental steps were performed with three replications and statistical results were obtained with the help of GraphPad Prism software version 9. *Conclusion:* According to the results, this pigment was effective against *Leishmania major* parasite, and its selective index on cells was 13.5 times (13.49), so more and more comprehensive studies to investigate the composition of prodigiosin in vitro and in vivo are suggested. **Keywords:** Prodigiosin pigment, *Serratia marcescens*, *Leishmania major*, Cell line, IC50

The effects of resveratrol on gene expression of TNF- α , TGF- β and PPAR- γ and glycemic control in patients with diabetic coronary heart disease

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نوع پذیرش: oral | کد مقاله: G-89673

Abstract: *Background:* The effects of resveratrol on gene expression of TNF- α , TGF- β and PPAR- γ and glycemic control in patients with diabetic coronary heart disease Asma Hoseini^{1*}, Gholamreza Namazi¹, Zatollah Asemi¹. Research Center for Biochemistry and Nutrition in Metabolic Diseases, Kashan University of Medical Sciences, Kashan, Iran *Background:* Type-2 diabetes (T2DM) is one of the largest public health problems entire the world. Despite the various treatments available now, the cases of diabetes and its complications are increasing. Coronary heart disease (CHD) is one of the most important complications related to T2DM. T2DM is associated with several metabolic complications, including dyslipidemia, hyperglycemia, insulin resistance and increased inflammatory cytokines. Also several genes are involved in the pathogenesis of diabetes and CHD, including PPAR- γ , TNF- α and TGF- β . *Aims:* This study was performed to evaluate the effects of resveratrol on gene expression of TNF- α , TGF- β and PPAR- γ and glycemic control in patients with diabetic coronary heart disease. *Materials and Methods:* This randomized, double-blind, placebo-controlled trial, registered in the Iranian Registry of Clinical Trials (IRCT20181029041490N1) was conducted on 56 patients with diabetic coronary heart disease, aged 40 to 75 years, at a cardiac clinic in Kashan, Iran. Participants were randomly divided into two groups to receive 500 mg of resveratrol per day (n = 28) or placebo (n = 28) for 4 weeks. *Conclusion:* 4-week supplementation of resveratrol in patients with both T2DM and CHD, upregulated gene expression of PPAR- γ . Additionally, resveratrol had beneficial effects on glycemic control as well as reduced fasting glucose and insulin resistance, and significantly increased insulin sensitivity when compared with the placebo. Resveratrol supplementation did not have any effect on gene expression of TNF- α and TGF- β . *Keywords:* Resveratrol, coronary heart disease, type 2 diabetes mellitus

Investigating the effects of quercetin and calorie restriction on the activity and expression of antioxidants in mice fed a high-fat diet

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نوع پذیرش: oral | کد مقاله: G-86103

Abstract: *Background:* effects of Calorie restriction along with quercetin on obesity-induced oxidative stress were investigated. Over the past decades, obesity has been one of the major public health threats in most countries. Some strategies, such as dietary intervention, caloric restriction (CR), and the use of antioxidant, have been propounded to reduce obesity-induced oxidative stress. In this study the effects of CR along with quercetin (QUER) on obesity-induced oxidative stress were investigated. To this end, thirty 8-week-old BALB/c mice were divided into five groups: normal diet, high-fat diet (HFD), HFD and QUER (15 mg Kg⁻¹, IP), HFD and CR and HFD with QUER and CR. Activities of catalase (CAT), paraoxonase (PON1), liver enzymes and lipid profile, and the expression of NQO1 were analyzed. The activity of CAT and PON1 were decreased in the HFD group. Treatment with QUER and CR brought about significant changes (P 0.05). To be more precise, this treatment relatively decreased liver enzymes, which was notable about ALT and ALP. Elevated levels of triglyceride and total cholesterol in the HFD group were reduced by QUER and CR, which was considerable about CR. CR, increased HDL-C and also lessened atherogenic lipids. High-fat diet decreased NQO1 gene expression, and it was observed that combination of QUER and CR significantly increased NQO1 gene expression (P 0.05). These results demonstrate that QUER, CR, and particularly their combination have the potential to reduce the destructive effects of HFD by improvement of oxidative stress status. Accordingly, CR and QUER are deemed appropriate strategies for improving liver function and the antioxidant system in obese people. **Keywords:** high-fat diet, calorie restriction, quercetin, catalase, paraoxonase, NQO1.

Evaluation of calprotectin and heparin binding protein in patients with COVID-19

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نوع پذیرش: oral | کد مقاله: G-02931

Abstract: Background: There are many serum biomarkers associated with infectious disease, in which Calprotectin and HBP1 seems to be related to the severity of clinical symptoms of COVID-19 disease. Materials and Methods: Serum samples of 35 hospitalized patients with COVID-19 were assessed for the level of the aforementioned biomarkers and also compared with the 35 positive controls. HBP and Calprotectin level Measurements were quantitatively detected using Creative Diagnostics ELISA kit according to the manufacturer's instruction and Levels of LDH and CRP were determined by Biochemistry Auto-analyzer (Hitachi-911), ferritin was measured using DiaPro diagnostic ELISA kit (DiaPro- Italy), and neutrophils and platelets were counted by a Sysmex Cell Counter (Sysmex KX-21- Japan). Results: Analysis of pharyngeal swab specimens from all participants showed the presence of SARS-CoV-2 viral RNA in only the patient's group (n = 35). There was no significant difference in the mean age of the patients (45.40±10.34) and healthy control (46.34± 11.71) subjects. Calprotectin was significantly higher in patients compared with controls. An increasing trend was also observed in the HBP level but it did not reach statistical significance. COVID-19 patients had a significantly higher level of ferritin, CRP, platelet and neutrophil counts, and LDH activity compared with healthy individuals. Conclusion: Our study indicate that Calprotectin and HBP1 relate to the severity of clinical symptoms of COVID-19 disease. However, more studies are needed in this field. Keywords: COVID-19, HBP, Calprotectin

Higher serum level of CTRP15 in patients with coronary artery disease is associated with disease severity, body mass index and insulin resistance

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نوع پذیرش: oral | کد مقاله: G-50723

Abstract: *Background:* CTRP15 is a prologue of adiponectin which has shown to have favourable effects on glucose and lipid metabolism. Studies have reported lower levels of CTRP15 in T2DM and metabolic syndrome; however, its circulating levels have not been evaluated in CAD patients. *Materials and Methods:* This case-control study was conducted on 190 angiographically confirmed coronary artery disease (CAD) patients and 70 controls. Serum levels of CTRP15, adiponectin, TNF- α , and IL-6 were measured using the ELISA technique. *Results:* CTRP15 was shown to occur in higher levels in CAD patients compared with controls. In CAD patients, CTRP15 showed a positive correlation with BMI, FBS, insulin, HOMA-IR, IL-6, and TNF- α and a negative correlation with HDL-C and adiponectin. *Conclusion:* Elevated levels of CTRP15 in CAD patients and the relation of CTRP15 with pathogenic conditions such as insulin resistance, inflammation, and decreased adiponectin and HDL-C suggest a possible compensatory response to these conditions in CAD patients **Keywords:** CTRP; adiponectin; atherosclerosis; adipose tissue; inflammation

Promising anti-breast cancer activity of a novel analogue of 4-thiazolidinones via apoptosis induction in in vitro and in vivo models

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انستیتو پاستور ایران^۱

دانشگاه آزاد واحد علوم دارویی^۲

نوع پذیرش: oral | کد مقاله: G-61805

Abstract: *Background:* Novel lead compounds as anticancer agents with ability to circumvent emerging drug resistance have recently gained a great deal of attention. Thiazolidinones are among such compounds with well-established biological activity in the field of oncology. Here, we evaluated the potential of some synthesized compounds with thiazolidinone structure to kill triple negative breast cancer (TNBC). *Methods:* Hep-G2, HT-29 and MDA-MB-231 cell lines were used in this study. MTT, soft agar colony formation, matrigel invasion assay, flowcytometry, DAPI staining, Real-time PCR and western blotting experiments were carried out to explore the potential activity against TNBC and also elucidate the possible mechanism of cell death induction. For in vivo studies, 4T1 cells were inoculated into the fat pad mammary of female BALB/c mice and then the most potent compound in vitro was intraperitoneally administered for 20 days. Proliferation index and angiogenesis in tumor and lung tissues were examined using immunohistochemistry. *Results:* The findings of anti-proliferative assay led to discovery of one compound with a high cytotoxic effect using colon, liver and breast cancer cells. Furthermore, MDA-MB-231 and 4T1 cell lines were employed to represent triple negative breast cancer (TNBC). Next, a number of in vitro and in vivo evaluations were performed to demonstrate the potential activity against TNBC and also elucidate the possible mechanism of cell death induction. Our in vitro outcomes exhibited an impressive anticancer activity for this compound toward MDA-MB-231 cells through inducing apoptosis and a remarkable anti-metastatic feature via suppressing MMP-9 expression as well. Consistently, the in vivo and immunohistopathologic evaluations demonstrated that the target compound significantly inhibited the 4T1 induced tumor growth and its metastasis to the lung.



چهاردهمین گنگره بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Conclusion: Altogether, among numerous thiazolidinone derivatives, our synthesized compound represented a promising anticancer agent for TNBC, which is a major concern in the developed and developing countries. **Keywords:** TNBC; Thiazolidinone; Apoptosis; Metastasis; BALB/c

Earlier Detection of Alzheimer's Disease based on a Novel Biomarker cis P-tau by a Label-Free Electrochemical Immunosensor

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نوع پذیرش: oral | کد مقاله: G-92038

Abstract: Early detection of cis phosphorylated tau (cis P-tau) may help as an effective treatment to control the progression of Alzheimer's disease (AD). Recently, we introduced for the first time a monoclonal antibody (mAb) with high affinity against cis P-tau. In this study, the cis P-tau mAb was utilized to develop a label-free immunosensor. The antibody was immobilized onto a gold electrode and the electrochemical responses to the analyte were acquired by electrochemical impedance spectroscopy (EIS), cyclic voltammetry (CV), and differential pulse voltammetry (DPV). The immunosensor was capable of selective detection of cis P-tau among non-specific targets like trans P-tau and major plasma proteins. A wide concentration range (10^{-14} M– 3.0×10^{-9} M) of cis P-tau was measured in PBS and human serum matrices with a limit of detection of 0.02 and 0.05 pM, respectively. Clinical applicability of the immunosensor was suggested by its long-term storage stability and successful detection of cis P-tau in real samples of cerebrospinal fluid (CSF) and blood serum collected from human patients at different stages of AD. These results suggest that this simple immunosensor may find great application in clinical settings for early detection of AD which is an unmet urgent need in today's healthcare services.

The Successful Experience of a Knowledge-based Company in the Production of Biological Products:

Dr. Hossein Zolfagharian¹ © @

¹ Member of the Board of Directors of Masoondarou Company

نوع پذیرش: oral | کد مقاله: G-54208

Abstract: The biological products are drugs that are derived from biological sources including vaccines, therapeutic sera, products derived from plasma and products derived from recombinant technology, monoclonal antibody and products derived from tissue and cells. Biological products are prepared from hosts such as bacterial cells, viruses, yeasts and other microorganisms through multiple processes and modern biotechnology methods. Today, biological products in the world are focus by many investors and different countries because of their essential role in the prevention and treatment of diseases. Masoondarou pharmaceutical company was established in 2007 as a knowledge base company , that succeed in producing biotechnological drugs and vaccines for humam by advanced technical knowledge , it also works by providing new drugs with the help of sophisticated technology to improve community health. Masoondarou pharmaceutical company has produced several biological products in our country for first time with own scientific experiences, as a successful model. Masoondarou is the first and only pharmaceutical company in Iran that produces monovalent and polyvalent antitoxins of Clostridium botulinum, Haemophilus influenzae type B conjugate vaccine and Clostridium botulinum toxin type A .The products of Masoondarou were manufactured according to American and European Standards. We have high production capacity to fully meeting the needs of the country. One of the biological products produced by this company is botulinum antitoxin, which is considered the only treatment for botulism, and due to the complex technology, there are few manufacturers at the global level and it is considered as one of the rare and strategic products. Masoondarou Company has designed, optimized and implemented all stages of manufacturing of the mentioned product at the semi-industrial and industrial level with local knowledge to meet the urgent needs of the country, and for the first time, clinical trial studies have been conducted classically in the country and entered the market with the approval of the Ministry of Health. Since 2007, all the needs of the country have been provided by the company, and the production capacity can be upgraded to whatever extent the country needs.

Comparison of Clinical and histological findings between patients with rectal and cecal cancer

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نوع پذیرش: oral | کد مقاله: G-57264

Abstract: *Background:* Genetic and environmental factors and social factors that determine health and socio-economic status can probably be effective in the prevalence, incidence, mortality, and survival rate of colorectal cancer. Therefore, the present study was conducted to compare the findings of patients with rectal cancer and cecal cancer. *Materials and Methods:* This study was of a cross-sectional type, it was performed on all patients who underwent colonoscopies in Ayatollah Rouhani and Shahid Beheshti Hospitals in Babol city (2007-2017). The diagnosis of rectal and cecal cancer was performed on patients, too. The data collection tool included a checklist of demographic characteristics, questions about symptoms, time of visit, and duration of symptoms. Data were analyzed statistically using statistical package for the social sciences (SPSS)-19, frequency distribution, Analysis of variance, t-test (p<0.05). *Results:* Among 117 cases of colorectal cancer, the files of 97 patients (average age: 59.69 ± 14.11), including 33 cases of cecal cancer and 64 cases of rectal cancer, were examined. Among the patients, 55 (56.7%) were male and 42 (43.3%) were female. The A relationship between gender (p=0.04) and smoking (p=0.041) with rectal cancer was observed. Male gender (OR=2.42; CI: 1.03-5.71) and smoking (OR=2.70; CI: 1.14-6.13) have been associated with an increased risk of rectal cancer. Rectal bleeding (OR=2.78; CI: 1.16-6.67) in patients with rectal cancer (64.1%) was significantly (p=0.021) more than in patients with cecum cancer (39.4%). The prevalence of abdominal pain (OR=2.60; CI: 1.08-6.20) in cecum cancer (36.4%) was significantly (p=0.031) higher than in rectal cancer (26.6%). Poorly differentiated histology grade (OR=4.11; CI: 1.31-12.93) was seen more in cecum cancer (27.3%) than in rectal cancer (10.9%). The average age of patients with cecum cancer (63.67 ± 14.82) was higher than that of patients with rectal cancer (57.64 ± 13.40) (P=0.041). *Conclusion:* Summary of the overall findings and the importance of the study (Times New Roman, font size12). **Keywords:** Rectal Cancer, Cecal Cancer, Patients Findings

Biological dosimetry in the events of nuclear and radiological accidents

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نوع پذیرش: oral | کد مقاله: G-08431

Abstract: Human is under constant exposure to ionizing radiation from natural or man-made radioactive materials. However, in case of nuclear and radiation accidents a large number of individuals would be exposed to a substantial dose of ionizing radiation. In case of a radiation accident, the first information comes especially from physical dose reconstruction, blood count data and from the clinical symptoms that exposed persons might display. Therefore, dosimetry is essential to distinguish between those who are exposed and are not exposed to radiation in order to provide them with timely medical treatment. Thus, accurate assessment of the radiation dose in shortest possible time is especially important for successful and effective triage and medical management. Biological dosimetry has become a valuable tool when person does not have personal radiation measuring devices or when those devices cannot provide important information due to the inter-individual variation in biological response to radiation. Biological dosimetry implies using different biophysical, cellular, hematological, immunological, biochemical, molecular or cytogenetic methods for radiation dose estimation. From these methods, different cytogenetic assays (including dicentric (DC)-, micronuclei ((MN-, premature chromosome condensation (PCC)-assay, and fluorescent in situ hybridization (FISH)) are of much interest because of their specificity and sensitivity to radiation. Three techniques- DC assay, MN assay and FISH-have been standardized to date for monitoring and quantifying the resulting chromosomal aberrations in peripheral blood lymphocytes (PBL) in order to estimate radiation absorbed dose. PCC analysis is under active consideration for standardization. Among these, DCA assay in PBL is considered as the 'gold standard' for biological dosimetry for radiation emergency medicine because of its proven utility in the past large-scale nuclear incidents or accidents such as the Chernobyl accident in 1986, the Goiania accident in 1987, the Tokaimura accident in 1999 and the Fukushima accident in 2011. More recently, molecular biomarker methods such as the gamma-H2AX assay have been proposed. Moreover, utilization of other genetic (transcriptomic) and epigenetics biomarkers (such as miRNA, long non-coding RNA, circular RNA) for biological dosimetry is under investigation because of high-thruput nature of these assays. All the available methods as well as the dicentric gold standard assay, suffer from limitations. Therefore, search for a suitable biomarker and assay is underway. The range of biodosimetry options now available have led to proposals for a multi-parametric approach to investigate overexposed subjects.

The need for coordinated activities in research and technology development of diagnostic products

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نوع پذیرش: oral | کد مقاله: G-90158

Abstract: Background: Science and technology exhibits a very strong relationship. Countries those having better science and technology education will end up to better products and knowledge base economy. Creating the critical mass of educated as well as researchers is one of the most important parameter in creating the technology environment. Other effective tools in technology development would be the use of platforms such as universities, incubators, and accelerators. Investments in such infrastructures will surely increase the chance of success in development of such platforms. In well developed countries 3 to 5 percent of total GDP is invested on research. A big part of this amount is funded by governmental institutions. Although a considerable amount of budget comes from public sector also. In this way there is a good relationship between the public and private sector in supporting research for the development of technology and products which in first place is developed to cope with the needs of society. In Iran the authorities have tried their best to increase the investment in science and technology program to the level up to 2 percent of total GDP, which however never ended up to be more than 0.6 %. In addition the relevant authorities committed to support the establishment of 50.000 companies and startups in 8 years which can accommodate 500.000 employment with a turnover of some 500.000 billion toman equivalent to annual construction budget of the country. Unfortunately this has not been achieved either. It is understood that not supporting the small startups, specially not procuring their products and services and importing similar goods produced by those companies are among the most important reasons for not achieving the level of self-dependency for knowledge base companies. Conclusion: Based on analysis a total turnover of 140 thousand billion toman exists in laboratory section. Assuming creating 3000 technology based company which can create as much as 50 billion toman / year is very much achievable. In this talk I will try to elaborate some ground to which we should plane to work on clinical diagnosis products. **Keywords:** science based economy, technology development, Clinical diagnosis

Alterations of oxidative stress indices in various obesity phenotypes

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نوع پذیرش: oral | کد مقاله: G-64912

Abstract: Background: The rapid prevalence of obesity not only imposes a significant economic burden on the health system but also predisposes it to various metabolic abnormalities. Recent investigations have elucidated that the incidence of obesity-related diseases depends not only on excessive body weight but also on several metabolic health criteria such as insulin sensitivity, waist circumference, blood pressure, and the levels of HDL-C and triglyceride. Therefore, according to a classification based on BMI and also mentioned metabolic health criteria, individuals can be divided into four classes including metabolically healthy non-obese (MHNO), metabolically unhealthy non-obese (MUNO), metabolically healthy obese (MHO), and metabolically unhealthy obese (MUO). Plus, recent investigations have suggested that the occurrence of oxidative stress is widely associated with the pathogenesis of obesity and its related complications including diabetes, cardiovascular diseases, and liver failure. Moreover, the concentrations of diverse oxidative stress parameters seem to vary amongst healthy/unhealthy obese and non-obese individuals (in terms of BMI and metabolic health criteria). Regarding the critical role of oxidative stress in the pathogenesis of different metabolic disorders, in the present study we aimed to evaluate several pivotal oxidative stress parameters in order to achieve an illustrative prognosis of the prospective abnormalities in people with different types of obesity. Materials and Methods: In the present study, A total of 199 male patients with different BMI ranges and also discrepant metabolic criteria were divided into four groups including MHNO, MUNO, MHO, and MUO. Thus, the activity of various antioxidant enzymes including catalase and superoxide dismutase as an appropriate approach to determine the capacity of plasma antioxidant factors to counteract oxidative stress was investigated. Furthermore, simultaneous with escalated oxidative stress and concomitant with aggravated damage to protein and lipid content of erythrocytic membrane, the concentration of plasma protein carbonyl content and malondialdehyde as potential surrogate markers of protein and lipid oxidation, respectively were appraised. Results: According to our findings, the activity of superoxide dismutase was significantly higher in MHNO phenotype compared with MHO and MUO individuals and also displayed a noticeably higher value in MUNO phenotype compared with MHO subjects. Besides, the activity of catalase was significantly higher in the MHNO phenotype compared with MHO and MUO individuals. Moreover, MUNO patients demonstrated a significantly greater catalase activity compared with MHO and MUO phenotypes. On the contrary, the levels of plasma malondialdehyde demonstrated a significant increase in MUO patients compared with other phenotypes. Besides, the concentrations of plasma protein carbonyl content were significantly higher in MUNO patients compared with MHNO and MHO phenotypes. Additionally, protein carbonyl levels were found to be remarkably elevated in MUO patients compared with MHNO and MHO individuals.



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Conclusion: To conclude, along with the emergence of obesity and increased BMI, the activity of catalase and superoxide dismutase enzymes was found to get drastically plummeted in obese patients compared with non-obese subjects. Furthermore, the levels of plasma protein carbonyl content as well as malondialdehyde underwent a phenomenal upsurge along with the advent of diverse metabolic disorders in metabolically unhealthy phenotypes. **Keywords:** Obesity phenotypes, BMI, Oxidative stress. **Keywords ?**

Coronavirus influences on CRP, ESR, BUN, and Creatinine blood biochemical markers

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نوع پذیرش: oral | کد مقاله: G-49837

Abstract: *Introduction:* Covid-19 is a viral infectious disorder caused by the SARS-CoV-2 virus and mainly targets the respiratory system. This virus exerts its effects by binding to the receptors of the angiotensin-converting enzyme. These receptors are primarily present in several body organs, such as the liver, Kidney, pancreas, heart, lungs, intestine, and brain. In addition to this virus's effects on the lungs, it also influences the mentioned organs, which can lead to further symptoms, and as a result, this virus causes alteration in blood chemical biomarkers, such as CRP, ESR, BUN, and Creatinine. Due to the specificity of some of these biomarkers, serum level assessment indicates the damage to a particular tissue caused by the Covid -19 virus. Our study was performed through the measurement of some of the aforementioned chemical biomarkers on 764 patients infected with the Covid-19 virus and were referred to Pardis Laboratory of Pathobiology and Genetics in Mashhad. Among these 764 people, 764 persons had CRP test, ESR test was performed on 571 individuals, and BUN and Creatinine were assessed in 180 specimens. *Materials and Methods:* In order to investigate the Coronavirus, oral and nasopharyngeal samples were taken from the oronasopharynx area of people who were referred to the Laboratory. The Coronavirus RdRp and N genes expression were measured with real-time PCR and the commercial Pishtaz Teb diagnostic kit. Among positive results, 764 patients who had biochemical tests were selected. For CRP, BUN, and Creatinine assessment, Aptech, Audit, and Biomed colorimetric commercial kits were used consecutively via an autoanalyzer type BS800. ESR measurement was executed by an analyzer named Linear. *Results:* The number of 419 (54.84%) patients out of 764 had an increased level of CRP. ESR level was higher in 137 (23.99%) individuals out of 571. Among 180 persons who had BUN and Creatinine tests, 33 (18.33%) and 25 (13.88%) had abnormal results, respectively. *Conclusion:* Some studies revealed that serum CRP levels could increase significantly in the early stages of Covid-19 infection. Therefore, it can be considered as a prognostic marker of this viral disorder. In addition, the higher amount of CRP indicates more severity of Coronavirus infection. Several investigations on the relationship between Covid -19 and ESR measures showed that the level of ESR could not rise due to the infection with Coronavirus. For that reason, ESR is not even considered as a prognostic marker. Kidney



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dysfunction markers, BUN, and Creatinine were assessed in a number of studies that were increased in Coronavirus infected patients after the indication of symptoms of the ailment which might be variable from 2 to 14 days. **Keywords:** Coronavirus, CRP, ESR, BUN, Creatinine

Somatic TERT promoter mutations and expression of H-TERT in liver tissues with HBV related Hepatocellular carcinoma

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نوع پذیرش: oral | کد مقاله: G-46391

Abstract: *Background:* Hepatocellular carcinoma is the most common cause of liver cancer and the fifth most common cancer worldwide. Genetic alteration of signal transduction pathways plays an important role in the development of this cancer. Telomerase is involved in the maintenance of the length of telomeres and thereby consistency of cell proliferation and so it is important in the development of cancers. Some mutations in the Telomerase reverse transcriptase promoter are suggested as factors increasing the Telomerase expression. The Hepatitis B virus is a carcinogenic pathogen known as a risk factor for HCC. In this study, we evaluate the mutation of the TERT promoter in HBV-infected HCC patients. *Method:* Fresh frozen and formalin-fixed paraffin-embedded liver tissues was used for this study. The genomic DNA was extracted, next a semi-nested PCR test was conducted for amplification of TERT promoter region. Direct sequencing was implemented for discrimination of mutations. A SYBR green based Real-time PCR assay was used to measure the H-TERT expression level. Statistical analysis has been conducted using SPSS. *Result:* Totally, 83 patients positive for HBV (58M/25F) were enrolled with the mean age of 61.2 ± 11.6 +. In addition, 42 individuals negative for Hepatitis seromarkers have been included. Mutations in TERT promoter region were included: T-245C (20%), C-124T (16.6%), and G-31T (13.3%) mutations; at position -146 there was not any mutations. The Real-time PCR has indicated a significant increase in the expression of H-TERT in HCC patients, especially those with a mutation at -124 compared with normal controls. *Conclusion:* Our results depict a remarkable role of mutations in the TERT promoter in



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the higher expression of H-TERT and consequent development of HCC. Monitoring these mutations may help clinicians to predict the risk of HCC in patients with HBV infection. **Keywords:** Telomerase, TERT, mutation, Hepatocellular Carcinoma, Hepatitis B Virus

آدرس دبیرخانه:

تهران، خیابان کارگر شمالی، رویروی مرکز قلب تهران،
کوچه دانش ثانی، بعد از تقاطع صالحی، پلاک ۱۵، واحد ۲

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The Leukocyte Expression Level of LncRNA LINC00987 Is Correlated with Physiopathology of COVID-19 Disease

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نوع پذیرش: oral | کد مقاله: G-28390

Background: *Background:* The pandemic emergence of coronavirus disease 2019 (COVID-19) infection by severe acute respiratory syndrome coronavirus- 2 (SARS-CoV-2) left a high death rate in the worldwide. The cellular and molecular physiopathology of the disease is often unknown, and this issue has made it more difficult to plan appropriate therapeutic and prognosis targets. Evidence obtained from recent research shows that expression alterations of long non-coding RNAs (lncRNAs), especially in immune cells, play important roles in the pathogenesis of SARS-CoV-2 infection. In the current case-control study, we investigated the expression levels of LINC00987 as an immune-related lncRNA in peripheral blood leukocytes of patients with severe COVID-19 compared to healthy controls. *Materials and Methods:* We included a population of 50 patients with severe form of the COVID-19 and 50 healthy individuals during May 2020 until January 2020. After RNA extraction from peripheral blood leukocytes, expression level of LINC00987 was determined by real-time PCR technique. *Results:* The findings revealed that LINC00987 has a significantly increased level in patients compared to healthy controls ($P < 0.001$). We also observed that the expression of this lncRNA is upregulated in patients with cough complications compared to patients without cough sign ($P = 0.039$). While patients with fever tremor had a reduced level of it compared to patients without fever ($P = 0.016$). *Conclusion:* These observations show that lncRNA LINC00987 may be a key non-coding gene in the immune regulation, whose functional dysregulation play an important role in the pathophysiology of the COVID-19. Therefore, it can be introduced as a potential therapeutic, diagnostic and prognostic target by conducting further investigations. *Keywords:* LINC00987, lncRNA, COVID-19, SARS-CoV-2

Role of Circ-FOXO3 and miR-23a in radiosensitivity of breast cancer

Elahe Abdollahi, Hossein Mozdarani¹ © @

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نوع پذیرش: oral | کد مقاله: G-37624

Abstract: *Background:* Radiosensitivity of cells prior to radiation therapy (RT) in breast cancer (BC) patients allows appropriate switching between routinely used treatment regimens and reduces adverse side effects in exposed patients. *Materials and Methods:* In this study, blood was collected from 60 women diagnosed with Invasive Ductal Carcinoma (IDC) BC (mean age: 47 ± 9.93) and 30 healthy women (mean age: 44.43 ± 6.7). A standard G2 assay was performed to predict cellular radiosensitivity. qPCR was performed to examine the expression levels of circ-FOXO3 and miR-23a in peripheral blood mononuclear cells (PBMCs). The sensitivity and specificity of the mentioned RNAs were evaluated by plotting Receiver Operating Characteristic (ROC) curves. Binary logistic regression was performed to identify the involvement of RNAs in BC and cellular radiosensitivity (CR) in BC patients. Meanwhile, qPCR was used to compare differential RNA expression in the radiosensitive MCF-7 and radioresistant MDA-MB-231 cell lines. An annexin V FITC/PI binding assay was used to measure cell apoptosis 24 and 48 hours after 2, 4, and 8 Gy irradiation. *Results:* The frequencies of spontaneous and radiation-induced chromatid breaks (CB) were significantly different between control and patient groups ($p < 0.05$). A cut-off value was determined to distinguish between patients with and without cellular radiosensitivity. Circ-FOXO3 was significantly downregulated and miR-23a was significantly upregulated in BC patients. RNA expression levels were directly associated with CR. Cell line results showed that circ-FOXO3 overexpression induced apoptosis in the MCF-7 cell line and miR-23a overexpression inhibited apoptosis in the MDA-MB-231 cell line. Evaluation of the ROC curves revealed that both RNAs had acceptable specificity and sensitivity in predicting BC and CR in BC patients. Binary logistic regression showed that both RNAs were also successful in predicting BC. *Conclusion:* Although only circ-FOXO3 has been shown to predict CR in BC patients, circ-FOXO3 may function as a tumor suppressor and miR-23a may function as OncomiR in BC. circ-FOXO3 and miR-23a, along with other important biomarkers, may be promising potential biomarkers for BC prediction. Furthermore, Circ-FOXO3 could be a potential biomarker for predicting CR in BC patient. **Keywords:** breast cancer; G2 assay; cellular radiosensitivity; circ-FOXO3; miR-23a.

Whole Exome Sequencing, qRT-PCR, and Stereochemical analysis of the c.679C>T variant in the COLQ gene, causing Congenital Myasthenic Syndrome in an Iranian family

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نوع پذیرش: oral | کد مقاله: G-39746

Abstract: *Introduction:* Congenital myasthenic syndromes are rare heterogeneous disorders of autosomal inheritance caused by genetic defects that leads to skeletal muscle weakness and abnormal fatigability. The onset is usually from birth to childhood. Mutations in the collagen-like tail subunit (COLQ) are the most explained etiology in synaptic CMS, causing defected acetylcholinesterase. *Material and methods:* We performed whole whole-exome sequencing on the affected proband and gene expression assay by qRT-PCR on whole family members, and then we performed a stereochemical analysis of COLQ protein. *Case presentation:* A 15-year-old boy, born in the western region of Iran (Kurdistan) with consanguineous parents, was presented with muscle weakness, ophthalmoplegia, and bilateral ptosis. He was unable to run and jump during the first years of his life. As he was growing up, he required assistance to do his physical activities, such as climbing stairs. *Conclusions:* This case was diagnosed with a rare COLQ gene mutation, which shows the significance of genetic testing in congenital myasthenic syndromes. By the whole sequencing, we could identify the c.679CT variant in the COLQ gene, changing the Argenin codon to stop codon at position 227 (p.Arg227Ter), causing deficiency of COLQ tail of acetylcholinesterase in the neuromuscular junction and leading to acetylcholinesterase deficiency. **Keywords ?**

A novel large exon deletion in GFAP gene, Adult Alexander disease in Iran

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نوع پذیرش: oral | کد مقاله: G-85962

Abstract: *Background and Objectives:* Alexander disease is a heterogenous group of diseases with various manifestations based on age of disease onset. This rare leukodystrophy syndrome with mutations in GFAP Gene could present with developmental delay and seizure in infantile form to ataxia and bulbar palsy in adulthood. However psychiatric symptoms are not well-defined and usually evaluate after disease diagnosis not before disease investigations. *Material and methods:* Our patient is a fifty-two-year-old Iranian woman with history of depression from about 17 years ago, suicidal attempt two years ago and ingestion a large amount of opium with the intention of suicide 2 months ago who was presented with disorientation and probably delirious state in the last interview. *Results:* Eventually in comprehensive investigations, white matter hyperintensity and leukodystrophy was diagnosed and ultimately to determine the cause of these changes with gene study, whole Exon deletion of GFAP Gene and Late Onset Alexander disease was determined. *Discussion & Conclusion:* Neurological-onset manifestation of Alexander disease specifically late onset form is the most common clinical picture of disease and was seen in about 90% of patients but psychiatric symptoms are not well-known and psychiatric-onset disease was not described yet. On the other hand, various Gene Mutation were described in Late Onset Alexander Disease, however large whole Exon deletion which was revealed in our patient is a novel mutation and significantly need to be declared. Here authors describe a late onset Alexander disease with psychiatric onset symptoms and novel large Exon deletion in GFAP Gene. **Keywords:** Alexander disease, Late-onset, GFAP mutation, Psychiatric symptoms, Leukodystrophy

CRISPR/CAS9: From Tumor Genome Modification to CAR-T Cell Immunotherapy

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نوع پذیرش: oral | کد مقاله: G-51946

Abstract: *Background:* Today, various genome editing technologies such as zinc finger nucleases (ZFNs), effective transcription activator nucleases (TALENs), and CRISPR systems are used to conduct clinical trials and treat various diseases such as AIDS and types of cancer. The CRISPR system is one of the most advanced genome editing tools. In addition to its simplicity, flexibility, and cost-effectiveness, it has opened a new perspective for treating human diseases and can be used to silence or disrupt any specific genome location. This system relies on RNA-DNA recognition and can fight oncogenic infections, modulate gene expression and treat various cancers. CAR-T cell therapy is a gene therapy in which T lymphocytes eradicate cancer cells; combining this type with CRISPR technology can provide a practical guideline for successful cancer treatment. *Method:* For this review, electronic medical databases such as PubMed and Google Scholar were used as search engines. The search was performed using the keywords CRISPR/Cas9, CAR-T cell therapy, and Immunotherapy for cancers. Finally, selected articles related to the last five years. *Conclusion:* The challenges of using CAR-T cells in treating cancers include insufficient quantity, low quality of autologous T cells, exhaustion of CAR-Ts, neurotoxicity, cytokine release syndrome (CRS), B cell aplasia, tumor lysis syndrome, and anaphylaxis. Currently, preclinical studies of CRISPR-edited CAR-T cells are showing promising results. Identifying harmful regulatory genes in CAR-T cells and targeting them with CRISPR/Cas9 technology can improve cancer treatment in the future. **Keywords:** CRISPR/Cas9; CAR-T cell therapy; Immunotherapy for cancers

APOA4 gene as a prognostic factor in colorectal cancer associated with ulcerative colitis

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نوع پذیرش: oral | کد مقاله: G-40138

Abstract: *Background:* Inflammatory bowel diseases such as ulcerative colitis (UC) are more at risk of developing colorectal cancer (CRC) than others. Traditional techniques in the diagnosis of cancers, including colonoscopy, X-ray, computed tomography (CT), MRI, PET/CT, etc., mainly focus on morphological analysis of cells and tissues. Therefore, it is very important to develop new and rapid approaches with high accuracy and sensitivity that can detect single or parallel biomarkers, especially in the early stages of the disease. Overall, the development of clinically useful biomarkers able to identify a subset of colitis patients may be recognized as a potential biomarker for the analysis of colitis-associated neoplasia in the early stage of the disease. *Materials and Methods:* In this study, the dataset GSE50788 from the GEO database was studied. Then the utilization of R software program and package “limma” and in accordance to adj p-value and |LogFc|1, DEGs are identified. To analyze the network received in STRING, the Cytoscape program (CytoHubba tool) and a total of 4 parameters EcCentricity, EPC, MNC, and Degree were used; hence the Hub gene was recognized. Finally, the DAVID database was used to find out the gene ontology and enrichment analysis. *Results:* According to the investigations carried out in the GEO database regarding the finding of HUB gene in the development of CRC-related diseases, including UC, as well as advanced and numerous searches related to the identification of CRC-related biomarkers in different databases, CYP2C9, CYP3A4, CYP3A5, and APOA4 gene was identified as the potential biomarkers involved in the progression of ulcerative colitis into CRC. *Conclusion:* The results of the current study led to the identification of biomarkers in the progression from colitis to colorectal cancer that, subject to further analysis and more detailed experiments, could be used as a diagnostic biomarker and therapeutic target. Based on this study, the APOA4 gene, which was previously known to be an effective agent in the development of colitis, was introduced as one of the most prognostic factors for CRC. *Keywords:* Colorectal Neoplasms, Diagnosis, APOA4 gene

Effectiveness of clinical exome sequencing in the diagnosis of genetic etiologies in Iranian patients with neurological manifestations

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نوع پذیرش: oral | کد مقاله: G-25740

Abstract: *Background:* Neurological syndromes, clinically and genetically heterogeneous disorders, are increasingly being unraveled by using high-throughput technologies. The aim of this study was to apply Exome sequencing (ES) as a diagnostic tool to investigate genetic causes of Iranian patients suffering from neurological symptoms. *Methods:* In this study, pediatric patients with neurological abnormalities were ascertained and submitted to clinical examinations including Magnetic resonance imaging (MRI), Electrocardiogram (ECG) and karyotype tests. Biochemical and hematological tests were then conducted. Creatine kinase (CK) level in serum, acylcarnitine profile in plasma and organic acids and acylglycine profile in urine were evaluated by spectrophotometry, (MS/MS) and (GC-MS and LC-MS/MS), respectively. Since there are a number of disease-associated genes, ES was applied to elucidate the genetic etiology of the neurological manifestations in patients and family member, followed by co-segregation studies. Structural modeling and other in-silico analyses were done to predict the pathogenicity of the candidate variants. Interpretation of the identified variants were performed according to the American college of medical genetics (ACMG) guidelines. This study was approved by the ethics committee of Isfahan University of Medical Sciences (ethics codes: IR.MUI.MED.REC.1399.203 and IR.ARI.MUI.REC.1400.011). *Results:* ES results on a 3.5-year-old girl from a non-consanguineous couple suffering from congenital muscular dystrophy together with autism-like behaviors and cardiomyopathy showed a novel variant (c.3936_3937delAT, p.Tyr1313LeufsTer4) in the LAMA2 gene. Hypotonia and feeding difficulties were the early symptoms. ECG showed atrial septal defect. Plasma CK levels increased to 2721 IU/l (normal 230 IU/l). Due to some unusual behaviors including failure to show facial expressions, difficulties in making eye contact and not responding to her name, the patient was suggested to do autism screening tests. MCHAT (score: 11/23) and MCHAT R/F (score: 13/20) results were positive and the patient was at high-risk of autism. MRI results showed bilateral symmetrical centrum semiovale WM T2-FLAIR hyperintensity. Another proband was a 15-year-old boy with primary microcephaly, intellectual disability, facial anomalies and signs of craniosynostosis from an Iranian first cousin once removed family. His brother and cousin also suffered from primary microcephaly. ES of the proband identified a hemizygous missense mutation in the ATRX gene (c.5182GC, p.Ala1728Pro). Interestingly, the previously reported Iranian patient with the same genotype was diagnosed without microcephaly. The last proband was an 8-year-old girl diagnosed based on the clinical demonstrations of ataxia telangiectasia. The homozygous



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disease-causing variant was identified in the ATM gene (c.829GT, p.Glu277Ter) using targeted next-generation sequencing. Karyotype and biochemical profiles were normal in all patients. These families with increased risk for a child with neurological disorders could be subjected to pre-implantation genetic diagnosis or prenatal diagnosis to prevent their recurrence. **Conclusion:** Combination of clinical evaluation and molecular genetic diagnosis via ES is a helpful strategy to resolve the genetic etiology of neurogenetic disorders. **Keywords:** LAMA2, ATRX, ATM, exome sequencing

Clinical Evaluation and Molecular Analysis of Angelman Syndrome Recurrence in an Iranian Pedigree with Multiplex Cases

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نوع پذیرش: oral | کد مقاله: G-61237

Abstract: *Background:* Angelman syndrome (AS) is a rare genetic condition mainly affecting the development of the nervous system leading to intellectual disability, speech disorders, and developmental delay caused by the loss of the functional maternal copy of the UBE3A gene located on 15q11.2–q13. UBE3A has exclusive expression in the brain, and its disruption could derive from an imprinting defect, a mutation or deletion of the maternal allele, or paternal uniparental disomy (UPD) of chromosome 15. *Materials and Methods:* Two 17- and 14-year-old Iranian siblings with severe developmental delay and intellectual disability were analyzed to confirm the AS diagnosis. Clinical evaluation was performed, followed by G-banding karyotype, FISH analysis for SNRPN/IC locus, and investigation of the methylation pattern in 15q11-q13 using PCR amplification following McrBC and NotI treatment. *Results:* Medical history of four-generation was normal, as well as G-banding karyotype and FISH analysis; however, it was established that the methylation pattern of the 15q11-q13 was impaired in both siblings. *Conclusion:* despite the fact that AS is often a sporadic disease and recurrence is rare, through a staged genetic evaluation, we confirmed the diagnosis of AS in two siblings with a normal four-generation background caused by either UPD or maternal germline mosaicism. *Keywords?*

Pulmonary Delivery of Levamisole Nanoparticles as an Immunomodulator Affecting Th and a Potential ADAM10 Inhibitor to Ameliorate Severe Allergic Asthma

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نوع پذیرش: oral | کد مقاله: G-61750

Abstract: Asthma is a common chronic lung disease without absolute treatment, and hypersensitivity reactions and type 2 immune responses are responsible for asthma pathophysiology. ADAM10 as a metalloproteinase transmembrane protein is critical for development of Th2 responses, and levamisole as an anthelmintic drug has immunomodulatory effects, which not only regulates ADAM10 activity but also can suppress the bone marrow and neutrophil production. Therefore, in the present study, nanoparticles were used as a levamisole delivery system to reduce bone marrow suppression, and the immunomodulatory and ADAM10 inhibitory effects of levamisole were studied in allergic asthma. Asthmatic mice were treated with PLGA-levamisole nanoparticles. Then, AHR, BALF, and blood cell counts, levels of the IgG1 subclass, total and OVA-specific IgE, IL2, IL-4, IL-5, IL-10, IL-13, IL-17, IL-25, IL-33, INF- γ , and TNF- α , gene expression of FoxP3, T-bet, ROR γ t, PU.1, GATA3, Fc ϵ R2, CysLT1R, eotaxin, and ADAM10, and lung histopathology were evaluated. PLGA-LMHC1 with considered characteristics could control airway hyper-responsiveness, eosinophils in the BALF, levels of immunoglobulins, Th2-, Th9-, and Th17-derived cytokines and pivotal genes, eosinophilic inflammation, hyperplasia of the goblet cell, and hyperproduction of mucus and could increase Th1- and Treg-derived cytokines and also pivotal genes. It could also modulate the ADAM10 activity and had no effect on the number of neutrophils in the bloodstream. The novel safe nanodrug had no side effect on the bone marrow to produce neutrophils and could control the allegro-immuno-inflammatory response of asthma. **Keywords?**

Construction of recombinant scFv library against lymphocyte function-associated antigen-1 (LFA_1) for targeted exosome delivery to cancer T lymphocytes

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نوع پذیرش: oral | کد مقاله: G-86293

Abstract: *Background:* Due to the prevalence of blood-based cancers and the problems caused by immune diseases targeted drug delivery to T lymphocytes has been considered an interesting field for scientists. One of the most important interactions discovered among immune cell-derived exosomes is the entry of dendritic cell-derived exosomes into activated T lymphocytes through the intercellular binding of the intercellular adhesion molecule (ICAM-1) to its cognate receptor, lymphocyte function associated antigen-1 (LFA-1). This study intended to isolate a high-affinity single-chain variable fragment (scFv) specific for the LFA-1 out of a library constructed from LFA-1-immunized mice using the phage display technique. After that, the scFv antibody will use for targeted exosome delivery to cancer T lymphocytes. *Materials and Methods:* After expression, purification, dialysis and concentration of the LFA-1 protein, BALB/c mice were immunized. RNA was extracted and purified from the immune spleen tissues and cDNA was synthesized. Library of about 1100 bp scFv was created using overlap-extension PCR using the heavy chain primer and light chain primer. The SfiI restriction sites were introduced at the both ends of the scFv fragments, then they were cloned into the pComb-3XSS phagemid vector following enzymatic digestion to develop phage library. After phage rescue, phage concentration and titration were determined. 3 rounds of biopanning were done. Polyclonal and monoclonal phage ELISA were performed to select the scFv with the highest binding capacity to LFA-1. The selected scFv was sequenced, subcloned into the pET28a (+) vector, its expression was optimized, characterized by some techniques ultimately. *Results:* The results of ELISA, Western blot, and in silico studies of selected scFv antibody, showed that there was a significant interaction of the scFv with the LFA-1 receptor. *Conclusion:* The finding demonstrated, a high-affinity LFA-1-specific scFv can be applied for the redirection of cargo-loaded targeted exosomes to activated T lymphocytes for therapeutic purpose. *Keywords?*

Investigation of apigenin-3 acetate vs apigenin and methyl-prednisolone-acetate in inhibiting proliferation and gene expression of Th1 cells in patients with Multiple Sclerosis

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نوع پذیرش: oral | کد مقاله: G-71308

Abstract: *Background:* In spite of the advances in therapeutic modalities, the morbidity due to multiple sclerosis (MS) remains high. Therefore, a large body of research endeavouring to discover or develop novel therapies with improved efficacy for treating MS patients. In the present study, we examined the immunomodulatory effects of apigenin on PBMCs isolated from MS patients. We also developed an acetylated form of apigenin (apigenin-3-acetate) to improve its blood-brain barrier permeability and compared its anti-inflammatory properties with original apigenin and methyl-prednisolone-acetate (as a standard therapy) as a potential option in treating MS patients. *Methods:* The current study was an experimental-interventional type. The IC₅₀ was determined for apigenin-3-acetate, apigenin and methyl-prednisolone-acetate with peripheral blood mononuclear cells (PBMCs) of healthy volunteers (n=5). The gene expression of T-box transcription factor (TBX21 or T-bet) and IFN- γ , as well as the proliferation of T cells isolated from MS patients' PBMCs (n=5), were examined in co-cultures of apigenin-3-acetate, apigenin and methyl-prednisolone-acetate after 48 hours of treatment using quantitative real-time PCR. *Results:* The results showed that apigenin-3-acetate, apigenin and methyl-prednisolone-acetate at concentrations of 80, 80 and 2.5 μ M were able to inhibit Th1 cells proliferation after 48 hours respectively (P= 0.001, P=0.036, and P=0.074), also inhibited T-bet (P= 0.015, P= 0.019, and P=0.022) and IFN- γ (P= 0.0001) genes expression after 48 hours of treatment, and apigenin-3-acetate had comparative immunomodulatory effects compared to apigenin, and methyl-prednisolone-acetate respectively. *Conclusions:* Our findings suggest that apigenin has the potential could induce anti-inflammatory effects, in part, by blocking the proliferation of IFN- γ production by Th1 cells. Moreover, comparative immunomodulatory effects were found for the acetylated version of apigenin apigenin-3-acetate vs apigenin and methyl-prednisolone-acetate. *Keywords?*

Pathological evaluation of lesions caused by *Leishmania major* during treatment with bone marrow mesenchymal stem cells in BALB/c mouse model

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Background: *Leishmania major* is the cause of cutaneous leishmaniasis, which leads to skin lesions in the patient. Currently, the use of chemical drugs is the first line of treatment, which in addition to being painful, it has many side effects. Recently, the use of mesenchymal stem cells (MSCs) to repair various skin wounds of non-infectious origin has been considered. In the present study, the regenerative role of these cells in the healing process of leishmaniasis lesion was evaluated through examination of tissue sections.

Materials and methods: The standard strain of *Leishmania major* parasite was injected into the base of the tail of BALB/c female mice aged 6-8 weeks, after three weeks and grouping of animals (control, treatment with MSCs and standard drug glucantim), the number of 10^6 MSCs (derived from bone marrow) were injected in the surrounding areas of the lesion, the size of the wound was checked weekly, and on days 10, 20, 30, skin tissue, spleen and liver were sampled for histopathological examination.

Results: A significant decrease in lesion size was observed in the groups treated with MSCs and (MSCs+ glucantim) compared to the group receiving the standard drug. Regeneration of skin appendages, revitalization of the epidermis layer, reduction in the number of inflammatory cells and granulation tissue were also evident at the end of the treatment period in the group treated with MSCs. Considering the involvement of liver and spleen in BALB/c mice with cutaneous leishmaniasis, examination of the tissue sections of these organs also confirmed the effectiveness of MSCs on wound healing through migration to the site of inflammation.

Conclusion: Considering the reduction of lesion size and improvement at the end of the treatment period, MSCs can be useful in the healing process of skin wounds caused by infectious agents including *Leishmania major* parasite.

Keywords: MSCs, cutaneous leishmaniasis, BALB/c mice

The effects of exosome-induced alternative macrophages on the bacterial load levels in CLP-induced sepsis mice

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نوع پذیرش: oral | کد مقاله: G-96841

Abstract: *Background:* Considering the role of inflammation in the outcome of sepsis and liver damage, this study was designed to assess the effect of alternative macrophages induced by exosomes on the dynamics of inflammatory responses in the sepsis mouse model. *Materials and Methods:* Cecal Ligation and Puncture (CLP) model was used to induce sepsis in mice. C57BL/6 mice were divided into sham, CLP-induced sepsis mice injected with saline, CLP-induced sepsis mice injected with alternative macrophages induced by exosomes, and CLP-induced sepsis mice injected with undifferentiated peritoneal macrophages. Blood and lavage of peritoneal samples were obtained as bacterial load. *Results:* In sepsis mice, alternative macrophages induced by exosomes significantly reduced bacterial load compared with undifferentiated peritoneal macrophages. *Conclusion:* Intraperitoneal administration of alternative macrophages induced by exosomes in sepsis mice demonstrated a positive effect on inflammatory responses. Exosome-induced alternative macrophages reduced inflammatory mediators. **Keywords:** Cecal Ligation and Puncture (CLP), exosomes, alternative macrophages

Diagnostic Role of MicroRNA-146a in Patients with Rheumatoid Arthritis: Involvement of Oleuropein

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نوع پذیرش: oral | کد مقاله: G-38276

Abstract: *Background:* Rheumatoid arthritis (RA) is a common progressive autoimmune disorder that causes chronic inflammation of the joints and damage to other organs. Previous studies have reported the potential role of miRNA-146a in the pathogenesis of RA. In addition, anti-inflammatory and modulatory effects of oleuropein (OLEU) on the expression pattern of microRNAs (miRNAs) have been shown in different diseases. Therefore, this study aimed to determine both the sensitivity and specificity of miRNA-146a and evaluate the potential effects of OLEU on the expression levels of miRNA-146a and TNF- α in RA patients. *Material and methods:* Participants were divided into 2 groups: RA (n = 45) and healthy controls (n = 30). The isolated peripheral blood mononuclear cells (PBMCs) samples were treated with different concentrations of OLEU; and the expression of TNF- α , anti-citrullinated protein, and miRNA-146a was evaluated by enzyme-linked immunoassay and real-time polymerase chain reaction, respectively. In addition, the sensitivity and specificity of miRNA-146a were determined in RA patients using the receiver operating characteristic (ROC) curve analysis. *Results:* Our findings revealed a positive correlation between the expression of miRNA-146a level with the serum levels of C-reactive protein (CRP) and rheumatoid factor (RF) in RA patients. In addition, OLEU treatment decreased the levels of TNF- α and miRNA-146a expression in treated PBMCs samples compared with untreated cells. The ROC curve analysis showed an 85% sensitivity and 100% specificity of miRNA-146a in RA patients. *Conclusion:* Therefore, miRNA-146a can be used as a useful biomarker for RA diagnosis, particularly for early detection. In addition, OLEU could suppresses inflammation in RA patients through regulation of miRNA-146a. **Keywords:** Anti-citrullinated protein; miRNA-146a; Oleuropein; TNF- α ; Rheumatoid arthritis

Cellular and Humoral Immune Responses against AS03-Inactivated SARS-CoV-2 Vaccine

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نوع پذیرش: oral | کد مقاله: G-64817

Abstract: Several vaccines in the world are commercialized versus COVID-19 infection. One of these vaccines is inactivated SARS-CoV-2 vaccine which are formulated in Alum adjuvant that are not capable in the induction of cellular immune responses. In the present study inactivated SARS-CoV-2 virus was formulated in AS03 adjuvant and the immunogenicity was compared with the Alum-based vaccine. Experimental 6-8-week-old BALB/c mice were immunized three times with three weeks interval with AS03- and Alum-based vaccines along with PBS as a control group. Lymphocyte proliferation of spleen cells was performed by BrdU method, IL-4 and IFN- γ cytokines were assessed on the spleen cell culture supernatant by quantitative ELISA kits. Specific total IgG and IgG1/IgG2a were assessed with an optimized indirect ELISA. The results showed that the vaccine formulated in AS03 adjuvant lead to a significant lymphocyte proliferation response versus Alum-based and PBS control group. In addition, the cytokines responses showed a Th1 platform in our vaccine formulation. Furthermore, IgG response showed an improvement versus the other experimental groups. **Keywords?**

Neutralizing antibodies against recombinant RBD Inhibit SARS CoV-2 binding to ACE2 expression cells

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نوع پذیرش: oral | کد مقاله: G-34968

Abstract: *Background:* The spike protein, especially RBD has been reported as one of the most critical targets for vaccine design strategies against the SARS CoV-2 infection. RBD binds the ACE2 surface receptor containing host cell, resulting in entering the viral genome and replication of viral particle which damages the host cells. Therefore, RBD plays a key role in initiating and spreading viral infection in host cells. Hence neutralizing antibodies against this protein can inhibit SARS-CoV-2 to ACE2 receptor binding. The aim of this study was to investigate the binding of recombinant RBD (rRBD) to ACE2 and the effect of the neutralizing antibodies against rRBD on this binding. *Method:* Both bioinformatics and in vitro methods were used. Molecular docking of rRBD-ACE2 was performed by Auto Dock v4.2. rRBD gene was cloned, then the protein was expressed and injected into 4 groups of mice (BALB/c) to select the best dose-response. Stimulation of the humoral and cellular immune system was assessed by ELISA. Histological studies were performed to rule out complications of rRBD injection. The neutralizing property of antibodies produced against SARS CoV-2 was evaluated by VNT. The binding of rRBD to ACE2 and effect of the neutralizing antibodies produced against rRBD on this binding were evaluated by flow cytometry. *Result:* In molecular docking, binding of rRBD-ACE2 was confirmed. It was shown that the mice serum antibodies which produced against rRBD protein after injection, have ability to neutralize the SARS CoV-2. The binding of rRBD protein to ACE2 cell surface receptors as well as the inhibitory effect of neutralizing antibodies on this binding were also confirmed. *Conclusion:* The protein has the ability to produce antibodies with virus-neutralizing properties inhibiting binding of the virus to the ACE2 receptor. Therefore, due to the neutralizing properties of antibodies against SARS CoV-2, this protein was shown to have potentials to be used as recombinant vaccine based on spike protein. **Keywords?**

Development and Validation of an Anti-cyclic citrullinated peptide IgG Detection ELISA Kit

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نوع پذیرش: oral | کد مقاله: G-35281

Abstract: *Background:* Rheumatoid arthritis (RA) is a chronic inflammation of the synovium can lead to joint destruction, disability, and reduced quality of life. The most common serological test for the diagnosis of RA is the rheumatoid factor (RF) test. Although it has a good sensitivity, it is not specific, as it is often seen in healthy individuals and patients with other rheumatic, inflammatory, autoimmune, or chronic infections. But anti-cyclic citrullinated peptide (CCP) is present early in RA disease, often with the absence of clinical symptoms. These findings indicate an important role for anti-CCP IgG in the diagnosis of RA in the early stages of RA. The aim of this study was the development of an ELISA kit for the quantitative detection of IgG specific to CCP that is considered as an aid in the diagnosis of RA. *Materials and Methods:* The assay is designed and developed based on an indirect solid-phase ELISA. In this assay, streptavidin was coated in solid phase and the optimum amount of biotinylated CCP and serum sample were added to the streptavidin-coated wells. After 60 min incubation at RT, the HRP-conjugate anti-human IgG (30 min) and then chromogen-substrate were added. Finally, the resulting color was measured spectrophotometrically at 450 nm. In order to confirm the validity of the designed kit, 205 serum samples of RA patients who attended one of the referral rheumatology hospitals were checked in parallel by a commercial relevant kit. In addition, 215 healthy serum samples were used to find expected values. Test precision, interference, linearity and recovery were also checked for the designed anti-CCP IgG kit. *Results:* In this study, we successfully designed an indirect ELISA kit for detection of anti-CCP IgG. Comparison study showed that the developed kit had 94.0% correlation by the commercial competitor kit. The calculated LOD of the kit was 0.6 RU/mL. It was also shown that 98% of healthy included subjects had an anti-CCP IgG value lower than 11.0 RU/mL. Furthermore, intra-assay and inter-assay precision tests were lower than 8.9 and 11.2, respectively. The developed kit has no interference with hemoglobin, triglyceride and bilirubin at 1 mg/mL, 3000 mg/dL and 20 ng/gL in the serum samples, respectively. The linearity was accepted at 1:16 dilution of the sample. The recovery of two mixed sera with different amount of anti-CCP IgG was also accepted in 80-120% range. *Conclusion:* The designed ELISA kit can efficiently detect the anti-CCP IgG in human serum. The validation results confirm the kit performance in precise and accurate detection of anti-CCP IgG that could be a tool in diagnosis of RA patients. *Keywords:* Anti-CCP IgG, rheumatoid arthritis, ELISA, development

Effects of azithromycin (AZT) and extracellular vesicles derived from mesenchymal stem cells (MSC-EVs) injection on the neutrophil to lymphocyte ratio (NLR) in a mouse model of sepsis

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نوع پذیرش: oral | کد مقاله: G-50421

Abstract: *Background:* Extracellular vesicles derived from mesenchymal stem cells (MSC-EVs) showed promising immunomodulatory results in different inflammatory and autoimmune diseases. Moreover, macrolides including azithromycin (AZT) showed relative immunomodulatory effects on immune system. Neutrophil to lymphocyte ratio (NLR) is a great sign showing the trend of recovery from sepsis and the effectiveness of immunomodulatory medications. Therefore, study we aim to study the combinational therapy of these two agents together in a mouse cecal ligation and puncture (CLP) model of sepsis and investigate the effectiveness of this regimen. *Materials and Methods:* C57BL/6 female mice were randomly divided into the sham group, the cecal ligation and puncture (CLP) group, the AZT group, the MSC-EVs group, and the AZT+MSC-EVs group. The CLP group underwent abdominal surgery and received sterile saline via intravenous injection (i.v.), the AZT group received 100 mg/kg AZT via intraperitoneal injection (i.p.), the MSC-EVs group received 200 mg/kg of MSC-EVs via i.v. injection, and the AZT+MSC-EVs group received i.p. injection of 100 mg/kg of AZT and a tail vein injection of 200 mg/kg of MSC-EVs. After 24 hours, mice were euthanized by exsanguination under anesthesia. With only one drop, the blood was smeared onto a slide and after staining with the giemsa stain, the leukocytes were calculated and differentiated. *Results:* Only the group receiving both MSC-EVs and AZT showed significantly reduced NLR in comparison with the CLP group. *Conclusion:* The co-administration of AZT and MSC-EVs with the dose of 100 mg/kg and 200 mg/kg, respectively, can be beneficial by intensively exerting the



چهاردهمین گنگره بین المللی آزمایشگاه و بالین

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immunomodulatory effects on immune system and this combination can be more effective than the administration of each medications alone. **Keywords:** Extracellular Vesicles, Exosomes, Mesenchymal stem cells, Sepsis, NLR

آدرس دبیرخانه:

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Are cryptic/rare *Aspergillus* spp. kicking off a new antifungal resistance crisis?

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نوع پذیرش: oral | کد مقاله: G-71584

Abstract: *Background:* Among the aspergilli, *Aspergillus pseudonomius*, *Aspergillus alliaceus* and *Aspergillus minisclerotigenes* in section Flavi and *Aspergillus tubingensis*, *Aspergillus welwitschiae* and *Aspergillus luchuensis/awamori* in section Nigri are the rare/cryptic species recognized besides clinically relevant ones. Although the rare species pursue the analogous phenotypic algorithm, they take variances both in their phylogenetic positions and in the antifungal susceptibility trend that determines their treatment protocols. Hence, we designed a study on 213 clinical *Aspergillus* isolates of sections Flavi and Nigri. *Materials and Methods:* Samples collected from sputum, ears and nails of patients with invasive and non-invasive aspergillosis. After culturing on PDA, purification and DNA extraction, barcoding of β -tubulin gene was employed to species identification at the molecular level. An in vitro AFST by testing amphotericin B, itraconazole, voriconazole, posaconazole, caspofungin, micafungin and anidulafungin was also enforced in accordance with the CLSI-M38-A3 guideline. *Results:* The rarest species were isolated from ears (55/213), sputum (43/213) and nails (5/213), respectively. A total of 62/213 (29.1%) isolates belonging to rare species were identified: *A. pseudonomius* (n=1), *A. Alliaceus* (n=1), *A. Minisclerotigenes* (n=1) in section Flavi and *A. tubingensis* (n=49), *A. Welwitschiae* (n=5), *A. luchuensis/awamori* (n=3) and *A. Japonicus* (n=2) in section Nigri. In section Flavi, *Aspergillus alliaceus* responded to amphotericin B at a high MIC (16 μ g mL⁻¹) and in section Nigri, one of the three *Aspergillus luchuensis/awamori* isolates responded to itraconazole at a MIC 16 μ g mL⁻¹. Interestingly, for all *Aspergillus welwitschiae* isolates, the MIC₅₀ and MIC₉₀ of itraconazole were both 16 μ g mL⁻¹. *Conclusion:* The emergence of highly-resistance rare/cryptic *Aspergillus* spp. warns that species misidentification unquestionably leading to an incorrect antifungal susceptibility pattern. Consequently, prophylaxis and the definition of inappropriate treatment protocols make entering a new phase of crises caused by antifungal resistance. **Keywords:** *Aspergillus*, cryptic/rare species, β -tubulin gene, antifungal susceptibility test

The Value of Nasal and Oral Clinical Examination in Febrile Neutropenic Patients for Initiating Antifungal Therapy as a Preemptive Method

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نوع پذیرش: oral | کد مقاله: G-65941

Abstract: *Background:* Invasive fungal infections (IFIs) are complications that lead to mortality and morbidity in hematologic malignancies. The time of starting antifungal therapy is vital. Preemptive antifungal therapy has appeared recently as a new policy for the management of IFIs based on noninvasive ways in neutropenic patients. *Methods:* We enrolled leukemia patients with neutropenia after chemotherapy in Imam Khomeini Hospital Complex, Tehran, Iran. Patients who entered the neutropenic phase were divided into two categories (empirical and preemptive) for receiving antifungal agents. The patients were clinically examined in the preemptive group every day to find IFIs. As soon as clinical evidence of IFIs was observed, antifungal was prescribed. The empirical group patients received antifungals based on the ward protocol. Based on the data in each group, the diagnostic and therapeutic results of cases are followed-up to 3 months. To compare percentages between the two groups, the chi-squared test was used. And to compare two means between the two groups, the independent t-test was used. All the statistical analyses were done in the Statistical Package for the Social Sciences (SPSS) version 24 software (IBM Corporation, Armonk, New York, USA). *Results:* We assessed 132 leukemic patients with inclusion and exclusion criteria. Eventually, 80 patients were enrolled. The mean age was 35.52 years. Demographics data and distribution of leukemia type show no significant differences between the two groups. Despite a higher percentage of IFIs discovered in the preemptive group than the empirical group (25 vs. 18.75%, respectively), but data show no significant differences. The average days of IFIs diagnosis since the beginning of neutropenia in the empirical group were 9.5 days while in the preemptive group, the average days were 5.4 days (p 0.05). Totally, there were 15 patients with a proven IFI in each group (40% in the empirical group and 60% in the preemptive group). Results significantly show an increase in surgical sinus debridement in the empirical groups (83.3%) vs. the preemptive groups (55.5%), (p 0.05). The mortality rate differed significantly among the two groups; it was 7.5% in the preemptive group and 25% in the empirical group (p 0.05).



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Conclusion: Daily oral and nasal cavities examination to find the symptoms of IFIs and then start preemptive antifungal agents may be able to lead to accurate diagnosis, earlier treatment, and decreasing sinus surgery debridement in leukemia patients with neutropenia. **Keywords?**

آدرس دبیرخانه:

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Gene expression changes may be useful for designing novel platelet-based therapies for thrombosis-associated invasive Aspergillosis

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نوع پذیرش: oral | کد مقاله: G-58601

Abstract: *Background:* *Aspergillus fumigatus* is the most common species causing invasive aspergillosis (IA), a life-threatening infection with more than 80% mortality. A specific feature of invasive aspergillosis is the fungal invasion of the blood vessels. This angioinvasion is seen in involved tissues during hematogenously disseminated aspergillosis. Angioinvasion results in intravascular thrombosis and tissue infarction, which produces a necrotic area as an excellent food source for the fungus. Interaction between *A. fumigatus* and human blood platelets leads to intravascular thrombosis. To better understand *A. fumigatus* pathogenesis during thrombosis, we aimed to study the dysregulation of fungus genes involved in interactions between the aspergillus and blood platelets. *Methods:* A bioinformatic pipeline on microarray gene expression dataset, including analysis of differentially expressed genes (DEGs) using Limma R package and their molecular function, as well as biological pathways identification, was conducted to find the effective genes involved in IA. After the bioinformatics analysis, in vitro validation phase was done by the quantitative reverse transcriptase-PCR analysis and evaluated the gene expression changes following fungal exposure to blood platelets at time series. Platelets were exposed to hyphae for various incubation times. Untreated hyphae served as control. The platelet-fungus contact was evaluated using an inverted light microscope. *Results:* Three genes encoding aspartic endopeptidases including (Pep1), (Asp f 13), and (β -glucanase) was the standing candidates. The invasion-promoting fungal proteinase-encoding genes were down-regulated after 30 min of hyphal incubation with blood platelets; and then up-regulated at 60 and 180 min, although only Pep1 was greater than the control at the 60 and 180 min time points. Also, the same genes were downregulated in more clinical isolates relative to the standard strain CBS 144.89. Platelet aggregation was seen as early as 15 min and increased over time. After 180 min, 95% of the hyphae were surrounded by platelet aggregates. *Conclusion:* Our findings delineate the possible induction of fungal-encoded proteinases by blood platelets. This provides a new research line into *A. fumigatus*' molecular pathogenesis.



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Such insight into IA pathogenesis might also guide researchers toward novel platelet-based therapies that involve molecular interventions, especially in IA patients. **Keywords:** Gene Expression; *Aspergillus fumigatus*; Blood Platelets, Thrombosis

A case of peritonitis caused by fusarium and Candida species

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نوع پذیرش: oral | کد مقاله: G-06738

Abstract: Fungal peritonitis (FP) is a rare, but potentially devastating complication in patients undergoing peritoneal dialysis. It is often refractory to treatment and results in serious morbidity and mortality. We present a case of a 40-year-old female with a history of ascites, fever, abdominal pain, and antibiotic treatment failure. A culture of peritoneal fluid specimens revealed fusarium along with Candida as the causative agent of ascites. Treatment with voriconazole and amphotericin B is very successful in eliminating the infection caused by fusarium but led to a temporary good clinical response. As Candida did not respond to the aforementioned antifungals and continued to spread, then, further treatment for persistent Candida was needed. Accordingly, sampling was also performed from pericardial fluid and bone marrow. After the microscopic and macroscopic examination, no involvement with fungal elements was observed in pericardial fluid, but Candida was found in the bone marrow of the patient, and treatment was started. The emergence of less common but medically important fungal pathogens contributes to the rate of morbidity and mortality, especially in the increasingly expanding population of immunocompromised patients as well as its diagnosis is difficult to ascertain. In addition, appropriate treatment should be administered. **Keywords?**

Immunological response to COVID-19 and its role as a predisposing factor in invasive aspergillosis

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نوع پذیرش: oral | کد مقاله: G-01875

Abstract: The world is involved with a pandemic coronavirus disease 2019 (COVID-19) caused by severe acute respiratory syndrome coronavirus 2. The clinical manifestations of reported COVID-19-associated pulmonary impairments range from asymptomatic infections to a pneumonia-induced acute respiratory distress syndrome that requires mechanical ventilation. Fungal superinfections complicating the clinical course remain underexplored. Angiotensin-converting enzyme 2, the receptor for COVID-19 that is mainly expressed in airway epithelia and lung parenchyma, is considered an important regulator of innate immunity. With regard to the viral-cell interaction, imbalanced immune regulation between protective and altered responses caused by the exacerbation of inflammatory responses should be considered a major contributor to secondary pulmonary aspergillosis. In addition, the complex inherited factors, age-related changes, and lifestyle may also affect immune responses. The complication and persistence of invasive aspergillosis have been well described in patients with severe influenza or COVID-19. However, there is a scarcity of information about the immunological mechanisms predisposing patients with COVID-19 to fungal co-infections. Therefore, this study was conducted to investigate the aforementioned domain. **Keywords?**

Rhino-orbital mucormycosis caused by *Syncephalastrum racemosum* in a diabetic patient with COVID-19 in Babol

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نوع پذیرش: oral | کد مقاله: G-69437

Abstract: *Background:* Invasive mucormycosis is a rare mycosis that affects most cases of uncontrolled diabetes and has a high mortality rate. Patients with COVID-19 are at high risk of invasive mucormycosis because of using anti-inflammatory drugs such as corticosteroids and dexamethasone. The main common etiological agent of rhino-orbital mucormycosis is *Rhizopus* species followed by *Rhizomucor* spp. and *Mucor* spp. *Case presentation:* 73-year-old diabetic female was referred to Ayatollah Rouhani Hospital in Babol, with a confirmation of COVID-19 based on positive RT-PCR and CT of the lungs. Due to severe lung complications, she has received methylprednisolone. Twenty days after the hospitalization, nasal involvement and left orbital swelling was observed. By sinus endoscopic surgery, debridement was done and histopathology indicated wide hyphae lacking septa. The sequenced PCR product displayed *Syncephalastrum racemosum*. In the antifungal susceptibility test, amphotericin B showed good activity against *S. racemosum* and the patient survived with timely treatment. *Conclusion:* This is the first case of rhino-orbital mucormycosis reported by *S. racemosum* in COVID-19 patients and *S. racemosum* can be considered as one of the etiological factors of rhino-orbital mucormycosis in COVID-19 cases. **Keywords:** COVID-19, Mucormycosis, *Syncephalastrum racemosum*

A case of fatal post-COVID-19 Sino-orbital Mucormycosis in a Diabetic Patient as a Complications of COVID-19 treatment

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نوع پذیرش: oral | کد مقاله: G-17820

Abstract: Background: Coronavirus disease 2019 (COVID-19) infections can be related to a vast range of fungal and bacterial super-infections. Here we presented a case of post-COVID-19 mucormycosis during the course of corticosteroid therapy. Case Presentation: A 63-year-old woman with diabetes mellitus was diagnosed with COVID-19 and treated with dexamethasone, remdesivir, and ivermectin as part of COVID-19 protocol management. On the seventh day after discharge, she was re-admitted to the hospital with dyspnea and lethargy. On the third day of re-admission, the patient complained of unilateral facial and orbital pain. A diagnosis of mucormycosis was established after histopathology and mycological assessment. Even though she had undergone surgical debridement and afterward received 3 mg/kg/day amphotericin B, she passed away. Based on the sequencing of ITS rDNA, the fungus was identified as *Rhizopus arrhizus*. The antifungal susceptibility testing was performed according to the CLSI M38-A3 guideline. The minimum inhibitory concentration (MIC) values were 0.016 µg/mL for amphotericin B, 0.031 µg/mL for posaconazole, 0.25 µg/mL for isavuconazole, 1 µg/mL for itraconazole, and 8 µg/mL for voriconazole. Conclusion: Early diagnosis and treatment of mucormycosis are critical to achieving



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better outcomes. Rapid diagnosis, timely treatment with antifungals, and the appropriate surgical procedure are necessary to improve mucormycosis outcomes in COVID-19 patients. **Keywords:** Mucormycosis, Zygomycosis, Sino-orbital, COVID-19, Diabetes mellitus, Corticosteroids

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Demodiosis. A neglected, reemerge or new emerge dermoparasitic disease

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نوع پذیرش: oral | کد مقاله: G-85039

Abstract: *Background:* Demodiosis in humans caused by two species of Demodex called folliculorum and brevis. Demodex live inside the sebaceous glands and hair follicles. After mating they burrow into the skin, laying eggs, introducing infection to the skin. The disease is seen in male and female. Although, there is no clinical symptoms in individuals with normal immunity system, but in many cases, dermatitis, rough, dry and scaly skin rosacea, particularly asymmetrical papulopustular or granulomatous variants and in some cases, perioral dermatitis, blepharitis are observed. In recent years we examined many patients referred to the laboratory with clinical symptoms of dermatophytosis, rosacea or unknown dermatitis. *Case series:* Two hundred and twenty suspected patients from different cities of Khuzestan province with dermatitis referred to Iran- Zamin medical diagnostic laboratory for fungi examination. Sampling by scraping from the skin of face or scalp lesions and slide preparation with 20 % KOH was carried out. *Results:* In microscopic examination of the slides, Demodex species was observed. Out of 220 cases, 170 (77.2%) were female and 50 (22.8%) were male. In 5 cases, co- infection of demodiosis and Tinea versicolor, two cases with Tinea faciei, one case with cutaneous leishmaniasis, one case with lupus erythematosus and one case had acute lymphoid leukemia. In sinus discharge of a patient with COVID-19, many Demodex follicularum was seen. The age of patients was from 8 months to 81 year (mean: 33 year). All patients were misdiagnosed as acne, rosacea and dermatophytosis clinically and treated for dermatophytosis or dermatitis for months and years, but no cure happened. *Conclusion:* Misdiagnosis of demodiosis with dermatitis, dermatophytosis and rosacea and mistreatment had not successful cure and suggested that before any treatment, the cause of disease must be clarified. Demodiosis is a neglected dermoparasitic disease and should be considered. **Keywords:** Demodiosis, dermatitis, rosacea,

Nanoemulsion of Spiramycin against Tachyzoites of Toxoplasma Gondii, RH Strain: Preparation, Toxicology, and Efficacy Studies

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نوع پذیرش: oral | کد مقاله: G-81759

Abstract: *Background:* Toxoplasma infection is caused by Toxoplasma gondii, which is an intracellular protozoan parasite. This infection consequently lead to fetal death or various congenital disabilities during pregnancy in patients. Spiramycin (Spi), a macrolide antibiotic concentrating on the placenta, is typically recommended for T.gondii infection in pregnant women. The present study aimed to prepare the nanoemulsion of spiramycin (NE-Spi) and to evaluate the activity of this formulation in tachyzoites of T.gondii, RH strain. *Methods:* For the purposes of this study, NE-Spi was prepared by spontaneous emulsification. Vero cells were then cultured and the effects of this nanoemulsion on the viability of cultured cells were measured using MTT assay. To estimate the effects of NE-Spi on tachyzoites of T.gondii, RH strain, different concentrations (including 250, 125, 62.5, and 31.25µg/ml) of NE-Spi, S-Spi (suspension of spiramycin), and NE (nanoemulsion without any spiramycin) were added to tachyzoites and then stored for 30, 60, 90, 120 minutes and also 24 hours in 250µg/ml concentration at room temperature. Finally, Tachyzoites mortality rates were evaluated by trypan blue staining. Of note, Flow cytometry was conducted to confirm the obtained results. *Results:* The final particle size of the synthesized NE-Spi was calculated to be 11.3 nm by DLS and TEM. Thereafter, using MTT assay, in 62.5µg/ml concentration of NE-Spi, the Vero cells viability was obtained as 82%. The highest mortality rates of tachyzoites of T.gondii, RH strain were observed at 250µg/ml concentration and after 120 min of exposure, but it was not significantly different from 24 hours of exposure. According to the results of this study, S-Spi and NE had no significant effects on mortality rates of tachyzoites compared to NE-Spi. *Conclusion:* The results of this study show the in-vitro efficacy of NE-Spi on mortality rates of tachyzoites of T.gondii, RH strain. *Keywords:* Nanoemulsion, Spiramycin, Toxoplasma gondii, Tachyzoites, RH strain

Isolation, identification, and phylogenetic analysis of potentially pathogenic free-living amoebae isolated from oral cavity of child labor in Iran

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نوع پذیرش: oral | کد مقاله: G-82154

Abstract: *Background:* FLA, including *Acanthamoeba* spp. is known as an opportunistic pathogen. FLA has been isolated from water, soil and environments. Child labor refers to the exploitation of children through any work that deprives them of their childhood. The population of street children are increasing in poor and developing countries. For the first time, this study investigates the presence of pathogenic FLA in the oral cavity of child labor. *Materials and Methods:* Oral swabs were collected from 100 child labor in Iran. All swabs were cultured in a sterile condition in a non-nutrient agar (1.5%). Morphological and molecular tests was applied for positive plates. PCR was performed to detect *Acanthamoeba*, *Vahlkampfiids*, *Vermamoeba* and *Balamuthia mandrillaris* using specific primer sets. Genetic associations among sequenced genotypes inferred by the 18S rRNA gene obtained by MEGA X and a phylogenetic tree were constructed using the maximum likelihood model. *Results:* Out of 100 samples collected from labor children, 18 (18%) samples showed positive outgrowth of *Acanthamoeba* based on the page key sequencing of the DF3 region. Sequence similarity showed that 3 isolates (AW5, AW8 and AW13) belonged to *Acanthamoeba* T5 genotype, 10 isolates (AW1, AW2, AW3, AW4, AW6, AW7, AW9, W10, AW11, AW12) belonged to T4 genotype, 1 isolate (AW14) belonged to T9 genotype. Moreover, AW13 isolate also infected with *Naegleria Americana*. *Conclusion:* For the first time, this study reports *Acanthamoeba* genotypes isolated from the oral cavity of child labor in Iran. The present study is the first report of *Acanthamoeba* T9 and T5 genotype with *Naegleria Americana* in mucosal tissue worldwide. Our findings indicate



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that Acanthamoeba can colonize in child labor oral cavity. As most of the isolated strains were highly pathogenic these children may develop fatal infections. However, supplementary and comprehensive studies are recommended. **Keywords:** Free living amoeba, Acanthamoeba, Naegleria, child labor, Iran

Identification and multilocus genotyping of *Toxoplasma gondii* isolates from congenital infection in north of Iran

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نوع پذیرش: oral | کد مقاله: G-06359

Abstract: *Background:* Congenital toxoplasmosis can cause severe consequences in the fetus, such as spontaneous abortion which is affected by parasite strain. Also, recent studies revealed the high genetic diversity of *Toxoplasma gondii*. This study aims to investigate the serological status of *T. gondii* in pregnant women, multilocus genotyping in aborted fetuses' tissue, and archived formalin-fixed paraffin-embedded placenta. *Materials and Methods:* This study was performed on 100 pregnant women with spontaneous abortion and their aborted fetuses, and 250 of the archived placentae in Iran. The blood and tissue were examined for seroprevalence and genotype determination of *T. gondii* using ELISA and multilocus nested-PCR-RFLP, respectively. *Results:* Anti-*T. gondii* IgG and IgM were detected in 68 samples (68%) and 1 (1%) out of 100 serums. *Toxoplasma* DNA was identified in 1 (1%) aborted fetuses' tissue and 32 (12.8%) placenta samples. Overall, ten positive DNA samples were successfully genotyped, and five genotypes were recognized (ToxoDB#1, #2, #10, #27, and #48). *Conclusion:* The obtained results indicated congenital toxoplasmosis is a severe risk in this region. As type I is highly pathogen and can lead to severe complications, the prevention of the infection should be considered in seronegative pregnant women. *Keywords?*

Comparison of four different antigens originated from *Echinococcus granulosus sensu stricto* for sero-diagnosis of cyst stages in human liver cystic echinococcosis

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نوع پذیرش: oral | کد مقاله: G-65984

Abstract: *Background:* Cystic echinococcosis (CE) is an important zoonotic parasitic disease caused by the larval stage or of the tapeworm *Echinococcus granulosus sensu lato*. Due to treatment protocols for different liver cysts, diagnosis of cyst stages is very important. Different antigens have been used for CE diagnosis. However, which one is more sensitive and effective for the diagnosis of specific CE stages is not known well. The present study aimed to compare HCF, LHCF, antigen B (AgB) and LAgB originated from *E. granulosus sensu stricto* (G1-G3) genotype, for sero-diagnosis of active, transitional and inactive human liver CE using ELISA technique. *Materials and Methods:* The HCF was collected aseptically from liver CE cysts of sheep. The cysts were characterized by PCR and sequencing for genotype specification. Four types of antigens were used: HCF, LHCF, AgB and LAgB originated from *E. granulosus sensu stricto* (G1-G3) genotype. Thirty-three serum samples from active, transitional, and inactive human cysts were collected. A total of 48 samples from other parasitic diseases and 60 samples from healthy subjects as negative controls were checked using four antigens by ELISA method. *Results:* The results showed the best diagnostic sensitivity with 96.97% was observed by anti-LHCF IgG ELISA test. The best specificity with 95.37% was observed in ELISA test using LAgB. *Conclusion:* Simultaneous test of sera with anti-LHCF IgG ELISA and anti-LAgB IgG ELISA would be the best in the diagnosis of human liver cystic echinococcosis. *Keywords:* Cystic echinococcosis; Ultrasonography; *Echinococcus granulosus sensu stricto*; Antigens; Human

Proteomics evaluation of human sera in patients' undergone pulmonary cystic echinococcosis

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نوع پذیرش: oral | کد مقاله: G-74132

Abstract: *Background:* Cystic echinococcosis (CE)/hydatidosis is an important zoonotic parasitic disease caused by the larval stage of *Echinococcus granulosus sensu lato*. The disease is a major health problem all over the world. Finding specific and sensitive biomarkers for follow up of CE in patients after surgery is essential. Using proteomics methods, the present study aimed to evaluate post-surgical treatment by finding probable biomarker/s in the serum of human lungs CE. *Materials and Methods:* A total of 24 human sera were tested. These sera were included eight confirmed lung/s CE patients sera before surgery (BS), eight sera 12 months post-surgery (12MPS) as well as eight control sera from healthy people. Proteomics methods including 2DE and LC-MS/MS were performed on the specimens followed by bioinformatics analysis. Differentially expressed proteins (DEP) were detected and, separately integrated with Protein-Protein Interaction (PPI) data to construct the PPI network. *Results:* A total of 171 protein spots were detected in three groups including: BS, 12MPS and control groups; of which a total of 106 DEP have been expressed based on fold changes=2 and p-value0.05. More analysis was performed and a total of 10 protein spots were selected for identification by mass spectrometry showed the following proteins: APOA1, BGN, SPP2, EAF1 ACOXL, MRPL55, MCTP2, SEPTIN1, B4GALNT1, and ZNF843. Based on centrality parameters of the PPI network (degree and betweenness) five Hub-bottlenecks proteins with significant centrality values, were found including APOA1, BGN, SPP2, EAF1 and ACOXL. *Conclusion:* This study showed five proteins as hub-bottleneck proteins; of which APOA1 was more prominent. It can be concluded that change in expression of them in patients' sera could be used as indicator tool for following-up lungs CE patients. **Keywords:** Proteomics, Lungs cystic echinococcosis, follow-up, 2-DE, LC-MS/MS

A Convenient and Sensitive kDNA-PCR for Screening of Leishmania infantum Latent Infection Among Blood Donors in a Highly Endemic Focus, Northwestern Iran

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نوع پذیرش: oral | کد مقاله: G-13840

Abstract: Background: Recent global evidences showed that asymptomatic blood donor carriers of Leishmania infection will appear as a threat for blood transfusions recipients in endemic areas. As yet, there is no appropriate diagnostic procedure for detecting infection of blood donors in blood banks. Materials and Methods: The present study was aimed to apply various current diagnostic tests among blood donors in an endemic area of visceral leishmaniasis (VL), Ardabil Province, northwestern Iran. Blood samples were gathered from 860 blood donors in endemic areas of the province between 2017 and 2018, at eight blood donation centers. These samples was assessed using microculture, serological (DAT and rK39-ICT) and molecular based (conventional kDNA-PCR and HRMPCR) tests. Results: Of 860 eligible donors, 24 (2.8%) were seropositive for VL by DAT, and 388 (45%) were positive by kDNA-PCR. Moreover, 19 (19/860) were positive for both of them. Out of 19 subjects, 5.3% (1/19) was positive by rK39-ICT, 10.5% (2/19), and 79% (15/19) were detected positive in microculture and HRM-PCR methods, respectively. Nineteen donors were followed up for 2 years, of which 16 (84.2%) had a serological conversion, and 4 (21%) were positive by kDNA-PCR. The sensitivity of kDNA-PCR, and HRM-PCR procedures in detecting Leishmania parasite was found to be 98.7%, and 79%, respectively. Conclusions: Our findings justify the



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use of kDNA-PCR as a convenient and sensitive tool for screening subjects with leishmanial latent infection in blood banks at least in endemic regions. In these areas, however, a PCR-based test should be used to validate Leishmania infection among seropositive donors.

Keywords: Blood donor, DAT, kDNA-PCR, HRM-PCR, Microculture

Evaluation of Dihydrofolate Reductase (Dhfr) Gene, Related to Plasmodium Falciparum Pyrimethamine Resistance in Imported Malaria Cases in Iran

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نوع پذیرش: oral | کد مقاله: G-29834

Abstract: *Background:* Antimalarial drug resistance is one of the important challenges for governments in the fight against malaria. Molecular surveillance of antimalarial drug resistance supports early detection of how the recommended treatments work. This allows immediate action to reduce any threat and prevent it from spreading. Therefore, the aim of this study was to evaluate the frequency of dihydrofolate reductase (dhfr) mutants in Plasmodium falciparum resistance to pyrimethamine in Iranian malaria patients. *Materials and Methods:* In 2020, 27 patients (22 males and 5 females) with imported P.falciparum cases were studied. The nested-PCR technique first confirmed the species in all samples and then amplification was done by the semi-nested-PCR method in order to detect single nucleotide polymorphisms (SNPs) in dhfr gene related to pyrimethamine resistance. *Results:* All samples in the 18S rRNA gene had species-specific bands for P. falciparum strains. In the sequence analysis of pf dhfr gene amplification after comparison with the standard strain (wild type), 21 patients had a double mutation (C59R+S108N) and six patients had a triple mutation (N51I+C59R+S108N) of pyrimethamine resistance. *Conclusion:* The results of this study showed that the susceptibility



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of *P. falciparum* to pyrimethamine in the treatment of malaria is significantly reducing. These findings can raise concerns about pyrimethamine resistance in *P. falciparum*. Due to the high emergence of double and triple mutants related to pyrimethamine resistance, the malaria surveillance and treatment systems in Iran, the use of pyrimethamine should be considered.

Keywords?

آدرس دبیرخانه:

تهران، خیابان کارگر شمالی، رویروی مرکز قلب تهران،
کوچه دانش ثانی، بعد از تقاطع صالحی، پلاک ۱۵، واحد ۲

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Comparison of proteome characterization of active (CE1 & CE2) and transitional (CE3) stages of human cystic echinococcosis and determination of immuno-dominant proteins by proteomics and immunoblotting

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نوع پذیرش: oral | کد مقاله: G-10479

Abstract: *Background:* Cystic echinococcosis (CE) is caused by metacestode of Echinococcus granulosus sensu lato raises a significant public health issue. The prognosis of CE depends on a number of factors such as cyst stage, location of cyst, and the number of cysts that make it difficult to manage this disease which need identification. In this regard, proteomics can facilitate the identification of potential molecular markers for the development of diagnosis and monitoring tools. *Materials and Methods:* In present study, the analysis of protein profiles and their differentiation at CE1, CE2, and CE3 stages of single fertile hepatic human CE and the identification of prominent proteins from HCF of 2-DE gel by tandem matrix-assisted laser desorption/ionization time-of-flight (MALDI-TOF/TOF) is described. The immunoblot protein using sera from patients from CE1 to CE3 stages was then determined. *Results:* Approximately 236 protein spots in the range of 3-10 pI representative of the hydatid cyst fluid (HCF) stages were resolved on Coomassie-stained 2DE gels. The results showed differential expression patterns depending on the cyst stages. The proteins identified also showed a difference in protein profile of the HCF proteins depending on the stages of CE. MALDI-TOF/TOF analysis identified four specific proteins for CE1 stage included Homeobox protein EMX2, Probable crossover junction endonuclease EME2, Neuronal vesicle trafficking-associated protein 1, and Neuropeptide-like protein C4orf48. Five specific protein including Peptidyl-prolyl cis-trans isomerase, Fibrillin 1, Neurogenic locus notch protein, BTB/POZ domain-containing protein KCTD16, and Hemoglobin subunit beta for the CE2 stage and Palmitoyltransferase ZDHHC23 for CE3 stage identified. *Conclusion:* specific proteins were identified for each stage of liver hydatid cyst, which may be effective in the mechanisms of conversion of stages to each other (active to inactive). **Keywords:** Proteomics, Liver cystic echinococcosis, 2-DE, Cyst stage

Toxoplasma gondii in Individuals Occupationally Exposed to Livestock and Raw Meat: A Case-Control Seroprevalence Study

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*Corresponding Author: Seyed Hossein Hejazi: hejazi@med.mui.ac.ir, Department of Parasitology and Mycology, School of Medicine, Isfahan University of Medical Sciences, Hezar Jerib St. Isfahan; 8174673461; Iran; **Background:** *Toxoplasma gondii* is an obligate intracellular parasite with global distribution. This food-related disease is a facultative heterogenous protozoan with a complex life cycle. It has multiple transmission routes, capable of infecting all warm-blooded animals, including humans. The overall prevalence of this protozoa is directly related to eating habits, environmental climate, and contact with the hosts of this parasite. In Western Europe, the overall prevalence is 30 to 50%. The prevalence of over 80% is due to the specific type of diet in Eastern/Central Europe and Latin America. It has also been observed in the Middle East and Africa due to environmental health issues, suitable climate, and contact with the main hosts (felines) and areas of Southeast Asia. This coccidial protozoan in Iran is also widely prevalent in the main hosts (50-59%) and intermediate hosts (20-50%). Most existing studies on the seroepidemiology of *Toxoplasma* have focused on immunocompromised patients, pregnant women, and childbearing age. Special occupational groups dealing with risk factors should not be ignored. To clarify the knowledge of this important zoonosis, we aimed to ascertain if Individuals occupationally exposed to animals or raw meat and viscera (IOE) in livestock fields and slaughterhouses were more prone to *T. gondii* seropositivity than controls by developing a case-control study on anti-*T. gondii* IgM and anti-*T. gondii* IgG. **Materials and Methods:** After providing the necessary information to the subjects, they entered the study by completing the consent form. At the beginning of the study, each sample (n = 802) was coding; then, all the tests continued with the code number of each individual. Participants' information (n = 401) included four slaughterhouses in Isfahan province. The sera samples of the control group, from anonymous volunteers without all kinds of autoimmune and inflammatory diseases (n = 401), matched. All procedures were approved by the Research Ethical Committee of Isfahan University of Medical Sciences with ethics number IR.MUI.MED.REC.1400.372. All sera samples were individually tested for the presence of anti-*T. gondii* IgM and anti-*T. gondii* IgG antibodies using a commercial semiquantitative enzyme immunoassay (*Toxoplasma* ELISA IgG G1027, M1027, Edition 2020, Vircell, Granada, Spain). **Results:** From the whole sera samples tested, seroprevalence in the IOE and control groups was (4/401) 1.2% and (14/401) 3.5% for anti-*T. gondii* IgM and (185/401) 46.1% and (126/401) 31.4% for anti-*T. gondii* IgG antibodies, respectively. Chi-square analysis showed the difference in anti-*T. gondii* seroprevalence between IOE and controls is statistically significant ($p < 0.001$). **Conclusion:** Previous studies on IOE society are limited to cross-sectional studies in the north and northeast of Iran, which respectively estimated the anti-*T. gondii* IgG prevalence of contamination in farmers and shepherds is 80.7%, and in butchers and slaughterhouse workers is 58.2%. Also, a cross-sectional study on 53 butchers in the west of Iran showed 11.32% anti-*T. gondii* IgG seropositive. During a case-control study in southwest Iran, butcher contamination was estimated at 41.8% and in the control community at 28.8%. Our findings, like these studies, support a potentially significant association between *T. gondii* seropositivity and animal occupational exposure. **Keywords:** Occupational exposure, Seroprevalence, antibodies, One Health, Zoonotic

Organophosphate Poisoning: Review of Prognosis and Management

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نوع پذیرش: oral | کد مقاله: G-16705

Abstract: Introduction: The high annual mortality rate of organophosphorus (OP) poisoning indicates that the treatment is mostly ineffective in this regard. For this reason, the present study was conducted with the aim of reviewing the prognosis and management of organophosphorus poisoning. Methods: We systematically searched and retrieved the relevant articles using keywords on the online databases, including Embase, Scopus, PubMed, Web of Science, and Cochrane databases up to December 1st, 2021. The retrieved records underwent a title/abstract and full-text screening process, and the eligible papers were identified. Result: It has been suggested to add calcium channel blocking drugs or magnesium sulfate to normal care to decrease the release of acetylcholine at cholinergic synapse. Moreover, the diagnosis of OP poisoning is chiefly based on clinical evidence. Oximes and atropine are the recognized antidotes of OP. However, low-priced medications such as magnesium sulfate and sodium bicarbonate as well as novel adjunct therapies have been introduced recently. Furthermore, antioxidants are recommended for managing OP poisoning. In addition, hemoperfusion, fresh frozen plasma, and K-oximes are a number of innovative management modalities that deserve further evaluations. However, prevention seems to be the most effective management modality in this respect. Therefore, the present study aimed at briefly discussing the controversies in the OP poisoning management and presenting recent advances in its management and prognosis. Conclusion: The results of this study revealed that multiple factors including type of exposure, AChE plasma

level, time of hospitalization, and severity confirming OP poisoning should be considered to provide the best treatment strategy. **Keywords?**

Toxicity effect of synthesized platinum Schiff bases on SKBR3 cell line in breast cancer

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نوع پذیرش: oral | کد مقاله: G-72561

Abstract: Background: Breast cancer is a prevalent disease which has not been completely treated by chemotherapy. The aim of this study was to investigate the effect of the cytotoxicity of Schiff bases derived from platinum (II) on breast cancer cell line (SKBR3) and analysis of expression of genes involving molecular pathway. Methods: In this study, at first cytotoxicity of carboplatin (as the main drug of chemotherapy) and Schiff base derived from platinum (II) (12.5, 52 and 50 μ M) on SKBR3 cell line was investigated using MTT and 50% concentration of inhibition (IC50) was determined. After cell treatment with concentrations of 12.5, 25 and 50 μ M of compounds, RNA was extracted and cDNA was synthesized and gene expression of various cellular pathways such as Apoptosis (Bcl2 and Bax) and autophagy (ATG5, Beclin and Topoisomerase 1, LC3 and Hif1) was evaluated using Real-time PCR method. Results: Cell treatment with platinum (II) Schiff bases complexes in various concentrations showed that complex A had the greatest toxicity compared to other studied compounds. The synthesized complexes through inhibition of genes expression of Hif1 and Topoisomerase 1 may affect cell toxicity of SKBR3. Conclusion: Regarding the induction of cell cytotoxicity of breast cancer cell line by platinum (II) Schiff bases, it may be concluded that these medicine may be an appropriate option for treatment of breast cancer. **Keywords:** Cell toxicity, Gene Expression, Carboplatin

Challenges in Laboratory Detection of Synthetic Cannabinoids

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نوع پذیرش: oral | کد مقاله: G-96758

Abstract: *Background:* Synthetic cannabinoids (SCs) as a major type of New Psychoactive Substances (NPS) are highly abused, worldwide. SCs act as endocannabinoids (CB) receptor full agonists and have unpredictable toxicity and abuse potential. In this article, the challenges of SCs in forensic and clinical toxicology have been reviewed. *Method:* A literature search was performed on PubMed and Google Scholar databases. The terms used for the search were: "synthetic cannabinoids", "Analysis" OR "Detection". The search was limited to years 2018 to December 2022 and the retrieved articles were reviewed. *Results:* The identification of SCs in biosamples is very difficult. These may concern the lack of knowledge on chemical structure and metabolism data and lack of certifies reference materials of available SCs. Analysis of SCs in biosamples in the clinical and forensic setting need to sophisticated analytical instruments. Liquid gas chromatography tandem mass spectrometry (LC-MS/MS), matrix-assisted laser desorption/ionization-time of flight mass spectrometry (MALDY-TOF-MS), ultra-high performance liquid chromatography/high-resolution time-of-flight mass spectrometry (UHPLC-HR-TOFMS) and LC-ESI-MS/MS, have been used to detect SCs and their metabolites in serum, whole blood, urine, hair samples. *Conclusion:* Analysis of SCs is not included in the routine forensic/clinical drug testing. Therefore, sophisticated laboratory as a national or regional reference lab for detection of these substances are recommended. **Keywords?**

Alcohol false positive results in non-alcoholic diabetic patients

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نوع پذیرش: oral | کد مقاله: G-53209

Abstract: Among the drugs tested in workplace drug screening program the most abused one causing the greatest hazard is ethanol. Urine alcohol testing has the advantage of being inexpensive and easy to run but it also suffers from a number of disadvantages. Non-alcoholic diabetics who are evaluated for alcohol consumption may be falsely categorized with alcoholic people. Diabetic persons suffer from a weakened immune function and cannot properly fight against foreign agents. For this reason, bacterial and candidial urinary tract infections are frequently seen among these patients. Glucose is frequently present in urine of diabetics and sometimes transiently present in non-diabetic urine. Candida albicans is yeast which is known to ferment glucose into alcohol. This creates a falsely positive test result for alcohol detection for these patients. Another false positive result may occur during working with Breath analyzer for alcohol detection. Some diabetics have a high levels of blood acetone because of high rate of fatty acid catabolism. Acetone can produce a false positive result in Breath analyzer-based tests. Most laboratories that perform urine alcohol testing should be aware of such cases and test/report the presence of glucose in urine samples. Finally, positive results from an immunoassay test should be followed by gas chromatography/mass spectrometry (GC/MS) for the confirmation of alcohol consumption. **Keywords?**

Emerging diseases: nature or man?

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نوع پذیرش: oral | کد مقاله: G-96501

Abstract: Background: The main characteristics of biological agents; High morbidity and mortality, Ability to transmit from human to human, Low infectious dose and the ability to spread very quickly through the air (aerosol), Late diagnosis, Lack of effective vaccine in the world, The ability to cause concern, Availability and ease of production, Environmental stability, The existence of sufficient information in the field of research and development, Ability to become a weapon. Materials and Methods: The US Centers for Disease Control and Prevention (CDC) divides potential biological hazards into 3 categories: A, B, and C. Results: Group A: • They are the most dangerous because they are easily transmitted and spread from one person to another. They cause many deaths and have the greatest impact on public health. They cause public fear and social disorder. • Anthrax, botulism, plague, smallpox, rabbit fever, viral hemorrhagic fevers, arenaviruses: Lassa, bunyaviruses: Crimean Congo, filoviruses: Ebola, Marburg Category B: • Brucellosis, Clostridium perfringens epsilon toxin, threats to food security (Salmonella, Escherichia coli, Shigella), equine and human infectious diseases, melioidosis, pitazosis, Q fever, ricin toxin, staphylococcal enterotoxin B, typhoid fever (Rickettsia provazki), viral encephalitis, Water safety threats (Vibrio cholera, Cryptosporidium parum) Category C: • Emerging infectious diseases such as Nipah, Hantavirus, Sars, Corona, Pandemic Influenza. Conclusion: Viruses like Corona are more likely to be man-made than natural. **Keywords:** Disease, emerging, nature, human, bioterrorism

Phosphine toxicity management, Review of new findings

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نوع پذیرش: oral | کد مقاله: G-40736

Abstract: *Background:* Aluminum phosphide (AIP) is a highly toxic pesticide that unfortunately using for suicidal attempts. The chemical reaction of water and AIP induces a toxic gas, Phosphine. Phosphine could easily inhibit cytochrome C which induces oxidative stress leading to the generation of free radicals and resulting in cell death. There is no specific antidote against phosphine. Thus several compounds were suggested and evaluated. In this article, we review the latest proposed and evaluated compounds for this poisoning. *Materials and Methods:* For this purpose, different databases were searched and 75 papers were selected and summarized from the nearly 700 articles which were published from 2000 until now on Phosphine toxicity. *Results:* Apart from factors such as the type, number, and method of use, the lag time between consumption and therapeutic measures determines prognosis. Among the many proposed methods for decontamination, gastric emptying along with the prescription of various oils (such as coconut oil, liquid paraffin, and Olive oil) and sodium bicarbonate gavage were used and recommended more than the other methods. Although the use of potassium permanganate solution was used in some reports, there were no positive results regarding its use. The correction of acidosis with bicarbonate and shock with vasopressors are the most important supportive treatment. The beneficial effects of applying magnesium sulfate and N-acetyl cysteine have been confirmed in numerous human and animal studies, and in many studies, they have been used as a basic treatment for patients. However, calcium supplemental administration had been reported in some case series, but there was no clinical trial. Although there were reports of the effectiveness of vitamin C and hydroxyethyl starch, stronger studies had not confirmed their use. Trimetazidine, hyperinsulinemia-euglycemia, and L-carnitine are compounds and methods whose beneficial effects have been reported in case reports and clinical trials. Extracorporeal techniques such as hemodialysis, peritoneal dialysis, hemoperfusion, continuous renal replacement therapy (CRRT), automated red blood cell exchange, and plasmapheresis were reported in case reports and case series. We compare them in this paper. Extracorporeal Membrane Oxygenation (ECMO) is a procedure for which there have been promising reports in severe cases. Some clinical trials are underway about it. Several compounds were evaluated in animal models or were reported in a few case reports, but none has been confirmed. *Conclusion:* Rapid management of the patient and decontamination with



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oily compounds and bicarbonate along with correction acidosis and shock and administration of intravenous N-acetyl cysteine, magnesium sulfate, Trimetazidine, hyperinsulinemia-euglycemia, and L-carnitine are recommended. ECMO is useful in severe cases. **Keywords?**

آدرس دبیرخانه:

تهران، خیابان کارگر شمالی، رویروی مرکز قلب تهران،
کوچه دانش ثانی، بعد از تقاطع صالحی، پلاک ۱۵، واحد ۲

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Investigating the relationship between HLA-DBPB1 gene polymorphism (rs9277534 A / G, rs3117229 T / C) and chronic hepatitis B

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نوع پذیرش: oral | کد مقاله: G-46938

Abstract: Background: Hepatitis B virus infection is one of the most important causes of liver damage and can lead to chronic infection, resulting in liver cirrhosis and liver cancer. More than 350 million people in the world suffer from chronic infection of the virus. Successful cleansing and the removal of infection from the body or the progression of the disease to chronic disease depends on the genetic history of the host immune system. One of the most important genetic factors in HLA antigens is that they play a role in immune pathogenesis, cleansing of infection and various diseases. HLA antigens, especially HLA_DPBI, are key factors in self-removing viral infections, especially HBVs. The purpose of this study was to investigate the relationship between rs9277534 A / G polymorphisms and rs3117229 C / T polymorphisms in the HLA_DPBI and chronic hepatitis B gene. Materials and Methods: In this case-control study, a zoonotic DNA of 300 patients with chronic hepatitis B, 300 healthy individuals and 120 spontaneous cleaners were extracted. The genotypes related to the single-nucleotide polymorphism rs9277534 (AG) and (T / C) rs3117229 were sequenced by the PCR-RFLP method. Result: Frequency of genotypes GG, GA, AA and G and A alleles rs9277534 in patients were 67%, 26.7%, 6.3% and 80%, 20%, respectively, The healthy group was 60%, 35.3%, 4.7%, 78%, 22% And in the clear group, 65%, 26%, 9%, 79% and 21%, respectively, were calculated. After genotypic stages and statistical analysis, there was no significant difference between the normal and the healthy group. Conclusion: In this study, there was no significant relationship between HLA-DPB1 gene and chronic hepatitis B polymorphism (rs9277534 A / G) and (rs3117229) polymorphism. It seems that these snp's do not play a significant role in the potential for chronic hepatitis B infection. **Keywords**

Selective APC-targeting of a novel Fc-fusion multi-immunodominant recombinant protein (tTax-tEnv: mFcγ2a) for HTLV-1 vaccine development

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نوع پذیرش: oral | کد مقاله: G-28157

Abstract: *Background:* HTLV-1 causes two life-threatening diseases: adult T-cell leukaemia/lymphoma and HTLV-1-associated myelopathy/tropical spastic paraparesis. Due to the lack of proper treatment, an effective HTLV-1 vaccine is urgently needed. *Main methods:* DNA sequences of 11–19 and 178–186 amino acids of HTLV-1-Tax and SP2 and P21 were fused to the mouse-Fcγ2a, or His-tag called tTax-tEnv:mFcγ2a and tTax-tEnv:His, respectively. These constructs were produced in *Pichia pastoris*, and their immunogenicity and protective properties were assessed in a mouse challenging model with an HTLV-1-MT2 cell line. *Results:* The immunogenicity assessments showed significant increase in IFN-γ production in animals receiving tTax-tEnv: mFcγ2a (1537.2 ± 292.83 pg/mL) compared to tTax-tEnv:His (120.28 ± 23.9 , p equal 0.02). IL-12 production also increased in group receiving tTax-tEnv: mFcγ2a than tTax-tEnv: His group, (23 ± 2.6 vs 1.5 ± 0.6 , p equal 0.01), respectively. The IFN-γ and IL-12 levels in the Fc-immunised group were negatively correlated with PVL (R equal -0.82, p less than 0.04) and (R equal -0.87, p equal 0.05), respectively. While, IL-4 was increased by tTax-tEnv: His (21.16 ± 1.76 pg/mL) compared to tTax-tEnv: mFcγ2a (13.7 ± 1.49 , p equal 0.019) with a negative significant correlation to PVL (R equal -0.95, p equal 0.001). *Significance:* The mouse challenging assay with tTax-tEnv: mFcγ2a showed 50 % complete protection and a 50 % low level of HTLV-1-PVL compared to the positive control receiving HTLV-1-MT2 (p equal 0.001). Challenging experiments for the His-tag protein showed the same outcome (p equal 0.002) but by different mechanisms. The



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Fc-fusion construct induced more robust Th1, and His-tag protein shifted more to Th2 immune responses. Therefore, inducing both T helper responses, but a Th1/Th2 balance in favour of Th1 might be necessary for appropriate protection against HTLV-1 infection, spreading via cell-to-cell contact manner. **Keywords?**

آدرس دبیرخانه:

تهران، خیابان کارگر شمالی، رویروی مرکز قلب تهران،
کوچه دانش ثانی، بعد از تقاطع صالحی، پلاک ۱۵، واحد ۲

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Effect of minocycline in COVID-19 patients: A randomized clinical trial

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نوع پذیرش: oral | کد مقاله: G-08951

Abstract: *Background:* Minocycline, a semi-synthetic antibiotic belonging to the tetracycline class, is a potential therapeutic option for COVID-19 because of its anti-inflammatory and immunomodulatory properties. Moreover, its antioxidant, antiapoptotic and antiviral effects have been demonstrated. In the present study, the efficacy of minocycline in therapy of patients with COVID-19 has been evaluated. *Methods:* A randomized, double-blind placebo-controlled clinical trial was performed in Mashhad, Iran. 40 outpatients were randomized to treatment with either minocycline or placebo, in a 1:1 ratio with 20 patients in each group. Standard therapy was used in both groups and patients in the treatment group received oral minocycline 100 mg twice daily additionally for 14 days. Patients in both groups were observed for improvements in clinical symptoms, lymphocytes, leukocytes, CRP, and SpO₂ on day 3, 7, 14 after initiation of treatment. *Results:* A total of 40 patients with similar demographics and disease characteristics were enrolled. Results showed that the time interval until improvement of clinical symptoms was significantly decreased in the minocycline group (6.85 ± 0.79 , day) compared to the placebo group (10.95 ± 1.18 , day) ($P=0.006$). Furthermore, the time interval for leukocytes to reach the normal range was significantly decreased in the minocycline group (3.95 ± 0.59 , day) compared to the placebo group (6.72 ± 1.25 , day) ($P=0.046$). *Conclusion:* In this randomized, double-blind, placebo-controlled study, minocycline (100 mg, 14 days BID) decreased the duration of clinical symptoms improvement along with the WBC normalizing interval in outpatients with COVID-19 disease. **Keywords:** COVID-19 disease, minocycline, clinical symptoms, white blood cell. *Keywords?*

The first evidence of Seoul Hantavirus, Hepatitis E virus, and rabies virus in Norway rats (*Rattus norvegicus*) captured from urban areas of Tehran, Iran

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نوع پذیرش: oral | کد مقاله: G-70358

Abstract: *Background:* Zoonotic infections are considered a global health challenge despite effective treatment regimens and appropriate health policies. Norway rats may be an important source for the transmission of many zoonotic pathogens. The present study is the first study to investigate the presence and frequency of Seoul Hantavirus, Hepatitis E virus, and rabies virus in Norway rats captured from urban areas of Tehran, Iran. *Methods:* In the present study, 100 *R. norvegicus* were captured during one year from five districts of Tehran, Iran. Liver samples were collected from rodents and serum was recovered after centrifugation. The presence of specific IgG antibodies against Rabies virus was detected using a commercial qualitative rat ELISA kit. A conventional RT-PCR assay was employed to detect the presence of SEOV and HEV in the commensal *R. norvegicus* population. *Results:* The results of the ELSA assay showed that 1% ($n = 1/100$) of the 100 *R. norvegicus* captured in Tehran carried Rabies virus. This pathogen was detected only from the northern (5%; $1/20$) part of Tehran. Results of the RT-PCR method showed that the highest frequency (35%; $7/20$) among *R. norvegicus* collected from the south part of Tehran related to HEV. Also, tested positive for SEOV was 12%, repeatedly. Overall, the surveyed zoonotic microorganisms had the highest ($n = 7/20$; 35%) and lowest ($n = 1/20$; 5%) frequency rates in the southern and northern parts of Tehran, respectively. *Conclusion:* The results accentuate the necessity of implementing rodent control programs and regular disinfection as well as avoiding contact with rodent populations in urban environments. **Keywords?**

High prevalence of SARS-CoV-2 and influenza A virus (H1N1) coinfection in dead patients in Northeastern Iran

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نوع پذیرش: oral | کد مقاله: G-62197

Abstract: *Background:* In the last months of 2019, an outbreak of fatal respiratory disease started in Wuhan, China, and quickly spread to other parts of the world. It was named COVID-19, and to date, thousands of cases of infection and death have been reported worldwide. This disease is associated with a wide range of symptoms, which makes an accurate diagnosis of it difficult. During the previous severe acute respiratory syndrome (SARS) pandemic in 2003, researchers found that the patients with fever, cough, or sore throat had a 5% influenza virus-positive rate. This finding made us think that the wide range of symptoms and also the relatively high prevalence of death in our patients may be due to the coinfection with other viruses. Thus, we evaluated the coinfection of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) with other respiratory viruses in dead patients in North Khorasan. *Materials and Methods:* We evaluated the presence of influenza A/B virus, human metapneumovirus, bocavirus, adenovirus, respiratory syncytial virus (RSV), and parainfluenza viruses in 105 SARS-CoV-2 positive dead patients, using polymerase chain reaction (PCR) and reverse transcription PCR tests. *Results:* We found coinfection with influenza virus in 22.3%, RSV, and bocavirus in 9.7%, parainfluenza viruses in 3.9%, human metapneumovirus in 2.9%, and finally adenovirus in 1.9% of SARS-CoV-2 positive dead cases. *Conclusion:* Our findings highlight a high prevalence of coinfection with influenza A virus and the monopoly of coinfection with Human metapneumovirus in children. **Keywords:** coinfection, human metapneumovirus, influenza virus, respiratory syncytial virus, SARS-Cov-2

Mutations in HBV- S gene and overlapping RT region in association to hepatocellular carcinoma

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نوع پذیرش: oral | کد مقاله: G-32740

Abstract: *Background:* Chronic hepatitis B virus (CHB) infection is a major health problem and leading cause of hepatocellular carcinoma (HCC) worldwide. Among the viral risk factors of HCC, variations within HBsAg coding region has been recently considered with HCC. Mutations in RT are dominant treatment responsive factor that is associated to replication rate and liver disease progress. So, we aimed to investigate the mutation profile of s and RT gene of HBV in the liver tissue of patients with HCC from Iran. *Method:* This was a cross-sectional work performed from 02/2018 to 03/2020, among Iranian patients with HCC, liver cirrhosis and normal liver (LC). Preserved FFPE samples and fresh Needle biopsies were collected from liver tissues with HCC. Tissue samples were subjected for DNA extraction, next PCR test was performed to amplify HBV S gene. Mutations were detected by direct Sanger sequencing. *Results:* In overall there were 79 samples positive for HBsAg, among which 68 cases were positive for HBV-DNA including HCC (n: 39), LC (n: 18) and normal (n: 11). The mean intrahepatic viral load was $9 \times 10^5 \pm 6 \times 10^6$ copies/ μ l, and the HBV genotype was D among the all samples. In S gene Q30E, P120S, Q129H, T126I/S, D144E, V190F, W201L and P203L were predominant mutation. The observance of P120S and D144E were significantly associated with HCC. In RT region G26R, P34L/S, A38G, V142L, R152G/W and C198F were prominent mutations. Among mutations of RT, V142L and R152G/W were seen mostly in HCC group that were associated with higher viral load. *Conclusion:* We detected 23% amino acid changes in S region. Two mutation at amino acid 120 and 144 on S gene were associated with HCC. Further investigations are recommended to further clarify the relationship and interaction between mutations in HBV genome and HCC progression. **Keywords:** HBV, S gene, HBsAg, RT, mutation, HCC, liver cirrhosis, Iran

Investigating the role of co-infections between Epstein-Barr virus (EBV) and Human Papillomavirus (HPV) types 16 and 18 in cervical cancer development

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نوع پذیرش: oral | کد مقاله: G-70953

Abstract: *Background:* The majority of newly diagnosed instances of cervical cancer are caused by high-risk human papillomavirus types 16 and 18 (HPV-16 & HPV-18). Additional elements must be present for HPV to induce cervical cancer. One of these factors can be simultaneous infection with other cancer-causing viruses. The aim of this study is to determine the prevalence of co-infection with EBV and human papillomaviruses HPV-16 & HPV-18 in women with intraepithelial neoplasia and squamous cell carcinoma of the cervix and compare it with the non-cancerous control group. *Materials and Methods:* The present study was conducted on 258 cervical samples, related to paraffin (204 samples) and fresh (54 samples) tissues. Viral load of viruses by absolute quantification method and by Real Time-PCR technique in chronic cervicitis samples (control group) (141 samples) and cervical intraepithelial neoplasia (CIN I) samples (26 samples), CIN II (29 samples), CIN III (36 samples) and cervical cancer (26 samples) were evaluated. *Results:* In the present study, HPV-16 was prevalent in the control group (19.85%), CIN I group (34.61%), CIN II group (51.72%), CIN III group (69.45%), and SCC group (73%). HPV-16 significantly increases the chance of having CIN II, CIN III, and SCC compared to the control group (P0.001). The results of Bayesian logistic regression analysis showed that infection with HPV-18 increases the risk of CIN II (P=0.008) and CIN III (P=0.013) compared to the control

group. Co-infection of EBV and HPV-16 was observed in 12.56% of control group samples and 11.73% of SCC group samples, which was not statistically significant difference ($P=0.212$). Although CIN III and SCC had a higher prevalence of HPV-18 and EBV co-infection than controls, this difference was not statistically significant ($P=0.616$). The difference in the mean HPV-16 viral load per cell between the control group and the CIN-I ($P=0.0012$), CIN-II ($P=0.0035$), CIN-III ($P=0.0001$) and SCC ($P=0.0001$) groups was significant. The difference between the mean number of HPV-18 copies per cell between the control group and the CIN-III and SCC groups was significant ($P=0.013$). Also, the control group had a higher EBV viral load per cell than the premalignant and malignant groups ($P=0.033$). **Conclusion:** Overall, in line with previous studies, this study found a link between the prevalence and viral load of HPV-16 and HPV-18 and cervical cancer progression. The difference in the prevalence of co-infection of EBV with HPV-16 and EBV with HPV-18 in the premalignant and malignant groups with the control group was not statistically significant and therefore could not support the hypothesis that EBV may be a cofactor in the occurrence of cervical cancer to confirm the role of HPV16/18. However, the high viral load of EBV in control group compared to CIN I, CIN II, CIN III and cervical cancer samples can cautiously suggest the hit and run hypothesis regarding EBV in the progression to cervical cancer. Therefore, more research is needed to understand EBV infection in the cervix and its role in cancer progression. **Keywords:** Cervical cancer, Human Papilloma Virus type 16, Human Papilloma Virus type 18, Epstein - Barr virus

The use of two strains of Newcastle virus in the prevention of liver cancer

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نوع پذیرش: oral | کد مقاله: G-35470

Abstract: *Background:* Primary liver cancer, mostly hepatocellular carcinoma, remains difficult-to-treat cancer and is globally the sixth-most frequent cancer and the fourth-leading cause of death from cancer. Treatment options may include surgery, targeted therapy, and radiation therapy, and in certain cases, a liver transplant may be used. Currently, oncolytic viruses (OVs) offer the promise of selective cancer therapy via direct and immune-mediated mechanisms. One of the goals of cancer therapies is to target tumor cells selectively and spare adjacent healthy tissue from destruction. OVs are helpful anti-tumor agents killing dividing tumor cells but not normal tissue. Newcastle disease virus (NDV) can lyse human cancer cells directly. NDV is a paramyxovirus that is pathogenic in birds but causes only mild flulike symptoms in human beings also NDV is a single-stranded RNA virus that replicates in the cytoplasm of infected cells without affecting host DNA, reducing the risk of undesired recombination events. We tried to use two strains of the NDV virus to investigate its effect on the control of hepatocellular carcinoma. *Materials and Methods:* The Hitchner B1 (NDV/B1) nonpathogenic, chicken vaccine strain of the NDV virus was purchased and suspended in PBS. Lasota strain (Razi Vaccine and Serum Research Institute) was grown in 9 days' embryonic eggs at allantoic fluids for 13 days. On the 13th day, allantoic fluid was collected. The titer of both of them was determined by Hemagglutination (HA) test with 0.5% chicken RBC. The HepG2 cell line was cultured as liver cancer cells in high glucose DMEM with 10% FBS. When cells reached 70% confluence, cells were seeded 104 cells per well in a 96-well plate, then treated with Lasota strain, B1 strain, and Lasota strain plus B1. After 24 hours, apoptosis was analyzed *Results:* Simultaneous use of two viruses increased its effectiveness and apoptosis occurred in liver cancer cells. Newcastle viruses from two different strains



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showed that they are suitable candidates for cancer treatment. *Conclusion:* It may be possible to use two strains of the same virus strain to increase effectiveness in cancer

Keywords: Liver cancer, Newcastle disease virus, apoptosis, treat cancer

Investigation of Respiratory Viruses Infection in Patients Referred by Respiratory Disease

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نوع پذیرش: oral | کد مقاله: G-18643

Abstract: *Background:* Second to COVID19 pandemic, other viral respiratory infections are still important causes of human diseases or co-infections. The classical URI symptoms include sorethroat, sneezing, rhinorrhea, nasal congestion, sinus pain, cough, headache, myalgia, loss of appetite, chills, and fever. Meanwhile, due to widespread COVID19 infection, differentiating viral respiratory infection symptoms remains challenging. Hence, the present study was carried out to investigate the common respiratory viruses in patients with respiratory illness diagnosed negative for SARS-CoV2 in primary screening. *Method:* In a cross-sectional study, we collected samples identified negative for SARS-CoV2 via an in-house Realtime PCR as primary screening. Then, the second Real time PCR was carried out using HiTeq 17 Viro Respiratory pathogen One Step RT-PCR Kit (Genova, Bonda Faravar, Iran). As for the kit, the analytical specificity was 100%, diagnostic specificity was 95%, diagnostic sensitivity was 95%, and analytical sensitivity (limit of detection (LOD)) was 100 copy/ul for SARS-CoV-2, 200 copy/ul for Flu A and Flu A/H1N1, 250 copy/ul for Flu B and HCoV-NL63, 300 copy/ul for HRSV, HCoV-229E and HMPV, 350 copy/ul for HCoV-HKU1, 500 copy/ul for HPIV-1, -2, -3, HAdV and HBoV-1, -2, -3. *Results:* From a total of 549 specimens in primary screening, specimens from 311 individuals (mean age \pm SD: 48.2 ± 21.7 y, range: 1-97 y) underwent second PCR. Among these, 161 (51.7%) were female. Totally, 67 (21.5%) cases (mean age \pm SD: 45.7 ± 18.1 y) were found positive for respiratory viruses panel in the second PCR. According to the results of PCR, we discovered that 67 (21.5%) cases (41 (61.1%) female and 26 (38.9%) males; Mean age \pm SD 45.7 ± 18.1 ; range: 13-82 y) were positive for respiratory viruses panel. Detected viral infections included HCoV-OC43/HKU1: 5.1% (16/67), Flu A: 4.5% (14/67), SARS-CoV2: 3.2% (10/67), HCoV-229E/NL63: 2.8% (9/67), HMPV: 1.6% (5/67), HPIV-1, -2, -3: 1.2% (4/67), HRSV: 0.9% (3/67), and HAdV: 0.6% (2/67) (Figure 2). The co-infection was detected in 4 samples (1.2%) among the studied cases. The co-infections included COVID19-HMPV (0.6%, 2/67), OC43/HKU1-Flu A (0.3%, 1/67), and COVID19-NL63/229E (0.3%, 1/67). Pure positive rate of respiratory viruses infection in patients with negative SARS-CoV2 was observed to be 18.3% (57/311). Of 57 positive cases, 25 (43.8%) individuals were identified by non SARS-CoV2 coronaviruses infection (HCoV-OC43/HKU1, HCoV-229E/NL63), which rate them as predominant infections followed by Flu A virus (20.8%, 14/57). In addition, sorethroat (0.028), headache ($p=0.016$), and body pain ($p=0.0001$) were statistically the most significant symptoms in studied cases. The specificity and sensitivity of the primary screening assay were 100% and 89%,



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respectively. **Conclusion:** According to the findings of our study, respiratory viruses infections and co-infection, other than SARS-CoV2, were 18.3% and 1.2% frequent, respectively. Interestingly, near half of our positive cases (43.8%) were identified by non-SARS-CoV2 coronaviruses (OC43, E229, NL63, and HKUI) followed by influenza A virus (20.8%). However, for more comprehensive results, we recommend using greater sample size. **Keywords?**

آدرس دبیرخانه:

تهران، خیابان کارگر شمالی، رویروی مرکز قلب تهران،
کوچه دانش ثانی، بعد از تقاطع صالحی، پلاک ۱۵، واحد ۲

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Assessment of virucidal activity of Ag-NPs and ethanol 70% toward HSV-1

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Background: The viruses infecting humans are undeniably capable of causing asymptomatic or acute severe and often lethal diseases, in the other hand they can be manipulated to be beneficial to human health. The virus act as a double-edged sword for human life. Although the viruses cause severe and persistent disease, such as CNS disorder and several cancers, but, some other viruses offer the potential to cure cancer, correct genetic disorders, or fight pathogenic viral infections. The 2019 outbreak of severe acute respiratory syndrome (SARS-CoV-2 pandemic was a global challenge worldwide, and approving disinfectant to render the environment virus free are needed. Since viruses can spread directly and indirectly, it is essential to use proper disinfection to decrease viral transmission. Lipophilic disinfectants play an active role in inactivation and reduction of the virus infectivity of enveloped viruses. IBV and HSV-1 can be appropriate surrogate models to assess the virucidal activity against SARS-CoV-2 in the absence of equipped with proper BSL cabinet. The aim of this research was to evaluate the virucidal activity of Ag-NPs and ethanol 70% toward HSV-1.

Material and method: To assay the probable toxic effect of disinfectants on Vero cells a cytotoxicity assay was performed. The DLS analysis and FE-SEM were used to assessment of the Ag-NPs characterization. Afterward suspension test was carried out on the HSV-1 virus for the alcohol-based disinfectant and the silver nanoparticle disinfectant at the target times (30", 5, 10, 20, 40, 80 and 160 minutes). Finally, the virus titers and log reduction were calculated by the tissue culture infective dose (TCID₅₀) endpoint method.

Result: Approximately 7-log reduction of HSV-1 in suspension test was showed by usage of ethanol 70%. Ag-NPs in suspension test showed at least 4-log and maximum 6-log reduction of HSV-1 titer. Both disinfectants inactive HSV-1 within indicated time.

Conclusion: our findings showed that Ag-NPs and 70% ethanol have great inhibitory activity toward HSV-1 and reduced virus activity in infected Vero cells. To test their virucidal activity, suspension methods were used. Our result would seem to suggest that HSV-1 appeared as the relevant candidates to test the virucidal activity of lipophilic disinfectants toward enveloped



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virus; like SARS COV2 and may provide useful supplemental information about SARS COV2 susceptibility to disinfectants.

Key words: HSV-1, Ag-NPs, Ethanol 70%, Disinfectants

آدرس دبیرخانه:

تهران، خیابان کارگر شمالی، رویروی مرکز قلب تهران،
کوچه دانش ثانی، بعد از تقاطع صالحی، پلاک ۱۵، واحد ۲

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Epstein-Barr virus nuclear antigen 1 increases the expression of HPV type 18 E6 and E7 oncogenes in the HeLa cell line

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Abstract: *Background:* Epstein-Barr virus (EBV) is one of the top viral carcinogens. EBV nuclear antigen-1 (EBNA1) is a critical protein of EBV which can affect different cellular and viral genes expression. In this study, we assessed the impact of the EBNA1 protein on the HPV-18 E6 and E7 oncogene expression patterns in the HeLa cell line. *Materials and Methods:* Three groups of HeLa cells—one with the EBNA1 plasmid transfected, one with a control plasmid, and one without transfection—were created. In EBNA1 and control plasmid transfected groups, hygromycin B treatment was used to choose cells with stable EBNA1 expression. Real-time PCR assay was applied to measure expression changes of the E6, and E7 oncogenes in each of the three groups. *Results:* HeLa cells transfected with the EBNA1 plasmid showed significantly higher levels of HPV-18 E6 (P=0.02) and E7 (P=0.02) gene expression than cells transfected with the control plasmid. In fact, the presence of EBNA1 increased the expression of these two viral oncogenes twofold and threefold, respectively. Additionally, EBNA1 led to the development of enormous HeLa cells that were packed with cytoplasm and nuclei. *Conclusion:* EBNA1 could increase the expression levels of HPV-18 E6 and E7 oncogenes in the HeLa cells. According to these results, cervical cells that are simultaneously infected with HPV-18 and EBV may develop cervical cancer more quickly. **Keywords:** Cervical carcinoma, Human Papillomavirus, Epstein-Barr Virus, EBNA1

Comparative RNA-sequencing transcriptome analysis of peripheral blood mononuclear cells in Cervical Cancer

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نوع پذیرش: oral | کد مقاله: G-48712

Abstract: *Background:* Human papillomavirus (HPV) is a causative agent of cervical cancer, and is major etiologic agent of all the cases. The purpose of this investigation was to use RNA-sequencing (RNA-seq) to screen the appropriate differentially expressed genes (DEGs) in the PBMCs for the progressive cervical cancer. *Materials and Methods:* Here we carried out RNA-seq gene expression profiling of 45 peripheral blood mononuclear cells (PBMCs) from Tabriz (northwest of Iran) women, of the disease from cervical intraepithelial neoplasia I (CIN), CIN-II, CIN-III, healthy control (n= 15), and identified distinct RNA-seq gene expression signatures. The cDNA libraries were paired-end sequenced using an Illumina HiSeq 4000. All raw RNA-sequencing data analyses were performed using conventional RNA-sequencing analysis tools. Next, gene ontology analyses were carried out to elucidate the biological processes of DEGs. Finally, relative transcript abundance of selected DEGs was verified using qRT-PCR on additional validation groups. *Results:* Specifically, 14, 192, and 895 DEGs were identified for CIN-I, CIN-II and CIN-III, when compared with the healthy subjects. Overall, immune and inflammatory pathways were found to be significantly upregulated in patients with progressive stage. Additionally, we identified candidate signatures of disease progression such as CCL-2, CCL-5, IL-6, IL-10, TNF- α , and ANXA1 among others that were validated by qRT-PCR in the samples used for RNA-seq studies as well in an independent set of additional samples. *Conclusion:* This study provides us with new insights into the biological function and potential cervical cancer and could facilitate the development of diagnostic markers of cervical cancer progression. *Keywords:* Human papillomavirus, differentially expressed genes, Peripheral blood mononuclear cells, Biomarker

Study prevalence of respiratory viruses other than SARS-COV-2 by 2021-2022

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نوع پذیرش: oral | کد مقاله: G-75813

Abstract: *Background:* Due to the fact that even during COVID-19 pandemic, other viral respiratory infections are still important and they can be misdiagnosed as COVID-19, the prevalence of these viruses is required to be evaluated, especially during the COVID-19 peaks. Thereby, not only the prevalence of viral infections that cause the same respiratory symptoms to COVID-19 is measured, but also the diagnostic errors rate made by depending on the patients' symptoms are being determined. *Methods:* A cross-sectional study is carried out on the referred patients to the Mehr hospital, under observation of Iran University that had the respiratory infection symptoms but were negative for SARS-CoV-2 PCR result. The negative samples for SARS-CoV2, from Mar 2021 to Jul 2022 that were tested by Real-time PCR as primary screening, were collected. A second Real Time PCR was being done by HiTeq 17 Viro Respiratory pathogen One Step RT-PCR Kit to determine the presence and genotype of other respiratory viruses. To evaluate, the demographic data of the patients with positive samples were analyzed by SPSS v16 and the P-value less than 0.05 considered to be statistically significant. Other parametric variables such as mean age of the patients were analyzed by t-test and Mann-Whitney-Wilcoxon analysis. *Result:* Among the 549 samples included in the initial screening, a second PCR was performed for 311 samples, the mean and standard deviation of their age was 48.2 ± 21.7 years (range 1-97 years), and 161 of them (51.7%) were women. In general, during evaluating the prevalence and determining the genotype of respiratory viruses, including OC43/HKU1/229E/NL63/ influenza A virus and coronavirus, 52 samples were positive, and the average age and standard deviation of all positive patients were 19.014 ± 44.96 years. The prevalence of each virus included 5% for OC43/HKU1, 3% for 229E/NL63, 4% for Covid-19, 5% for influenza A, and 5% for other viruses. Fever, body aches, and fatigue were prominent symptoms in the studied patients. Thus, by performing relevant analyses, there was no significant relationship between age group and type of virus (p-value=0.1); There was a significant relationship between the sampling season and the type of viral infection (p-



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value=0.003); Based on sore throat, there was a significant relationship between the group infected with 229E/NL63. Therefore, significantly more sore throats have been reported in people infected with these coronaviruses. **Keywords?**

آدرس دبیرخانه:

تهران، خیابان کارگر شمالی، رویروی مرکز قلب تهران،
کوچه دانش ثانی، بعد از تقاطع صالحی، پلاک ۱۵، واحد ۲

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EBNA1 upregulates MDM2 and MDM4 genes expression in Burkitt's lymphoma cell line

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نوع پذیرش: oral | کد مقاله: G-17609

Abstract: *Background:* Suppression of p53 is a key mechanism in Epstein-Barr virus (EBV)-associated cancers. The interaction between EBV nuclear antigen-1 (EBNA1) and cellular USP7 protein is a critical route in p53 suppression. In this study, we aimed to see how EBNA1 affects the expression of p53-inhibiting genes like MDM2 and MDM4. *Materials and Methods:* The BL28 cell line (which has p53 wild type and is negative for EBV) was transfected with the PCEP4 plasmid that harbors the EBNA1 gene. The transfection was accomplished using the electroporation method. After 24 hours, the cell culture was treated with Hygromycin B (350 g/mL) for 16 days to select transfected cells with stable EBNA1 expression. Real-time PCR was used to assess MDM2 and MDM4 expression. *Results:* The qRT-PCR assay indicated that MDM2 (P=0.028) and MDM4 (P=0.028) are considerably more expressed in EBNA1-containing cells than in control plasmid transfected cells. *Conclusion:* It seems that EBNA1 could strongly upregulate p53-inhibiting genes, including MDM2 and MDM4. This finding indicates that EBNA1 might suppress p53 in latency type I cancers like Burkitt's lymphoma by upregulating several p53-inhibiting genes. **Keywords?**

Susceptibility of the Iranian population to SARS-CoV-2 infection based on variants of angiotensin I converting enzyme 2

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نوع پذیرش: oral | کد مقاله: G-61725

Abstract: Background: Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) is a newly formed coronavirus with more than 3 million cases and thousands of deaths. Variations in the viral receptor Human angiotensin-converting enzyme 2 (ACE2) may specify the susceptibility of a certain population. Therefore, it was aimed to evaluate the role of ACE2 polymorphisms in the interaction between virus receptors and the susceptibility of viral infections among the Iranian population *Materials and Methods:* The Crystallographic Structure of ACE2 was recovered from the Protein Database (PDB). Single nucleotide polymorphisms (SNPs) of ACE2 among the Iranian population were collected from the Iranome database. Missense mutations in the N-terminal peptidase domain were selected for the analysis. The molecular docking was conducted using the ClusPro web server. Docking tests and binding sites were further investigated using UCSF Chimera and MGLTools software. *Results:* Seventeen missense SNPs were found at ACE2 of which seven substitutions at the peptidase domain were chosen for docking. ACE2 variant S331F with -1003.7Kcal.mol⁻¹ had highest interaction energy with the viral glycoprotein. Viral glycoprotein had the lowest interaction energy (-972.2 Kcal.mol⁻¹) with the ACE2 mutant V485L. Fewer atoms were also involved in the interaction of viral glycoprotein with the mutant ACE2 V485L. Other substitutions had the same interaction energy with SARS-CoV-2 spike glycoprotein. *Conclusion:* Some populations may have some ACE2 variants that affect the susceptibility to SARS-CoV-2 infection. The V485L variant of ACE2 could be a natural resistance mutation among the Iranian population. In addition, variant S331F can increase slightly the susceptibility to infection with the virus. Considering the significance of these hotspots on ACE2, targeting these sites may be beneficial for treatment processes. **Keywords:** SARS-CoV-2; Human angiotensin-converting enzyme 2; SARS-CoV-2 spike glycoprotein; Natural resistance variant; Molecular docking

Clinical characteristics of SARS-CoV-2 infection during pregnancy and its Perinatal Outcomes

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نوع پذیرش: oral | کد مقاله: G-81620

Abstract: *Background:* With the onset of the severe acute respiratory syndrome coronavirus-2 pandemic, there were controversial theories regarding the potential consequences of the virus on pregnant women and delivery outcomes. During the past three years, a great diversity of literature reported various data regarding covid-infected mothers and pregnancy-related complications including preterm birth, stillbirth, preeclampsia, cesarean delivery, etc., however; the exact influences which can be exerted by the virus and possibility of vertical transmission, still remained obscure. Here we described the clinical features and outcomes of delivery in 16 laboratory confirmed COVID-19-infected mothers referring to a hospital in northern Iran from August 2020 to December 2021. *Materials and Methods:* Clinical records, laboratory results, and chest CT scans in addition to such samples as maternal peripheral blood, umbilical cord blood, placental blood, vaginal secretion, placental tissue, breast milk after first lactation, and neonatal throat swab and peripheral blood were collected to answer the questions raised on the possibility of vertical transmission of COVID-19 and transferring maternal immunity to the neonates, all the aforementioned specimen were evaluated based on molecular and serological assays. *Results:* Among 16 pregnant women with the gestational age range 26-38 weeks, 10 and 6 underwent caesarean and vaginal delivery, respectively, also 16 livebirths, and 2 fatal distress were registered; however, 3 newborns died after delivery (5-6 and 7-8, 1 and 5 min Apgar scores). In 10 out of the 16 patients, fever was reported before delivery and 2 patients had postpartum fever. Moreover, other symptoms of upper respiratory tract infection were reported as follow: cough (11), myalgia (7), sore throat (2) and chest pain (3), Dyspnea (7) and headache (2). Additionally, the results of laboratory tests include: lymphopenia (1.0×10^9 cells per L) in 2 cases, high levels of C-reactive protein (10 mg/L) in 11 cases, elevated concentration of ALT or AST in 5 cases, increased white cell counts ($11.0 \times 10^9/L$) in 4 cases. There were no SARS-CoV-2 in vaginal secretions and placental tissue. In serological tests of mothers' blood (15 IgG positive and 4 IgM positive), breast milk (1 IgM positive), Umbilical cord blood (2 IgG positive), placental blood (2 IgG positive) and neonatal blood (2 IgG positive) were observed. Chest CT scan of abnormal cases revealed typical signs of viral pneumonia, such as decreased diffuse and bilateral ground-glass opacities, patchy lung consolidation, blurred borders, and lesions merged into strips in some cases. *Conclusion:* According to the current investigation there is outstanding associations between COVID infection, the risk of adverse pregnancy



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outcomes and preterm birth; however, any sign of intrauterine vertical transmission of COVID-19 hasn't reported. What's more, the observed clinical characteristics didn't specify to COVID-infected pregnant women. These results also suggests the possibility of passive IgG transfer from the infected mothers to their neonates. **Keywords?**

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Evaluation of MicroRNAs expression pattern (miR-28, miR-181a, miR-34a, and miR-31) in Patients with COVID-19 Admitted to ICU, and Diabetic COVID-19 patients

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نوع پذیرش: oral | کد مقاله: G-82963

Abstract: *Background:* MicroRNAs, or miRNAs, with regulatory performance in inflammatory responses and infection are the prevalent manifestations of severe Coronavirus disease (COVID-19). This study aimed to evaluate whether PBMC miRNAs are diagnostic biomarkers to screen the ICU COVID-19 and diabetic-COVID-19 subjects. *Material and Methods:* Candidate miRNAs were selected through previous studies, and then the PBMC levels of selected miRNAs (miR-28, miR-31, miR-34a, and miR-181a) were measured via quantitative reverse transcription PCR. The diagnostic value of miRNAs was determined by the receiver operating characteristic (ROC) curve. The bioinformatics analysis was utilized to predict the DEMs genes and relevant bio-functions. *Results:* The COVID-19 patients admitted to ICU had significantly greater levels of selected miRNAs compared to non-hospitalized COVID-19 and healthy people. Besides, the mean miR-28 and miR-34a expression levels in the diabetic-COVID-19 group were significantly upregulated when compared with the non-diabetic COVID-19 group. ROC analyses demonstrated the role of miR-28, -miR-34a, and -181a as new biomarkers to discriminate the non-hospitalized COVID-19 group from the COVID-19 patients admitted to ICU samples, and also miR-34a can probably act as a useful biomarker for screening diabetic COVID-19 patients. Using bioinformatics analyses,



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we found the performance of target transcripts in many bio-processes and diverse metabolic routes such as the regulation of multiple inflammatory parameters. **Conclusion:** The difference in miRNA expression patterns between the studied groups suggested that miR-28, miR-34a, and miR181a could be helpful as potent biomarkers for diagnosing and controlling the COVID-19. **Keywords:** SARS-CoV-2, COVID-19, microRNA, Diabetes, Biomarker

Possible Role of HPV/EBV Coinfections in Anoikis Resistance and Development in Prostate Cancer

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نوع پذیرش: oral | کد مقاله: G-68250

Abstract: *Background:* This study aimed to evaluate the possible role of human papillomavirus (HPV) and Epstein-Barr virus (EBV) coinfection as an etiological factor for prostate cancer (PCa) development. *Methods:* This case-control study was conducted on 67 patients with PCa and 40 control subjects. The expression levels of cellular and viral factors involved in inflammation, tumor progression, and metastasis were quantified, using the enzyme-linked immunosorbent assay (ELISA) and quantitative real-time polymerase chain reaction (qRT-PCR) assay. *Results:* The EBV/HPV coinfection was reported in 14.9% of patients in the case group and 7.5% of the control subjects. The high-risk types of HPV, that is, HPV 16 and HPV 18, were responsible for 50% and 30% of HPV/EBV-coinfected PCa cases (n=10), respectively. No significant relationship was observed between PCa and HPV/EBV coinfection (OR=2.9, 95% CI: 0.18-45.2, P=0.31). However, the highest percentage of HPV genome integration was found in the HPV/EBV-coinfected PCa group (8/10; 80%). Also, the mean expression levels of inflammatory factors (IL-17, IL-6, TNF- α , NF- κ B, VEGF, ROS, and RNS), anti-apoptotic mediators (Bcl-2 and survivin), and anti-anoikis factors (Twist and N-cadherin) were significantly higher in the HPV/EBV-coinfected PCa group, compared to the non-coinfected PCa cases. Nevertheless, the tumor-suppressor proteins (p53 and pRb) and E-cadherin (inhibitor of anoikis resistance) showed significant downregulations in the HPV/EBV-coinfected PCa group, compared to the non-coinfected PCa cases. *Conclusion:* The HPV/EBV coinfection may be an etiological factor for PCa through modulation of cellular behaviors. **Keywords?**

Exosome Functionalization by Chondroitin Sulfate through Hydrophobic Insertion

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نوع پذیرش: oral | کد مقاله: G-12703

Abstract: *Background:* Exosomes are promising drug delivery platform candidates because of their intrinsic function of carrying various molecules from donor cells to recipient cells. However, the preferential accumulation of exosomes in the liver and spleen is a serious challenge of exosome-based delivery platforms. The surface alternation of exosomes by various targeting ligands is a practical solution to solve this problem and employ exosomes for cancer-specific drug delivery. One strategy to conjugate different targeting ligands to the surface of exosomes is hydrophobic insertion. Here, the surface of exosomes is modified with chondroitin sulfate (CS) because of the tendency of this polysaccharide to cancer cells overexpressing CD44. *Materials and Methods:* We tried to improve the targeting ability of HEK-derived exosomes through chemical modification of their surface. Chondroitin sulfate, a CD44-specific ligand, was functionalized with alpha-tocopherol succinate (TOS) and octadecylamine (ODA) to exploit their lipid chain in order to facilitate exosome surface decoration through hydrophobic insertion. The CS-TOS conjugate is generated by coupling TOS with CS. Carboxylic acid groups of TOS were activated by the addition of 1-Ethyl-3-(3-dimethylaminopropyl) carbodiimide hydrochloride (EDC·HCl) and N-hydroxysuccinimide (NHS) to the TOS dissolved in dimethylformamide. The TOS solution with activated carboxylic acid groups then was added to the CS dissolved in formamide, and the mixture was stirred vigorously at ambient temperature in darkness for two days. The product finally was isolated by freeze-drying. The CS-ODA molecule was synthesized by the carbodiimide reaction between amine groups of ODA and carboxylic acid groups of CS. Exosomes were extracted from HEK cell culture with the EXOCIB kit, and CS-TOS and CS-ODA were expressed on their surface through incubation for 48 h at 37 °C, followed by low-speed centrifugation to remove unbound ligands. The morphology, zeta potential, and the average size of naïve exosomes and modified exosomes were determined with transmission electron microscopy and dynamic light scattering. *Results:* CS-TOS was synthesized by ester bond formation between the carboxyl group of TOS and the hydroxyl group of CS. The conjugation of TOS to CS was confirmed by FT-IR analysis, and the peak at 1722 cm⁻¹ was caused because of C=O of the newly formed ester, and the absorption peak at 1650 cm⁻¹ corresponded to the C-O of the carboxyl group. It was demonstrated that the decoration of exosomes with CS-TOS did not change their morphology. However, the alternation of exosomes increased their size from 112.7 to 123.6, but the negative charge of CS shifted the zeta potential of exosomes from -7.01 to -13.24. The change in the exosome's average diameter and zeta potential confirmed their modification. *Conclusion:* In summary, a novel targeted delivery



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approach by modification of HEK-derived exosomes with CS is introduced. TOS-CS is conjugated to the surface of exosomes because of the lipophilic chain of TOS, and it is hypothesized that this modification will improve exosomes' tendency toward cancer cells overexpressing CD44.

Keywords?

آدرس دبیرخانه:

تهران، خیابان کارگر شمالی، رویروی مرکز قلب تهران،
کوچه دانش ثانی، بعد از تقاطع صالحی، پلاک ۱۵، واحد ۲

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Synthesized carbon dot nanoparticles from natural carbon source for cancer cell imaging and photothermal therapy

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نوع پذیرش: oral | کد مقاله: G-93574

Abstract: *Background:* Cancer as one of the most common and malignant diseases requires to take new treatment techniques to overcome the traditional treatment's drawbacks. Nanoparticle-based therapies with individual and tunable properties can be considered promising cancer theranostic treatments. Carbon dots (CDs) via heteroatom doping, provide optical absorbance in the near-infrared (NIR) range for selective cancer photothermal therapy (PTT) and strong fluorescence to cell imaging. *Materials and Methods:* In this study, a one-step and cost-effective hydrothermal technique was designed to create copper-doped carbon dots (CuCDs). CuSO₄ was used as the doping component in combination with tomato extract as the carbon source. The characterization of synthesized nanoparticles was analyzed by electron microscopy, dynamic light scattering (DLS), and FTIR. The optical properties and cell imaging potential were investigated by PL emission spectroscopy, fluorescence microscopy, and UV-vis absorption in different wavelengths. Cellular uptake, cytotoxicity, and PTT efficiency were examined on 4T1 breast cancer cells. *Results:* According to microscopy and spectroscopy investigations, spherical and monodisperse CuCDs had diameters under 10 nm with a strong fluorescence exhibition and a significant single absorption peak at 810 nm. CuCDs were highly uptake by the cells and induced cell death when they were under an 800 nm laser. This is demonstrated by their low in vitro cytotoxicity and the caused cell PTT with efficient photothermal conversion. After cell internalization of CuCDs, they had intense and brilliant fluorescence inside the cancer cells. *Conclusion:* Tomato extract and CuSO₄ precursors were used in a one-step, low-cost, simple, and quick hydrothermal method to create the Cu-doped CDs as a novel form of PTT agent. With a single absorbance peak at 810 nm, size below 10 nm, and good cellular uptake, the CuCDs exhibit a pretty effective photothermal conversion. As exposed to an 800 laser, CuCDs by great heat generation exhibits a good thermal ablation impact on 4T1 breast cancer cells. Besides this, by intracellular brilliant fluorescence, they have theranostic potential in cancer treatment. **Keywords:** Carbon dots (CDs), Nanoparticle, Photothermal therapy, Cell imaging

Effect of crocin and saffron on patients with type 2 Diabetes a Placebo- controlled 'triple-blinded clinical trial

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نوع پذیرش: oral | کد مقاله: G-62319

Abstract: *Objective:* The purpose of this study was to evaluate the effect of Saffron and its active ingredient, crocin, as a natural antioxidant in the treatment of type II diabetes. *Methods:* A total of 150 uncontrolled type 2 (non-insulin-dependent) diabetic patients were selected based on inclusion criteria, randomly divided into three groups (crocin, saffron and placebo) for three months' clinical trial. Fasting blood glucose (FBS), insulin level, glycosylated hemoglobin (HbA1c), lipid profile, kidney and liver function tests were performed before and three months after the study. The patients were followed every two weeks for possible clinical side effects. *Results:* Our results showed that after three months of treatment with crocin and saffron, FBS and HbA1c decreased whereas; FBS reduction was only significant in the crocin and placebo groups (P-value 0.05). Also, reduction of HbA1c was significant only in the crocin and saffron groups. Comparison between groups showed that treatment with crocin led to a significant reduction in HbA1c compared to saffron and placebo. In addition, changes in lipid profile were not significant in any of the three groups. Also, there was no significant difference in liver and liver parameters in all three groups. Inter-group comparison of insulin levels showed significant difference only between the saffron and placebo groups. *Conclusion:* Crocin can be effective in controlling the level of HbA1c in patients with type 2 diabetes and, can improve the side effects of high blood sugar. *Keywords?*



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Blood coagulation disorders in Iranian population; a systematic review

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نوع پذیرش: پوستر | کد مقاله: G-45708

Abstract: Abstract Objective: Blood coagulation disorders are one of the causes of mortality. Investigating the coagulation disorders can help laboratory specialists and clinician in diagnostic and treatment. This systematic review study was conducted to investigate blood coagulation disorders in Iranian population. Methods: Searches in electronic databases such as Web of Science, Pubmed, Scopus, SID, ProQuest, and Magiran from 10 May 1990 to 10 May 2019 were performed based on Prisma guidelines. Also, according to the inclusion criteria, cross-sectional, cohort, experimental, and case-control studies included without gender and language restriction. Participants were also being patients with coagulation disorders. The risk of bias assessed using the NOS (Newcastle–Ottawa scale) tool. Results: After screening and selection, 16 studies were selected for data extraction. The most common blood coagulation disorder in southern of Iran was defect in factor XIII (52%). Also, C562T C (100%) and C559T C (17.8%) mutations had the highest frequency. In addition, the C1691G A, in factor V Leiden was the most common mutation (14.2%). The most common factor XIII polymorphism among the Iranian Azerbaijanis was Val34Leu (52.2%). Conclusion: Investigate blood coagulation disorders in Iranian population show that, the most important coagulation disorders is factor XIII deficiency, which is associated with intracerebral hemorrhage and abortion. The most common mutation in this defect was C562T C mutation. Key words: Iran, blood coagulation disorders, Mutation, Systematic review

The role of hematological parameters in predicting the death of hospitalized patients with COVID-19

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Abstract: Background: The role of the hematologic indicators in the identification of severe or critical patients requires further investigation. In this study, we focused on predicting Covid-19 patients at risk of progression using blood parameters. Methods: We performed a retrospective study including 444 patients with confirmed Covid-19. Hematological parameters were evaluated. The logistic regression analysis was performed with step-wise method with dependent variables such as intensive care units admission, partial pressure of oxygen saturation, and mortality. Also, independent variables such as hematological parameters, age and sex to assess variables that are likely to predict patients at risk of progression. Results: Patients in intensive care units had significantly higher mean absolute neutrophil count than outpatients (P 0.001). There was a statistically significant difference in the mean absolute lymphocyte count between dead and survived patients. (P = 0.015). Multivariate analysis confirmed the positive association of the white blood cells (P 0.001), ANC absolute neutrophil count (P 0.004), red cell distribution width (P 0.001), and lactate dehydrogenase (P = 0.007) to be positively associated with the admission of Covid-19 patients in the intensive care units & the absolute monocyte count (P = 0.012, Odds ratios = 0.100, CI95% = 0.066-0.605) to be negatively associated with mortality. Conclusion: Based on the results of our study, it is recommended to use hematological data to make clinical decisions and evaluate the patient's prognosis. Keywords: COVID-19, Neutrophils, Novel coronavirus, Monocytes

Dual effects of Resveratrol on the Expression and Secretion of Angiogenic Factors

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Abstract: Abstract Objective: Angiogenesis is an essential process in the growth, development, and transition of tumors from dormancy to proliferating state. Resveratrol (RSV), as a natural polyphenolic compound, is claimed to be effective in regulating angiogenesis. This study aimed to evaluate the impact of RSV on the angiogenesis process in HUVECs (human umbilical vein endothelial cells) alone and co-cultured with Jurkat cells. Materials and methods: The effects of RSV on HUVECs and Jurkat cell viability and apoptosis were measured by MTT and Annexin-V/PI methods. HUVECs were co-cultured with pre-treated Jurkat cells and incubated for 24h, 48h and 72h. The angiogenesis process in HUVECs and Jurkat cells alone and in co-culture models was investigated by analyzing the expression of VEGF, VEGFR-2, and Interleukin-8 (IL-8) employing qPCR and ELISA. Results: RSV at low concentration (40µM) had no significant effects on apoptosis rate of HUVECs, but higher concentrations (80-160µM) increased apoptosis in co-culture method and HUVECs alone. RSV significantly reduced VEGFR2 and IL-8 gene expression also, IL-8 protein concentration in HUVECs, but the effects of this drug in the HUVECs-Jurkats co-culture were different. Expression of VEGF in Jurkat cells increased following treatment with RSV. Conclusion: RSV had direct anti-angiogenic effects on HUVECs. Unexpectedly its indirect effects were not significant on HUVECs-Jurkats co-culture. Results of our study showed, RSV may be effective in anti-angiogenesis therapy, but in some situations, it may induce angiogenesis. So, appropriate concentrations should achieve to minimize the unpredicted effects of RSV. Key words: Angiogenesis Inhibitors, Resveratrol, Co-culture, VEGFR2, VEGF, Interleukin-8

Blastocystis subtype 3; Predominant subtype among COVID-19 patients in Tehran, Iran

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Abstract: Background: Till now, there is no data about Blastocystis subtypes in COVID-19 patients. Therefore, the present study was done to evaluate the molecular prevalence of Blastocystis sp. and related risk factors in Iranian patients with COVID-19. Materials and Methods: Stool samples were gathered from 200 COVID-19 patients. Then, PCR and sequencing were used to detect Blastocystis sp. and their subtypes. Results: The frequency of Blastocystis sp. in patients with COVID-19 was 7.5% (15/200). Among them, Blastocystis ST3 was the most common subtype in the patients with COVID-19. Regarding associated factors for Blastocystis sp., we found significant differences regarding the residence (rural), loose and watery stool with diarrhea, and duration of treatment (6 weeks) in the COVID-19 group. Conclusion: Based on these results, health education, improved sanitation and good personal hygiene are highly recommended to prevent Blastocystis in COVID-19 patients. Key words:

Evaluation of Blood Pressure in Pediatric Survivors of Acute Lymphoblastic Leukemia and Healthy Children; A Case-control Study

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Abstract: Background: The exact prevalence of hypertension in children surviving acute lymphoblastic leukemia (ALL) has not been fully estimated. The aim of this study was to investigate the prevalence of arterial hypertension (AH) and to determine the risk factors for the development of AH in children surviving ALL with current treatments. Methods: A total of 150 patients (84 males, 66 females, with an age range of 1–16 years) were included in the study. Demographic and clinical information of patients were initially recorded. Hypertension is defined as average systolic blood pressure (BP) and/or diastolic BP that is greater than the 95th percentile for gender, age, and height. Results: The mean age at the assessment of BP was 11.3 and 9.8 years in the ALL and control group, respectively. A total of 20.6% of survivors of ALL and 10% of controls had high BP. Most patients in both groups had normal BP (65.3% patients in ALL group and 75.4% subjects in the control group). The number of patients with hypertension was significantly higher in ALL patients as compared with the control group ($P = 0.026$). Conclusion: The prevalence of AH in children surviving ALL is higher than in children in the general population, which emphasizes the need for regular monitoring of BP in children surviving ALL and intervention in the lifestyle of this population. Careful follow up of BP status is warranted for long term survivors of childhood cancer Keywords: Acute lymphoblastic leukemia, Children, Hypertension, Survivors

The effect and safety of olanzapine on nausea and vomiting in children receiving moderately emetogenic chemotherapy

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Abstract: Background: In order to improve the complete recovery of nausea and vomiting, we conducted a study with the aim of preventing acute and delayed nausea and vomiting in children undergoing moderate emetogenic chemotherapy. Materials and Methods: A clinical trial study was done on 130 children received chemotherapy. Patients received olanzapine and placebo. All groups received granisetron along with dexamethasone (DEX). The severity of chemotherapy-induced nausea and vomiting (CINV) induced by chemotherapy was compared in two groups. Results: The severity of nausea on the first, second, third, and fourth days was not significantly different (P .05) in two groups. The number of patients without vomiting was significantly different during the first 24 hours after chemotherapy between patients in the two groups (82.3% vs 64.5%; P = .016). Conclusion: This study showed that olanzapine, which acts as an inhibitor of neurotransmitters, had a favorable efficacy in controlling acute and delayed CINV. More studies with large sample size are needed to compare the effect of olanzapine with other agents including aprepitant, palonosetron in the prevention of CINV. Keywords: Aprepitant, Dexamethasone, Granisetron, NauseaVomiting Clinical Trials: IRCT20150119020715N6 Ethical committee code number: IR.ARAKMU.REC.1396.288



Management and prevention of red cell alloimmunization in pregnancy

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Abstract:

If the mother is RhD negative and the fetus RhD positive, the mother may react to fetal blood cells in her circulation by developing a template for producing anti-D antibodies. Rh Immune Globulin (RhIg) can be given to RhD-negative women to prevent sensitization and hence prevent HDN. The objective of this systematic review management and prevention of the red cell in all immunized pregnancy.

The effect of a novel dual kinase inhibitor on doxorubicin resistance K562 CML cell line

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Abstract:

Background: Philadelphia positive leukemia which is known as chronic myeloid leukemia, consists 25% of blood cancer cases. This chromosome activates tyrosine kinases that have been target of many tyrosine kinase inhibitors. Among numerated reasons for drug resistance in this disease, in addition to BCR-ABL1 mutations, downstream pathways have been indicated to have a role. In this study, using dual MEK/Aurora kinase inhibitor (BI-847325) we evaluated the effect of MAPK and aurora kinase pathway inhibitors on doxorubicin resistant K562 CML cell line (KDI/20). **Materials and Methods:** KDI/20 cell line was achieved by K562 cell line that had been subjected to increasing concentrations of doxorubicin to final concentration of 20 ng/ml. regarding characterization, parental K562 and modified cell line were both cultured at final concentration of doxorubicin. MTT test was performed in order to compare doxorubicin and BI-847325 IC50s. Cell cycle arrest and apoptosis were evaluated by flowcytometry while BAX, BCR-ABL1, C-MYC, CYCLIN-D1 and P21 were evaluated by real-time-PCR. **Results:** Resistance to doxorubicin showed 2.7-fold increase while KDI/20 resistance to BI-847325 increased 2.4-fold versus K562. Cell cycle arrest and apoptosis was seen in both KDI/20 and K562 cells after treatment. Also, both K562 and KDI/20 cell lines showed down regulation in BCL2. K562 showed upregulation in CYCLIN D1, P21, C-MYC and BAX while BCR-ABL 1 and BCL2 were downregulated. On other hand KDI/20 showed CYCLIN D1, P21 and C-MYC downregulation while upregulation in P21 and BAX. **Conclusion:** Apoptosis and cell cycle arrest following BI-847325 treatment were induced in both doxorubicin sensitive and resistant cell lines. **Key words:**

Frequency of Kell and Rh allo antibodies in Iranian thalassemia patients in Khorasan Razavi province, Iran

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نوع پذیرش: پوستر | کد مقاله: G-20351

Abstract: Background: Thalassemia is an inheritance disease with anemia and hemolysis. Blood transfusion is a routine treatment for thalassemia patients; alloimmunization is one of the complications of blood transfusion which is very serious for these patients, especially girls and young women. Materials & Methods: in this cross sectional study 446 thalassemia patients were examined. Demographic information of patients was extracted and recorded. The phenotype of ABO, Rh and Kell antigens (tube method) with antisera from IMMUNDIANOSTICA Company(Germany) and frequency of alloantibodies was determined. Results: 55.8% of studied individuals were male and 44.2% were female. Mean age of studied patients was 19.94 ± 10.63 . The allo-antibodies were detected in 7.5% of pack cell receivers. The most prevalent phenotype of ABO system was O blood group (37.4%), and The most abundant antigen of Rh group was 'e', which was found in 99.8% of studied population. The most frequent detected allo antibody was Anti K (38.2%); concerning kell phenotype, (K_k+) and (K+k+) were found in 99.3% and 0.7% of patients, respectively. The frequency of Anti-D, Anti-C, Anti-c and Anti-E was 23.5%, 14.7%, 2.9% and 14.7%, respectively. Conclusion: according to the results of this paper, finding the compatible pack cells in terms of Kell and Rh systems antigens in addition to ABO blood group is recommended to decrease the rate of alloantibodies in thalassemia patients. Key words: Thalassemia, Kell blood group system, Rh system, Antibody

Tissue factor related coagulopathies in SARS-CoV-2 infection

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نوع پذیرش: پوستر | کد مقاله: G-23967

Abstract: Tissue factor (TF) plays the major role in the activation of coagulation system during viral infection. In viral infections related coagulopathy multiple factors such as inflammatory cytokines and viral specific TLRs are involved, which consequently induce TF expression aberrantly. Proinflammatory cytokines and coagulation cascade dysregulation may occur in COVID-19 infection. Thromboembolisms are frequent in COVID-19 patients with the increased risk of some life-threatening complications such as myocardial infarction and pulmonary embolism. In this regard, elevation of proinflammatory cytokines such as IL-6, IL-1, TNF- α and cytokine storm increase the risk of platelet activation, clot formation and multiorgan failure that may eventually lead to death among the patients. SARS-CoV-2 can bind to angiotensin converting enzyme 2 (ACE2) on various cells such as lymphocyte, alveolar cells, monocytes/macrophages, and platelets. Platelet and monocytes/macrophages activation can affect coagulation cascade through releasing TF/FVIIa. TF expression/release may play a critical role in the development of COVID-19 coagulopathy. In this regard, the use of TF- VIIa complex inhibitor may reduce the coagulation abnormalities and mortality among COVID-19 patients. Keywords: Coagulopathy, SARS-CoV-2, COVID-19, Tissue factor, Thrombosis, Angiotensin converting enzyme, Angiotensin II

Prognostic value of hematological and biochemical laboratory parameters to predict SARS-COV-2 outcome

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نوع پذیرش: پوستر | کد مقاله: G-59481

Abstract: Background: Coronavirus disease 2019(COVID-19) is a respiratory syndrome symptomatically spanning from healthy carriers to patients with life-threatening complications and in some cases leads to death. Laboratory findings were introduced to predict the disease severity and outcome. Materials and Methods: This study used data of 201 patients who admitted to a teaching hospital, Ganjavian (Dezful, Iran) with positive RT-PCR test for SARS-COV-2 infection. Explanatory variables are considered, including age, sex, and length of hospitalization, comorbidity risk factors, and 33 other variables. The aim of this study was to introduce a model for predicting duration of hospitalization and mortality. Results: Evaluation of 33 laboratory parameters in the patients at admission time and following their outcome showed hypocalcemia and hyponatremia, decrease in MCV, monocytopenia and elevation in platelet count, aging and have comorbidity risk factors increase the hospitalization time and mortality. Conclusion: Hypocalcemia and hyponatremia, decrease in MCV, monocytopenia and elevation in platelet count, aging and have comorbidity risk factors can be used as a flash of light beside other prognostic factors to predict the disease severity. Key words: SARS-CoV-2, COVID-19, Prognosis, Ca, MCV, K, Comorbidity factors

The impression of ABO blood group on complications caused by covid-19 infection

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نوع پذیرش: پوستر | کد مقاله: G-12569

Abstract: Background: The 2019 coronavirus disease (COVID-19) has become a global pandemic. According to the World Health Organization (WHO), about 200 million cases of Covid-19 infection have been reported. Recently, several studies have investigated the association between ABO blood groups and the complications of COVID-19 infection. Therefore, the aim of this systematic review was to evaluate the available evidence regarding the susceptibility of ABO blood group to COVID-19 infection. Materials and Methods: Studies of The relationship between ABO's blood group and Covid-19 infection were searched in PubMed, Google Scholar, Scopus, and EMBASE until October 2022. Also A search was carried out in Medline and in MedRxive and BioRxive. Results: This systematic review demonstrates the ABO blood group's vulnerability to COVID-19 infection was significant. Blood groups A and B may be risk factors for COVID-19 infection, whereas the blood group O appears to be protective. We also found higher risk of infection in A group compared to non-A, but not with each group independently and a lower risk of infection in O group compared to non-O groups and to each individual group. Higher risk of infection in patients without anti-A or anti-B antibodies observed. O group showed a lower risk of infection compared to non-O groups but also with A, B, and AB. Group A, however, only showed a higher risk when comparing with non-A. The reason for the lower sensitivity of people with blood type O to be infected by viruses can be the natural anti-A and anti-B antibodies produced in people with blood type O, which potentially block the adhesion of the virus to cells. Conclusion: We found that the COVID-19 infection rate in persons with blood group A O B AB. Accordingly, this evidence-based systematic review study further indicates blood group A individuals' vulnerability to COVID-19 infection. Blood type AB is linked to a lower risk of COVID-19 infection. Keywords: Blood Group, COVID-19 infection, infection, Vulnerability.

Iron monitoring in thalassemia patients with persistent blood transfusions

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نوع پذیرش: پوستر | کد مقاله: G-16907

Abstract: Background: Thalassemia and hemoglobin disorders are an emerging global health burden, accounting for about 3.4% of deaths in children less than 5 years of age. The current therapeutic management of thalassemia is based on regular blood transfusions. Frequent transfusions can lead to the accumulation of iron that can result in liver cirrhosis, diabetes mellitus, arthritis, arrhythmias, cardiomyopathy, heart failure, and hypogonadism. Hepcidin (encoded by the *Hamp* gene) is a peptide hormone synthesized by hepatocytes, and it plays an important role in regulating systematic iron homeostasis. Since hepcidin deregulation is responsible for iron disorder-associated diseases, the purpose of this review is to summarize the recent findings on therapeutics targeting hepcidin. Materials and Methods: Searching electronic databases, including EMBASE, PubMed, and Scopus was conducted from 2017 to 2021. Results: The electronic literature searches yielded a total of 459 relevant articles on thalassemia that met our search criteria. After a review of the study abstracts, 43 were deemed appropriate for full-text review. 25 articles were excluded and 18 articles representing 15 different studies were included in the systematic review. Reasons for exclusion included not reporting survival data (n=6), not reporting comparative data (n=6), not reporting on iron overload (n=4), having less than 25 subjects (n=2), focusing on patients who underwent hematopoietic stem cell transplant (n=6), and, in 1 case, a duplicate article reporting the same data. Conclusion: We reviewed the pathogenesis of iron disorders and molecular mechanisms with relevance to hepcidin. We also recapitulated the current progress on hepcidin modulation including siRNAs, antibodies, chemical compounds, and plant extracts. Therefore, hepcidin is suggested as a novel therapeutic strategy in the management of iron for patients with persistent blood transfusion thalassemia. Keywords: Iron monitoring, thalassemia patients, persistent blood transfusions, hepcidin.

Investigating the relationship between red blood cell sedimentation rate (ESR) and acute appendicitis in patients referred to affiliated hospitals of Abadan University of Medical Sciences in 2017 and 2018.

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نوع پذیرش: پوستر | کد مقاله: G-15280

Abstract: Background: Acute appendicitis is one of the most common surgical emergencies, which is primarily diagnosed based on the patient's history and physical examination. Inflammatory parameters (i.e., CRP, leukocytes, and lymphocytes) prevent half of unnecessary surgeries and lead to fewer negative appendectomies. Sometimes the WBC count can be normal, but an elevated WBC count helps confirm appendicitis. CRP measurement has been effective in confirming appendicitis in most studies. Materials and methods: This study was conducted in a cross-sectional and retrospective manner. The study population was all patients who underwent appendectomy with a clinical diagnosis of acute appendicitis in 2018. Before surgery, complete blood and ESR tests were requested for all patients. In this study, ESR is higher than expected considering age and gender, for women it is obtained from the formula of $age + 2 / 10$ and for men from the formula of $age / 2$. Results: The ESR level increases on average in all the examined people in 65% of the cases and in 35% of the cases the ESR level is negative. The prevalence of ESR is not significantly different between males and females. Conclusion: The statistical results showed that laboratory factors such as WBC and ESR can be used in better diagnosis of acute appendicitis along with clinical symptoms. Keywords:

Immune thrombotic thrombocytopenia caused by Covid-19 vaccine

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نوع پذیرش: پوستر | کد مقاله: G-01679

Abstract: Background: The common reported adverse effects of COVID-19 vaccination consist of the injection site's local reaction followed by several non-specific flu-like symptoms. However, recent reports of thrombosis with thrombocytopenia syndrome (TTS) associated with adenovirus vector vaccines have raised concern. Objective: This is narrative review to investigate TTS after the Covid-19 vaccine. Materials and Methods: Studies of TTP after ChAdOx1 nCoV-19 or Ad26.COV2 vaccine were searched in PubMed, Scopus, Embase and Web of Science databases until August 2022. Summary effects between studies were observed regarding incidence, presentation, site of thrombosis, diagnostic findings, and clinical outcomes. Results: TTS, also known as vaccine-induced immune thrombotic thrombocytopenia, is a reaction associated with exposure to the ChAdOx1 nCoV-19 and Ad26.COV2 vaccine, which may result in thrombocytopenia and thrombotic events. There are several case series of patients diagnosed with TTS, but the overall incidence is rare. TTS is characterized by exposure to one of the aforementioned vaccines 4–30 days prior to presentation, followed by thrombosis, mild-to-severe thrombocytopenia, and a positive platelet factor-4 (PF4)-heparin enzyme-linked immunosorbent assay (ELISA). Thrombosis typically involves atypical locations, including cerebral venous thrombosis and splanchnic vein thrombosis. Evaluation should include complete blood count, peripheral smear, D-dimer, fibrinogen, coagulation panel, renal and liver function, and electrolytes, as well as PF4-heparin ELISA if available. Consultation with hematology is recommended if suspected or confirmed. Treatment may include intravenous immunoglobulin and anticoagulation, while avoiding heparin based agents and platelet transfusion. Conclusion: Health care providers should be familiar with the clinical presentations, pathophysiology, diagnostic criteria, and management consideration of TTS. Early diagnosis and quick initiation of the treatment may help to provide patients with a more favorable outcome. Keywords: ITP, Covid-19, Vaccine, Immune system, Thrombocytopenia

The implementation of patient blood management in surgery

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نوع پذیرش: پوستر | کد مقاله: G-98762

Abstract: Introduction: Patient blood management (PBM) is defined as the application of evidence-based diagnostic, preventive and therapeutic approaches designed to maintain hemoglobin concentration, optimize hemostasis and minimize blood loss to improve patient outcomes. We propose a protocol for the assessment of the evidence of diagnostic, preventive, and therapeutic approaches for the management of relevant outcomes in surgery of patients to create a framework for PBM implementation. Methods: Search Medline databases (PubMed, EMBASE, Web of Science, and CINAHL) were searched from 2018 to 2020. Result: Forty-nine publications matching the selection criteria and reporting results in the predefined areas were included in the final analysis. Conclusion: progress in the identification and implementation of best transfusion practices based on evidence-based systematic reviews suggests that, compared with a liberal allogenic blood transfusion policy, there was no evidence of negative consequences when following a restrictive blood transfusion policy. As PBM is being increasingly introduced in routine clinical practice, there is wide expectation that it will shape the practice of transfusion medicine, the modality of prescription, preparation, and administration of blood components as well as the relationship between different disciplines. PBM brings a paradigm shift in the concept of blood components which should be considered not only an important resource but also a possible risk factor, with increases in costs, a sometimes-limited availability: risky, costly, in limited supply, and their use can worsen negative patient outcomes. PBM aims to overcome the 'product-centered' concept of blood components and to have a 'patient-centered' approach that focuses on improving the health and well-being of the patient. Keywords: patient blood management, blood transfusion, therapeutic, General Surgery

Detection of Chronic Myeloid Leukemia by Application of Microfluidic system

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نوع پذیرش: پوستر | کد مقاله: G-91638

Abstract: Background: The use of protein biomarkers is common in disease diagnosis, such as cancer and infectious disease. Microfluidic system is a technology for performing rapid, low cost, precise diagnose. Point of care testing (POCT) is simple medical testing that can be performed at the time and place of patient care. It allows to diagnose the disease faster than conventional lab based test and therefor, allows for better immediate clinical management. It seems that can apply microfluidics base POCT in leukemia detection. Methods: PubMed and google scholar databases searched based on the keywords related to the aim of this study. Results: The early diagnosis of leukemia is important because it can increase the recovery rate and prevent spread of the disease by metastasis. Chronic myeloid leukemia (CML) is a myeloproliferative neoplasm that associated with chromosomal translocation called Philadelphia chromosome. This abnormal fusion gene generates a P210 KD protein that is specific for CML detection. Microfluidic based POCT platform can be used as innovative procedure for detection of Philadelphia P210 KD protein in biological fluid. It need a low volume of sample and provide a quick, accurate and user friendly methods. A portable microfluidic system was designed for the POCT detection of Alpha-fetoprotein (AFP), carcinoembryonic antigen (CEA) and carcinoma antigen 125 (CA125) protein biomarkers simultaneously which was rapid and sensitive multiplex detection. With integrating microfluidics into POCT, fluid manipulation and detection can be accomplished in one device with minimal sample consumption. Conclusion: The low cost, high sensitivity, and high throughput of microfluidics make it potentially beneficial in cancer field. To perform conventional medical testing, specialized laboratory equipment and skilled lab technician are required. Furthermore, this technology could be used in undeveloped area for timely and cost effective diagnosis. Thus, application of microfluidics for point of care system could be used to detection of P210 BCR-ABL1 protein in CML diagnosis. Keywords:

Application of Aerogel in Cell Free Fetal DNA Analysis

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نوع پذیرش: پوستر | کد مقاله: G-67803

Abstract: Background: Noninvasive prenatal diagnosis (NIPD) is based on cell free fetal DNA (cffDNA) analysis which is used to determine the fetal gender, RH genotyping, identification of some inherited disorders and aneuploidies. While the NIPD has substantial advantages for fetal RHD genotyping, low level of CffDNA in maternal blood poses a challenge and the extraction method is important because a reliable detection requires enough cffdna. So, what measures lead to better cffDNA separation? The use of Porous-based material strategies can be useful for the optimal isolation of DNA. Material and Methods: Information is collected from articles published in Scholar and PubMed databases. Result: Alloimmunization against RhD antigen is the leading cause of hemolytic disease of newborns and a proper prenatal diagnosis is important since the disease can be fatal to the newborn. There is approximately 11-13% fetal DNA in maternal blood. cffDNA are smaller than maternal DNA with a majority being 300 bp. So, it can be distinguished by its size and this separation model increases the ratio of fetal to maternal DNA. As maternal plasma has a small amount of ccfDNA, the need for highly specific and efficient DNA purification techniques is of course critical. Aerogel is the least dense particle ever known with high surface area, high porosity, and uniform pore size that its pore size is adjustable and can be used to separate fetal DNA from maternal DNA based on size. DNA extraction by trapping DNA molecules in tiny pores can have positive effects on DNA extraction Conclusion: Early detection of RhD in a fetus with cffDNA testing allows for early management of at risk pregnancy and reduces the need for anti-D medications. Fetal DNA consists of only a small portion of cffDNA. Therefore, DNA purification technique is important. The use of aerogel pore size based separation helps to obtain optimal extraction and cause accurate and sensitive diagnosis. Keywords:

Investigating the callback rate due to covid-19 in blood donors in Bushehr transfusion organization during 2019-2022

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نوع پذیرش: پوستر | کد مقاله: G-53498

Abstract: Background: The health and adequacy of blood products is the main goal of all blood transfusion bases, and counseling before donating blood, performing screening tests, the possibility of confidential self-removal, as well as callback cases (donor withdrawal after donating blood) are all health promotion methods and production products. And therefore, a study entitled "Investigation of the callback rate caused by Covid-19 in blood donors in Bushehr transfusion organization during 2019-2022. Materials and Methods All blood transfusion callbacks in Bushehr province from 2019 to 2022 were investigated and individual information was extracted from blood transfusion information software (Nagare) and donors who had symptoms of Covid-19 were interviewed by phone and their condition was checked. And they were divided into 3 definite positive-doubtful-definite negative groups. Results Out of 95,441 blood transfusion donors in Bushehr province, 79 people have been called back, of which 46 of the reports were related to Covid. Most of their products have been withdrawn from the consumption cycle, and only 4 cases of RBC (8.70%), 13 cases of PLT (28.2 %), 1 case of FFP (2.17%) has been used in hospital. Also, based on a telephone interview with 46 people with symptoms of covid (19), 13% were definite positive, 34% were suspicious, and 52% were definite negative. Of this number of definite positive cases, no product has been used. Conclusion The number of callbacks due to cold symptoms increased from 2019 to 2022 compared to previous years, and the callback screening system prevented the distribution of 87% of blood products that had symptoms of covid after donating blood. Keywords: Covid 19, call back, Blood donor

Investigating the causes of exemption related to covid-19 in donors in Bushehr transfusion organization during 2019-2022

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نوع پذیرش: پوستر | کد مقاله: G-38745

Abstract: Background With the outbreak of acute respiratory disease in 2019 and considering the risks caused by this disease and the vital role of blood donation and the quality and health of blood products, a study was conducted by examining the causes of immunity related to Covid-19 in donors in Bushehr transfusion organization during 2019-2022. Materials and Methods: This retrospective cohort study was conducted from 2019 to 2022 on the callback cases of blood donors in Bushehr, which was collected from blood transfusion technical software (negare). With a telephone interview, cases of exemption due to Covid-19 were examined. Results: The number of blood donors in Bushehr province was 95,441 people, of which 79 people had callback cases. Out of this number, 46 people had symptoms caused by covid. Also, based on a telephone interview with 46 people with covid symptoms, 13% of positive cases were confirmed. 34% were suspicious, 52% were definite negative. And cases of immunity due to covid were in blood group A (39%), B (17%), AB (2.17%), and O (50%). Conclusion According to the callback system in blood transfusion, 78% of the spread of blood products due to covid immunity has been prevented. And the callback screening system has been effective in preventing the spread of Covid-19 during blood transfusion. Keywords: Covid 19, call back, Blood donor, Blood transition

Sterlite examination of the arm of blood donors in Bushehr transfusion organization in 2022

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نوع پذیرش: پوستر | کد مقاله: G-08357

Abstract: Background Disinfecting the skin in the blood collection area is one of the important steps to reduce microbial contamination in blood donation, and due to the importance of healthy blood and blood products, the optimal preparation method of Sterlite examination of the arm of blood donors in Bushehr transfusion organization in 2022. Materials and Methods During 6 months, 32 samples were taken daily using swab after sterilization with 2% Chlorhexidine and 70% Isopropyl disinfectant solution, sampling was done from the arm area and then in the Thioglycolate environment for one week in an incubator at 37 degrees Celsius. It was placed and if there is turbidity in the blood agar medium for 48 hours with three conditions of aerobic jar, anaerobic jar and CO2 jar. Results In this study, which was conducted with Chlorhexidine 2% and Isopropyl 70% disinfectant during 6 months with Thioglycolate Broth culture medium, no signs of the presence of microbes appeared and the cultures of all microbial samples were reported negative. Conclusion: The results of sterility quality control of donors' arms show the proper performance of sterilization and the desired quality of the disinfectant, and considering the importance of microbial transfer through blood, It is recommended to perform sterilization of donors' arms carefully. Keywords: Blood donor, Blood transition, Sterlite examination

Aerogel-Platform Engineered based on Panel of Anti-miRNAs as a diagnostic tool in laboratory

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نوع پذیرش: پوستر | کد مقاله: G-52864

Abstract: Background: Emerging evidence has suggested that circulating miRNAs can serve as invasive putative biomarkers for most type of cancers. On the other hand, a new generation of bio-based aerogels has been attracted much consideration research during the last years, especially in emerging areas associated biomedical sciences. Due to their unique properties, as well as ease of functionalization, a widespread range of applications has been proposed and developed for biopolymer aerogels. But how microRNA and Aerogels can have been connected? Methods: Information was collected based on keywords related to the purpose of this research from the study of articles on PubMed and Google Scholar sites. Results: The aerogel-based biopolymers are three-dimensional (3D) porous solid networks structure that have attracted much interest and represented as a promising class of biomaterials for various biomedical applications such as, due to their porosity, permeability, high surface area, biocompatibility, and biomimetic structures. Aerogels highlights their major applications in wound healing, bone regeneration, thermal insulation, drug delivery, and showing excellent coagulation. Besides, they can be used as photocatalysts, biosensor, supercapacitor, water treatment. And conversely, miRNAs, tiny regulators with fantastic functions, involves in pathogenies of many threatening diseases. But their measurement in laboratory has faced with serious problem. So how supposed to Aerogels become a building-up element for measuring of miRNAs? We endeavored completely to create a useful idea for this limitation. Based on the characteristics of photocatalysts of aerogels and interconnected porous structure, the photometric reaction can be designed with Anti -miRNA coated in pores that the specificity of the results reaches the optimal level. Conclusion: miRNAs have imitation in field of being biomarkers particularly due to their small size. Despite presence of the diagnostic kit for miRNAs, there are still problems such as optimal extraction, presence of dimers and confusing them with miRNAs, and etc. This is where aerogels can become a research hotspot in designing a diagnostic kit for miRNAs. Aerogels as high-performance biomaterial with adsorption capacity that have been regarded as a bridge connecting the nano and macro worlds. Keywords:

Novel treatment of TKIs as a better therapeutic supplement in ALL

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نوع پذیرش: پوستر | کد مقاله: G-08951

Abstract: Background: Philadelphia-chromosome positive acute lymphoblastic leukemia (Ph+ ALL) is the most common subtype of B-ALL in adults and its incidence increases with age. Fortunately, development of increasingly powerful tyrosine kinase inhibitors (TKIs) from the beginning of the 2000's dramatically improved the prognosis of Ph+ ALL patients with complete response rates above 90%, deep molecular responses and prolonged survival, altogether with good tolerance. TKIs became the keystone of Ph+ ALL management and their great efficacy led to develop reduced-intensity chemotherapy backbones. Subsequent introduction of blinatumomab allowed going further with development of chemo free strategies. Tyrosine kinase inhibitors (TKIs) have become an integral part of front-line therapy for Philadelphia chromosome-positive (Ph+) acute lymphoblastic leukemia (ALL). Ph+ ALL serves as the first model system for truly targeted treatment. Although the choice of the most effective TKI is not yet settled, the best results are shown with TKIs incorporated early, daily and continuously with chemotherapy. Current complete remission rates reach 90% and long-term survival rates attain 50–60%. The primary goal of treatment is the achievement of early deep molecular remission as the achievement of complete molecular remission (CMR) at 3 months has been demonstrated to be predictive of higher long-term survival. The probability of attaining this goal by a more potent TKIs like dasatinib or ponatinib is higher, thus we recommend the use of second- or third-generation TKIs over imatinib. If the past decade has witnessed the TKI revolution, the next will welcome a fine-tuning of TKI use, with the definition of rational decision algorithms taking into account biological and clinical prognostic/predictive factors, both at diagnosis and dynamically during the course of treatment. With improved genomic sequencing and the development of novel molecular, immunological and cellular therapy, we are now entering an exciting era of precision medicine for ALL. Replacing toxic chemotherapy with precisely targeted therapy promises to improve not only the cure rate of this disease, but also the quality of life of patients. In this review, we discuss a number of recently approved novel therapies for ALL, including new approaches with targeted tyrosine kinase inhibitors. This review also will focus on these amazing recent advances as well as novel therapeutic strategies in adult Ph+ ALL. Conclusion and Result: The advent of TKIs in the management of Ph+ ALL has dramatically improved the prognosis of patients. With the use of more potent TKIs like ponatinib in combination with chemotherapy in the frontline setting, the long-term OS is now reaching 80%, compared to as low as 10% in the pre-TKI era. In conclusion, outcome of Ph+ ALL patients dramatically improved over the past 20 years with the development of imatinib and subsequent 2G/3G-TKIs as well as monoclonal antibodies. Consistent efforts have been made to decrease toxicity to the point of chemo free strategies, allowing managing elderly/comorbid patients with clinical benefit. Keywords:

Free mitochondrial DNA as a new quality indicator in platelet concentrations

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نوع پذیرش: پوستر | کد مقاله: G-32074

Abstract: Background: Platelet concentrates are administered to prevent bleeding in cancer and stop bleeding in surgery and trauma. The quality of platelet concentrations has a primary effect on raising the recipient's platelet count and the incidence of complications after platelet transfusion. During the storage time of platelet concentration, platelets undergo structural, biochemical, and functional modifications called platelet storage lesions (PSLs). Platelet storage lesions decrease PC quality, which could lead to various complications. Free mitochondrial DNA in milieu of PCs stimulates the recipient's innate immune system and produces adverse transfusion reactions. Given that, free mitochondrial DNA could have predictive applications in PCs. In this study, we investigated the potential role of free mitochondrial DNA as a new quality indicator of platelet concentrations. Methods: The research was performed on PUBMED and Google Scholar databases between 2010 and 2022 using keywords such as: "Platelet concentration AND free mitochondrial DNA" and "Platelet concentration AND quality." Results: It was found that higher levels of free mitochondrial DNA in blood products were associated with higher adverse transfusion reactions. Conclusion: Free mitochondrial DNA in platelet concentrates is one of the predictors of adverse transfusion reactions. Therefore, investigating the mechanism which leads to free mitochondrial DNA release can help us to reduce adverse transfusion reactions and produce and transfuse higher quality PCs to recipients. Moreover, free mitochondrial DNA can be measured in PCs as a quality indicator. Keywords:

The contributory roles of the CXCL12/CXCR4/CXCR7 axis in normal and malignant hematopoiesis: A possible therapeutic target in hematologic malignancies

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نوع پذیرش: پوستر | کد مقاله: G-70592

Abstract: C-X-C motif chemokine 12 (CXCL12), also known as stromal cell-derived factor-1 (SDF-1), is produced by the bone marrow microenvironment. This chemokine binds and activates its cognate receptors C-X-C chemokine receptor type 4 (CXCR4) and C-X-C chemokine receptor type 7 (CXCR7) to widely regulate cell proliferation, survival, differentiation, as well as homing and mobilization of hematopoietic stem cells (HSCs) in specialized niches within the bone marrow. Given this key role in hematopoiesis, it comes as no surprise that any aberrancies in CXCL12/CXCR4 or CXCL12/CXCR7 pathways might lead to excessive proliferation of HSCs, an event that leads to the development of leukemia. So far, numerous therapeutic interventions have been developed to harness CXCL12/CXCR4 and CXCL12/CXCR7 axes in leukemic cells. Plerixafor, BKT140, LY2510924, PF-06747143, ulocuplumab, and NOX-A12 are among the most well-known CXCR4 and CXCL12 modulators that their therapeutic efficacies have been evaluated in different pre-clinical and clinical studies of hematologic malignancies. To have an overview of the importance of CXCL12/CXCR4 and CXCL12/CXCR7 axes in the pathogenesis of leukemia and to gather information about the latest advances as well as challenges in targeting these axes in clinical settings, the present review has begun with a discussion about how aberrant expression of CXCL12/CXCR4 and CXCL12/CXCR7 pathways might regulate leukemogenesis and ended by outlining the key news of preclinical and clinical investigations in leukemia treatment. **Keywords:**



CRISPR/Cas9, a promising approach for the treatment of β -thalassemia; A Systematic Review

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نوع پذیرش: پوستر | کد مقاله: G-54189

Abstract: The CRISPR/Cas9 techniques are easily programmable, fast, more powerful, and efficient at generating a mutation compared to previous gene therapy methods. β -thalassemia is the most common autosomal recessive disorder worldwide. Appropriate genomic changes in the β gene can be modified to alleviate the symptoms of the disease by using the CRISPR/Cas9 system. PubMed, Scopus, MEDLINE, Web of Science, and SID databases were searched in Persian and English from February 2000 to September 2022. Finally, 39 articles had inclusion criteria which were reviewed by two separate individuals. Among the reviewed articles, articles were divided into 3 categories. The first group increased the expression of hemoglobin F. The second group corrected the mutation causing β -thalassemia. The third group took the reduction of the alpha globin chain. Studies have shown that the genome of β -thalassemia patients can be modified using the CRISPR/Cas9 technique, and this approach might be promising for the treatment of β -thalassemia. Keywords:

The relationship between secreted frizzled related protein-1 methylation with complete remission and relapse in patients with Acute Myeloblastic Leukemia

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نوع پذیرش: پوستر | کد مقاله: G-69537

Abstract: Background: In recent years, epigenetic disorders including methylation of tumor suppressor genes like secreted frizzled related proteins (SFRPs) family genes have also been shown to play a role in Acute Myeloblastic Leukemia (AML) pathogenesis. This study assesses the relationship between SFRP-1 methylation with complete remission and relapse in patients with AML. Materials and Methods: Peripheral blood samples were drawn from 25 healthy individuals as negative control group and from 43 patients with newly diagnosed AML. Isolated DNA was treated with sodium bisulphite and analyzed by methylation-specific polymerase chain reaction. Statistical Package for the Social Sciences 21 was used for statistical analysis. Results: Six out of 43 people had a recurrence, among which two patients were attributed to methylated SFRP-1 gene. There is no any significant association between methylation of SFRP-1 gene and relapse of patients. Conclusion: We showed that there is no significant relationship between SFRP-1 gene methylation and complete remission and relapse of patients. Keywords:

The relationship between immunophenotypes of leukemic cells in Patients with AML with methylation of secreted frizzled related protein-1

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نوع پذیرش: پوستر | کد مقاله: G-10983

Abstract: Background: Acute myeloid leukemia (AML) is a clonal disorder of hematopoietic stem cells that is associated with the infiltration of blasts in the peripheral blood and bone marrow. In recent years, epigenetic disorders including methylation of secreted frizzled related proteins (SFRPs) family genes have also been shown to play a role in AML pathogenesis. This study assesses the relationship between SFRP-1 methylation with immunophenotypes of leukemic cells in patients with AML. Materials and Methods: Peripheral blood samples were drawn from 43 patients with newly diagnosed AML. The methylation status of SFRP-1 gene was examined using methylation-specific PCR technique. Statistical Package for the Social Sciences 21 was used for statistical analysis. Results: SFRP-1 methylation had significant association with CD34 (P = 0/045) and CD14 (P = 0/046) expression. While no other antigen expression showed association with SFRP-1 methylation Conclusion: We showed that SFRP-1 methylation is related with increased expression of CD34 and CD14 antigens. Keywords:

Evaluating the effect of cinnamon and rosuvastatin, on the formation of foam cells in macrophages co-cultured with platelets.

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نوع پذیرش: پوستر | کد مقاله: G-58412

Abstract: Background: Atherosclerosis is a progressive inflammatory disease caused by the deposition of lipids in the arterial endothelial cells. Various medications, including rosuvastatin, are recommended to treat atherosclerosis, on the other hand, Cinnamon extract has been shown to treat atherosclerosis by modulating macrophage activation. According to these properties, we evaluate the synergistic effect of cinnamon and rosuvastatin on the formation of foam cells in the macrophages derived from U937 cells. Materials and Methods: To investigate the toxicity of rosuvastatin and cinnamon, MTT assay was employed. The formation of foam cells was evaluated by Oil red O staining. Flow cytometry was employed to determine CD 163 marker. RQ-PCR was used to determine the expression level of the genes involved in cholesterol metabolism in foam cells. Data were analyzed using t-student and ANOVA tests. Results: Our findings indicated that the foam cells formation significantly decreased in the presence of rosuvastatin and cinnamon extraction. Expression of the CD163 on the foam cell surface was also increased during exposure to these two agents. The expression level of LXR and PPAR γ genes in foam cells in accompanied by platelet and ox-LDL was significantly increased (p0.01).but the expression of SRA was reduced. The expression of SRB1 and ACAT1 significantly increased (p0.01). But the expression of SRA was reduced. Conclusion: Both cinnamon and rosuvastatin could robustly induce M2 macrophages with anti-inflammatory properties and reduce foam cell formation, suggesting that the combination of two agents may treat atherosclerosis. Keywords: Rosuvastatin, Cinnamon, Platelet, Foam cell

Solubilization, Isolation and identification of Rhc antigen from donor erythrocyte membranes: an experimental study

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نوع پذیرش: پوستر | کد مقاله: G-58304

Abstract: Introduction: Rh blood group is one of the most complex human blood group systems, which plays a very important role in blood transfusion medicine. In this study, we tried to obtain Rhc antigen from the membrane of RhD negative red blood cells by maintaining the primary structure. Methods: In this experimental study, two methods were used for antigen purification. In the first method, RBCs are placed in a Lysis buffer that contains EDTA, Tris, Nonidet P-40 and protease inhibitor (phenylmethylsulfonyl fluoride (PMSF). This buffer breaks down the RBC membrane and releases the proteins. After 1h incubation, it was centrifuged at 14000 g for 15 min. Then the supernatant was separated and the precipitate was removed. The obtained solution was transferred into dialysis bags and dialyzed in the phosphate buffer for 24 h. Finally, the solubilized membrane proteins were stored at -30°C. In the second method, 50 ml of packed RBCs was frozen at -70°C. After 24 h, they were melted at room temperature. This process was repeated for three times. The broken RBCs were centrifuged at 1000 g for 10 min and the pellet was collected and washed. Consequently, the solubilization buffer including Nonidet P-40 and 0.2 mM PMSF were added to the pellet and placed on a shaker for several hours. Finally, after centrifugation, the supernatant solution was separated and the precipitate was discarded. Dialysis was done and the samples were passed through a 0.4 µL filter and stored at -30°C. Rhc antigen was purified by affinity chromatography and the eluted protein was concentrated by Corning concentrator tube. ELISA and SDS-PAGE methods were used to evaluate the purified antigens. Results: The results showed that both methods can be used for the membrane solubilization of RBCs. On the other hand, the results of ELISA method showed that the obtained antigens had the ability to react with the Rhc-specific antibody. In addition, SDS-PAGE results showed that the size of the antigen-related band was in the desired range. Conclusion: It seems that lysis buffer containing the non-ionic detergent of Nonidet P-40, can be suitable for the membrane solubilization of RBCs. Keyword: Rhc, Blood Group, Membrane Solubilization

Beneficial effects of blueberry against phenylhydrazine-induced anemia in mice

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نوع پذیرش: پوستر | کد مقاله: G-21453

Abstract: Background: Anemia is known as one of the most common blood disorder which affects billions of people in the worldwide. It has been known that current treatment strategies of anemia are with limitations and side effects. So, much attention has been paid to natural resources as complementary or alternative hematinic agents in recent years. In this regard, blueberry as highly rich source of bioactive phenolic compounds has been reported to have potent antioxidant effects. Present study aimed to examine the beneficial effects of blueberry on the phenylhydrazine-induced anemia in the experimental animals and its mechanism of action. Materials and Methods: Total 30 male albino mice (4-6 weeks old) were randomly divided into 3 groups: control, phenylhydrazine and blueberry groups. Animals in the blueberry group were orally received with 200 mg/kg body weight/day of blueberry for 14 days. Thereafter, phenylhydrazine was injected intraperitoneally (60 mg/kg body weight) to phenylhydrazine and blueberry groups. Blood samples were collected for hematologic tests and liver, kidney, intestine, bone marrow, and spleen samples were also collected. Iron homeostasis-related gene expressions has been checked by real-time PCR: hepcidin in liver, ferroportin in spleen and intestine. Results: Results showed that blueberry significantly increase in the number of reticulocytes, the erythroid progenitors, compared to that of in phenylhydrazine group. Simultaneously, plasma iron and Hb levels was significantly decreased in the blueberry group in comparison with the phenylhydrazine group. Additionally, mRNA expression of hepcidin in liver was significantly decreased whereas ferroportin expressions in spleen and intestine were significantly increased in the blueberry group. Conclusion: Present study suggests that blueberry treatment decreased hepcidin expression in liver and increased ferroportin expressions in the intestine and spleen. Therefore, blueberry may have beneficial role in anemia via regulating iron homeostasis and promoting erythroid differentiation. Keywords: Blueberry, Anemia, Phenylhydrazine

Platelet-Derived Microparticles in Leukemia

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نوع پذیرش: پوستر | کد مقاله: G-07195

Abstract: During cell activation, apoptosis, or injury platelets shed their membrane fragments in the form of microparticles. Platelet microparticles (PMPs) account for 70-90% of all circulating microparticles. These microparticles take part in the initiation and progression of thrombosis in different ways in hematological malignancies. Microparticles are being evaluated as therapeutic options for leukemia. PMPs can modulate cancer. PMPs lead to chemoresistance in acute myelogenous leukemia (AML). Daniel Cacic et al, co-incubated PMPs with THP-1 cells, and then PUMA proteins were measured before/ after treatment with daunorubicin (DNR), the results showed that PMPs led to downregulation of the pro-apoptotic PUMA protein. PMPs could reduce the activation of Caspase-8 and Caspase-9 by DNR. Thus, their results indicated that AML cells may be protected against apoptosis by PMP through the downregulation of PUMA that participates in the intrinsic apoptotic pathway. Dr. Yaftian et al, evaluated the reaction of isolated peripheral blood mononuclear cells (PBMCs) from whole blood of childhood B-precursor acute lymphoblastic leukemia patients (pre-B-ALL) in the face of PMPs. The results indicated that PMPs have induced apoptosis in PBMCs isolated from pre-B-ALL patients. Therapeutic application of PMPs in acute leukemia. Recently scientists showed that microparticles can be used as novel therapeutic vehicles for the delivery of drugs and RNA interference. Microparticles can overcome biological barriers such as the blood-brain barrier and they are poorly immunogenic as well. Daniel Cacic et al, used PMP as drug delivery vehicle. They incubated HL60 cell line with PMP-Doxorubicin, and the results showed greater toxicity by PMP-Dox compared to free Dox. PMPs as a biomarker in leukemia Shosaku Nomura et al, assessed 103 MM patients and evaluated PMPs in these patients. They showed that there was no significant difference in PMPs among patients and healthy control, there was no significant changes before and after treatment in the level of PMPs also patients who did not achieve complete response, had significantly higher percentages of PMPs. In addition, PMPs were positively associated with increased numbers of bony lesions. Conclusion and Perspectives In this review, we demonstrate the roles of PMPs in acute leukemia. However, with the limited number of studies on the role of PMPs in leukemia, it is essential to characterize PMPs as a biomarker in leukemia. Keywords:

Red cell distribution width as a differential parameter between iron deficiency anemia and α -thalassemia: an empirical approach

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نوع پذیرش: پوسنر | کد مقاله: G-19034

Abstract: Background: Iron deficiency anemia (IDA) and thalassemia minor are the most common hypochromic microcytic anemias in the world. Different formulas have been proposed to differentiate IDA from beta thalassemia minor. However, yet no formula has been proposed to differentiate IDA from alpha thalassemia minor, and Hb electrophoresis is not helpful in this hemoglobinopathy. Materials and Methods: an empirical approach. Results: Red cell distribution width (RDW) as indicator of changes in red blood cell size is primarily employed to differentiate IDA from other microcytic anemias. An empirical approach involving iron therapy over 1 month has shown that an increase in Hb concentration by 1 g/dL over this period is indicative of IDA, while no changes in Hb concentration are suggestive of alpha thalassemia. Conclusion: RDW measured after iron therapy in order to differentiate IDA and related disorders from alpha thalassemia is a better index than an increased reticulocyte count. Due to the high prevalence of IDA and costly and time-consuming nature of specific diagnostic tests, the RDW index is considered as a very sensitive and cost-effective tool in the differential diagnosis of IDA. Keywords:

Extramedullary hematopoiesis in β -thalassemia major patient: a case report and review of the literature

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نوع پذیرش: پوستر | کد مقاله: G-36175

Abstract: Background: Extramedullary hematopoiesis (EMH), as a compensatory phenomenon, refers to the blood cell formation outside of the bone marrow that occurs once the cells in the circulatory system fail to meet individuals' needs. EMH is rare in moderate to severe beta thalassemia because most symptomatic patients are effectively managed with transfusion. However, patients that fail to receive transfusions like β -thalassemia intermedia (β -TI) as indicated are at increased risk for developing EMH. Case Presentation: This paper describes the case of a 15-year-old female adolescent with β -thalassemia major (β -TM), suffering from a rare form of EMH affecting the sinus cavities, characterized by headache, sinusitis, and nasal obstruction, as confirmed by physical-pathological examinations and computerized tomography (CT) scan findings. The EMH in this patient could be significantly attributed to the lack of regular blood transfusions in recent years. Conclusion: It was concluded that β -TM along with the occurrence of EMH in the sinus cavities had led to a complex case, carrying a heavy burden of the disease for the patient. Keywords:

RED BLOOD CELL ALLOIMMUNIZATION IN IRANIAN PREGNANT WOMEN

مهرداد گل محمدی، دکتر ارزو اوودی، فرناز مارالی، محرم احمد نژاد ©¹

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نوع پذیرش: پوستر | کد مقاله: G-70213

Abstract: Background: Hemolytic Diseases of the Fetus or New born (HDFN) is considered as one of the life threatening diseases for fetus and infants. This disorder is due to the cross of maternal alloantibodies through placenta which causes hemolysis, hyperbilirubinemia and in some cases kernicterus. In this study the prevalence of specific alloantibodies in Iranian pregnant women was evaluated. Aims: Determination the prevalence of significant and insignificant RBC alloantibodies among pregnant women in Iran. Methods: A retrospective study was conducted to characterize the prevalence of unexpected clinically significant and insignificant alloantibodies in pregnant females who were referred to immunohematology reference laboratory of Iran between 30 March 2018 and 31 December 2021. Data were obtained from 570 sera positive pregnant women, which included results of antibody screens and antibody identification. Results: Data of 570 pregnant women with positive antibody screening results were analyzed to calculate the frequency of unexpected alloantibodies. The most frequent identified significant alloantibody was anti-D 225(39.7%), followed by anti-E 58(10.1%) and anti-C 39(6.8%). The frequency of anti-Kell and anti-M was equal at 23(4%). The next most frequent antibody was anti-P with 14 (2.42%). 7 (1.22%) out of 570 patients had anti-Leb, this was followed by anti-jka with 4(0.7%). The frequency of anti-jkb, anti-Fyb, anti-S and anti-e was equal at 2 (0.35%). Only 1 (0.17%) out of 570 patients had anti-Lea as well as anti-Fya and anti-I in their blood samples. 166 (29.15%) of 570 patients had only clinically insignificant red cell alloantibodies, including 80 females with RhIG induced anti-D and 84 women with nonspecific cold antibody. 378 (66.3%) out of 570 sera positive women, with 8 different specificities, had at least one antibody known to cause HDFN. 50 (8.7%) of the patient had multiple antibody specificities. A breakdown of those antibodies is showed in table 1. Antibody No. D+C 23 c+jkb 1 D+C+E 4 c+jka 1 D+E 3 E+c+jkb 1 c+E 2 D+Kell 1 D+C+Kell 1 D+C+jka 2 E+Leb 1 Fya+jkb 1 Kell+Fyb 1 D+C+M 2 D+S 2 c+E+Kell 1 Kell+Kpa 1 E+Kell 2 Table 1 Summary / Conclusions: Detection of various clinically significant and insignificant alloantibodies in Iranian pregnant women, were shown that red blood cell alloimmunization is still remained as a major complication in pregnancy. It is suggested that antibody screening and identification should be carried out during pregnancy to prevent the fatal complications of HDFN. Keywords:

Evaluation of novel treatments for advanced and relapsed/refractory Hodgkin lymphoma

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نوع پذیرش: پوستر | کد مقاله: G-02859

Abstract: Background: Most patients with Hodgkin lymphoma (HL) are cured with initial therapy, but 10% to 15% of patients with early-stage disease and 15% to 30% of patients advanced disease suffer from relapsed or refractory disease. Recent breakthroughs in understanding the mechanisms of oncogenicity, interactions within the tumor microenvironment and identifying various factors of tumor recurrence and their impact on disease recurrence, have resulted in development of novel therapies of patients with HL. However, still an unmet need there is in those with advanced and relapsed/refractory Hodgkin lymphoma and in this review, we intend an overview of new and developing agents. Materials and Methods: Our basic research first was in Google Scholar and PubMed databases. Then advancedly searched in Blood, Leukemia and Lymphoma, Journal of Hematology & Oncology and American Journal of Hematology journals by related key words such as "Hodgkin Lymphoma", "Novel Treatment", "Relapse", "refractory" from 2015 to 2023. After overview, 262 related results were found that 20 its articles were analyzed (compatible with the Inclusion and exclusion criteria). Results: Brentuximab vedotin (BV) has been developed for the treatment of newly diagnosed classical HL, relapsed/refractory HL or consolidation after autologous stem cell transplantation (ASCT). Notably, BV treatment combined with doxorubicin, vinblastine, and dacarbazine treatment has been established as standard treatment for newly diagnosed advanced-stage. Also BV and the checkpoint inhibitors nivolumab and pembrolizumab are very effective with limited side effects and after ASCT is beneficial in patients at high risk for relapse. Other studies showed in patients who have relapsed after ASCT or are refractory to first-line therapy, salvage treatment has incorporated brentuximab vedotin or PD-1 checkpoint inhibitors to improve response rates of cytotoxic chemotherapy thereby improving the probability of a successful ASCT. Conclusion: Additionally, promising new therapeutics are emerging are currently the treatment landscape for this challenging patient population, Such as CD25-directed ADC therapy and CD30-directed chimeric antigen receptor T cells. Keywords: Hodgkin Lymphoma; Novel Treatment; Relapse; refractory

The effect of royal jelly on BAX and BCL-2 apoptosis proteins in different tissues of male rats

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نوع پذیرش: پوستر | کد مقاله: G-94276

Abstract: Background: Nowadays, much attention is paid to the use of natural and biological therapies. Royal jelly (RJ), secreted from the mandible and pharyngeal glands of worker bees, has been widely used as a dietary supplement. It has a broad range of pharmaceutical activities, including antioxidant, antiaging, anti-tumor, and antiapoptotic. The aim of the current study was to investigate RJ impacts on the cell survival by measuring the amount of protein BCL2 and BAX on different tissues of rats. Methods: In this study 21 male Wistar rats were experimented. The animals were randomly divided into 3 groups consisting of 7 rats as follow: Group 1 was the control group who were administered distilled water for 30 days. Group 2 was treated with royal jelly at a concentration of 150 mg/kg for 30 days and group 3 was treated with RJ at a concentration of 300 mg/kg for the same duration. The contents of Bax and BCL-2 in the tissues Brain, Liver, Kidney, and lymphocytes were measured using ELISA method. Moreover, the Bradford method was used in order to measure the concentration of total protein of the tissues based on the standard protocols. Results: Although BAX and BCL-2 proteins showed irregular patterns, the ratio of BAX/BCL-2 declined in almost all the studied tissues with a significant decline in the rats' Liver and Kidney treated with RJ at the dose of 300 mg/kg and in the lymphocytes of the group administered 150 mg/kg of RJ. Conclusion: RJ appears to have potential anti-apoptotic effects on the rats' tissues studied via regulating the levels of BAX and BCL-2 proteins. With regard to the ratio of BAX/BCL-2, it is sensible to conclude that RJ tends to positively impact the cell survival rate at the dose of 300 mg/kg in Brain, Liver, and Kidney. Nonetheless, this ratio decreased more significantly at the dose of 150 mg/kg in lymphocytes, showing more potential to survive Brain cells in this concentration. Key words: Apoptosis, BAX, BCL2 and Royal jelly

Evaluation of the Relationship between Maternal ABO Antibodies and Red Blood Cell Indices of Cord Blood Unit during 2019-2020 in Gonabad, Iran

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نوع پذیرش: پوستر | کد مقاله: G-64015

Abstract: Background: Hemolytic disease of the newborns (HDN) can be due to fetomaternal blood group incompatibility and might be associated with neonatal jaundice and kernicterus. Predicting the risk for severe HDN is crucial. The aim of this study was to assess the relationship between maternal anti ABO antibodies titers and cord blood complete blood count (CBC) indices. Materials and methods: This cross-sectional study was conducted on all mothers with negative indirect coombs test who were admitted for delivery in a university hospital in Gonabad, Iran during 2019-2020. Data including maternal age, gravid, and gestational age were recorded. Serum anti ABO antibody and blood group was assessed in all mothers and neonatal cord blood CBC indices, including hemoglobin, hematocrit, red cell distribution width (RDW), red blood cell (RBC) count and mean corpuscular volume (MCV) were recorded. Results: A total of 424 cases with mean maternal age of 28.88 ± 6.00 years were included in this study. Most common maternal and neonatal blood groups were O (34.4%) and B (35.1%), respectively. Anti ABO antibody titers above 1:64 was observed in 21% of the mothers. There was a significant difference in MCV, RDW and RBC between neonates with non-O blood group who were born from mothers with O blood group and other groups ($p < 0.05$). No correlation was observed between maternal characteristics and maternal anti ABO antibody titers and between cord blood CBC indices and maternal characteristics. Conclusions: This study showed that some cord blood CBC indices were related to maternal and neonatal blood groups. Keywords: ABO antibody; red blood cell indices; cord blood

Evaluation of the Causes of Mild Gestational Thrombocytopenia and its Relationship with Blood Groups and Rh in Pregnant Women in 2018, Gonabad, Iran

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نوع پذیرش: پوستر | کد مقاله: G-27698

Abstract: Background: Thrombocytopenia is common disorder in pregnancy that may affect the outcome of pregnancy. The aim of this study was to assess the causes of mild thrombocytopenia in pregnancy and its relationship with blood group and Rh in pregnant women of Gonabad Municipality in 2017. Materials and methods: This analytic cross-sectional study was conducted on 480 pregnant women referred to Allameh Behloul Hospital in Gonabad in 2017. The data including age, cause of thrombocytopenia, blood group, Rh, place of residence, parity and gestational age at labor were recorded from patient files. Data were analyzed by SPSS software. Results: Out of the 480 cases studied, 38 (7.9%) had thrombocytopenia. Gestational thrombocytopenia was the most common cause of thrombocytopenia (33, 86.8%) followed by idiopathic thrombocytopenic purpura (ITP) (3, 7.9%) and gestational hypertension (2, 5.3%). There was no significant relationship between cause of thrombocytopenia and blood groups ($P = 0.504$) and Rh ($P = 0.279$). There was no significant relationship between blood groups and RH and presence of thrombocytopenia ($p=0.701$ and $p=0.316$, respectively). Conclusions: Gestational thrombocytopenia was the most common cause of thrombocytopenia in our study. No significant relationship was observed neither between thrombocytopenia and blood groups and Rh nor between causes of thrombocytopenia and these parameters. Keywords: thrombocytopenia; blood groups; gestational thrombocytopenia; pregnancy

The effect of riboflavin/ultraviolet light on pathogen reduction in human platelet lysate and its function as a cell culture supplement

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Abstract: Background: Due to the increasing use of platelet lysates (hPL) as a cell culture supplement and the importance of pathogen inactivation (PI) for biologically sourced products, finding an effective PI process for hPL that increases the product safety and maintains its efficacy as a cell culture supplement is essential. Aims: The main objective is to introduce an effective PI process for pathogen-free hPL production with optimal efficiency in the manufacturing of cell therapy products. Methods: hPL was prepared by repeated freeze-thaw cycle using expired Platelets. The ability of riboflavin/ultraviolet (RB / UV) radiation to inactivate a group of viruses (HSV, VSV, and Polio) and bacteria (E. coli and S. aureus) in the infected batches of hPL were evaluated. The in vitro function of PI-hPL was assessed in the process of growth, colony formation, immunophenotype, and differentiation capacity of human placenta-derived mesenchymal stem cells (PLMSCs). Conclusion: Photochemical treatment with RB and UV light was an effective PI process in all groups. It also did not show any adverse effect on the PLMSCs' growth, proliferation rate, colony formation, immunophenotype, and their differentiation capacity. To increase the safety of cell therapy products, this PI method can be used for hPL manufacturing. However, further optimization of this method is necessary to deal with in vivo situations. Keywords: Cell therapy, Pathogen inactivation, Platelet lysis, Riboflavin, Ultraviolet radiation

The Efficacy of ATRA and ATO in combination with chemotherapy in Acute Promyelocytic Leukemia

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Abstract: Background: Acute promyelocytic leukemia (APL) a subtype of Acute Myeloid Leukemia accounts that 10-15% of newly diagnosed. APL is characterized by T(15;17) and obstructs the differentiation of granulocyte cells. APL Patients often experience fatal bleeding due to disseminated intravascular coagulation and the release of high levels of pro-coagulation factor from APL granules. Even though the ATRA monotherapy with a response rate of more than 90% is used as the fastest drug regimen to control APL, but due to the short duration of response to this drug (about 3 to 6 months); it's necessary to the combined treatment regimens with chemotherapy. Our aim, investigation effect of the combination of ATRA and ATO with Chemotherapy on complete remission in acute promyelocytic leukemia. Methods: In the research was based on PubMed and Google Scholar databases by related key words from 2015 to 2022. Key words were such as: Acute Myeloid Leukemia, Acute promyelocytic leukemia, ATRA and Chemotherapy. According to advanced search with the mentioned keywords, 1471 articles were obtained. Eventually, 50 articles were evaluated based on criteria such as the statistical population, their journal and article type. Results: Based on the clinical trials studies, were conducted several groups were studied to evaluate the performance of therapeutic combinations. Two target groups were selected for the combination of chemotherapy and ATRA; which were suggested for chemotherapy and ATRA drug regimens sequentially {complete remission (CR):95%, 2-year disease-free survival (EFS):77%, overall survival (OS):81%} and chemotherapy and ATRA simultaneously {CR:94% , EFS:84%, OS:84%}. In other studies, for the effectiveness of the drug combinations with ATO, three groups were subjected to clinical trials. the combined regimen of intravenous ATO and ATRA for the first group{CR:88%}, the intravenous ATO and ATRA and GO or IDA regimen for the second group{CR:88%}, and the combination of ATRA and oral ATO(60mg/kg/day) for the third group{CR:99% , 3-year disease-free survival (DFS):98% , OS:99%} have been presented as effective treatments for APL. Conclusion: The results obtained from the studies that the simultaneous administration of chemotherapy and ATRA and the combined treatment of ATRA with oral ATO significantly showed complete survival with less recurrence of the disease. However, more studies are needed in this field for a detailed investigation of the effect of the proposed drug regimens on APL control and the discovery of new therapeutic compounds with better performance. Keywords: Acute Myeloid Leukemia, Acute promyelocytic leukemia, ATRA and Chemotherapy.

The Role of Extracellular vesicles in Complications of Thalassemia patients

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نوع پذیرش: پوستر | کد مقاله: G-03241

Abstract: Background: Thalassemia is the most common monogenic disorder of red blood cells caused by defects in the synthesis of globin chains. Thalassemia phenotypes have a wide spectrum of clinical manifestations and vary from severe anemia requiring regular blood transfusions to clinically asymptomatic states. Common complications in thalassemia patients include iron overload, thrombosis, cardiac morbidity, vascular dysfunction, inflammation, and organ dysfunction. Extracellular vesicles (EVs) are small membrane vesicles that are released from the plasma membrane of various types of cells. EVs are classified into subgroups based on size: exosomes, microparticles (MPs), and apoptotic bodies, and play a role in cell signaling pathways and intercellular communication. In this study, the effect of EVs on the complications that occur in patients with thalassemia is reviewed for the first time. Methods: This review article is a study of PubMed content from 1980 to 2022. The keywords used in this search were "Extracellular vesicles", "Cell-derived microparticles", "Exosomes", "Thalassemia" and "Complications". Results: EVs, especially red cell-derived MPs and platelet-derived MPs, can increase the risk of thrombotic events in patients with thalassemia through their effect on the induction of the coagulation cascade and increasing thrombin generation. It is possible that EVs, due to their role in the delivery of lactoferrin and transferrin to mammalian cells and ferritin-carrying exosomes may aggravate iron overload in patients with thalassemia. The increase of EVs-HSP70 (heat-shock protein 70) levels with a significant increase in ineffective erythropoiesis markers. It seems that EVs induce endothelial cells (ECs) dysfunction and increase the level of inflammatory cytokines through different mechanisms such as neutrophil migration, leukocyte-leukocyte interactions, activation of NF- κ B and JNK pathways, increased expression of E-selectin, P-selectin and adhesion molecules. Therefore they may play a role in increasing the severity of complications in thalassemia patients, especially cardiovascular complications and inflammatory responses. It has been determined that EVs increase apoptotic cells and caspase 3/7 activity and decrease cell viability in endothelial, hepatic, and pancreatic cells. These mechanisms are involved in the induction of organ dysfunction. Conclusion: In this study, it was found that EVs through different mechanisms can lead to the occurrence and aggravation of complications in thalassemia patients, including thrombotic events, iron overload, ineffective erythropoiesis, inflammation, vascular complications, cardiovascular diseases, and organ dysfunction. Therefore, EVs may play a role as biomarkers in monitoring the severity of complications of thalassemia patients. Keywords: Extracellular vesicles, Cell-derived microparticles, Exosomes, Thalassemia, Complications.

The role of exosomes in leukemia

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نوع پذیرش: پوستر | کد مقاله: G-82103

Abstract: Blood malignancies are one of the most challenging cancers in the terms of heavy treatment and high mortality. The factors and mechanisms involved in the occurrence of these diseases are very diverse and wide. The discussion of exosomes for helping to diagnosis and treatment of them has received much attention in recent years. Exosomes are secreted by most cells in different conditions and they are present in the biological fluids of body. The contents of them are very similar to the mother cells. So with these nanoparticles, the rapid progression of the malignant cells can be justified. The presence of anti-apoptotic proteins, various microRNAs, heat shock proteins, oncogenes, metastatic, resistance to chemotherapy agents has been proven in exosomes derived from malignant cells that can be involved in development of inflammatory phenotype of target cells in tumor microenvironment. For example, the presence of FMS-like tyrosine kinase 3 (FLT3), Nucleophosmin 1 (NPM 1), Insulin-like growth factor 1 receptor (IGF-1R) and Matrix metalloproteinase 9 (MMP9) has reported in exosomes derived from AML cells. On the other hand, using of exosomes will probably be very helpful in the treatment of different cancers. **Keywords:**

Are NETosis inhibitors useful for treating DIC?

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Abstract: Background: DIC (disseminated intravascular coagulation) is an unusual but very serious condition that result in abnormal blood clotting throughout a patient's body. A new mechanism for DIC pathogenesis has been identified - neutrophil extracellular traps (NETs). NETs play a key role in the interaction between inflammation, immunity, and thrombosis. The NET consists of histone proteins, DNA and other antibacterial proteins released by activated neutrophils that contribute to several pathological states. Materials and Methods: Relevant literature was identified by a PubMed search (2012-2022) of English language papers using the terms “: NETosis,” “Disseminated intravascular coagulation”, and “NETosis inhibitors”. Results: Several NET-associated diseases, including DIC, can be effectively treated with NET inhibitors, although patients should be monitored for recurrent infections, particularly those with compromised immune systems. Therefore, NET inhibitor drug formulations or enzymes with minimal side effects can be useful. Conclusions: This review demonstrated the presence of NETs early in the course of DIC, which may contribute to excessive and unbalanced thrombin generation. As a result, NETs may provide a diagnostic advantage in DIC detection and, eventually, an inhibitor of NETosis may offer therapeutic benefits for thrombosis inhibition. Key words: NETosis; DIC; Disseminated intravascular coagulation

Inhibitor development in patients with type 3 Von Willebrand disease, a comprehensive study on 99 Iranian patients

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Abstract: Background: Type 3 von Willebrand disease (VWD) is the most severe type of VWD affects one per 2-3 million individuals. Although on-demand therapy is the treatment of choice, primary or secondary prophylaxis could be considered for those at high risk of severe bleeding. Alloantibody formation is a rare but serious complication of replacement therapy that can be accompanied with anaphylaxis reaction following re-injection of factor concentrate. Methods: A total of 99 patients were included in the study based on the number of VWF/factor VIII concentrate injection and precise laboratory diagnosis by factor VIII coagulant activity (FVIII: C), VWF antigen (VWF: Ag), and VWF: ristocetin cofactor assay (VWF: RCo). VWF and FVIII inhibitor titers were determined by a modified Nijmegen–Bethesda assay Results: Of 99 patients, 19 (~19.5 %) were positive for inhibitor against von Willebrand factor (VWF), most high-titer (n: 10, 58%) responders. The mean age at the detection of inhibitor was 3.7 years old, and the mean time between the start of replacement therapy and inhibitor formation was 21 years. Of 19 patients 3 were successfully managed by prophylaxis regimen with Haemate®, AryoSeven™, and FEIBA® while the majority didn't respond to treatment. The inhibitor formation was exacerbated clinical presentations in the study population, and hemarthrosis was observed in 41% of patients after inhibitor development, while before inhibitor development this phenomenon was observed only in 1 patient. Conclusions: Inhibitor formation is a relatively common complication in Iranian patients with type 3 VWD that can significantly exacerbate the clinical presentations. Early detection of major risk factors of inhibitor formation should be considered as a preventative program. Keywords: von Willebrand disease, inhibitor, Alloantibody, Type 3 von Willebrand disease

Evaluation of procoagulant platelet microparticles in Covid-19 patients with disseminated intravascular coagulopathy

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Abstract: Background: The discovery of new biomarkers in critically ill patients with Covid-19 can play an important role in the diagnosis, prognosis or even treatment of this disease. In the current study, the level of platelet derived MPs (PMPs) as coagulant new-biomarker was evaluated in patients with Covid-19 who suffered from DIC. Material and Methods: In this case-control study, 93 patients with Covid-19 and 25 healthy individuals were sampled after obtaining written consent. Determination and counting of MPs using CD61 and Annexin-V conjugated markers and the coagulation activity of MPs was also determined based on ELISA-based procoagulation activity assay. The hemostasis status of the patients was evaluated by prothrombin time (PT) and relative thromboplastin time (PTT) tests. In order to evaluate the fibrinolytic system, D-Dimer level was also measured. Complete blood count (CBC) evaluation was also done using Sysmax hematology analyzer. Results: In the examination of coagulation indices, it was shown that there is a statistically significant difference in the amount of PT, PTT, fibrinogen, D-Dimer between patients and healthy subjects ($p < 0.01$). Flow cytometry results showed that most MPs originate from the type of platelets (CD61) and their levels in the non-surviving patients group were significantly higher than the surviving patients ($p < 0.001$) and the control group ($p < 0.001$). Also, the procoagulation activity of MPs in the group of non-surviving patients was significantly higher than that of surviving patients ($p < 0.001$), and the control group ($p < 0.001$) and was correlated with the number of Annexin V+ MPs ($p < 0.001$). Conclusion: The function of coagulation system in patients with Covid-19 is significantly increased compared to healthy volunteers. The measurement of coagulation variables can be helpful in determining the prognosis of critically ill patients with Covid-19. Key words: Covid-19, Coagulation, Microparticles

Evaluation of circulating microparticles pattern in B-thalassemia patients with Covid-19

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Abstract: Background: Cell derived microparticles (MPs) are membrane derived vesicles that have key roles in inflammation, coagulation, and vascular function. Thalassemia is one of the most common single gene disorders in the world that causes anemia. On the other hand, there is very little information about the 2019 coronavirus disease in patients with thalassemia. This study was conducted with the aim of determining the pattern of MPs in beta thalassemic patients with confirmed Covid-19 infection. Material and Methods: In this forward and retrospective cohort study, 19 beta-thalassemic patients with Covid-19, 20 thalassemic patients who were not infected with Covid, and 20 healthy individuals were sampled after obtaining written consent. Evaluation of complete blood count (CBC), biochemical parameters, as well as the total number of microparticles, procoagulant MPs, and the types derived from platelet, erythrocyte, and leukocyte were determined by flow cytometry. Results: The mean age of thalassemic patients with Covid-19 was 27.1 years and in the thalassemic patients without Covid-19, and healthy subjects were 29.1, and 30 years, respectively. There was a statistically significant differences in the CBC parameters, Retic count, frequency of NRBC, as well as Leukocyte and platelet count between patients with Covid-19 and normal volunteers. Based on the flowcytometry results, the majority of MPs originate from platelets (CD61+). All MPs were significantly increased in thalassemic patients with Covid-19 compared to those with thalassemia and healthy groups. Conclusion: Changes in blood factors and MPs in thalassemic patients with covid-19 are significant. Therefore, measuring these variables can be helpful in determining the prognosis of thalassemic patients with Covid-19. Keywords: Covid-19, Microparticle, Thalassemia

Studying of emerging immunotherapies in Acute Myeloblastic Leukemia with poor prognosis

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Abstract: Background: Acute myeloblastic leukemia (AML) leads to the production and proliferation of abnormal blast cells from the bone marrow (BM) and is an aggressive and heterogene disease, poor prognosis due to various genetic alterations and abnormalities that complicate approaches to treatment. Immunotherapy has become a powerful clinical strategy for treating cancer. Advances in immunotherapy employ monoclonal and bispecific antibodies, chimeric antigen receptor (CAR) T cells, immune checkpoint inhibitors (ICIs) and vaccines provide an alternative pathway for AML treatment. In this Review, we present current evidence of immunotherapeutic in AML with poor prognosis. Materials and Methods: Our study was based on Pubmed and Google Scholar databases by related key words such as: Acute Myeloblastic leukemia, Immunotherapy, AML and targeted therapy from December 2015 to 2022. After advanced search, 480 results were found which 12 articles were compatible with the Inclusion criteria were analyzed. Results: Recent studies have suggested the potential clinical benefits of immunotherapy against AML such as targeting CD33, CD123, and CLL-1, also immune checkpoint inhibitors (anti PD-1 and anti CTLA4 antibodies) with or without conventional chemotherapy. Early-phase clinical trials of CAR-T or NK cells for relapsed/refractory (poor prognosis) AML exhibited complete remission (CR) or marked reduction of BM blasts in a few enrolled patients. Bi-/tri-specific antibodies (bispecific T-cell engager and dual-affinity retargeting) showed 11–67% CR rates with 13–78% risk of cytokine releasing syndrome. Conventional chemotherapy in combination with anti-PD-1/anti-CTLA4 antibody for poor prognosis AML showed 10–36% CR rates with 7–24 month-long median survival. As well as other study showed that gilteritinib and CUDC-907 (a dual inhibitor of PI3K and histone deacetylases) synergistically induce apoptosis in FLT3-ITD AML cell lines and primary patient samples and have striking in vivo efficacy. Conclusion: There is no doubt that the landscape of treating AML is becoming more and more complex. However further advances and clinical applications of immunotherapy for AML are awaited. Also, should be better investigated other emerging treatment methods besides immunotherapy, such as stem cell therapy, exosome and microvesicles derived from mesenchymal stem cells and even gene therapy. Keywords: Acute Myeloblastic leukemia, Immunotherapy, AML and targeted therapy

Gene Editing-based technologies in Beta thalassemia

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Abstract: Background: It is estimated that 1.5% of the global population and 2 to 3 million of people in Iran are the carriers of a hereditary blood disorder called beta thalassemia. Since these patients face irreparable complications, gene editing-based technologies are considered. This approach can be conducted by some genetic modifications in Hematopoietic stem cells (HSCs) with CRISPR/Cas9 system, Prime editing, Base editors, Zinc finger nucleases (ZFNs) and transcription activator-like effector nucleases (TALENs). This study aims to investigate and compare the various types of gene editing-based technologies. Methods: A total of 30 studies related to gene therapy and β -thalassemia published from January 2021 till September 2022 was conducted using MEDLINE and SCOPUS. Results: Most studies were focused on the naturally occurring hereditary persistence of fetal hemoglobin (HPFH) by reactivation of fetal γ -globin by reduction of the BCL11A gene expression or by modification of β -globin genes in HSCs by CRISPR/Cas9 system and ZFNs. CRISPR/Cas9, a natural system in bacteria, recognizes the sequence adjacent to PAMs by single guide RNA (sgRNA) and uses Cas9 as an endonuclease. Although some pre-clinical studies reported various off-target mutations but this system is simple for design even for multiple gene editing and it has low cytotoxicity along with high specificity and efficiency. Another type of gene editing tools, prime editing, consists of two components, impaired Cas9 endonuclease fused to a engineered reverse transcriptase and a prime-editing guide RNA (pegRNA). This system has multiple editing capabilities, such as: single base editing, insertion and deletion of multiple bases. Some studies reported potential indels mutation and immunogenicity of this editing tool. Base editors use sgRNA to find the target adjacent to PAMs. Most studies reported this system as a single base editor without double strand break (DSB) and off-target mutations. ZFNs utilize zinc finger proteins to find the target sequence and Fok I endonucleases for cleavage. Since ZFNs have the large range of recognitions site, many off target mutations have been reported. ST-400 as a developed ZFN regulating fetal to adult hemoglobin switch is used in different clinical trials. TALENs use TALE for the recognition of the target site and Fok I endonucleases for the cleavage. This system is easy to design while it is very expensive. Most articles demonstrated that ZFNs and TALENs edit many loci in multiple cell types while TALENs have less cytotoxicity. Conclusion: Although gene therapy has some limitations such as design difficulties and also potential risks like off-target mutations, but gene therapy can be a revolution for definitive treatment of children with β -thalassemia all over the world. Keywords: Gene therapy, β -thalassemia, CRISPR, ZFNs, TALENs

Valuation the effect of mesenchymal stem cell derived exosomes on male infertile as a novel treatment

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نوع پذیرش: پوستر | کد مقاله: G-63049

Abstract: Background: Infertility is now discussed to be a global health issue affecting about 15% of couples worldwide and It may arise from agents relevant to the male (30%), including varicocele, undescended testes, testicular cancer, and azoospermia. The novel experimental methods of the infertility treatment are stem cell and exosome applications. Because of the limitations using live cells injections and also the therapeutic effect of their paracrine substances, Mesenchymal Stem Cells derived exosomes (MSC-EXO) containing bioactive molecules have been recently used in studies of infertility treatment. In this review, we evaluate the effect of MSC-EXO on male infertile as a novel therapy. Materials and Methods: Our study was based on PUBMED, GOOGLESCHOLAR and SCOPUS databases by related key words such as: “exosome”, “Mesenchymal Stem Cell”, “male Infertility” and “treatment” from 2015 to 2022. After advanced search, we found 104 results in these databases res which 15 articles were compatible with the inclusion and exclusion criteria were analyzed. Results: MSC-EXO exhibit regenerative, anti-apoptotic, anti inflammatory and anti-hypoxic characteristics. They can induce cell proliferation, cell viability, migration, oogenesis, spermatogenesis, capacitation and acrosome reaction. Studies results have shown the MSC-EXO ability to regenerate the damaged sperm, treating asthenozoospermia by their repairing molecules and counteracting with the reactive oxygen species. Also, it has been reported that MSC-EXO are able to induce the process of spermatogenesis in the testes of infertile animal models. Conclusion: Male infertility is very complicated pathogenically and there is no ideal method for its treatment. These findings indicate that may be exosomes secreted by mesenchymal stem cells helpful in the novel treatments of male infertility. Keywords:

Association between HbS and RBC index and WBC in sickle cell disease.

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نوع پذیرش: پوستر | کد مقاله: G-12078

Abstract: Background: Hemoglobin S is the most current variant of hemoglobin in South west of Iran. A single substitution of valine for glutamic acid at the sixth position in the β - chain causes a significant change in the physical characteristics of this hemoglobin. In this epidemiological study, hematologic profiles and also the prevalence of HbS amongst patients with hemoglobinopathy in Bushehr was investigated. The aim of this study was to explore the potential association between presence of hemoglobin S with MCV and WBC as hematological indexes in adults suffering sickle cell disease in Bushehr. Material methods: In an analytical-descriptive cross-sectional study that was performed on 102 anemic patients who have been referred to Mehr clinical laboratory in Bushehr. Capillary hemoglobin electrophoresis were carried out for all sample patients, and also they were investigated from hematological parameters viewpoint by Sysmex XN-1000 hematology analyzer. Patient's results of hemoglobin electrophoresis and hematological indexes were assessed by SPSS software version 22. Statistical differences were considered significant at a 0.05 significance level, and all. Data were reported as the mean \pm standard deviation (SD). Result: From total 102 adult patients with an average age of 27.31 ± 2.45 years old enrolled in the study, 32 person were HbS carrier including 24 heterozygous person and 8 person with Hb SS genotype who suffered sickle cell anemia. The mean HbS of the 32 participants with SCD was 44.97 ± 17.33 . HbS demonstrated a positive correlation with WBC ($r=0.35$), MCV ($r=0.37$), ferritin ($r=0.53$) and also a negative correlation with RBC ($r=-0.52$), Hb ($r=-0.40$), HCT ($r=-0.50$). Conclusion: The result suggest there were significant inverse correlations between presence of HbS and RBC count, Hb concentration, HCT, MCHC indexes. Furthermore, there were significant direct correlations between presence of HbS in the patients, and MCV and WBC count. It is also recommended to evaluate biochemical profiles of SCD patients to explore more relationships with hematologic indexes in these patients. Key word: ferritin, sickle cell disease, hemoglobin S, hematological parameters, Bushehr

Relationship between fetal hemoglobin and various hematological indices in sickle cell disease in Bushehr, Iran

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نوع پذیرش: پوستر | کد مقاله: G-07619

Abstract: Background: Fetal hemoglobin (Hb F, $\alpha_2\gamma_2$) moderate the sickle cell anemia (SCA) phenotype by delaying the polymerization of sickle hemoglobin (Hb S, $\alpha_2\beta_s2$). The study examined the levels of Hb F and its relationship with various hematological indices were evaluated in people with sickle cell disease (SCD) who were referred to a laboratory in Bushehr city. Materials and methods: The present study was a cross-sectional study conducted on sickle cell patients who were referred to Mehr Bushehr Laboratory for hematological tests and hemoglobin electrophoresis. Hemoglobin F level was measured by Sebia capillary electrophoresis and hematological parameters were determined by Sysmex XN-1000 hematology analyzer. All statistical analyses were conducted using SPSS software. Statistical differences were considered significant at a 0.05 significance level, and all data were reported as the mean \pm standard error of mean (SEM). Results: We studied thirty-two patients with sickle cell disease with an average age of 27.31 ± 2.45 years participated in the study. There were 17 (53.1%) females and 15 (46.9%) males for Hb SS and Hb AS groups. The Hb F level of the 32 participants with SCD was 8.05 ± 2.10 . The mean Hb concentration, hematocrit (HCT) and total red blood cell count were 13.28 ± 0.74 , 38.15 ± 1.66 and 4.85 ± 0.15 respectively. Hb F had a positive correlation with MCHC ($r = 0.26$), WBC ($r = 0.39$) and PLT count ($r = 0.18$) and an inverse correlation with RBC count ($r = -0.42$), Hb concentration ($r = -0.69$), HCT ($r = -0.74$), MCV ($r = -0.24$) and MCH ($r = -0.26$). Conclusion: Our study showed that Hb F had an inverse correlation with RBC count, Hb concentration, HCT, MCV and MCH, as well as direct correlation with MCHC, WBC and PLT count. It is also recommended to investigate the level of Hb F and its relationship with hematological indices in other hemoglobinopathies, especially Hb D. Keyword: fetal hemoglobin, sickle cell disease, hematological indices, Bushehr

Crimean-Congo Hemorrhagic Fever: prevention and control

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Abstract: Background: Crimean-Congo hemorrhagic fever (CCHF) is a re-emerging tick-borne viral hemorrhagic fever (VHF) centered in parts of Asia, Europe, and Africa. CCHF was discovered in the 1940s and caused a severe form of hemorrhagic fever with a fatality rate of up to 40%. Since 2000, the outbreaks have increased significantly in Turkey, Iran, Russia, Uganda, and Pakistan. The virus responsible for the disease is the Crimean-Congo hemorrhagic fever virus (CCHFV), which is a negative-sense ssRNA virus that belongs to the genus Nairovirus in the Bunyaviridae family. The virus is primarily spread through the bite of infected ticks of Hyalomma genus. The virus is transmitted to animals through the bite of an infected tick, whereas animal-to-human transmission can occur either by tick bites or through exposure to infected livestock, particularly in the case of farmers, slaughterhouse workers, and veterinarians. Human-to-human transmission is done through direct contact with blood or body fluids from an infected person. Confirmation of infection can be achieved by the detection of viral nucleic acid, the detection of viral antigen, virus isolation or the demonstration of an antibody response. Prevention and control of CCHF infection are achieved by avoiding or reducing exposure to infected ticks by using approved tick repellent on the skin and clothing. Individuals should also avoid close physical contact with CCHF-infected people. It is important for health-care workers to use standard infection control precautions for patients with suspected or confirmed CCHF or their specimens. Methods: We conducted all searches between January 2010 and December 2022. A literature search was accomplished for published eligible articles with MEDLINE/PubMed and Embase databases using the keywords "CCHFV," "Crimean Congo Hemorrhagic Fever," "Diagnosis," "Management," "Prevention". Results: CCHF is clinically difficult to diagnose, and finding rapid diagnostic methods for CCHFV is a crucial step toward protecting healthy people and treating patients more quickly. The diagnosis of human CCHF can be confirmed by directly detecting the presence of CCHFV in viral culture, reverse-transcription PCR (RT-PCR), viral antigen detection assay or measuring the serological responses in the acute infection phase. The choice of which detection technique should be employed for diagnosis with the highest level of sensitivity and specificity depends on the illness stage and available specimens. Despite the fact that all of these laboratory techniques are reliable and sensitive, there are some limitations, such as the requirement for special equipment, laboratories with a high level of biosafety, and expert staff. Due to the lack of these detection techniques in underdeveloped countries, the transmission load (sample-to-person or indirect transmission) is significantly higher in these areas. A novel approach to controlling the morbidity of CCHF is therapeutic intervention of CCHFV life cycle in either tick vectors or infected animal or human hosts. Conclusion: The public health threat posed by CCHF has been rising around the world. Thus, to reduce the ongoing and emerging threats posed by CCHFV, a strategic framework for the prevention and control of CCHF must be created and put into action. Keywords: Crimean-Congo hemorrhagic fever, CCHF, diagnosis, control

The procoagulant role of microparticles in the diagnosis of DIC in patients with covid-19

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Abstract: Background: Covid-19 is an infectious disease caused by the Sars-Covid-2 virus. The main symptoms of the disease are fever, cough, and fatigue. In the severe form of the disease, one week after the onset of the disease, symptoms such as shortness of breath and hypoxia are observed. In such conditions, the disease can progress to coagulation disorders and even multi-organ failure. Microparticles (MPs) are cell membrane derived fragments which are an important factor in physiological and pathological processes such as viral diseases. Materials and Methods: A systematic search was performed to identify studies published in multiple databases (science direct, PubMed, ProQuest, google, Google Scholar) up to 2022, and recently published abstracts were also reviewed. Using the key words such as covid- 19, microparticles, DIC Results: In the conditions of inflammation, the production of MPs increases the level of inflammatory cytokines such as IL1-IL6, IL8 and TNF- α , and following the increase of these cytokines, the amount of inflammation and MPs production increases and leads to the occurrence of an inflammatory cascade, which is followed by DIC, in This state , the coagulation system in the various vessels of the body is pathologically activated and eventually the blood flow of the organs is disturbed, as a result it is very dangerous and fatal. Studies show that the level of platelet-derived microparticles (PMPs) in patients who have been diagnosed with DIC as a result of covid has increased. Conclusion: Determining the number of MPs as an efficient biomarker may help us in diagnosis and prognosis of DIC in patients with covid disease prior to CRP and ESR. Keywords: Covid-19, microparticles, DIC

Cell-derived microparticles as prognostic biomarker in multiple sclerosis

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Abstract: Background: Cell derived microparticles (MPs) are submicron cell membrane derived fragments that extended in lots of physiological conditions like apoptosis, and cell activation, or pathological conditions such as cardiovascular diseases, cancer, multiple sclerosis (MS) and many other diseases. MPs play a significant function in physiological procedures like inflammation, coagulation, and vascular function, and can be used as diagnostic and prognostic biomarkers in many disease. We aimed to investigate the MPs property in MS. Materials and Methods: A systematic search was performed to identify studies published in multiple databases (PubMed, ProQuest, Cochrane and google Scholar) up to 2022, and researchers have analyzed all the relevant data through the SCOPUS search engine using “Advance search” option and key words such as MS, microparticles, and endothelial. Results: When lymphocytes and macrophages are activated and produce inflammatory factors, small vesicles called endothelial-derived microparticles are released from the cytoplasmic membrane of the cerebral endothelial cells. Increased Endothelial cell derived MPs (EnMPs) counts were stated in MS. Overproduction of EnMPs in cerebrospinal fluid (CSF) has been mentioned in lots of patients, and these particles is probably one of the main factor in the development of MS. Drugs used to treat MS, such as interferons, lessen the release of a number of EnMPs. Therefore, it is probably that EnMPs can be used as a functional and sensitive biomarker for the diagnosis and prognosis of the MS. Conclusion: The clinical importance of MPs in various diseases is increasing day by day. Endothelial dysfunction is evident in the exacerbation of MS. Prompt diagnosis can be very helpful. It is hoped that in the future, with more studies on EnMPs as diagnostic biomarkers, progress can be made in the diagnosis and treatment of MS. Keywords: Multiple sclerosis, Microparticles, Endothelial cell

Association of tumor markers with anemia

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نوع پذیرش: پوستر | کد مقاله: G-87365

Abstract: Background: Tumor markers are a group of molecules used to diagnose of certain diseases, including cancer. These molecules can alter cellular pathways, including those associated with some anemias, by expressing or influencing certain cellular mediators. Materials and Methods: The present study is based on the data obtained from the PubMed database (1970-2022) using the keywords “Tumor markers”, Anemia” and “Iron”. Results: In this study, it was found that some tumor markers can affect hepcidin expression and iron uptake by altering cell pathways like the increase in serum CA-15.3 levels in patients with megaloblastic anemia is probably due to B12 deficiency, which is secreted by apoptotic megaloblastic erythroblasts. Some tumor markers can control iron metabolism like estrogen by reduces iron absorption in the intestine and consequently estrogen deficiency conditions increase the body’s iron stores due to accelerated absorption of iron through the intestine. Therefore, estrogen participates in iron metabolism by acting on hepcidin and ferroprotein. Other tumor markers like Progesterone Receptor Membrane Component 1 (PGRMC1) can also act as a sensor to regulate Heme production. This hemoprotein directly coordinates FECH activity with stabilizing or destabilizing mitochondrial heme contents. Another group of tumor marker such as progesterone can reduce iron levels by increasing hepcidin expression during binding to PGRMC. Several other tumor markers also increase in some anemias that can sometimes be used to diagnose and confirm the type of anemia. The role of some tumor markers remains unclear despite the increase in some anemias. Conclusion: In general, some tumor markers are involved in the pathophysiology of a number of anemias or help diagnose anemia. However, studies on the role of tumor markers in the diagnosis, development or progression of anemias are very limited. Keywords: Tumor markers, Anemia, Iron, Heparin.

Introduction to Angiogenesis Methods

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نوع پذیرش: پوستر | کد مقاله: G-51972

Abstract: Background: Angiogenesis as an essential process in the growth and development is controlled by pro and anti-angiogenic factor. New blood vessels maturation and stabilization are normal in physiological angiogenesis, but tumor cells have abnormal vascular structures, irregular blood flow, increased vascular permeability, and late maturation. Pathologic angiogenesis occurs when the balance between angiogenesis-related factors is disrupted and causes uncontrolled angiogenesis. Recently, accumulating studies have indicated that leukemic cells express receptors for these factors, leading to regulate of their proliferation and differentiation by modulating gene expression. Recently, angiogenic factors become potential targets to control the development of hematological malignancies. The vascular endothelial growth factor (VEGF) family and its receptors are primary signaling mediators that play important roles in angiogenesis. Although different tests have been described with some advantages and limitations the purpose of this study was to introduce the most appropriate methods Materials and Methods: Considering the development of non-invasive procedures various models, including in vitro, in vivo, and in ova were investigated with an emphasis on in vitro techniques of angiogenesis. However, convenience and availability were preferable. Results: Most studies relied on various models, including in vitro, in vivo, and in ova using both pro- and anti-angiogenic agents. Quantified techniques (2D and 3D) including Tube Formation and wound healing Assay along with fluorescent labeling were introduced as the best visualization methods. Conclusion: This presentation introduce the most convenient methods for the visualization and quantification of angiogenesis with emphasis on the existing in vitro techniques of angiogenesis. Keywords: Angiogenesis, angiogenesis in vitro assays, visualization techniques

Evaluation of attitudes and barriers toward blood donation in volunteer blood donors in Mashhad city (North-east of Iran)

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Abstract: Background: Blood transfusion services responsible for providing blood products. Due to population growth requirement to blood products is increasing. Knowing parameters, which affects people decision to donate blood, will help to respond to this demand. This study was designed to assess the attitudes and barriers toward blood donation among volunteer donors in Mashhad city (Northeast of Iran). Materials and Methods: This study was performed in Iranian blood transfusion organization (IBTO) centers in Mashhad city. A total of 640 volunteer blood donors including first time and frequent donors attended in this study. A Questionnaire consisted of multi-choice questions, was provided to participants. Results: Among 640 participants, 80% of them completed the questionnaire and returned it. 474(92.5%) of participants were male and 38(7.4%) of them were female. 114 of them were first time donors and the others had donated blood before. The most important motivations for blood donation include: altruism in 249 (91.88%) and 76 (85.40%) frequent and first-time donors respectively. Moreover, other factors like social behavior were indicated in 126 (58.86%) and 47 (78.34%) of frequent and first-time donors respectively. Asking people to donate blood was effective motivator for blood donation in 172 (53.70%) and 72 (80.90%) of frequent and first-time donors respectively. Nevertheless, lack of time (73.80%) was the most important barrier to blood donation among first-time donors. Conclusion: The results of this study showed that altruism is the most important motivations of blood donation. Paying attention to the motivations or barriers of blood donation in donors can play an important role in attracting and retaining donors and thus increasing and maintaining blood reserves. Key words: Blood donation, Volunteer blood donor, Attitude, Barrier



HLADRB1*07:01, *12 Alleles Association with Alloantibody Production in Transfusion-Dependent Thalassemia Patients

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نوع پذیرش: پوستر | کد مقاله: G-64231

Abstract: Background: Transfusion is a lifesaving treatment for lots of patients. However, in chronic blood recipients such as thalassemia patients, there are high concerns about alloantibody production that affects the quality of their life. Therefore, research on risk factors of alloimmunization has been started and followed. This study aimed at the determination of correlation probability between HLADRB1*07:01, *12 alleles and alloimmunization in Iranian thalassemia patients. Materials and Methods: The present study was conducted on 60 alloimmunized and 60 non-alloimmunized transfusion-dependent thalassemia patients. Antibody screening and identification tests were carried out using the tube method. HLA-DRB1 genotyping was done using a single specific primer-polymerase chain reaction (PCR-SSP) confirmed by Sequencing for positive samples. Results: The results of antibody screening showed that the most prevalent alloantibodies were Anti-K (46.7%), and followed by Anti-E (32.5%), Anti-C (15.8%), Anti-D (13.3%), respectively. Data analysis showed that there is no significant relationship between DRB1*07:01 frequency among responder and non-responder groups ($p=0.195$). There was a significant association between HLA-DRB1*12 and alloimmunization as well as antibody specification ($p=0.05$, OR=2.071, CI: 1.716-2.501). Conclusion: The findings of this study represented that there is a significant relationship between HLADRB1*12 and Kell and E alloantibodies. Although more developed studies on other HLA alleles are demanded, these findings can be valuable in determining important alloimmunization risk factors to better management of transfusion complications. Keywords: Thalassemia, Alloimmunization, HLA-DRB1

Effect of Chemotherapy on the Level of CCL2 in Patients' serum suffering from Acute Myeloid Leukemia with Monocytic Differentiation

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نوع پذیرش: پوستر | کد مقاله: G-64798

Abstract: Background: Acute myeloid leukemia (AML) is a bone marrow and peripheral blood malignancy. Some chemokines take part in the migration, progression and tumor initiation. CCL2 has a poor prognosis in AML patients because promotes tumor growth. We examined the effects of chemotherapy drugs on the level of CCL2 in AML patients' serum. Methods: This project was a case-control study, blood samples were collected from 25 AML (M5 and M4) patients before/after the first stage of the chemotherapy regimen (7+3) and 25 healthy individuals. The level of CCL2 was measured by ELISA kits. SPSS 22 was used for data analysis (two-sample t-test and paired t-test). Results: The level of CCL2 was significantly higher in the patients before chemotherapy than in the healthy controls. After chemotherapy, the level of CCL2 reduced significantly and there is no difference between patients after chemotherapy and healthy controls in the level of CCL2. Conclusion: The chemotherapy regimen (7+3) can effectively inhibit CCL2 in AML patients.

Effect of Chemotherapy on the Level of CXCL1 and CXCL10 in Patients' serum suffering from Acute Myeloid Leukemia with Monocytic Differentiation

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نوع پذیرش: پوستر | کد مقاله: G-06397

Abstract: Background: Acute myeloid leukemia (AML) is caused by various mechanisms. Chemokines have roles in the migration, initiation, survival, and progression of AML cells, also treatment in AML patients. Leukemia cells produce CXCL10 chemokine that attracts natural killer cells to eradicate cancer cells. CXCL1 has an indirect role in the progression of cancer. This project investigated the effects of chemotherapy drugs on serum levels of CXCL1 and CXCL10 in AML patients. Methods: From M4/M5 AML patients (n=25) taken blood samples before/after the first stage of a chemotherapy regimen (7+3). ELISA kits were used for measuring serum levels of the chemokines. Two-sample and paired T-test in SPSS 22 software were used for data analysis. Results: The patients attained partial response to the chemotherapy. The serum level of CXCL10 was high in patients but reduced following chemotherapy. However, the serum level of CXCL1 did not change in the patients before and after chemotherapy towards each other. Conclusion: CXCL1 levels do not change in AML patients before/after the chemotherapy, although chemotherapy could reduce CXCL10 levels in AML patients. Keywords:

Granulocyte dysmorphisms in symptomatic COVID-19 patients

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نوع پذیرش: پوستر | کد مقاله: G-85061

Abstract: Background: Since the beginning of COVID-19 pandemic, many groups reports a variety of morphologic abnormalities in affected patients. Like other viral infections, early attention is paid to atypical reactive lymphocytes as the main morphologic abnormality. However, myeloid cells also show striking changes(3). An investigation for myelodysplastic syndrome is usually prompted by abnormal hematologic findings. Blood smear demonstrates various cytopenias and dysplastic changes(1). The morphologist should have considered the reactive source of dysplasia, including; drugs, infections, inflammatory disorders, and non-malignant hematologic disease(2). In a cohort of RT-PCR confirmed COVID patient's(n=82), we examined the blood smear morphology to clarify the abnormal findings. Materials and Methods: Blood smear examination was performed by two experienced morphologists for each smears. Informed consents were taken from all patients. Results: In the present study, frequent MDS type dysplastic changes are getting our attention. Patients demographic data and morphologic abnormalities are summarized in table 1. Detached nuclear lobes and Howell-jolly-like bodies are identified in some patients (figure1.A). In addition to MDS, this abnormal morphology is reported in HIV patients. Hypogranular neutrophils are frequently evident (figure1.B). Neutrophils with the simultaneous pseudo-pelger-huet nucleus and agranular cytoplasm are found in some patients(figure.1.C); this abnormality is a specific MDS-type neutrophil change. In line with our finding, Zini et al. also reported hypogranular and MPO deficient neutrophils in a small group of COVID-19 patients (3). Irregularly nuclear projections are relatively common (Figure1.D). This type of change is more specific for MDS than reactive conditions. One patient shows immature granulocytes with uneven granule distribution (Figure1.E). In MDS context, dysplastic immature granulocytes are more common in bone marrow smears; however, it could be evident in blood smears of high-grade MDS. Hypersegmented neutrophil was a relatively common finding (figure1.F). This morphology is not specific to MDS, and usually found in megaloblastic anemia, uremia and severe iron deficiency. Abnormal long and thin nuclear filaments were also identified (Figure1.H). Few cells with myelokathexis-like thin interlobar strands were observed. A ring-shaped nucleus is a well-known neutrophil dysplasia in MDS. We document this anomaly, too (Figure1.G). Conclusion: According to our findings, to make a final diagnosis for any patient who are suspected of having MDS, it should be ruled out an active COVID-19 infection. Keywords: COVID-19, Blood smear, Morphology, Dysplasia Table1. Demographic data. Age; ranges (median) 25-93 (51.2) Y Sex F=31(38%)/M=51(62%) WBC; range (median) 2200-34700 (9464) / μ l Hb; range (median) 7.1-19.9 (14.1) g/dl PLT; range (median) 12-691 (213) $\times 10^3/\mu$ l Frequency of morphologic abnormalities; n(%) Hypogranulation 6(7.3%) pseudo-pelger nuclear lobulation 4(4.8%) Abnormal chromatin clamping 6(7.3%) Abnormal immature granulocyte 1(1.2%) Howell-jolly like bodies & detached nuclear segments 5(6.0%) Hypersegmented neutrophil & nuclear border irregularity 8(9.7%) Elongated and thin nuclear filaments 5(6.0%) Ring form nucleus 1(1.2%) Figure1. Granulocyte dysmorphisms in COVID-19. Keywords:

Investigating the effect of oleuropein and genistein on the rate of apoptosis in acute myeloid leukemia cell lines (HL-60 and KG1)

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نوع پذیرش: پوستر | کد مقاله: G-17586

Abstract: Background: Acute myeloid leukemia, the most prevalent adult form of leukemia, resulting in a significant number of deaths annually. Common treatments of this disease are usually associated with the risk of recurrence and overall toxicity. In order to reduce the side effects of chemical medications, the use of herbal remedies has grown in importance in recent years. Oleuropein and genistein are among the flavonoids with anti-cancer effects. In this study the rate of apoptosis and the expression of the BAX and BCL2 genes in HL-60 and KG1 cell lines were measured using both Oleuropein and genistein alone and in combination. Methods: In a 37-degree incubator with 95% humidity and 5% CO₂, the HL-60 and KG1 cell lines were cultured in RPMI1640 culture medium with 10% FBS. The MTT test was then used to determine the IC₅₀ dose for oleuropein and genistein in each of the cell lines. The cells were treated with genistein and oleuropein on their own and in combination. Following 12, 24 and 48 hours of cell treatment, the amount of apoptosis induced in each of the cell lines was measured using flow cytometry. Also, after RNA extraction and cDNA synthesis, expression of BAX and BCL2 genes was assessed using Real Time PCR. Results: When compared to the control group, the KG1 cell line's apoptosis levels increased after 24, 48 and 72 hours of treatment, with the highest levels occurring 24 hours after treatment. Additionally, the groups that received treatment with both genistein and oleuropein combination had the greatest apoptosis. BCL2 gene expression is lowest, and BAX gene expression is highest 24 hours after treatment. After 24 and 48 hours of treatment, there were no significant changes in the amount of apoptosis in the HL-60 cell line treated with oleuropein. However, there were significant changes in the apoptosis in the cell line treated with genistein and the combination of two drugs compared to the control group. After 72 hours of treatment, there were no significant changes in the apoptosis. In addition, compared to 72 hours after treatment, the expression levels of BCL2 and BAX decreased and increased 24 and 48 hours later, respectively, in the case of the combination of two drugs compared to the single case. Conclusion: The results showed that oleuropein and genistein increased apoptosis and BAX gene expression and decreased BCL2 gene expression in acute myeloid leukemia cell lines. Apoptosis can also be induced by combining two agents at lower doses. Keywords: Oleuropein, Genistein, Apoptosis, Acute Myeloid Leukemia



A review of the interaction between the coagulation-fibrinolytic system and cancer

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نوع پذیرش: پوستر | کد مقاله: G-50813

Abstract: Background: Interaction between cancer cells and the coagulation-fibrinolytic system could have reciprocal effects on both groups. Coagulation-fibrinolytic is a process that regulates the homeostasis of the body, and this process can be disrupted by several factors; one of the most important of which is cancer. In contrast, the coagulation-fibrinolytic system can also act as a factor in cancer growth and metastasis. Our aim in this study is to investigate this relationship. Materials and Methods: The present study is based on Pubmed database information (2010-2022) using the words "Cancer", "Coagulation", "Platelet" and "Tissue factor". Results: Cancer cells disrupt the coagulation process by activating pro-oncogenic factors or inhibiting tumor suppressors, thereby inducing changes in platelets and coagulation factors, and increasing proteins involved in coagulation. These aberrations in the coagulation system result in coagulation abnormalities such as venous thromboembolism (VTE) and disseminated intravascular coagulation (DIC). In various cancers, the activity of the coagulation and fibrinolytic systems increases, leading to an increase in coagulation and fibrinolysis factors. These factors are closely related to tumor size, tumor stage, cancer progression and metastasis. Conclusion: The coagulation-fibrinolytic system is closely related to cancers, so that coagulation-fibrinolytic agents can both lead to cancer progression and can be used as a marker for the prognosis of some cancers. Keywords:

Hypoxia inducible factor: a crucial molecule in cancer

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

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نوع پذیرش: پوستر | کد مقاله: G-30258

Abstract: Background: Hypoxia is one of the factors that contribute to the development of a range of cancers, including leukemia. Hypoxia plays a crucial role in various physiological processes. Aim: This article reviews the roles and relationships between the hypoxia-inducible factor (HIF) (gene and protein) and cancer. Method: A review of studies found in internet databases such as Google Scholar, PubMed, and Scopus was done. All relevant English-language studies published between 2010 and 2020 were found by conducting internet-based searches on these databases for HIF1 α , HIF2 α , HIF1 α , cancer, gene therapy, and malignancy. Result: HIF adapts the hypoxic cells by instilling particular genes for this compromise in the cell. Hypoxia-exposed cells reduce protein synthesis, limit proliferation, and eventually die. In addition, hypoxia can completely inhibit tumor cell growth in vitro. Sustained hypoxia alters the cell cycle and influences how cells respond to radiation and medicines, with the degree of inhibition varying depending on the severity and length of the hypoxia. The cell cycle of the most of tumor cells stops immediately when exposed to hypoxia. Hypoxia can also cause both neoplastic and normal cells to commit suicide planned cell death (apoptosis). Hypoxia does not only slow tumor progression but also stops it from growing. Although activating other factors, such as HIF, can trigger a cascade of events that allows tumor cells to proliferate and grow. Subsequently, hypoxia helps other factors, such as HIF, to progress to the tumor. HIF levels rise in tumors. Although activating other factors, such as HIF, can start a chain reaction that causes tumor cells to multiply and develop. Hypoxia then facilitates the progression of other factors, such as HIF, to the tumor. Conclusion: Based on previous research, this study found that HIF can induce angiogenesis, metastasis, proliferation, survival, and increased tumor metabolism cells. HIF has been widely investigated in the treatment of cancer in recent years. Despite significant research, the mechanism of the HIF gene and protein in cancer is still unknown. Keywords: Cancer, hypoxia, biomarker, gene therapy, malignancy

SPRED-1 expression level in adult Acute Myeloid Leukemia

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Abstract: Background: Acute myeloid leukemia is a heterogenous malignancy which is caused by different molecular alterations in hematopoietic stem cells. One of these alterations is seen in tumor suppressor genes which cause loss-of-function effects. SPRED1 is tumor suppressor gene which is negatively regulate the MAP kinase activation and even heamatopoiesis. SPRED1 is highly expressed in heamtopoeitic stem cells. Therefore, loss of function mutation or alteration in expression of SPRED1 could lead to increased proliferation and finally cause leukemia. So, we aimed to evaluate the expression level of SPRED1 in adult patients with acute myeloid leukemia. Materials and Methods: This case-control study was approved by AJA University of medical sciences with approval id IR.AJAUMS.REC.1399.131. Written informed consent was obtained from all participant. 5 cc of blood sample were collected from 62 adult patients initially diagnosed with acute myeloid leukemia and 32 healthy individuals without any underlying disease. Total RNA was extracted from buffy coat of each sample using RiboeX (GeneAll, South Korea). Then RNAs were reverse transcribed to cDNA with RevertAid First Strand cDNA Synthesis Kit (Thermo Fisher, USA). Finally real-time PCR was carried out to determine the relative expression level of SPRED1 (ABI, USA). Abl-1 gene was selected as an internal control to normalize the data. $\Delta\Delta CT$ model was used to evaluate the relative fold change of SPRED1 gene. Data were analyzed using t-test and GraphPad Prism (Version 7.04) and P-value less than 0.01% and 0.001% was considered as significant. Results: Patients included in this study were 37 male and 25 female with mean age of 41.48 and healthy individuals were 19 male and 13 female. According to FAB classification, 48.3 percent of patients were M3 AML and 51.7 percent of them were non-M3 AML. The expression level of SPRED1 gene in patient samples were significantly lower than control group (0.115 vs. 0.0323) (P-value0.001%). Conclusion: Significant down-regulation of SPRED1 in adult patients with AML confirmed the tumor suppressor role of SPRED1. Consistent with our study, down-regulation of SPRED1 was reported in pediatric leukemia, colon cancer, and hepatocellular carcinoma and breast cancer. So, this shows that SPRED1 is involved in underlying mechanism of leukemogenesis and could be used as a marker for leukemia transformation. Keywords: Leukemia, SPRED1, tumor suppressor gene

Recent advances in the roles of exosomal microRNAs (exomiRs) in Hematologic Neoplasms: Pathogenesis, diagnosis, and treatment

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نوع پذیرش: پوستر | کد مقاله: G-19504

Abstract: In clinical diagnosis, the capability of exosomes to serve as biomarkers is one of the most important biological functions of exosomes. The superior stability of exosome biomarkers makes them superior to those isolated from traditional samples such as serum and urine. Almost all body fluids contain exosomes, which contain proteins, nucleic acids, and lipids. Several molecular components of exosomes, including exosome proteins and microRNAs (miRNAs), are promising diagnostic biomarkers. These exosomes may carry genetic information by containing messenger RNA (mRNA) and miRNA, small non-coding RNAs. miRNAs act as repressors of translation by regulating genes. miRNAs unusual expression has been detected in hematologic Neoplasms. Additionally, miRNAs found within exosomes have been linked with specific diseases, including hematologic neoplasms. Numerous studies suggest that circulating exosomes contain miRNAs similar to those found in parental cancer cells. Studies suggests that miRNAs are loaded into exosomes and secreted by almost all cell types. miRNAs are transported to recipient cells through exosomes. Exosomal miRNAs can be utilized as mediators of cell-to-cell communication. Exosomes are considered as cancer immunotherapy. The interaction of exosomes with tumor cells and immune cells has received a great attention in the field of tumor immunology. Keywords:

Examining the diagnostic test of D-dimer in the diagnosis of venous thromboembolism and pulmonary embolism as its main complication: A systematic review

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نوع پذیرش: پوستر | کد مقاله: G-75810

Abstract: Introduction Pulmonary embolism (PE), as the main complication of venous thromboembolism (VTE), occurs when a blood clot passes through the veins, settles in the pulmonary arteries and leads to blockage. The risk group for pulmonary embolism is people with cancer, people who have been inactive for long periods, people who have recently undergone surgery, and pregnant women. Early diagnosis of pulmonary embolism plays an effective role in saving the patient's life. The D-dimer test is one of the tests used by doctors to diagnose pulmonary embolism (PE) as a complication of Venous Thromboembolism. This study was conducted with the aim of examining the diagnostic test of D-dimer in the diagnosis of venous thromboembolism and pulmonary embolism as its main complication. Method This study was a systematic review that was conducted in 2022. It has been done using the keywords (D-dimer), (Venous Thromboembolism), (Pulmonary Embolisms), (PE), (Diagnosis) in the reliable databases of PubMed, Scopus, Web of Sciences with a time limit of 2017 to 2022. To ensure the completeness of the search results, the sources of the articles have been reviewed and after removing duplicate titles from the endnote software and checking the titles and abstracts, related articles were reviewed using JBi tools. After checking the quality of the articles, the findings were entered in the desired checklist. Results D-dimer is one of several protein fragments that are separated from the clot by the activity of plasmin enzyme and move in the bloodstream. During clot formation, two pieces of fibrin D are connected through covalent bonding by the coagulation cascade, especially factor XIII. This engineered fragment creates specific epitopes that are recognized in the D-dimer test by monoclonal antibodies to confirm the presence of the coagulation cascade generating thrombin. Today, the D-dimer test is used to decide whether to continue or stop anticoagulation in people with intractable venous thromboembolism. In healthy people, there are low levels of D-dimer, which increases with age. In almost all cases of acute venous thromboembolism, an increase in D-dimer is observed. But since in any process that increases the production and breakdown of fibrin, the level of D-dimer also increases, high levels of D-dimer are not a specific test to confirm Pulmonary Embolisms. The D-dimer test has a high sensitivity, but despite the high sensitivity of the D-dimer test, there has been a high level of false positive results, especially in people over 65 years old. Considering the high false positive values in the D-dimer test, the negative result of this test has a diagnostic value in ruling out pulmonary embolism, but its positive result alone does not indicate pulmonary embolism. Discuss The D-dimer test is one of the safe and cost-effective tests in rejecting the diagnosis of Pulmonary Embolisms, especially in people who prevent imaging tests. The D-dimer test has no diagnostic value to confirm pulmonary embolism, especially in the elderly population over 65 years old, and other diagnostic tests such as imaging tests should be used for these people. Keywords:

The Functions of the HIF Gene in Kidney and Liver Diseases

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نوع پذیرش: پوستر | کد مقاله: G-39720

Abstract: Abstract: Background: Tissue hypoxia is a pathologic feature of many human diseases including cancer, myocardial infarction, stroke, liver, and kidney disease. Method: A review of studies found in internet databases such as Google Scholar, PubMed, and Scopus was done. All relevant English-language studies published between 2010 and 2020 were found by conducting internet-based searches on these databases for HIF1 α , HIF2 α , HIF1 α , liver injury, liver disease, Kidney disease. Result: Hypoxia inducible factors (HIFs) are a group of transcriptional regulators that impact the body's homeostatic response to low oxygen levels. HIF stabilization and transcription activation of hypoxia-induced genes are a central mechanism of hypoxia adaptation. Anemia (Anemia) is one of the common complications of chronic kidney disease and one of the reasons for this is the shortage of erythropoietin (EPO). The kidney is the main physiologic source of erythropoietin in the adult and responds to decreases in tissue oxygenation with increased EPO production. HIF activation through hypoxia-dependent and hypoxia-independent signals have been reported in liver disease of diverse etiologies. Inappropriate HIF activation is associated with the progression of many human diseases, including kidney cancer. Conclusion: In this study we review the investigations that demonstrate a role for HIFs in the development of Kidney and Liver Diseases. HIFs are a significant cause of a variety of liver and kidney disorders, and more cellular and molecular research is needed to better understand how this molecule functions. Key words: HIF, liver disease, kidney disease

Normal Ranges of Hematological Parameters Among Young Adults Referring for Premarital Screening for Thalassemia; An Overlooked Practice in Zabol, Sistan and Balochestan province, Iran

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نوع پذیرش: پوستر | کد مقاله: G-13078

Abstract: Background: There is a high prevalence of hemoglobinopathies, including thalassemia, in Sistan and Baluchestan province of Iran. It is important to appropriately screen young adults to control the birth of new cases with thalassemia. In many less-equipped centers, this practice relies on cell blood count only. Here we investigated the hematological parameters of the couples referring to the Central Laboratory of Sistan, Zabol, for premarital screening for thalassemia. . Materials and Methods: This was a descriptive cross-sectional study conducted in Zabol city, Sistan and Baluchestan province of Iran from August 2020 to August 2021. Complete blood count (CBC) parameters of 2926 young adults were collected using a Sysmex KX-21 device and were compared with available reference intervals according to Clinical and Laboratory Standards Institute. Results: The means of age of women and men were 38.84 ± 16.32 and 36.64 ± 14.14 years, respectively. The average values for each parameter in the studied population were: RBC (4.78 ± 0.55), hemoglobin (13.19 ± 2.46 g/dL), hematocrit ($40.11 \pm 3.57\%$), MCV (85.16 ± 28.33), neutrophil (52.12 ± 9.98), lymphocyte (37.84 ± 9.03), mixed leukocytes (10.00 ± 3.51), platelets (244.02 ± 62.32). The mean values of hemoglobin (14.48 ± 5.17 vs. 12.69 ± 1.39 g/dL), hematocrit (43.01 ± 3.89 vs. $38.97 \pm 3.45\%$), serum ferritin (115.4 ± 74.3 vs. 69.20 ± 12.36 g/dL), TIBC (316.84 ± 1.38 vs. 320.95 ± 41.01 , $P=0.01$), and serum iron (85.05 ± 28.51 vs. 76.25 ± 28.22 , $P=0.02$) were significantly lower in women than in men. Conclusion: The relatively low hemoglobin in females referring for premarital screening for thalassemia ring the bell for healthcare experts to carefully examine these cases for possibility of thalassemia minor after excluding other common possible reasons such as iron deficiency anemia using iron studies and hemoglobin electrophoresis. Keywords: hemoglobinopathy screening, thalassemia, normal ranges

Prevention of iron deficiency anemia in toddlers 6-24 months old by taking iron supplements

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نوع پذیرش: پوستر | کد مقاله: G-54796

Abstract: Background: Iron deficiency anemia (IDA) is the most common micronutrient deficiency affecting nearly one-third of the population and is the leading cause of anemia worldwide. IDA is one of the most common anemias, especially in children 4 to 23 months. Aims: The aim of this study was to investigate the effectiveness of two iron supplements, ferrous sulfate (G1) and ferrous gluconate (G2), for children aged 6 to 24 months. Methods: A randomized, single-blind clinical trial was performed; enrolling 129 toddlers aged 4 to 6 months old. Randomization of patients in this study was stratified by factors known to influence hematologic parameters, including age, weight (at baseline), and exclusive breastfeeding to ensure the balance between treatment groups. After obtaining informed consent and based on the type of iron supplement received, 120 healthy toddlers are categorized into 2 groups: G1 group (n=60), toddlers received 2 mg/kg/day G1 supplementation, and G2 group (n=60), toddlers received 2 mg/kg/day G2 supplementation. The trial was registered at the Registry of Clinical Trials as IRCT20190902044674N1. Conclusion: Comparison of hematological parameters of G1 group toddlers before the start of prophylaxis (at baseline) and after 6 months of supplementation showed that there was a significant increase in hemoglobin level ($P = 0.002$), hematocrit ($P = 0.004$), red blood cells count ($P = 0.021$), and ferritin level ($P = 0.001$). Comparison of hematological parameters of G2 group toddlers before the start of prophylaxis (at baseline) and after 6 months of supplementation showed that there was a significant increase in hemoglobin level ($P = 0.001$), hematocrit ($P = 0.004$), red blood cells count ($P = 0.011$), and ferritin level ($P = 0.001$). Therefore, ferrous sulfate and ferrous gluconate supplements can be effective in the prophylaxis of iron deficiency and IDA in toddlers. Keywords:

Mesenchymal stem cell-derived microvesicles affect proliferation and apoptosis of Acute Myeloid Leukemia

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نوع پذیرش: پوستر | کد مقاله: G-49520

Abstract: Background: Acute myeloid leukemia (AML) is a predominant blood malignancy with high mortality and severe morbidity. In recent years, Novel reagents or biologicals for the therapy of AML are urgently needed, and microvesicles isolated from mesenchymal stem cells (MSC-MVs) have been identified as candidate biomarkers for disease diagnosis and prognosis. In this study, we evaluated the effects of MSC-MVs on cell proliferation and apoptosis AML cells in vitro and in vivo. Materials and Methods: The current research is a narrative review type, in order to achieve the study objectives, articles were searched in scientific databases including Google Scholar, Scopus, Pubmed from 2013 to 2022 with using key words such as: Acute Myeloid Leukemia, Mesenchymal stem cell, Microvesicles and Apoptosis. After searching, 71 results were obtained and according to the topic and purpose of the study, duplicate and unrelated articles removed and 15 articles with full text were included in the study. Results: Findings showed that MSC-MVs inhibited proliferation of K56 and HL60 cells in a concentration-dependent manner. MSC-MVs reduced the ratio of Bcl/Bax, enhanced the autophagy proteins level of Beclin-1 and LC3-II. Other studies showed that MSC-MVs can inhibit T24 cells proliferative viability via cell cycle arrest and induce apoptosis in T24 cells in vitro and in vivo, suppressed cell proliferation and cell cycle progression, and also significantly enhanced cell apoptosis in KG-1a cells. MSC-MVs down regulated phosphorylation of Akt protein kinase and up-regulated cleaved Caspase 3 during the process of anti-proliferation and pro apoptosis in T24 cells. MSC-MVs increased the expression of BID and BAX and decreased expression of BCL2, indicating the induction of intrinsic apoptosis in NB4. In contrast, MSC-EVs increased the expression of the death receptor gene TRAILR2 and cell cycle regulator genes P21 and CCNE2 in K562. Conclusion: These results demonstrate that MSC-MVs suppress cell proliferation and cycle progression and promote cell apoptosis in leukemia cells and thus may have potential for the development of supportive therapies for leukemia. Keywords: Acute Myeloid Leukemia; Mesenchymal stem cell; Microvesicles and Apoptosis

Regulation cell proliferation and apoptosis of acute myeloid leukemia cell cells by Exosomes released from derived-Mesenchymal Stem Cell

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نوع پذیرش: پوستر | کد مقاله: G-21680

Abstract: Background: Acute myeloid leukemia (AML) is a malignant hematological disease, originating from hematopoiesis stem cell differentiation obstruction and clonal proliferation. Recently studies suggest that mesenchymal stem cells (MSC) possess antitumor properties; exosomes are considered as a novel avenue intercellular communication, which may be a mediator in MSC-related antitumor effect. Our aim in this study, investigation the role of MSC-derived exosomes in the regulation of leukemic cell growth and apoptosis was. Materials and Methods: In this narrative review were used PubMed, Google Scholar databases. The keywords that were used included Mesenchymal stem cell, Exosomes, Acute Myeloid Leukemia and cell proliferation and apoptosis. Articles from 2012 to 2022 were reviewed. After advanced searching, we analyzed the articles that matched our inclusion and exclusion criteria among the displayed results. Results: In overall 50 articles were obtained and according to the topic, the study aim and type of the study, duplicate and unrelated studies removed and 13 articles were analysed in this the research. MSC-derived exosomes mediate intercellular communication as cell-derived extracellular signalling organelles that transmit specific information from cell of origin to target cells. MSC-derived exosomes exerted a pro-apoptotic and/or necrotic effect on NB4 and K562 cells and increased the expression of anti-tumor factors in both cell lines compared to control. In other studies revealed that MSC-derived exosomal miR-425-5p significantly inhibited cell viability, Edu positive cells, invasion and migration, and induced apoptosis of AML cells. MSC-derived exosomes effectively suppressed cell proliferation and cell cycle progression, and also significantly enhanced cell apoptosis in KG-1a cells. Also Quan Xiao et.al observed that MSC-derived exosomes promotes autophagy in nucleus pulposus cells (NPCs) and inhibits the release of inflammatory factors such as IL-1 β and TNF- α in LPS-treated NPCs and inhibits apoptosis in NPCs. Further studies showed that BMSC-Exo inhibited the Akt-mTOR pathway. Conclusion: In conclusion, MSC-derived exosomes induce leukemic cell apoptosis, suppress cell proliferation and cycle progression. Our study establishes a basis for a MSCs derived exosomes-based leukemia treatment. Keywords: Mesenchymal stem cell, Exosomes, Acute Myeloid Leukemia and cell proliferation and apoptosis.

Relationship between liver enzyme levels and clinical status of patients admitted to the pediatric ward: A cross-sectional study

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نوع پذیرش: پوستر | کد مقاله: G-59324

Abstract: Background: Most liver diseases are diagnosed accidentally during routine tests. Liver function tests cannot be easily ignored because some of these patients may develop a progressive and life-threatening liver disease in the future. Methods: This cross-sectional study was conducted among patients over 30 days hospitalized in the pediatric ward and referred to the gastrointestinal clinic of Shahid Rahimi Hospital in Khorramabad during 2019-2020 according to the tests recorded in the hospitalization file of patients with elevated liver enzymes. Based on the history recorded in previous files and also taking the history of hospitalized patients during the research, we will look for the causes of increased liver enzymes. Results: In this study, 64 patients with elevated liver enzymes were studied, which were divided into four categories. Causes of liver disease include cirrhosis, sclerosing cholangitis, autoimmune hepatitis, fatty liver, choledochal cyst, hepatitis A, billiary atresia, PF1C, choledochal stone, Gilbert syndrome, portal vein thrombosis, and crigler-najjar. Metabolic causes include tyrosinemia, hyperphosphatasia, GSD, hyperlipidemia syndrome, CF, alagille syndrome, Wilson, alpha 1 antitrypsin deficiency. Infectious causes include covid- 19, herpes gingivostomatitis, Kawasaki and infectious mononucleosis. As well as Seizures, Duchenne, celiac disease, cardiomyopathy, scorpion stings, hypothyroidism, favism, patients who died before the final diagnosis, and patients who did not reach a definitive diagnosis by the end of the study were classified as miscellaneous. Conclusion: The most common cause of elevated liver enzymes was hepatic causes and secondarily metabolic causes. Increased liver enzymes were significantly associated with the disease process, the method of diagnosis. While there was no significant relationship with age and sex of the subjects, visit status, medical history, family history, history of maternal illness during pregnancy, parental relationship. As well as the cause of increased liver enzymes was not significantly associated with ALT, AST, ASMA, CERULOPLASMIN, BILI, PT, INR, LKM, G6PD, TSH, TG, GGT, IGG and AAT. While it was significantly associated with ALP, CPK and LDH levels. Keywords: ALP, ALT, AST, Enzyme Liver, pediatric



Association between sLDH and Mobilization in Autologous Hematopoietic stem cell transplantation

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نوع پذیرش: پوستر | کد مقاله: G-78492

Abstract: Background: Autologous hematopoietic stem cell transplantation (auto-HSCT) is considered as one of the most important treatment options for many hematological malignancies. The outcome of transplantation is significantly affected by successful hematopoietic stem cell mobilization from bone marrow niche into circulation. The purpose of this study was to investigate the impact of Serum lactate dehydrogenase (sLDH) on mobilization outcomes in patients undergoing auto-HSCT. Materials and Methods: 195 patients who received an auto-HSCT were enrolled in this retrospective study. We collected demographic and laboratory data, such as complete blood count (CBC), post-apheresis CD34+ cell count and sLDH levels. Using the receiver-operating characteristic, the predictive values of pre-mobilization LDH for CD34+ cell in apheresis yield was analyzed. Results: Our data did not demonstrate any significant association between pre-mobilization sLDH and CD34+ cell count in apheresis product. However, it was figured out that some of CBC parameters including PLT and HCT on admission day, associated with successful mobilization. Conclusion: Successful engraftment is highly depended on the quantity of mobilized stem cells. Further investigations may provide more insights into the association between sLDH and other biomarkers for estimating the apheresis harvest. Keywords: Autologous hematopoietic stem cell transplantation, lactate dehydrogenase, successful mobilization

New applications of Cell Free DNA detection techniques in Noninvasive prenatal testing for thalassemia

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نوع پذیرش: پوستر | کد مقاله: G-23541

Abstract: Background: Noninvasive prenatal testing (NIPT) procedures for rhesus D type, sex determination, aneuploidies, and single-gene disorders, among other genetic fetal screening, were inspired by the finding of circulating cell-free fetal DNA (cff-DNA) in maternal plasma. Thalassemias are one of the most frequent hereditary diseases, and they have a large social and economic impact in high-risk populations. Methods: Articles indexed in Google scholar and Pubmed databases, according to MeSH available keywords for “Cell free DNA” AND “Prenatal screening” AND “Thalassemia” during 2020 to 2023 were included. Finally, 11 articles were selected based on the criteria of the research. Results: If the test for paternal inheritance is negative, NIPT using maternal cff-DNA and allele-specific ARMS RT-PCR can be used to screen paternally inherited β -thalassemia mutant alleles and prevent pregnant women from invasive therapies. The COLD-PCR approach could be regarded a cost-effective screening option for detecting the paternal HBB gene IVS-II-1 (GA) (HBB: c.315+1GA) mutation in maternal plasma cff-DNA. Droplet Digital PCR (ddPCR) is a simple and sensitive diagnostic technique for NIPT of paternally and maternally inherited β^+ IVSI-110 and β^0 mutations, as well as other single point mutations that cause monogenic diseases. For SEA deletion α^0 thalassemia, this assay has the potential to become a reliable and efficient NIPD. The semiconductor sequencing platform allows for NIPD of hemoglobin Bart hydrops fetalis via maternal plasma dispensed with parental haplotyping, allowing for early screening for maternal genotyping of α -thalassemia, fetal aneuploidies in chromosomes 13/18/21, and hemoglobin Bart hydrops fetalis detection in a single sample of maternal plasma. Next-generation sequencing (NGS) and haplotype-assisted analysis are two possible assays for non-invasive prenatal diagnosis of α - and β -thalassemia. As a first-line screening method, the carrier screen with reflex single-gene non-invasive prenatal test (sgNIPT) increases the detection of α -thalassemia affected fetuses. TAG-seq is a new NIPT approach that combines fetal aneuploidy screening with the identification of de novo FGFR3 mutations and paternal HBB mutations. Conclusion: The use of cell free DNA approaches for screening at-risk fetus can prevent unnecessary invasive procedures identifying common mutations in thalassemia. Keywords: Cell free DNA; Prenatal screening; Thalassemia

Relationship between hemoglobin D trait and hematological parameters

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نوع پذیرش: پوستر | کد مقاله: G-46078

Abstract: Abstract Background: Hereditary hemoglobinopathies, the most common monogenic hemoglobin (Hb) disorders, result in a variety of clinical consequences. It has been observed that various Hb variants and thalassemias are found common to specific ethnic groups and regions. Haemoglobin D is one of the most common hemoglobinopathies, which can be inherited as a homozygous or a heterozygous trait with other haemoglobinopathies. Hemoglobin D (Hb D, beta 22 Glu--Gln) is a beta-chain variant that was first described in 1973 in Iran. This study examined the relationship between hemoglobin D and hematological parameters in people who were referred to a laboratory in Bushehr city. Materials and methods: The present study was a cross-sectional study conducted on hemoglobin D patients who were referred to Mehr Bushehr Laboratory for hematological tests and hemoglobin electrophoresis. Hemoglobin D level was measured by Sebia capillary electrophoresis and hematological parameters were determined by Sysmex XN-1000 hematology analyzer. All statistical analyses were conducted using SPSS software. Statistical differences were considered significant at a 0.05 significance level, and all data were reported as the mean \pm standard error of mean (SEM). Results: out of 102 patients with hemoglobinopathy, cases of hemoglobin D (7.76%) were identified. an average age of participate was 24.3 ± 4.01 . There were 4 (50.0%) females and 4 (50.0%) males for Hb D group. Hb D had a positive correlation with WBC count ($r = 0.15$), Hb ($r = 0.36$), HCT ($r = 0.18$), MCV ($r = 0.74$) and MCH ($r = 0.52$) and an inverse correlation with RBC count ($r = -0.09$), MCHC ($r = -0.01$) and PLT count ($r = -0.25$). Conclusion: Our study showed that Hb D had an inverse correlation with MCHC, RBC and PLT count, as well as direct correlation with WBC count, Hb, HCT, MCV and MCH. Key words: thalassemia, hemoglobin D, hematological parameters, Bushehr.



The effect of the PLR and NLR on the patients with Immune thrombocytopenia (ITP)

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نوع پذیرش: پوستر | کد مقاله: G-37098

Abstract: Immune thrombocytopenia (ITP) is an acquired autoimmune disease characterized by a complex interaction of multiple aspects of the immune system. The clinical manifestations of ITP are low platelet counts with potentially spontaneous bruising, petechial rash, mucosal bleeding or even life-threatening hemorrhage. ITP is phenotypically heterogeneous with numerous potential triggers, including genetic, environmental and precipitating events, contributing to autoantiplaquet antibody production and the multifaceted immune response. Pathogenesis of ITP involves multifactorial autoimmune mechanisms of both humoral and cellular immunity. In this present study, our goal is to explore the association between PLR (Platelet to Lymphocyte ratio) and NLR (Neutrophil to Lymphocyte ratio) in patients with ITP. We speculate that PLR and NLR might be a risk factor for ITP patients. Keywords:

An introduction to a new version of semi-automated coagulometer and its primary performance evaluation

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Abstract

Background: Herein, we aimed to introduce and primarily analyze performance evaluation of the new version of a semi-automated coagulometer (PS-ProMax4) which has been recently invented in Iran.

Methods: Three hundred plasma samples were obtained from outpatients samples referred to a medical laboratory for check-up routine. Coagulometer performance was evaluated by measuring partial thromboplastin time (PTT) and prothrombin time (PT) at the medical decision levels using *Thermo Scientific™ Pacific Hemostasis™* PT and PTT reagents. Commercially available lyophilized control samples for normal, low and, medium pathological values were used as control in each set of runs.

Results: Among 300 enrolled samples, five PT and PTT tests were identified as abnormal and the rest of them were determined in the normal ranges. All the results were confirmed in the same laboratory using semi-automated coagulometer START Max. The mean of PT and PTT tests for normal samples were 14 and 30 ± 1.5 , and for abnormal samples were 19 ± 0.3 and 59 ± 0.7 , respectively.

Conclusion: Perfect precision in the detection of normal and abnormal samples using lesser patient and kit samples by means of the new PS-ProMax4 coagulometer not only can alleviate per-test costs, but also can speed up the procedure time compared to the other old versions of semi-automated coagulometer. Further studies are going to be performed on a larger population size including different pathologic samples. **Keywords:** Semi-automated coagulometer (PS-ProMax4), PT, PTT, evaluation

New insights of anti-angiogenesis strategies in multiple myeloma treatment

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نوع پذیرش: پوستر | کد مقاله: G-18275

Abstract: Background: Angiogenesis is enhanced in the bone marrow of MM in parallel with tumor progression. In MM, as well as in other aggressive tumors, the vessel wall is lined with only cancer cells as a mosaic of cancer cells and endothelial cells. This phenomenon is called “vasculogenesis mimicry”. The observation of an increased BM angiogenesis in MM, an overexpression of angiogenic cytokines, and their correlation with disease activity, overall survival and the development of new antiangiogenic compounds, led to consider angiogenesis as a new target in the treatment of MM. Method: Relevant literature was identified by a PubMed search (2000-2023) of English language papers using the terms: “Angiogenesis”, “Anti-angiogenesis”, “Tumor growth inhibitors”, “Multiple myeloma”. Result: A number of antiangiogenic therapeutic strategies such as Proteasome inhibitors, Tyrosine Kinase Inhibitors, Bisphosphonate, Interleukins, Immunomodulatory drugs, Histone deacetylase inhibitors (HDACi), Monoclonal Antibodies, and other new treatments have been evaluated in myeloma with varying degrees of efficacy. Conclusion: The principal drawback in the management of anti-angiogenic drugs in the treatment of MM is that several angiogenic molecules may be synthesized by tumor cells, and that tumor cells may depend on different factors for its supply. A very common side effect of anti-angiogenic therapy is hypertension, which is associated with nitric oxide changes, pruning of normal vessels, as well as effects on renal salt homeostasis. Toxic peripheral neuropathy represents a dose-limiting debilitating side effect of the treatment of MM with thalidomide, bortezomib and lenalidomide. Keywords: Angiogenesis, Anti-angiogenesis, Tumor growth inhibitors, Multiple myeloma

Investigation of serum ferritin level in dialysis patients of Soodeh Medical Center in 1401

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دانشجوی کارشناسی ارشد هماتولوژی - دانشگاه علوم پزشکی تهران، مدیر آکادمی سوده^۱

نوع پذیرش: پوستر | کد مقاله: G-53971

مقدمه: آنمی یکی از معضلات اصلی بیماران همو دیالیزی است که با عوارض بسیاری همراه است تولید ناکافی EPO علت اصلی آنمی در این بیماران می باشد. کاهش ذخایر آهن، یا کاهش در دسترس بودن آن، شایع ترین علت مقاومت به EPO است. از آنجا که کاهش و Over Load آهن هر دو دارای عوارض مخرب است اندازه گیری وضعیت آهن در بیماران همو دیالیز امری بسیار ضروری می باشد. مواد و روشها: جامعه آماری در این مطالعه تمام بیماران تحت دیالیز در مرکز درمانی سوده در سال ۱۴۰۱ که تحت درمان با EPO هستند، می باشد. داده های لازم شامل مشخصات بیماران از جمله سن و جنس، هم چنین میزان فریتین سرم بیماران که هر سه ماه یک بار اندازه گیری شده است. بعد از اندازه گیری سطح سرمی فریتین با تکنیک الایزا توسط آزمایشگاه مرکز با دستگاه الایزا فول اتومات تحت سیستم کنترل کیفی استاندارد، داده ها وارد نرم افزار اکسل شد و مورد تحلیل و بررسی قرار گرفت. نتایج: ۳۹۲ نفر در این مطالعه مورد بررسی قرار گرفتند که ۱۷۹ نفر از این تعداد زن و ۲۱۳ نفر مرد می باشند. از این تعداد ۱۰۳ نفر از افراد فریتین بالاتر از رنج عادی طبق رفرنس رنج کیت داشتند. به عبارتی ۲۶,۲۷ درصد بیماران همو دیالیزی تحت درمان با EPO ذخایر آهن بیش از حد مجاز دارند. که از این تعداد ۳۸ درصد زن و ۶۲ درصد مرد می باشند. نتیجه گیری: باتوجه به بالا بودن ذخیره ی آهن در ۲۶,۲۷ درصد بیماران، نیاز مبرم به بررسی آهن در بیماران و بررسی وضعیت ایشان پیشنهاد می شود. این مطالعه در حال انجام بوده و بررسی اطلاعات سطح سرمی آهن و TIBC و Hb و Hct در حال انجام می باشد. واژه های کلیدی: همو دیالیز، اریتروپویتین، ذخیره ی آهن

Co-Delivery of Doxycycline and Hydroxychloroquine Using CdTe-Labeled Solid Lipid Nanoparticles for Treatment of Brucellosis

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Background: Brucellosis is a systemic disease in both acute and chronic forms which can affect any organ or tissue in the body. One of the biggest issues in treating this disease is its relapse. In this study, a complete treatment of brucellosis was evaluated using enhanced performance of doxycycline and hydroxychloroquine drugs by using solid lipid nanoparticles (SLN) conjugated cadmium-telluride quantum dots..

Materials and Methods: The double emulsion method was used to prepare SLN and cadmium-telluride quantum dots. The physicochemical properties of NPs were determined. The effect of nanoparticle-loaded antibiotics against *Brucella melitensis* was determined by well diffusion, minimum inhibitory concentration (MIC), cell culture, and animal studies.

Results: The means of particle size, PDI, zeta potential, drugs loading, and encapsulation efficiency were 214 ± 25 nm, 0.385 ± 0.022 , -18.7 ± 2.3 mV, $17.7 \pm 1.5\%$, and $94.15 \pm 2.6\%$, respectively. The results of FTIR and DSC showed that no chemical reaction occurred between the components of the NPs. The effect of free drug and NPs on bacteria was the same by well diffusion and MIC method. Drug-loaded NPs significantly reduced the number of CFUs in the cell line and acute and chronic brucellosis compared to the free drug

Conclusion: In conclusion, the synthesized nanoparticles were safe and green. With the slow release of the drug (100 h), the accumulation of the drug at the bacterial site increases and causes a greater effect on the *B. melitensis* and improves the disease of brucellosis. The use of synthesized nanodrugs in this study had promising therapeutic results.

Keywords: brucellosis, *Brucella melitensis*, solid lipid nanoparticles, doxycycline, hydroxychloroquine

Bacterial contamination of external surface of cockroaches and their antibiotic resistance in hospitals of Hamadan, IRAN

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Background: To determine the type of cockroaches contaminated by bacterial species and their antibiotic resistance in different hospitals of Hamadan city.

Materials and Methods: This cross sectional study was carried out on 179 samples of cockroaches collected from hospitals in Hamadan city, Iran. The body surface was washed with physiological sterile serum and the solution was centrifuged at 2000 rpm for five minutes. Bacteria were identified using the phenotypic method. Antibiotic resistance of bacteria against various antibiotics was checked with disk diffusion method. Data were analyzed using SPSS version20 software. Chi-square test was applied for significance. P value <0.05 was regarded as significant.

Results: Out of 179 cockroaches, 117 (65.36%) and 62 (34.64%) were American and German cockroaches respectively. In total, 173 (96.64%) of them were contaminated with bacteria. Three hundred and fourteen (76%) and 99 (24%) strains of bacteria were isolated from both types of cockroaches. E. coli was the most common (119 cases) and Morganella was the lowest species found. Gram positive bacteria showed the highest antibiotic resistance to Clindamycin with 106 (79.7%) and Tetracycline with 43 (32.33%) highest susceptibility. Gram-negative bacteria had the highest resistance to Amoxicillin and the highest sensitivity to Norfloxacin.

Conclusion: Bacterial contamination of cockroaches in hospital environment is an important concern in health care systems. Moreover, antibiotic resistance observed in separated bacteria can enhance the pathogenicity of bacteria.

Keywords: Bacterial contamination, Antibiotic resistance, Cockroaches, Iran

SGLT2 inhibitors: a focus on lipotoxicity and cardiovascular diseases

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نوع پذیرش: پوستر | کد مقاله: G-89736

Abstract: In the first stage of atherosclerosis, excessive lipids and lipoproteins accumulate in the sub-endothelial matrix. This process is triggered by the accumulation of oxidized low-density lipoprotein (Ox-LDL), which stimulates the release of pro-inflammatory cytokines. Sodium-glucose co-transporter 2 inhibitors are a new class of glucose-lowering drugs. Furthermore, SGLT2 inhibitors affect lipid metabolism on several different levels. Methods: A systematic literature search was conducted to identify all studies that investigated the SGLT2 inhibitor therapy on lipid metabolism in the PubMed database. Results: According to Schernthaner et al. canagliflozin (300 mg/day) caused an 11.7% increase in LDL after 52 weeks of therapy in patients with type 2 diabetes mellitus. According to Basu et al., the cause of this possible increase in the LDL-C levels could be due to an increased lipoprotein-lipase (LpL) activity and because of a delayed turnover of LDL in the circulation. Canagliflozin reduced the expression of angiopoietin-like protein 4 (ANGPTL4), which is a known inhibitor of LpL in white and brown adipose, skeletal muscle, and heart tissues. Concerning HDL levels, according to Kamijo et al. after 12 weeks of canagliflozin administration (100 mg/day) the VLHDL and large high-density lipoprotein (LHDL) values showed a significant increase, of 10.9% and 11.5% respectively. These beneficial changes might also contribute to the subsequent reduction of cardiovascular outcomes, caused by SGLT2 inhibitors. Conclusion: SGLT2 inhibitors decrease lipid accumulation in visceral fat, regulate the serum lipoprotein levels, beneficially change the ratio of LDL particles, reduce lipid oxidation, and shift substrate utilization towards the usage of ketone bodies, which are more efficient in myocardial metabolism, affect the β -oxidation and the transportation of lipid molecules in the cells. These findings may show that even though SGLT2 inhibitors are used primarily for the treatment of patients with type 2 diabetes, they may not be restricted merely to these indications soon. Keywords:

The antibiotics resistance in *Klebsiella pneumoniae* in Tabriz, Iran

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نوع پذیرش: پوستر | کد مقاله: ۲۱۰۸G-5

Abstract: Background: *Klebsiella pneumoniae* is one of the most important causes of nosocomial and community-acquired infections. The study was conducted to examine the drug resistance in clinical isolates of *K. pneumoniae* in teaching hospitals in Tabriz, Iran. Methods: Seventy *K. pneumoniae* were isolated from the different wards of teaching hospitals in Tabriz, Iran from 2020 to 2022. Antibiotic susceptibility testing was done by Disk Diffusion Agar assay and to study the resistance genes, PCR was used. Results: Ampicillin was the highest resistance drug (99.4%) and 87% of isolates were multi-drug resistant (MDR). The *qepA*, *oqxB*, and *oqxA* genes were found 92%, 83.5%, and 67%, respectively. Seventy-four isolates were resistant to co-trimoxazole and the rate of resistance genes was *sul1* in 78%, followed by *sul2* (49%), *dfr* (19%), and *sul3* (11%). The most common aminoglycoside resistance genes were *ant3Ia*, *aac6Ib*, *aph3Ib*, and APHs in 34% 22%, 21%, and 20%, respectively. *fosA* (42%) was the most frequent resistance gene to fosfomycin followed by *fosC* (38%) and *fosX* (20%). The ESBLs gene was found to include *blaCTX-M-15* in 68%, followed by *blaSHV-1* (50%) and *blaSHV-11* (40%). We found *tetB* in 48%, *tetA* in 38%, *tetD* in 26%, and *tetC* in 18%. Conclusion: The most effective antibiotic against *K. pneumoniae* is tigecycline. The rate of drug resistance is high especially MDR among *K. pneumoniae* isolated from teaching hospitals of Tabriz which are ordinarily used in the management of *K. pneumoniae* infections. Keywords: Antibiotic, *Klebsiella pneumoniae*, multidrug-resistant, resistance genes

The status of anti-SARS-CoV-2 spike protein among PCR-confirmed COVID-19 Iranian population based on the voluntary blood donors- A cross sectional study

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نوع پذیرش: پوستر | کد مقاله: G-73504

Abstract: Background: Detection of specific IgG antibodies against SARS-CoV-2 S antigen can help estimate the number of people exposed to this virus in the past and assess the burden of infection. Recent research suggested that SARS-CoV-2 IgG antibodies persisted in patients for up to three or four months after natural infection. As of September 28, 2021, about 57% of Iran's population was unvaccinated against SARS-CoV-2. This study aimed to investigate the prevalence of natural immunity among the unvaccinated Iranian population with positive results in RT-PCR test based on blood donors, samples. Methods: A population-based cross-sectional study was conducted on unvaccinated Iranian blood donors with PCR-confirmed infection from 26 August 2021 to 15 September 2021 referred to blood transfusion centers in 31 main centers and some satellite centers over the country. A questionnaire was filled out by the trained physicians to gather the donors, information. SARS-COV-2 IgG antibody against spike protein was detected using EUROIMMUN Anti-SARS-CoV-2 ELISA (IgG) kit donated by World Health Organization. To extrapolate seroprevalence estimation from the blood donation samples to the general population, the weighted seroprevalence adjusted for test performance was estimated. Results: A total of 3339 participants were included. Of them, 1051(31.5%) were female. The median age was 35 years (IQR 15). Of the participants, 322 were previous positive COVID-19 PCR. The weighed and adjusted seroprevalence estimate of SARS-CoV-2 IgG antibodies was 78.18% (70.65-85.70). Conclusion: The study shows that in less than one-fourth of confirmed cases of COVID-19, SARS-CoV-2 anti-spike IgG were not detected. Decline antibody over time and lack of antibodies to SARS-CoV-2 due to illness severity, race/ethnicity, obesity, and drug therapy should be considered. Keywords:

Persistent Basal Ganglia Involvement in Aminoacylase-1 Deficiency: Expanding Imaging Findings and Review of Literature

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نوع پذیرش: پوسنر | کد مقاله: G-02174

Abstract: Aminoacylase-1 deficiency (ACY1D) is an autosomal recessive rare inborn error of metabolism, which is caused by disease causing variants in ACY1 gene. This disorder is characterized by increased urinary excretion of specific N-acetyl amino acids. Affected individuals demonstrate heterogeneous clinical manifestations which are primarily related to neurologic problems. Besides, in neuroimaging findings, corpus callosum hypoplasia, cerebellar vermis atrophy, and delayed myelination of cerebral white matter have been reported. Here, whole-exome sequencing was performed in order to identify disease-causing variants in an affected 5-year old male patient who presented with neurologic regression superimposed on neurodevelopmental delay following a febrile illness. He had inability to walk, cognitive impairment, speech delay, febrile-induced seizures, truncal hypotonia, and recurrent metabolic decompensation. All metabolic tests including serum ammonia, lactate, serum amino acids chromatography, metabolic screen (MS/MS), and urine organic acids profile were normal except for a moderate metabolic acidosis following a febrile illness. The results of serial brain magnetic resonance imaging (MRI) at age's 1 and 4.5 years revealed persistent bilateral and symmetric abnormal signals in basal ganglia mainly caudate and Globus pallidus nuclei with progression over the time, in addition to a mild supratentorial atrophy. A homozygous missense variant [ENST00000404366.7: c.1057C>T; p.(Arg353Cys)] was identified in the ACY1 gene, consistent with Aminoacylase-1 deficiency. Variant confirmation in patient and segregation analysis in his family were performed using Sanger sequencing method. Analysis by different in-silico prediction tools classified this variant as disease-causing. Our findings, expanded the phenotype spectrum of ACY1-related neurodegeneration by demonstrating persistent basal ganglia involvement. Keywords:

Investigating the inhibitory effect of the designed antibacterial peptide as a new antibiotic against metronidazole-resistant *Helicobacter pylori*

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نوع پذیرش: پوستر | کد مقاله: G-09273

Abstract: Background: *Helicobacter pylori* is an important risk factor in chronic gastritis, gastric ulcer and gastric cancer. The main purpose of this article is to investigate the effect of the designed antibacterial peptide that had inhibitory properties on the Oxygen-insensitive NADPH nitroreductase enzyme of *Helicobacter pylori* resistant to metronidazole. Materials and Methods: This research is a descriptive analytical study in which antimicrobial peptide, heliquet, hemopi databases and hex8 software were used to design antibacterial peptide as a new antibiotic against *Helicobacter pylori*. Results: Using the antimicrobial peptide database, the peptide MBP-1 (Maize Basic Peptide 1) It was selected with a length of 33 amino acids and by using the heliquet database and considering the criterion of minimizing oxidizable amino acids and checking in the hemopi database, a peptide with a length of 11 amino acids and the structure of RSGRGECRRQC was designed and using the HEX8 software, the inhibitory effect of the designed peptide compared to metronidazole on *Helicobacter pylori* was investigated and due to the more negative molecular docking energy of the designed peptide compared to metronidazole, this peptide showed stronger inhibitory effects against *Helicobacter pylori*. Conclusion: Due to the lower energy of the designed peptide compared to metronidazole, this peptide can be effective in inhibiting the oxygen-insensitive NADPH nitroreductase enzyme, which is effective in the resistance of *Helicobacter pylori* to metronidazole. To prevent the construction of the beta sheet of the second structure, are designed because it causes incomplete solubility of the constructed peptide. Cysteine, methionine, and tryptophan have a negative effect on the solubility and purity of the peptide because they tend to be oxidized and should be minimized. The number of hydrophobic amino acids (leucine, valine, isoleucine, methionine, phenylalanine and tryptophan) should be kept below 50%.
Keywords: antimicrobial peptide, helicobacter pylori, metronidazole resistance

Study on differences in virulence factors between Escherichia coli and Pseudomonas aeruginosa that cause urinary tract infections

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نوع پذیرش: پوستر | کد مقاله: G-31095

Abstract: Background: Urinary tract infections (UTIs) are one of the most frequent ambulatory bacterial infections with a lifetime incidence of 50 - 60% among adult females. Risk factors associated with the host include immune deficiency of the host, urinary tract abnormality, bladder dysfunction in type 2 diabetes, behavioral factors, and estrogen deficiency. Bacterial factors are also reported to be associated with UTI pathogenesis and progression. Methods: Studies were collected using different keyword combinations: Urinary Tract Infection, Virulence Factor, Escherichia coli, Pseudomonas aeruginosa, Elsevier and Pubmed, Science Direct, Web of Science, Google Scholar, and Scopus. Results: The surface protein regulation serves as a key tool in differentiating the pathogen isotypes. Furthermore, it might provide insights on novel diagnostic methods to detect uropathogen that are otherwise easily overlooked due to limited culture-based assays. Conclusion: In essence, this review shall provide an in-depth understanding on secretion of virulence factors of various uropathogens and their role in host-pathogen interaction, this knowledge might be useful in the development of therapeutics against uropathogens. P. aeruginosa and E.coli an increasingly problematic drug-resistant bacterium in today's world. Uropathogenic Escherichia coli (UPEC) and Pseudomonas aeruginosa express a multitude of virulence factors, which enable the bacteria to establish UTI. Keywords:

Urinary Tract Infections in During Pregnancy and Its Effect on the Delivery

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نوع پذیرش: پوستر | کد مقاله: G-07128

Abstract: Background: Urinary tract infections (UTIs) are the most common type of infection during pregnancy, affecting up to 10% of pregnant women. They are also recognized as the second most common ailment of pregnancy, after anemia. It is most commonly reported among pregnant women and is a known reason of morbidity during pregnancy worldwide, predominantly in developing countries. Methods: Studies were collected using different keyword combinations: Urinary Tract Infection, Pregnancy, and Fetus. The literature search strategy in this paper included searching PubMed, PMC, and Science Direct, Springer open, Google scholar and BioMed Central databases. Results: Women who had a UTI during pregnancy had more preterm deliveries than those without a UTI. Recurrent UTI was observed in 26.6% of women with UTI, while the incidence of pyelonephritis was relatively low in this group. The most common bacteria isolated from women with UTI were Group B Streptococcus, followed by Escherichia coli. They were sensitive to a wide range of antibiotics. Conclusion: According to our results, Women who have a urinary tract infection during pregnancy are more likely to give birth prematurely. However, with proper treatment, other complications such as pyelonephritis and undesirable perinatal outcomes can be minimized. Available evidence recommends routine screening for asymptomatic bacteriuria (ASB) in early pregnancy to minimize complications and identify women at increased risk of preterm birth. Keywords:

Screening, molecular identification and population diversity of Actinomycetes species isolated from meat and meat product of slaughterhouse, restaurant and meat store of a developing country, Iran.

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نوع پذیرش: پوستر | کد مقاله: G-03426

Abstract: Background: Actinomycetes can colonize the surfaces of tools and equipment and be transferred to the meat and meat product during manufacture, processing, handling and storage. Moreover, conventionally cleaning of meat not fully effective in eradicating microorganism to each product. Thereby, these opportunistic pathogens enter the human body and cause various infections. Due to this effort, the aim of current study was to screening and identification of Actinomycetes species from meat and meat product of Markazi province of Iran. Materials and methods: A total of 60 meat and meat product samples including: minced meat, mutton, beef, chicken, hamburgers and sausages were collected from slaughterhouses, butchers and restaurants of Markazi province of Iran. The samples were analyzed by using standard microbiologic protocols for isolation and characterization of Actinomycetes. The PCR amplification of hsp65 and 16SrRNA genes, and sequence analyses of 16SrRNA were used for the genus and species identification. Results A total of 21(35%) Actinomycetes isolates from 5 genus and 12 species were isolated from 60 samples. The most prevalent Actinomycetes were genus Mycobacterium with 6(28.6%) isolates (*M. avium* complex, *M. terrae*, *M. smegmatis*, and *M. novocasterense*) followed by genus Rhodococcus with 5(23.8%) isolates (*R. equi* and *R. erythropolis*) and genus Actinomyces with 4(19.1%) isolates (*A. ruminicola* and *A. viscosus*), genus Nocardia with 4 (19.1%) isolates (*N. asiatica*, *N. seriolae* and *N. niigatensis*) and genus Streptomyces with 2(9.5%) isolates (*S. albus*). Chicken and sausage samples with 6 and 1 isolates had highest and lowest level of contamination respectively. Conclusion The finding proves that meat and meat product have an important role as a reservoir for transmission of Actinomycetes to humans. Consequently, causing life threatening food borne disease such as gastrointestinal and cutaneous disorders. Hence, it is essential that basic hygiene measures are incorporated in cycle of meat production to ensure food safety.

Keywords:

Investigating the modulatory effects of *Lactobacillus crispatus* strain RIGLD-1 on *Helicobacter pylori*-triggered inflammation in gastric epithelial cells

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نوع پذیرش: پوسنر | کد مقاله: G-51798

Abstract: Background: Potential probiotic *Lactobacillus crispatus* bacteria are able to protect against *Helicobacter pylori* infection through ameliorating the inflammatory response in gastric epithelial cells. Materials and Methods: The effect of *L. crispatus* strain RIGLD-1 on mRNA expression level of IL-6, IL-8, IL-1 β , TNF- α , TGF- β , and IL-10 genes was investigated in *H. pylori*-stimulated AGS cells by RT-qPCR assay. ELISA was used to measure the production of IL-8 in the supernatant of treated AGS cells. The inhibitory effect of *L. crispatus* on *H. pylori* adhesion and invasion to AGS cells was also determined. Results: *L. crispatus* RIGLD-1 strain significantly downregulated the gene expression level of IL-6, IL-8, IL-1 β , and TNF- α and upregulated the gene expression level of TGF- β , and IL-10 in *H. pylori*-stimulated AGS cells after 24 hours of coinfection. Furthermore, *H. pylori*-induced IL-8 production was dramatically decreased after treatment with *L. crispatus*. Also, *L. crispatus* significantly inhibited the *H. pylori* adhesion and invasion to the gastric epithelial cells. Conclusion: The probiotic strains of *L. crispatus* can ameliorate *H. pylori*-induced inflammation and could be developed as an effective supplementation to the current treatment regimens administrated against *H. pylori* infection and its related gastric diseases. Keywords:

Investigating the antibiotic and biocide resistance and prevalence of qacAB, smr and norA genes in vancomycin-resistant enterococci isolated from Isfahan

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نوع پذیرش: پوستر | کد مقاله: G-05871

Abstract: Background: The widespread use of biocides in hospitals has increased the prevalence of resistant strains. Vancomycin-resistant enterococci (VRE) are one of the most common hospital pathogens due to antibiotic and biocide resistance, which has become of the major problems in hospitals. Determining the antibiotic resistance pattern of VRE isolates and the minimum inhibitory concentration of chlorhexidine and benzalkonium chloride, investigating the prevalence of biocide resistance genes norA, smr and qacAB and measuring the lethality time of biocides are among the goals of this study. Materials and Methods: In this study, 50 isolates of VRE were collected from teaching hospitals in Isfahan and confirmed by microbiological testing. Antibiotic susceptibility was determined by disk diffusion method and the minimum inhibitory concentration of benzalkonium chloride and chlorhexidine was determined by broth microdilution method. Prevalence of biocide resistance genes and determining the killing power of biocides were investigated by PCR and time-kill assay. Results: Among 50 clinical isolates, all isolates were resistant to ciprofloxacin and erythromycin and susceptible to linezolid. We reported the MIC range of benzalkonium chloride and chlorhexidine 4-8 µg/ml and 1-8 µg/ml respectively. norA, smr and qacAB genes were detected in 84%, 56% and 24% of the isolates. Conclusion: The Continuous control of antibiotic and biocide resistance because of the increase of biocide resistance genes in VRE isolates, allows us to prevent the further spread of hospital pathogens by choosing the appropriate antibiotic for treatment and using accurate concentrations of biocidal agents. Keywords:

Evaluation the bacterial contamination of personnel face masks working in a center of Corona hospitalized patients

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نوع پذیرش: پوستر | کد مقاله: G-93170

Abstract: Background: During the Corona Pandemic, the use of masks has increased a lot. While lack of observing system to hygiene protocols and the need to use PPE properly causes the transmission and spread of infection more including bacterial agents. Therefore, the purpose of this study is to investigate the degree of contamination and frequency of bacterial species isolated from surgical and N95 masks used by hospital personnel, as well as to investigate the antimicrobial susceptibility pattern of the isolates against routine antibiotics and disinfectants using both disk-diffusion and micro-dilution methods. Material and methods: A total number of 175 masks were collected from staff working in Sina hospital (Hamadan province, Iran) during the first six months of 2022. The bacterial contamination of masks were evaluated and identified using biochemical kits. Antimicrobial susceptibility testing of the isolates were done using Kirby-Bauer methods and MIC were assessed for each isolate against different disinfectants (Sodium hypochlorite 5%, Hydrogen Peroxide 3%, Ethanol 70% and Deconex). Results: Of 175 masks, 471 bacterial isolates were detected including 9 species. The most prevalent strain were Coagulase negative Staphylococcus (28%) followed by Acinetobacter (20.8%) and Pseudomonas (13.8%). While, Klebsiella and Enterococcus were the least frequent species with the rate of 3.8% and 1.2%, respectively. The data informed that 64.5% of the isolated were resistant to Ampicillin and highest susceptibility were observed for Imipenem (61.4%). The results of MIC methods indicates that all 471 strains were resistant to ethanol 70% and sensitive to hydrogen peroxide 3%. Furthermore, the mean average of Deconex inhibitory effect is lower than Sodium hypochlorite 5%. Conclusion: According to the results of this study the high prevalence of CoNS, Acinetobacter and Pseudomonas in hospital wards and also high resistance pattern they depicted against antibiotics specially Ampicillin and disinfectants. It is recommended the need to follow hygiene principles. Keywords:

Rapid identification of *Mycoplasma hominis* in women's endocervical samples referred to infertility hospital of Hamadan using PCR method.

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نوع پذیرش: پوستر | کد مقاله: G-48591

Abstract: Background: *Mycoplasma hominis* colonizes in the female genital tracts and can cause some genital disorders such as vaginitis, infertility, abortion, preterm delivery. The aim of this study was to compare PCR and culture methods to determine *Mycoplasma hominis* in the women's endocervical samples who were referred to infertility hospital of Hamadan (west of Iran) in 2016. Materials and Methods: 234 women who had at least one of the genital disorders symptoms such as vaginitis, infertility, abortion, preterm delivery were included in study. The endocervical samples were taken, using the sterile swab. The samples were cultured in a specific *Mycoplasma media* (PPLO) and were identified by culture results and PCR molecular techniques to detect the 16s rRNA gene. Descriptive statistics were used to analyze the data. Results: From 234 samples, 14 isolates (6%) were identified as *Mycoplasma hominis* by culture methods and 30 isolates (12/7%) were detected by PCR method. The prevalence of *Mycoplasma hominis* in the studied population was 13.7% in both methods. The genital tracts of 12.3% patients with vaginitis and 10.3% with infertility were colonized by *Mycoplasma hominis* species. The sensitivity of PCR method was 91.82%, while the sensitivity of culture method was 85.71%. Conclusion: The prevalence of *Mycoplasma hominis* in the studied population was significant, so further investigation is necessary. Our results also showed that PCR method was sensitive than culture method to detect *Mycoplasma hominis*, but agreement coefficient between culture and PCR method was very high ($k = 0.5$). Keywords: *Mycoplasma hominis*, vaginitis, abortion, Culture, PCR

The antibacterial activity of niosomal drug delivery system on the clinical isolate of staphylococcus aureus

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نوع پذیرش: پوستر | کد مقاله: G-25630

Abstract: Background: Staphylococcus aureus causes severe infections in human. The use of antibiotics for infectious diseases, in addition to side effects have caused a series of bacterial resistances. The aim of this research was to investigate the loading of gentamicin drug in noisome nanocarriers on the clinical isolate of Staphylococcus aureus. Materials and Methods: After gram staining, the other tests as catalase, coagulase, DNase and antibiogram were performed on Staphylococcus aureus (PTCC 1112 _ ATCC 6538) and collecting information to investigate the effect of three formalizations, based on Span 60, Tween 60 and cholesterol, on the synthesis of Noisome nano systems loaded with the antibiotic gentamicin by thin layer hydration method, and after characterizing the synthetic nano systems, antibacterial activity, they were evaluated by performing minimum inhibitory concentration (MIC) and inhibition zone tests. Results: All three formulations of noisome containing gentamicin contained more than 50% of the drug, and the antibacterial activity of the diluted drug in noisome had the same result as free gentamicin, and the drug was more stable and released. The drug was available for a longer period of time. Conclusion: This research showed that noisome are a suitable, targeted and effective drug delivery system for the treatment of many diseases and have a higher capability than conventional drug treatments. Keywords: Staphylococcus aureus, Gentamicin, Antibiotic, Nanosystem, Nisome

Antibacterial activity of chitosan based nanohybrid membranes against drug resistant bacterial isolates from burn wound infections

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نوع پذیرش: پوستر | کد مقاله: G-72964

Abstract: Background: Biocompatible and non-toxic properties of chitosan make it a candidate with excellent application prospects in developing wound dressing conjugate compounds. Materials and Methods: Six different chitosan-based nanohybrid membranes were evaluated against multidrug-resistant bacterial isolates. Different combinations of chitosan, ciprofloxacin (CIP), biofunctionalized montmorillonite (MMT), and montmorillonite with sulfate chains (SMMT) were provided, and their antibacterial activity was assessed using the colony count method Results: Totally, 27 drug-resistant isolates, including 6 methicillin-resistant *Staphylococcus aureus*, 7 vancomycin-resistant *Enterococcus faecalis*, 4 *Acinetobacter baumannii*, and 10 *Pseudomonas aeruginosa* isolates were identified from burn wound infections. Chitosan and montmorillonite did not show significant antibacterial effect ($p > 0.05$), but chitosan/SMMT/CIP was the most effective nanocomposite ($p < 0.01$). Chitosan-based nanocomposites with ciprofloxacin could effectively reduce the susceptibility of drug-resistant bacterial isolates. Conclusion: Bacterial targeting using nanosystems provides an opportunity for effective antibiotic treatment by improving antibacterial efficacy. Keywords:

Evaluation of the effect of Sarfosept Quick, sodium hypochlorite (Vitex), Intrahydrocor on Escherichia coli isolates

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نوع پذیرش: پوستر | کد مقاله: G-65213

Abstract: Background: Escherichia coli is an opportunistic and pathogenic microorganism that causes hospital infections. Pollution of environmental surfaces and its transmission is an effective factor in the development and spread of hospital infections, so it is necessary to eliminate bacteria from the hospital environment, especially E.coli. The use of disinfectants is effective in preventing and controlling hospital infections. In this research the effect of three disinfectants, Sarfosept Quick, sodium hypochlorite and Intrahydrocor with dilutions according to the manufacturer's instructions on the growth of a number of E.coli isolates from infectious urine samples. Materials and Methods: In this study 50 samples were collected from the general departments of the hospital. The presence of E.coli was confirmed by using biochemical and molecular methods with Lacz gene amplification by PCR technique and after culture. After culture, an approximate concentration of half McFarland was prepared from them. Then, the dilution effect of each disinfectant according to the instructions of the manufacturer was tested on 19 isolates by the Pour Plate Method in 5, 10, 15 minutes; the growth and non-growth of bacteria after these times were examined. Results: This research shown that the above three disinfectants inhibited the growth of all 19 strains of E.coli isolated, according to the dilutions recommended by the manufacturer and were effective on E.coli at all three times studied. They are 100% effective and efficient Conclusion: The dilutions proposed by the manufacturers of Surfosept Quick, Sodium hypochlorite (Vitex), Intrahydrocare are quite effective against Escherichia coli, and the results of our research were similar to some researches. Keywords:

Immunogenicity and cross-protective evaluation of chimeric OprF-OprI-PopB protein formulated with GM-CSF targeting *Pseudomonas aeruginosa*

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نوع پذیرش: پوستر | کد مقاله: G-26195

Abstract: Background and Aim. A vaccine versus *Pseudomonas aeruginosa* (*P. aeruginosa*) derived from outer membrane protein, including OprI and OprF, and the type three secretion system, consisting of PopB, can be protected from *Pseudomonas* infections. Due to enhancing the active immune response, the current study formulated FIB antigen with Granulocyte-macrophage colony-stimulating factor (GM-CSF) as a potent adjuvant. The purpose of this experiment was the construction, expression, and evaluation of recombinant protein containing OprF, OprI, and PopB (FIB) in the burned rat by measuring the levels of the subtypes of IgG and IgA antibody titers and the level of IL-17, IFN- γ , and IL-4 before and after challenge. Methods. The primitive sequencing and construction of the FIB protein were designed, prepared, and then synthesized via the BIOMATIK Company. Then, for the expression and purification of the recombinant protein, SDS-PAGE, western blotting, and chromatography via the Ni-NTA column were accomplished, dialyzed in PBS, and confirmed Bradford using protein assay. Female Wistar rats were divided into four groups, immunized with FIB protein, FIB+GM-CSF, GMCSF, and PBS; the response of antibody and cytokine assay were performed using ELISA. Results. The comparison of IgG1, IgG2a, IgG2b antibodies, and cytokines IL-17, IL-4, and IFN- γ levels indicated a higher rate of Th1 and Th2 oriented responses against *P. aeruginosa* chimeric FIB antigen. Based on our results, the FIB antigen was a potent IgA inducer in the presence of an adjuvant. As we compared the immunogenic response against FIB and FIB+GMCSF, our results revealed the valuable property of GM-CSF in expanding those responses. Furthermore, this substance enhanced the humoral and cell-mediated immune response against this opportunistic pathogen. Conclusion. Our findings highlighted that FIB plus GM-CSF immunization would be helpful as an immunogenic substance for treating *P. aeruginosa* infections. Keywords. Vaccine; *Pseudomonas aeruginosa*; OprF-OprI-PopB; GM-CSF; ELISA

Comparison of GeneXpert, Mycobacterial Culture, Smear Microscopy for Diagnosis of Pulmonary Tuberculosis In Reference Laboratory Of Mycobacterium Shiraz, Iran, 2019-2022

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نوع پذیرش: پوستر | کد مقاله: G-74521

Abstract: Objective To investigate the application value of GeneXpert, mycobacterial culture, smear microscopy in the detection of mycobacterium tuberculosis among tuberculosis suspicions patients. Methods A retrospective analysis was performed on the patients who referred to laboratory during 2019 to march 2022. The patients with positive tuberculosis culture or positive GeneXpert in pulmonary tuberculosis were selected as the case group, and those without tuberculosis served as the control group. The receiver operating characteristic (ROC) curve was used to evaluate the diagnostic value of GeneXpert, culture, smear microscopy ratio. Results For the patients with positive cultures as case, the sensitivity of GeneXpert, smear microscopy ratio was 92.16%, 80.00% respectively, the specificity was 100.00%, 86.00, respectively. For the patients with positive GeneXpert as case, the sensitivity of mycobacterial culture, smear microscopy was 95%, 80%, respectively, the specificity was 100.00%, 86.00, respectively. Conclusion The sensitivity and specificity of GeneXpert was best. The sensitivity and specificity of smear microscopy was lower. Gene Xpert is useful for rapid detection of TB especially in a high prevalence country. The results are superior to smear microscopy and comparable to culture with shorter turn-around time. Key words: pulmonary tuberculosis, GeneXpert, smear microscopy, culture

Evaluation of primary drug resistant Tuberculosis cases by conventional and molecular methods in Reference laboratory of Mycobacterium Shiraz, Iran, 2019-2022

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نوع پذیرش: پوستر | کد مقاله: G-68350

Abstract: Introduction & objectives: Drug resistant TB is major problem in world and Iran .Multidrug – resistant TB (MDR-TB) caused by resistant TB bacilli to at least Isoniazid and Rifampicin which is intrinsically resistant to drugs or can be appear by inconsistent or partial treatment or incomplete application of Dots program and increasing of TB/HIV cases. The aim of this survey was to evaluate intrinsical drug resistant cases in Shiraz Reference TB laboratory. Materials & Methods: During the study 328 new cases which were acid fast positive and confirmed as mycobacterium tuberculosis positive by gen expert method from southern provinces of Iran were subjected to Drug Sensitivity Test (DST) by proportional method in Lowenstein- Jensen media and compared with molecular method. Results: Among 328 cases, 294 cases were sensitive to Isoniazid, Rifampicin, and Ethambutol. 11 cases were resistant to Isoniazid and Rifampicin, 12 cases were monoresistant to isoniazid, 1 cases were resistant to Isoniazid and ethambutol.10 cases were monoresistant to Rifampicin. Conclusion: During 2019-2022 ratio of laboratory proven initial multidrug resistance in tuberculosis patients was 3.3%, monoresistant to Isoniazid was 3.65% and monoresistant to Rifampicin was 3.04% Resistance to Isoniazid and ethambutol was 1.1%. Keywords: Intrinsical MDR TB, Drug sensitivity test, proportional methods, Molecular

The bacterial etiology and Antibiotic resistance profile of Bloodstream Infections in the north of Khuzestan

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نوع پذیرش: پوستر | کد مقاله: G-13078

Abstract: Background: Septicemia is a severe and life-threatening infection caused by several pathogenic bacteria. The spread of antibiotic resistance in bacteria can make it difficult to treat patients. In this medical emergency, early diagnosis and antibiotic treatment play an important role in the prognosis of patients. In this study, the frequency and antibiotic resistance profile of bacterial isolated from blood cultures of patients referred to Dezful, Ganjavian Teaching Hospital were investigated. Materials and Methods: In this cross sectional study, blood culture samples were collected from hospitalized patients under standard conditions. The samples at 24 and 72 hours and the sixth day after the initial incubation were cultured on MacConkey and chocolate agar media in suitable atmospheres. The bacterial identification were used according gram staining and biochemical tests. Then initial and confirmatory antibiotic susceptibility testing for detection of Methicillin resistant S.aureus (MRSA), Vancomycin Resistance Entrococcus (VRE), Extended spectrum beta-lactamases (ESBLs) and resistance to colistin was performed according to CLSI 2022. Results: A total of 173 positive blood cultures were isolated from 88 men and 85 women patients. The most frequent bacteria were Escherichia coli, Staphylococcus aureus, Klebsiella pneumoniae, Enterobacter aerogenes and enterococci with 25.4%, 23.1%, 13.9%, 6.9% and 6.9%, respectively. In gram-positive isolates, the effective antibiotics were vancomycin, gentamycin and linezolid. MRSA and VRE strains were 70% and 36.3%, respectively. The resistance pattern of Enterobacteriaceae were as follows: meropenem 84.8%, amikacin 83%, gentamicin 83%, ciprofloxacin 71.3% and ceftriaxone 54% and 21.4% strains were ESBL producing. No colistin-resistant strains were isolated from Acinetobacter baumannii and Pseudomonas aeruginosa strains. Conclusion: Although vancomycin and colistin were observed the most effective antibiotics, the risk of their indiscriminate use and the occurrence of widespread resistance should be emphasized by the antibiotic stewardship committee in hospitals. Keywords: Blood culture, Antibiotic resistance, ESBL, MRSA, VRE.

Evaluation of the antibacterial effect of carvacrol alone and in combination with the antibiotic cefixime against *Escherichia coli* O157:H7.

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نوع پذیرش: پوستر | کد مقاله: G-37924

Abstract: Background: Today, the use of plant compounds and their derivatives such as extracts and essential oils to combat infectious agents is highly regarded by researchers. One of the active antimicrobial compounds with plant origin is carvacrol. The aim of the present study was to evaluate the antibacterial activity of carvacrol alone and in combination with the antibiotic cefixime against *Escherichia coli* O157:H7. Materials and Methods: The Antibacterial properties of carvacrol and cefixime were evaluated by determining the Minimum Inhibitory Concentration (MIC), Minimum Bactericidal Concentration (MBC) and disk diffusion method. The Checkerboard assay was used to evaluate the interaction between the carvacrol and cefixime and to determine the fractional inhibitory concentration. Results: The result showed that the MIC and MBC of carvacrol and cefixime against *E. coli* O157:H7 was 250, 250 µg/ml (MIC, MBC) and 128, 128 µg/ml (MIC, MBC) Respectively. In the checkerboard test, carvacrol had synergistic interaction with antibiotic cefixime against *E. coli* O157:H7 (FIC index=0/5). Conclusion: Due to the significant antibacterial activity of carvacrol, the present study introduces this agent as a new antibacterial drug with natural origin. In addition, since carvacrol significantly increased the antibacterial potential of cefixime (synergistic properties), carvacrol could be introduced as an effective compound to increase the antibacterial power of cefixime antibiotic. Keywords:

Association between integrons and metallo- β -lactamases in environmental *Acinetobacter baumannii* isolates in two hospitals

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نوع پذیرش: پوستر | کد مقاله: G-80479

Abstract: Background: *Acinetobacter baumannii* is considered a major cause of hospital-acquired infections. One of the important sources of infection with *A. baumannii* is surfaces contaminated with this bacterium in the hospital. This study was designed to evaluate association between integrons and metallo- β -lactamases (MBLs) in environmental *A. baumannii* isolates in two hospitals. Materials and Methods: Fifty-three carbapenem-resistant *A. baumannii* were isolated from the patients surrounding environmental surfaces in two hospitals. Antibiotic susceptibility testing of isolates was performed according to CLSI. The integrin class 1 and MBLs associated genes were assessed by PCR and sequencing. Results: All isolates were multidrug-resistant *A. baumannii* and none were resistant to colistin. The highest rates of resistance were obtained to ceftazidime, trimethoprim/sulfamethoxazole, imipenem, ciprofloxacin and gentamicin. The blaVIM, blaIMP MBLs genes and integrin class 1 were detected in 94.3%, 86.8% and 71.7% of *A. baumannii* isolates respectively. Conclusion: The high prevalence of metallo- β -lactamases producing *A. baumannii* harboring integrons in this study indicates the high potential of resistant strains for widespread expansion in the studied hospitals. Keywords: *Acinetobacter baumannii*, Metallo- β -lactamases, Integron

The high level resistance of carbapenemase and extended-spectrum β -lactamase producing *Escherichia coli* and *Klebsiella pneumoniae* isolates from nosocomial infections.

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نوع پذیرش: پوستر | کد مقاله: G-38652

Abstract: Background: *Escherichia coli* and *Klebsiella pneumoniae* bacteria with their specific resistance pattern to carbapenemase and extended-spectrum β -lactamase are the importance bacteria of nosocomial infections, therefore, identification and determining resistance to extended spectrum beta-lactamase (ESBLs) and carbapenemases to implement are essential to appropriate strategy and controlling nosocomial infections. Materials and Methods: Clinical samples from nosocomial infections were collected, then identify of bacterial were using phenotypic and biochemical examinations with standard methods. Overall, 57 *E.coli* and *K. pneumoniae* isolated from different infection sites were used to determine ESBLs and carbapenemases enzymes by phenotypical and moulocular (PCR) method. Results: Of 57 isolates of *E.coli* and *K. pneumoniae* overall, 43 (75.43%) ESBLs and 9 (15.79) isolates were Carbapenemases producers. Pcr showed high prevalence of the blaCTX-M 39 (90.69%) in ESBLs genes. Distribution of Carbapenemase gene the blaNDM 5(55.55%) *K. pneumoniae* isolates was detected. bla OXA-23 gene was observed in 4(44.44) *K. pneumoniae* and 1(11/11%) of *E. coli* isolate. The blaKPC and blaOXA-48 genes were detected in only 1(11.11%), *E. coli* isolate and *K.pneumoniae* isolate respectively. The blaVIM and blaIMP genes were not observed in any isolates. Conclusion: The interesting point of our study was the first identification of blaOXA-11, blaOXA-23, blaKPC and blaNDM-1 genes in *E.coli* and *K.pneumoniae* at ILAM city, which is very important due to high resistance to carbapenems and should be taken into consideration. Keywords: Nosocomial infection, *E. coli*, *K.pneumoniae*, ESBLs, Carbapenamase

Investigation of Bacterial toxins effects on malignant tissues

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نوع پذیرش: پوستر | کد مقاله: G-65190

Abstract: Background: One of the most important reason of mortality rate around the world, is suffering to different kinds of Cancer. Cancer is usually one of the third major factor of dying in human. Finding the best substances which have the lowest side effect for body cells, always was being an important aim for researchers. Some bacteria can produce toxic materials which can inhibit cell growth. It seems this is a new treatment for controlling malignancy. Material and Methods: This research is a review article and all data were collected by searching the MeSH terms like: bacterial toxins, anticancer, bacteriocins, etc in NCBI and PubMed using engines like as MEDLINE, Science Direct, ISI Web of Science. Results surveying on papers and articles revealed that some bacteria like Pseudomonas aeruginosa, Corynebacterium diphtheria, Streptococcus pyogenes and recently Bacillus turengensis, and many others bacteria produce specific materials which can inhibit cell growth on cancer's cells. Their mechanisms are different and they act on several ways. Conclusion: Finding new substances which have toxic effects on cancer's cell can be hopeful for patients whose loose their hope. This can replace instead of chemotherapy drugs and decreased their awful effects. Keywords:

Prevalence of Coagulase negative staphylococci (MRCoNS) strains isolated from patients with cancer

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نوع پذیرش: پوستر | کد مقاله: G-67201

Abstract: Background: Coagulase-negative staphylococci (CoNS) have emerged as major nosocomial pathogens especially in immunocompromised patients. This study aimed to determine the frequency of Methicillin-resistant coagulase-negative Staphylococci (MRCoNS) antibiotic resistance patterns. Materials and Methods: MRCoNS isolates were identified with cefoxitin disc (30 µg) on Mueller Hinton Agar (Merck, Germany) plates in accordance with the Clinical and Laboratory Standards Institute (CLSI) guidelines. The 16S rRNA (specifically detecting Staphylococcus species) and nuc (distinguishing *S. aureus* from CoNS) genes amplification was done by a multiplex-polymerase chain reaction (M-PCR) using sets of designed primers. Finally, the resistant isolates were confirmed as MRCoNS using PCR for amplification of *mecA* gene. Results: Out of the 307 clinical bacterial isolates, 79 (25.7%) isolates were confirmed as Staphylococcus species. According to PCR analysis, 41 isolates (51.9 %) were different coagulase-negative staphylococci (CoNS) species. 65.9% (27/41) and 34.1% (14/41) of isolates were confirmed as MRCoNS and methicillin-sensitive CoNS (MSCoNS), respectively. The antimicrobial susceptibility pattern for MRCoNS isolates were as follows: erythromycin 90.2%, clindamycin 70.7 %, cefoxitin 65.9 %, tetracycline 48.2 %, rifampicin 46.3 %, ciprofloxacin 46.3 %, cotrimoxazole 39.1 %, teicoplanin 12.2 %, and linezolid 9.8%. Conclusion: Recent data indicated the MRCoNS strains as the predominant Gram-positive pathogens isolated from various infections in cancer patients. It is recommended that regular monitoring programs be among the priorities of health policy makers in order to reduce the faster spread of resistant strains in the population of cancer patients and reduce the resulting mortality. Keywords: Cancer patients, Methicillin-resistance Staphylococcus aureus, antimicrobial resistance.

Genotypic investigation of the presence and identification of diffusely adherent Escherichia coli (DAEC) strains in human urinary pathogens.

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نوع پذیرش: پوستر | کد مقاله: G-50412

Abstract: Background: Urinary infection (UTI) is one of the most common hospital-acquired and community-acquired bacterial infections. The cause of 80 to 90% of urinary infections are extraintestinal Escherichia coli strains called uropathogenic Escherichia coli (UPEC) strains. Uropathogenic Escherichia coli strains consist of different types, including diffusely adherent Escherichia coli strains (DAEC). Diffusely adherent Escherichia coli is defined by a pattern of diffusely adhesion to HEP-2 or Hela epithelial cells. Diffuse adhesion phenotype, due to the production of adhesins by the afa/dra/daa genes encoded by the Afa/Dr/F1845 operons, respectively. Initially, this pathotype was described as associated with diarrhea in children aged 1 to 5 years, but the diffusely adherent pathotype of extraintestinal Escherichia coli is now recognized as a pathotype causing urinary infection. Materials and Methods: In this study, the genotypic investigation of the presence and identification of diffusely adherent strains of Escherichia coli in urinary pathogenic isolates and the ability to produce biofilm by these pathotypes were investigated. Checking the presence of this pathotype was done by PCR test and biofilm production by microplate test. Results: A total of 100 urinary isolates were analyzed by three separate PCRs to detect three afaBC/afaC/daaE genes. urinary isolates (23%) among the 100 available samples have been identified as containing the diffusely adherent Escherichia coli pathotype. The number of samples containing each of these three genes in the total urine samples is such that 21 samples (21%) contain the afaBC gene, 11 samples (11%) contained the afaC gene and 2 samples (2%) contained the daaE gene. The ability to produce biofilm by the diffusely adherent pathotype of Escherichia coli was evaluated poorly, which included 16 isolates (61.5%) and one sample of the diffusely adherent pathotype showed an average ability to produce biofilm, and none of the existing diffusely adherent pathotypes had the ability to produce biofilm. Conclusion: According to the investigations, we found that molecularly, a significant percentage of urinary strains fall into the diffuse adhesive pathotype category of Escherichia coli, although they are not strong in terms of biofilm production and fall into the weak biofilm producer category. In order to make a more accurate evaluation of Escherichia coli disseminated adhesive strains and its ability to produce biofilm, the evaluation of adhesion patterns of this isolate should be investigated in the future
Keywords: : Escherichia coli, diffusely adherent Escherichia coli, uropathogenic Escherichia coli,

Worldwide prevalence of extended-spectrum β -lactamases-producing uropathogenic Escherichia coli isolates among kidney transplant patients: a systematic review and meta-analysis

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نوع پذیرش: پوستر | کد مقاله: G-53762

Abstract: Background: A substantial proportion of urinary tract infection (UTI) usually impacting kidney transplant patients (KTP) is caused by the worldwide increase in extended-spectrum β -lactamases (ESBLs) and multi-drug resistance (MDR) of E. coli strains. For this reason, the current meta-analysis was conducted to summarize current evidence on the frequency of ESBL-producing UPEC among KTPs. Materials and Methods: A systematic search was conducted to identify studies meeting our inclusion criteria in the Web of Science, PubMed, Embase, and Scopus electronic databases between 2000 and 2021. Finally, 16 articles were selected for data extraction, and meta-analysis was performed using the metaprop program in the STATA (version 11) software. Results: From those studies, the pooled prevalence of ESBL-producing UPEC isolates was 40%. The subcategory analysis results based on continent indicated that Asian countries had the highest rate of ESBL-producing isolates with 45%, followed by 40%, 28%, and 16% in Europe, South America and North America, respectively. Conclusion: Uncomfortably, 40% of the UPECs in the current investigation were ESBL-producing isolates. These isolates pose a serious threat to public health because they can contribute to the spread of antimicrobial resistance in the local population and hasten the ineffectiveness of the majority of commonly prescribed antibiotics for the treatment of UTI in KTPs and other patients. Keywords: Escherichia coli, uropathogenic Escherichia coli, kidney transplant patients, extended-spectrum β -lactamases, ESBL

The effects of postbiotics of probiotic and protective cultures on proliferation and apoptosis of HCT-116 cells

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Abstract: Background: Postbiotics are microbial-derived bioactive compounds (by-products) which are produced during the growth and fermentation process of beneficial microorganisms in the food, gastrointestinal (GI) tract, or complex microbiological culture systems (commonly named extracellular extract or ECE) or after cell lysis (commonly named intracellular extract or ICE). Colorectal cancer (CRC) ranks third among cancers with respect to prevalence as one of the leading causes of cancer-related mortality worldwide. The novel strategy in CRC treatment should be oriented to utilization bioactive compounds like postbiotics aiming to improve the gut microbiome and host immune reactions, and offering adjuvants in the prevention of patients with CRC disease, which could be seen as improving the efficacy of treatment and could be explored to decrease the adverse outcome of available therapies. In current study, the potential effect of ECE and ICE derived from probiotic (*Lactobacillus sakei*; LS) and protective culture (FreshQ®; FQ) on proliferation and cell viability of HCT-116 human colorectal carcinoma cells were evaluated. **Materials and Methods:** Probiotic bacteria were cultivated in de Man, Rogosa and Sharpe (MRS) broth and afterwards postbiotics were isolated by centrifugation and sonication, then, the obtained solutions were lyophilized. HCT-116 cells were treated with various concentrations (1.25-20 mg/ml) of ECE and ICE derived from *Lactobacillus sakei* and FreshQ® (which are containing *Lactobacillus rhamnosus* and *Lactobacillus paracasei*) for 24 hours and then the effects of these compounds on cell cytotoxicity, proliferation and apoptosis were explored and measured by MTT, scratch test (wound healing) and acridine orange/ethidium bromide (AO/EB) assays. **Results:** Extracellular and intracellular extracts of LS and FQ induced a reduction in cell survival in a concentration-dependent manner ($P \leq 0.05$), while cells proliferation and migration was inhibited by extracellular and intracellular extracts of LS and FQ in wound healing assay. The results also represented that the postbiotics could induce apoptosis evidenced by AO/EB staining. **Conclusion:** Finally, in summing up the information and findings of this study, it can be concluded that postbiotics (extracellular and intracellular extract) derived from FreshQ® and *Lactobacillus sakei* can reduce survival (possibly by inducing apoptosis) of HCT-116 colon cancer cells and inhibit their proliferation. Further investigations are warranted to clarify the possible mechanism of action and the signaling pathways behind the induced effects which may offer support options in cancer prevention, control, and treatment protocols. **Keywords:** Postbiotic, Protective culture, Colorectal cancer, Proliferation, Apoptosis

Investigating the effect of shikonin carbon dot on the expression of bap and csuE genes in carbapenem-resistant *Acinetobacter baumannii*

© ۱ لیلیا عدالت خواه

دانشگاه تربیت مدرس^۱

نوع پذیرش: پوستر | کد مقاله: G-45786

Abstract: Background: *Acinetobacter baumannii* is a gram-negative bacterium that is increasingly recognized as an important cause of hospital infections such as bacteremia and ventilator-associated pneumonia. *Acinetobacter* infections are often difficult to treat with multi-drug resistant phenotypes such as resistance to broad-spectrum beta-lactams, aminoglycosides, and fluoroquinolones. This resistance is caused by the production of class D beta-lactamases with carbapenemase activity. Resistance to beta-lactams in *Acinetobacter baumannii* is attributed to the presence of genetic elements. Methods: In this study, the isolates of *Acinetobacter baumannii* were identified by checking the presence of ITS gene by PCR method. Antibiotic resistance in the isolates was done by disk diffusion method on Mullerhinton agar medium. Biofilm formation was investigated by microtiter plate method. PCR was used to identify genes related to biofilm formation, including bap and csuE, in carbapenem-resistant *Acinetobacter baumannii*. PCR method was used to detect the most common gene encoding Oxa23 antibiotic resistance. Isolation of *Acinetobacter baumannii* isolates producing carbapenemase enzymes was done using modified carbapenem inactivation method (mCIM) according to CLSI agenda 2021. Hydrothermal method was used to synthesize shikonin carbon dot. The antibacterial effects of shikonin carbon dot were done by MIC microdilution method and its anti-biofilm effects were done by microtiter plate method. The effect of shikonin carbon dot on the expression of bap and csuE genes of *Acinetobacter baumannii* isolates was investigated by real-time PCR technique using Cybergreen method. Results: Real-time PCR and data analysis, determined that the expression of bap and csuE genes in *A. baumannii* strains treated with MIC concentration (12.5 µg/ml) of shikonin nanoparticles decreased compared to control groups. Conclusion: Due to the inhibitory effect of shikonin against *A. baumannii* biofilm formation and genes expression, they can probably be used for prevent of biofilm formation in medical instrument or can be use for treatment of infections with or without antibiotic. Keywords:

Antimicrobial Susceptibility and Extended-spectrum β -lactamase Producing Escherichia coli Isolates in Tabriz city of Iran

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نوع پذیرش: پوستر | کد مقاله: G-34708

Abstract: Background: Escherichia coli (E.coli) is one of the prominent causes of several fatal diseases worldwide, which it's multidrug-resistant (MDR) strains face the public health with many problems by the Extended-spectrum β -lactamase (ESBLs) production. The rate of bacterial resistance can be different in various regions. This study aimed to determine the prevalence of ESBL-producing E. coli and assess their antimicrobial susceptibility in Tabriz, Iran. Materials and Methods: This study was conducted in the Imam Reza Hospital of Tabriz, from November 2021 to April 2022. A total of 400 E.coli isolates were collected from different clinical specimens. Antimicrobial susceptibility of the isolates was tested by the disk diffusion method. Determination of ESBL-producing bacteria was done by Double Disc Synergy Test (DDST) procedure according to CLSI guidelines. Data were analyzed on SPSS version 23. Results: Out of 400 E. coli isolated, 211 (52.75%) were collected from females and 189 (47.25 %) were from males. The mean age of patients was 52.1 ± 27.9 years. Overall, 279 (69.75%) confirmed as ESBL producer. Among ESBL producers, the highest antibiotic resistance was observed to ceftriaxone (92%) and the least was to imipenem (9%), respectively. Conclusion: The present study, showed a relatively high prevalence of ESBL-producing E. coli among patients referred to Imam Reza Hospital in Tabriz. Imipenem was confirmed as the most efficient antibiotic toward these bacteria, and ceftriaxone was the least effective agent. Keywords: Escherichia coli, Antibiotics, Antimicrobial Susceptibility, Extended-spectrum β -lactamase Research ethical code is: IR.TBZMED.REC.1398.779.

Prevalence of bacterial resistance in patients hospitalized in intensive care units

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نوع پذیرش: پوستر | کد مقاله: G-87049

Abstract: Introduction: Antimicrobial resistance is an essential challenge to global health and poses a serious threat to humans today. Some bacterial strains have resistance to almost all antibiotics. Thus, new antibacterial agents are needed to overcome resistant bacteria. Therefore, we aimed to regard the prevalence and antimicrobial sensitivity patterns of bacteria isolated from samples collected from patients at hospitalized in intensive care units. Methods: 500 culture samples of blood, urine, sputum and discharge fluids were collected from patients admitted to the intensive care unit of Rasoul Akram hospital from November 2021 to November 2022. All samples were studied by microscopic technics and biochemical tests. Then they were checked in all of them by specific media. The collected data were analyzed by SPSS-26 software. Result: Out of 500 patients who were admitted to intensive care unit, 250 patients had positive culture. That 175 (70%) were male and 75(30%) were female. The most prevalent isolates were Klebsiella pneumoniae (n= 85;33.9%), Acinetobacter(n=54;21.5%), Staphylococcus epidermidis (n=16; 6.4%), Pseudomonas aeruginosa (n=30 ;12%), Escherichia coli (n=30 ;12%), Staphylococcus aureus (n=27; 10.8%), Streptococcus milleri (n=2; 0.8%) and stenrophnonas maltophilla (n=6; 2.4%) (Figure A). High rates of antimicrobial resistance were detected across both Gram-negative bacteria. Klebsiella pneumoniae and Acinetobacter were resistant to several agents such as colistin (25%; 23%), amikacin (16%; 21%), ampicillin (12.5%; 12%), sulbactam (11%; 8%), ceftazidime (3%; 17%), tetracycline (14%; 5.4%), cefepime (8.5%; 5.6%) and gentamicin (10%; 8%) respectively (Figure B). Discussion and conclusion: Our results show that most of the microorganisms collected from patients are highly resistant to antibiotics. Also, Klebsiella pneumoniae (33.9%), and Acinetobacter (21.5%) were the most prevalent bacteria, with high rates of antimicrobial resistance to colistin and amikacin. Moreover, it is lower sensitivity to ceftazidime for Klebsiella pneumoniae and tetracycline for Acinetobacter. Further, identifying bacterial strains have resistant to antibiotics can cause to exclude the spread of antibiotic-resistant strains as this prevents the optimal treatment of bacterial infections and limit the choice of effective therapeutic options. Keywords: Antimicrobial resistance, Klebsiella pneumoniae, Acinetobacter, Antimicrobial sensitivity



Investigation the characteristics of Staphylococcus aureus isolated from Children's Medical center, Tehran



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نوع پذیرش: پوستر | کد مقاله: G-07149

Abstract: Staphylococcus aureus (*S. aureus*) can cause disease in almost all organs such as skin, bone (osteomyelitis), heart (endocarditis) and circulatory system (sepsis). *S. aureus* can cause a wide range of diseases in humans through its different virulence genes such as alpha toxin, proteins that damage immune cells such as hemolysins, and enterotoxins. *S. aureus* can be classified into two types, Methicillin-susceptible Staphylococcus aureus (MSSA) and Methicillin-resistant Staphylococcus aureus (MRSA), based on resistance to methicillin.

Emergence of linezolid-resistant *Staphylococcus epidermidis* in the COVID-19 hospitalized intubated patients in North Khorasan, Iran

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نوع پذیرش: پوستر | کد مقاله: G-62140

Abstract: Background: In the COVID-19 pandemic from 2019 to date, we confront secondary bacterial and viral infections in SARS-CoV2 infected patients, especially hospitalized patients. Coagulase-negative staphylococci, are commensals of the human body and can lead to infections in immunocompromised patients. The antimicrobial resistance is increasingly reported in coagulase-negative staphylococci, especially in *Staphylococcus epidermidis*. One of the most critical problems is resistance to linezolid in *S. epidermidis*, observed in Europe since 2014. The aim of this study was to evaluation of bacterial Co-infections and determination of antimicrobial resistance pattern of co-infection isolated strains in North Khorasan, Iran, in the last six-month period. Materials and Methods: An explanation of the study design and experimental method. Results: After microbiological evaluation of pulmonary samples of hospitalized intubated patients with signs of bacterial pneumonia, we found co-infection in 11 of 185 patients with *S. epidermidis*, *S. aureus*, and *Acinetobacter baumani*, respectively. Interestingly seven of nine *S. epidermidis* isolates were linezolid resistant. For identification of the isolates at the species level, we used phenotypic methods and also the Polymerase Chain Reaction (PCR) for the *atlE* gene. Selected isolates were characterized by determining their antimicrobial resistance patterns and using molecular methods including SCCmec typing, detection of *ica*, *mecA*, *vanA*, and *cfp* genes. Conclusion: The increasing linezolid resistance in bacterial strains becomes a real threat for patients, and monitoring such infections combined with surveillance and infection prevention programs is very important to decrease the number of linezolid-resistant staphylococcal strains. Keywords: SARS-CoV-2, staphylococcus epidermidis, co-infection, linezolid

The Prevalence of kfu, iutA, rmpA and K2 genes among ESBL-Producing Klebsiella Pneumoniae Isolated from Khorramabad, Iran

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نوع پذیرش: پوستر | کد مقاله: G-81037

Abstract: Abstract Background: Virulence factors play a significant role in the development of Klebsiella pneumoniae infections. The aim of current study was to investigate the prevalence of kfu, iutA, rmpA, and K2 genes among ESBL-producing Klebsiella pneumoniae isolated from Khorramabad, Iran. Materials and Methods: In this study, the extended-spectrum β -Lactamases (ESBL) screening phenotypic test was executed by disc diffusion technique and kfu, iutA, rmpA, and K2 genes detection by PCR. Results: From 110 K.pneumoniae strains isolated 57(51.8%) was ESBL producing strain. Out of 57 ESBL positive K.pneumoniae the frequency of kfu, iutA, rmpA, and K2 genes was 11(19.3%),24(42.1%),2(3.5%),3(5.3%), respectively. Conclusion: The results of this study showed that among the studied genes, kfu gene was more abundant in ESBL-Producing Klebsiella Pneumoniae isolated from clinical samples of Khorramabad hospitals. Keywords: Klebsiella Pneumoniae, Extended-Spectrum β -Lactamases (ESBL), Virulence genes



The Prevalence of Virulence Factors entB, mrkD, magA genes among ESBL-Producing Klebsiella Pneumoniae Isolated from Clinical Samples of Khorramabad Hospitals, Iran

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نوع پذیرش: پوستر | کد مقاله: G-56804

Abstract: Abstract Background: The purpose of our study was to investigate the prevalence of virulence factors entB, mrkD, magA genes among ESBL-producing Klebsiella pneumoniae isolated from clinical samples of Khorramabad hospitals, Iran. Materials and Methods: In this descriptive-analytical study, the extended-spectrum β -Lactamases (ESBL) screening phenotypic test was performed by disc diffusion method and virulence factor gene detection by PCR method of Klebsiella pneumoniae isolates isolated from clinical samples of selected hospitals in Khorramabad city in 2018. Data were statistically analyzed by SPSS version 21 software. Results: Out of 57 ESBL positive K.pneumoniae the frequency of entB, mrkD, magA genes was 44(77.2%),44(77.2%),2(3.5%),respectively. Conclusion: According to the results there is no relationship between the virulence genes and ESBL production. Keywords: Virulence Factors, Klebsiella Pneumoniae, Extended-spectrum β -Lactamases (ESBL)

Evaluation of the ybtS gene in ESBL-producing *Klebsiella pneumoniae* isolated from patients with nosocomial infections referred to teaching hospitals in Kurdistan province, Iran

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نوع پذیرش: پوستر | کد مقاله: G-52497

Abstract: Abstract Background: *Yersinia Bactin* plays an important role in the pathogenesis of *Klebsiella pneumoniae*. These virulence factors are encoded by genes such as ybt S, ent B, mrk D, K2, mag A, iut A, kfu, rmp A, all S. The aim of this study was to investigate the ybtS gene in ESBL-producing *Klebsiella pneumoniae* isolates isolated from patients with nosocomial infections referred to teaching hospitals in Kurdistan province, Iran. Materials and methods: *Klebsiella pneumoniae* isolates were collected from October 2014 to December 2015. Then Extended-spectrum beta-lactamases (ESBLs) producing isolates were isolated by phenotypic method. The detection of ybtS gene was done using specific primer and PCR technique. Results: Among the 70 isolates of *Klebsiella pneumoniae*, 88.57% (number = 62) were ESBL positive. The ybtS gene was not found in any of the ESBL-positive *Klebsiella pneumoniae* isolates. Conclusion: Several pathogenic factors contribute to the course of the disease, including the pathogenic factors of *Klebsiella pneumoniae* capsule, pili and siderophores such as enterobacter, aerobactin and siderophore hydroximate. Therefore, according to the results of the present study, another gene has played a role in the pathogenicity of the studied isolates. Keywords: *Klebsiella pneumoniae*, Extended-spectrum beta-lactamases (ESBLs), ybtS, polymerase chain reaction (PCR)

Antimicrobial susceptibility, and molecular detection of integrons, sulfonamides and trimethoprim resistance profile of extra drug resistant *Escherichia coli* isolates

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نوع پذیرش: پوستر | کد مقاله: G-61243

Abstract: Antimicrobial susceptibility, and molecular detection of integrons, sulfonamides and trimethoprim resistance profile of extra drug resistant *Escherichia coli* isolates Zahra Sabeti Noghabi 1, Vahid Soheili 2, Fatemeh Aflakiana, Gholamreza Hashemitabar 1*, Mahdi Askari Badouei 1*, 1- Department of Pathobiology, Faculty of Veterinary Medicine, Ferdowsi University of Mashhad, Mashhad, Iran 2- Department of Pharmaceutical Control, School of Pharmacy, Mashhad University of Medical Sciences, Mashhad, Iran Corresponding Author: hashemit@um.ac.ir; askari.m@um.ac.ir *Escherichia coli* is the causative agent for approximately 80% of Urinary tract infections (UTIs). UTI treatment has been resulted in overuse of antibiotics in hospitals, and subsequently the increasing antimicrobial resistance. This study aims to determine the frequency of XDR (extra drug resistance) and investigation the distribution of common sulfonamide- (sul1, sul2, sul3) and trimethoprim (dfrA1, dfrA12, dfrA14)-related resistance genes among *E. coli* isolates from UTI patient also for presence of class 1, and class 2 integrons (Int1 and Int2). For this, 120 uropathogenic-*E. coli* (UPEC) isolates which were recovered from UTI cases in Mashhad were assessed. Overall, 39 out of 120 isolates were identified as XDR as they were resistant to all classes of antibiotics tested except two or fewer comprising the quinolones, cephalosporins, penicillins, tetracyclines, and sulfonamide-trimethoprim. The antimicrobial susceptibility testing results have determined a substantial resistance rate against cloxacillin (98.3%), oxacillin (98.3%), and cephalexin (94.17%). According to the Polymerase-chain reaction (PCR) results, the sul1 and dfrA14 genes with the frequency of 35 (89.74%) and 28 (71.79%) were identified as the most prevalent resistant genes among XDR isolates. In addition, the int1 and int2 genes were detected among 23 (58.9%) and 8 (20.5%) XDR isolates, respectively. In conclusion, the substantial distribution of sul1 and dfrA14 genes was highlighted among XDR *E. coli* isolates recovered from UTI. Based on the present research findings, class I integrons play a major role in dissemination of resistance gene cassettes including sul and dfr in XDR isolates and need to be investigated in the future. Keywords: Antimicrobial resistance; *Escherichia coli*; XDR; Urinary tract infections (UTIs); sul genes; dfr genes; integrons.

Antibacterial potential of biosynthesized silver nanoparticles using Berberine extract against multidrug-resistant *Acinetobacter baumannii* and *Pseudomonas aeruginosa*

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نوع پذیرش: پوستر | کد مقاله: G-48507

Abstract: Background: The emergence of multidrug resistance in bacterial infections has limited the use of antibiotics. Helping the action of antibiotics is one of the needs of the day. Today, the biosynthesis of nanoparticles (NPs) is considered due to its safety and cost-effectiveness. In this study, we investigated the effect of biosynthesized silver nanoparticles (AgNPs) by Berberine plant extract against standard strains of multidrug-resistant (MDR) *Acinetobacter baumannii* and *Pseudomonas aeruginosa*. Material and Methods: UV-Vis, FTIR, FESEM/EDX, XRD, DLS, and Zeta potential techniques were used to confirm the biosynthesis of NPs. Then, disk diffusion agar (DDA) and minimum inhibitory concentration (MIC) tests were performed using common classes of standard antibiotics and AgNPs separately on the mentioned bacteria. The synergistic action between AgNPs and antibiotics was evaluated by the checkerboard method. Results: First, we obtained the confirmation results of the biosynthesis of AgNPs. According to the DDA test, both standard bacterial strains were sensitive to NPs and had an inhibition zone. Also, the MIC values showed that AgNPs inhibit the growth of bacteria at lower concentrations than antibiotics. On the other hand, the results obtained from checkerboard monitoring showed that AgNPs, in combination with conventional antibiotics, have a synergistic effect. Conclusion: The antibacterial sensitivity tests indicated that the desired bacterial strains could not grow even in low concentrations of AgNPs. This property can be applied in future programs to solve the drug resistance of microorganisms in bacterial diseases. Keywords: Silver nanoparticles, *Acinetobacter baumannii*, *Pseudomonas aeruginosa*, Biosynthesis, MIC

Distribution of pathogenic bacterial and antibiotic resistance patterns in clinical specimens in Ganjavian hospitals, Dezful, 2019-2022

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نوع پذیرش: پوستر | کد مقاله: G-15289

Abstract: Background: Almost everyone has a bacterial infection in their life. One of the major problems in the treatment of bacterial infections is the variable sensitivity of the isolates. Therefore, obtaining the epidemiology of infections and their drug resistance pattern is valuable for the planning of the stewardship committee, and this issue has been investigated in the present study. Materials and Methods: In this cross sectional study, during January 2019 through January 2022 clinical different specimens (blood, urine, CSF, wound, and respiratory secretions) were collected from hospitalized patients and cultured on Blood and MacConkey, and chocolate agar according bacteriology standard methods. In identification process were used gram staining and biochemical tests. Antimicrobial susceptibility testing were performed by disk diffusion method based on CLSI. Results: 4529 isolates were identified, including urine culture 47.2%, Blood culture 18.7%, respiratory secretions 14.5% and wound culture 11.1% by conventional methods. Among them, 96.5% (n= 4369) were bacterial and 3.5% (n=160) were candida albicans. The predominant bacteria were Escherichia coli (31.4%), Staphylococcus aureus (11.4%), Klebsiella pneumoniae 10.9%), and Enterococci (9.5%). Highest sensitivity rate of S.aureus strains was against aminoglycosides (78%), and in Enterobacteriaceae was carbapenems (87.6%) and about Acinetobacter baumannii and Pseudomonas aeruginosa was colistin (100%). The resistance trend of Enterobacteriaceae to third generation cephalosporins during the last four years was 63.6 to 72.3 percent and about fluoroquinolones 47.3 to 50.6 percent. This was 86.1 to 93.6 and 62.1 to 79.8 percent against penicillin and erythromycin in S.aureus, respectively. Conclusion: Our finding in the current study include the increasing trend of bacterial resistance to the most commonly used antibiotics, such as extended-spectrum cephalosporins, ciprofloxacin, penicillin, and erythromycin can provide guidance for designing of appropriate treatment guidelines in infectious diseases as well as in the supervisory decisions of the antibiotic stewardship committee. Keywords: Antibiotic resistance, Bacterial infection, antibiotic stewardship committee.

Novel laboratory diagnostic techniques for brucellosis

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نوع پذیرش: پوستر | کد مقاله: G-19546

Abstract: Background: Brucellosis is the most zoonotic infectious disease that transmitted from animals to humans, and caused by the Brucella genus as a Gram-negative bacterium. It seems to reemerging in recent years as a public health challenges and many studies have been executed on diagnostic techniques for brucellosis in the laboratory. Also, it is known as an acquired infection through laboratory in the world. To control the disease diagnosis assays are considered. This study presents novel laboratory diagnostic techniques for brucellosis. Methods: Four databases were used to explore the published research articles correlated to novel laboratory diagnostic techniques for brucellosis including PubMed, Web of Sciences, Scopus, Google Scholar databases using keywords Brucella, human brucellosis, diagnosis, serology test, protein, nucleic acid amplification for articles published between February 2017 and November 2022. Results: Many reports demonstrated some novel laboratory diagnostic techniques including: molecular (URS-PCR, Real-time RPA, DNA aptamer, LAMP assay, PSR assay, PMA-qPCR, RT-LAMP assay, PCR-RFLP and REP-PCR) and serological (Label-free electrochemical immunosensor, RVFT, quantum dot-based immunochromatographic test strip, mAbs, rOmp and LFA). Also, protein immunoassay and bacteriophage-detecting techniques leading to high sensitivity and specificity in comparison with Rose Bengal test (RBT), complement fixation test (CFT). The diagnostic antigen are Brucella species lipopolysaccharide (LPS) or outer membrane proteins (OMP) extracted from serum samples. Conclusion: The results of this study showed that molecular, serological, protein and bacteriophage immunoassays techniques are highly specific and sensitive methods used for detecting Brucellosis quickly without using complex equipment and grouped as reliable techniques. Keywords: Brucella, human brucellosis, diagnosis, serology test, protein, nucleic acid amplification

Novel laboratory diagnostic methods for macrolide resistance in *Mycoplasma genitalium*

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نوع پذیرش: پوستر | کد مقاله: G-70512

Abstract: Background: *Mycoplasma genitalium* is seen as a reemerging microorganism and belongs to genital mycoplasmas. It is responsible for sexually transmitted infections in men and women. Macrolide resistance increasingly appears in the worldwide, so detecting methods for samples resistance to macrolide are considered. This study refers to novel laboratory diagnostic methods for macrolide resistance in *Mycoplasma genitalium*. Methods: The published research articles related to novel laboratory diagnostic methods for macrolide resistance in *Mycoplasma genitalium* were searched in four databases including Web of Sciences, PubMed, Google Scholar and Scopus by using *Mycoplasma genitalium*, macrolide, resistance and diagnose as keywords from February 2017 to November 2022. Results: Many studies showed that novel laboratory diagnostic methods for macrolide resistance in *Mycoplasma genitalium* are Mg MacrolideR qPCR, Aptima MG (AMG), ResistancePlus MG (RPMG), ResistancePlus, RPMG Flex, MGMR PCR, Macrolide-R/MG ELITE MGB kit, MgpC-AsyHRM that among them some methods can identify macrolide resistance mutations. The specificity and sensitivity of these methods range from 94-98% and 95-100%, respectively. Conclusion: These methods provide high specificity and sensitivity, affordable and can be substituted in the current detection in laboratory. Therefore, using this methods as rapid detection and potent tools can control and therapy patients with macrolide resistance in *Mycoplasma genitalium* infections. Keywords: *Mycoplasma genitalium*, macrolide resistance, diagnostics

Identification of norA, qacAB and smr genes and determination of antibiotic and biocide resistance patterns in MRSA isolated from Isfahan

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نوع پذیرش: پوستر | کد مقاله: G-84752

Abstract: Background. Methicillin-resistant *Staphylococcus aureus* (MRSA) is a major cause of nosocomial infections, which have become a serious problem due to antibiotic resistance. In addition to antibiotic resistance, biocide resistance is also increasing due to the high use of biocides. The aim of this study was to investigate the pattern of antibiotic resistance and the prevalence of biocide resistance genes norA, qacA/B, smr and to determine the minimum inhibitory concentration of chlorhexidine digluconate (CHG) and benzalkonium chloride (BKC) in MRSA isolated from teaching hospitals in Isfahan, Iran. Materials and Methods. This study was conducted on 63 MRSA isolates collected from teaching hospitals in Isfahan, Iran. MRSA isolates were identified by phenotypic testing and confirmed by PCR. The susceptibility pattern was determined using disc diffusion for antibiotics and broth microdilution to determine the minimum inhibitory concentration (MIC) of CHG and BKC according to the Clinical and Laboratory Standards Institute (CLSI). The presence of biocide resistance genes was determined by PCR and the Time kill assay was performed to investigate the lethality of biocides. Results. MRSA isolates had MIC values of 0.5-4 µg/mL for BKC and 0.125-4 µg/mL for CHG. norA was the most common biocide resistance gene among 63 isolates (88.9%), followed by qacAB and smr with 28.6% and 22.2%. Among the isolates, the highest percentage of resistance was to penicillin, erythromycin, and doxycycline, respectively. Conclusion. Due to the high prevalence of MRSA isolates in hospitals and the role of this pathogen in nosocomial infections, continuous monitoring of antimicrobial resistance for appropriate antibiotic administration and continuous evaluation of biocide resistance due to the high prevalence of resistance genes and the use of precise concentrations of biocides for disinfection, it allows us to prevent further prevalence of resistant strains in hospital environments. Keywords:

Determining the antibiotic resistance pattern of *Acinetobacter baumannii* isolates obtained from patients referred to Isfahan hospitals

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Background: *Acinetobacter baumannii* is a non-fermenting gram negative coccobacillus which have been raised as one of the most important causes of hospital-related infections during the last three decades. *Acinetobacter baumannii* has existed in the hospital environment for a long time and causes nosocomial infections. *Acinetobacter* isolates with multiple drug resistance (MDR) have caused many problems in the treatment of infections, which seems to be caused by the indiscriminate use of drugs. The aim of this study was to assess the resistance pattern of the *Acinetobacter baumannii* strain in Isfahan city.

Materials and Methods: For 26 isolates of *Acinetobacter baumannii* obtained from patients referred to Isfahan hospitals, determining the antibiotic resistance pattern was done by antibiogram test through disc diffusion method according to the instructions of the National Laboratory Standards Committee using 10 different antibiotic discs. In order to perform the antibiogram test, after preparing a bacterial suspension, equivalent to a 0.5 McFarland standard, using Mueller Hinton agar medium and antibiotic discs, the lack of growth was checked after 24 hours.

Results: All 26 isolates of *Acinetobacter baumannii* were resistant to Imipenem, Ceftizidime, Gentamicin, Ciprofloxacin, Ceftriaxone, Tetracycline, Doxycycline, Amikacin, Tobramycin, and Piperacillin.

Conclusion: The results of this study provide very important information regarding the control and treatment of the mentioned organism for physicians, clinical specialists and the laboratory community. Due to high antibiotic resistance of *Acinetobacter baumannii*, it is better to take infection control in hospitals more seriously. We can also think of complementary treatments including phage therapy based on the results. It can be concluded that antibiotic resistance pattern is an important tool in management of microbial challenges.

Keywords: *Acinetobacter baumannii*, Antibiotic Resistance, Antibiogram Test, Multiple Drug Resistance

Molecular identification of *Acinetobacter baumannii* by PCR method in patients referred to Isfahan hospitals

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Background: *Acinetobacter baumannii* is an opportunistic pathogen and can cause a wide range of infections. The most common infections caused by *Acinetobacter baumannii* are ventilator-associated pneumonia and bacteremia, but it can cause other infections, including skin and soft tissue infections, secondary meningitis, brain abscesses, and osteomyelitis. Due to the time-consuming process of identifying this bacterium through bacteriological culture methods, late diagnosis can be the reason for the failure of the treatments for the infections caused by this pathogen. Therefore, the present study was conducted with the aim of molecular identification of *Acinetobacter baumannii* by PCR method.

Methods: In this cross-sectional descriptive study, 103 patients presented with problems of respiratory system, who had been referred to specialized hospitals in Isfahan, were included in the sampling process. bronchoalveolar lavage and stimulated sputum samples were collected using bronchoscopy procedure.

Results: Using the PCR method, the number of positive cases for the presence of *Acinetobacter baumannii* was 26 cases (25.24%). In the lavage and sputum samples, 27.5% of women and 41.66% of men had strains of *Acinetobacter baumannii*. The results of statistical analysis showed that there was no significant difference between the infection rates of women and men ($P>0.05$).

Conclusion: Early identification of the strains producing beta-lactamase enzymes such as *Acinetobacter baumannii*, is one of the important challenges in order to control and prevent the spread of resistant strains in hospitals; therefore, it is necessary to take appropriate measures to reduce the frequency of infected cases with *Acinetobacter baumannii* and one of the first issues in this field is the use of new and efficient methods of pathogen identification, diagnosis and treatment of the infections caused by this bacterium.

Keywords: *Acinetobacter baumannii*, Molecular Diagnosis, Polymerase Chain Reaction, Statistical Analysis

Epidemiological study of Carbapenem-Resistant Enterobacteriaceae in patients admitted to Sari Cardiovascular Hospital

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نوع پذیرش: پوستر | کد مقاله: G-36591

Abstract: Background: Enterobacteriaceae is a large family of Gram-negative bacteria, which can cause a variety of severe infections such as bloodstream, soft tissue infections, intra-abdominal, respiratory tract, and urinary tract infections. Enterobacteriaceae are constantly finding new ways to avoid the effect of antibiotics used to treat the infections they cause. Their high resistance to different groups of antibiotic is concerning as it is becoming prevalent as a health problem. Enterobacteriaceae are becoming increasingly resistant to many previously effective antibiotics and it makes them difficult to treat. The emergence and spread of carbapenem-resistant enterobacteriaceae (CRE) has become a serious threats to public health. In this research, enterobacteriaceae's resistance to carbapenem is studied in cardiovascular patients. The World Health Organization published a list of antibiotic-resistant bacteria in which carbapenem-resistant enterobacteriaceae (CRE) was in the critical priority group for an urgent need to develop new antibiotics. Methods: A total of 91 enterobacteriaceae-positive cultures was studied from July 2020 to March 2022. Antimicrobial susceptibility testing was performed on all samples and the carbapenem antibiotic disc used was Imipenem (IPM). Samples collected were blood, urine, endotracheal tube, sputum and wound from the patients in various wards. Results: 91 patients tested positive for enterobacteriaceae and 62 of them showed high level of resistance to carbapenem in Sari cardiovascular hospital. Conclusion: This study shows the level of resistant of carbapenem to enterobacteriaceae in hospital and emphasizes on the urgent need to develop new antibiotics to prevent spread of these pathogens. Keywords: enterobacteriaceae, carbapenem resistance, imipenem

Prevalence of Quinolone-Resistant Escherichia coli bacteria from patients hospitalized in Sari Fatemeh Zahra Hospital

معصومه باقری آسنانی^۱، @^۱ مریم اندیشگر، ©^۱ فرنوش فدایی، ^۱ مهناز نصراللهی، ^۱ روشنک حقیری سننه، ^۱ مائده کاظمی^۱

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نوع پذیرش: پوستر | کد مقاله: G-01835

Abstract: Background: Escherichia coli is the most common pathogen in hospital settings and is capable for causing intestinal and extra-intestinal infections. E. coli is a gram-negative bacillus known to be a part of normal intestinal flora but can also lead to a spectrum of disease from mild, self-limited gastroenteritis to renal failure and septic shock. Quinolones are one of the most common antibiotics which are also used to treat E. coli infections. However, the resistance of this bacteria to quinolones develops rapidly and spreads widely. Therefore, it has become increasingly urgent to enhance the potency of quinolones against it. The increased use of fluoroquinolones has led to resistance to these antibiotics and emergence of quinolone-resistant bacteria. This study shows an increase in the prevalence of resistance to ciprofloxacin among E. coli-positive cultures isolated from samples obtained from patients. Methods: 212 E. coli-positive cultures were studied from July 2020 to March 2022. Samples collected were urine, blood, endotracheal tube, sputum, blood, wound and CSF in patients. Antimicrobial susceptibility testing were performed and ciprofloxacin (CP) discs were used on all cultures. Results: 115 out of 212 E. coli-positive cultures were ciprofloxacin-resistant. Overall 54% of the clinical strains of Escherichia coli were resistant to ciprofloxacin. Conclusion: This study has shown an increasing prevalence of Quinolone-Resistant Escherichia coli in patients. 54% of Escherichia coli strains were resistant to ciprofloxacin. The spread of antibiotic resistance urges the need to develop new antibiotics in order to control the prevalence of E. coli. Keywords: Escherichia coli, antimicrobial resistance, quinolone-resistance

Digital technology for the emerging infection diseases diagnosis

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نوع پذیرش: پوستر | کد مقاله: G-80341

Abstract: Background and Aim: A review of the characteristics, advantages, and limitations of some key new methods in the diagnosis of infectious diseases will be organized by technology. New technologies have had the greatest impact in the fields of bacteriology and virology, but there are also promising new developments in mycology and parasitology. Methods: One of the main strengths of matrix-assisted laser ionization (MALDITOF) is that it allows culture organisms to be identified over days or even weeks in very slow cases. Organisms such as mycobacterium that are growing are not yet in routine clinical use, the use of MALDI-TOF to guide patient sampling, including urine and blood, and applications such as antibiotic resistance are good advances in this field. Nucleic acid-based technologies are also considered one of the most important achievements. In particular, there are a large number of testing platforms that provide early diagnosis directly from patient prototypes. Many of these are multiplexed to examine multiple pathogens simultaneously. An important part of the technologies are either in the category of "cognitive technologies" or "data analysis". The "cognitive technologies" group includes technologies such as artificial intelligence, expert systems, machine learning, artificial neural networks, but the "data analysis" section includes technologies such as big data analysis, data mining, parallel computing and Social media and mobile data analysis. Results: The specialized field of infectious diseases, which is mostly infectious diseases, is most active in the field of prevention and control of infections, it has epidemics and epidemics, hence the medical application in this field is very wide and all fields of education, research, prevention, includes consultation, diagnosis, treatment and control of infection. Early telemedicine approaches in diseases mostly focused on the treatment of HIV/AIDS, hepatitis C and tuberculosis, but later on the field of blood-borne diseases and Sexual contact has also expanded. Conclusion: Developing telehealth and telemedicine programs requires a variety of considerations, such as HIPAA health insurance, legal and professional licensure requirements, provider certification and licensure, scope of care, quality of service, and accountability. Issuing a treatment order. IDSA supports the optimal use of telehealth and medicine capacity to provide specialized, timely and cost-effective care for populations with limited resources. Several studies have shown the impact of communication technologies in disease management. Infectious diseases (mainly HIV) have. Keywords: Digital technology, infection diseases, emerging

Evaluation of antibiotic resistance and frequency of metallo-beta-lactamases in *Acinetobacter baumannii* complex isolated from clinical samples in west of Iran

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Abstract: Background: *Acinetobacter baumannii* is a Gram-negative, non-fermenting and multi-drug resistant coccobacillus, which mainly causes hospital-acquired infections. One of the most important reasons of its high prevalence compared to other non-fermenting Gram-negative bacteria is its wide range of antibiotic resistance mechanisms. The aim of this study was to determine the antibiotic resistance and frequency of metallo-beta-lactamases in *A. baumannii* complex strains isolated from clinical samples in west of Iran. Materials and Methods: In this cross-sectional study, 105 strains of *A. baumannii* complex isolated from infectious patients in educational and therapeutic hospitals of Sanandaj and Kermanshah were investigated during a period of 6 months. The strains were isolated from different clinical samples including urine, trachea, sputum, wound, blood and lung secretions. After identifying isolates using the biochemical tests, antibiotic susceptibility pattern of the isolates was determined by disk diffusion agar method, according to the CLSI 2020 guidelines. The presence of genes producing six metallo-beta-lactamases SPM, SIM, GIM, NDM, IMP and VIM was investigated by polymerase chain reaction (PCR) method. Results: The evaluation of the results of the antibiotic sensitivity tests of the strains showed that the highest antibiotic resistance rates were seen to cefotaxime 104 (99%), ciprofloxacin 95 (90%), meropenem 94 (89%), cefepime 90 (86%) and gentamicin 90 (86%), and the lowest antibiotic resistance was found for tetracycline 63 (60%) and trimethoprim/sulfamethoxazole 72 (68%). According to the increase in the resistance rate, the number and percentage of intermediate strains were as follows: tetracycline 31 (30%), cefepime 12 (11%), trimethoprim/sulfamethoxazole 8 (8%), ciprofloxacin 8 (8%), gentamicin 4 (4%), meropenem 2 (2%), cefotaxime 1 (1%). PCR results showed that 93 isolates (88.6%) contained VIM gene, while SIM, GIM, NDM, IMP and SPM genes were not found in any isolate. The level of resistance to meropenem, tetracycline, trimethoprim/sulfamethoxazole, cefotaxime, gentamicin, ciprofloxacin and cefepime in strains harboring VIM gene was 90 (96.8%), 60 (64.5%), 69 (74.2%), 93 (100%), 87 (93.5%), 92 (98.9%) and 86 (92.5%), and in strains without the VIM gene was 4 (33.3%), 3 (25%), 3 (25%), 11 (91.7%), 3 (25%), 3 (25%) and 4 (33.3%). Conclusion: Our study showed a high level of antibiotic resistance and the prevalence of metallo-beta-lactamase VIM in *A. baumannii* strains isolated from west of Iran. Considering the increase in the prevalence of *A. baumannii* nosocomial infections, the identification of antibiotic resistance mechanisms can help to design protective strategies such as infection control programs in different hospital wards and to deal with the problem of antibiotic resistance in this bacterium. Keywords: *Acinetobacter baumannii*, Metallo-beta-lactamase, Antibiotic resistance, VIM gene, Iran



The Effect of Medicinal Herbs on Helicobacter Pylori Infection

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نوع پذیرش: پوستر | کد مقاله: G-91725

Abstract: Background: Helicobacter pylori is one of the most common gastric pathogens that leads to gastric dysfunction, ulcers and cancer. Also, antibiotic resistance is growing as a serious problem that can interfere with the treatment of this disease. The use of plants as a source of medicinal agents has played a significant role since ancient times. The purpose of this study is to review the antimicrobial effects of medicinal herbs on Helicobacter pylori infection. Materials and Methods: This study is a review study by searching scientific databases such as Scopus, PubMed, Google Scholar, Embase from 2019 to 2023 by using the keywords Helicobacter pylori, herbal medicine, gastric cancer, gastric ulcer and Antibacterial effect, 63 articles related to inclusion criteria were extracted and then analyzed. Results: The results indicated that medicinal herbs including cinnamon (Cinnamomum verum), ginger (Zingiber officinale), thyme (Thymus vulgaris), garlic (Allium sativum) have anti-inflammatory and pro-inflammatory effects and lead to inhibition of cytokines such as IL-1 α , IL-1 β , IL-6, IL-12, IL-8, TNF α , IFN γ and also leads to inhibition of COX-2. But some studies showed that these medicinal herbs do not have significant antibacterial effects. Conclusion: we conclude that the mentioned medicinal herbs with anti-inflammatory effects as a complementary agent could be effective in the treatment of Helicobacter pylori infection, acceleration the treatment, and prevention of this disease. Keywords: Helicobacter pylori, medicinal herbs, gastric cancer, Antibacterial effect.

Helicobacter pylori: Antibiotic resistance and new therapeutic challenges

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نوع پذیرش: پوستر | کد مقاله: G-29786

Abstract: Background: *Helicobacter pylori* is a Gram-negative, spiralshaped, microaerophilic and neutrophil bacterium that has been associated with gastrointestinal diseases in humans and can lead to chronic gastrointestinal diseases such as dyspepsia, peptic ulcers, gastric adenocarcinoma and MALT lymphoma. The prevalence of *H. pylori* in the world is about 50%, although, its prevalence rate in developing countries even reaches 90%, therefore, considering the recent resistance of this bacterium to antibiotic treatments, there are many concerns and challenges in this regard. This narrative, non-systematic review provides an update on the new challenging aspects in the treatment of *H. pylori* and its antibiotic resistance. Materials and Methods: We performed an online search on PubMed and Google Scholar and other Web of Science with the keywords: *Helicobacter-pylori*, Antibiotic-resistance, Therapeutic-challenges, *H.pylori*-infection, *H.pylori*-treatment and summarized the antibiotic resistance, epidemiology, new treatment challenges in *H.pylori* infection. Results: We retrieved 63 published papers about *H. pylori* infection and treatment from January, 2021 to June, 2022. We found that the most commonly recommended treatment regimen is the Standard Triple Therapy (STT) containing two antibiotics (clarithromycin and a nitroimidazole or amoxicillin) and a stomach protector (omeprazole). However, multiple studies have shown that STT fails in more than one in five people. Therefore, researchers proposed this method with a bismuth-free sequential treatment (SEQ), containing a first phase with a dual treatment (amoxicillin and omeprazole) followed by a triple treatment phase (nitroimidazole, clarithromycin and omeprazole) to be replaced, as this method has also faced treatment resistance recently. Conclusion: *H. pylori* is a bacterium with more than 20 pathogenic tools and solutions to resist environmental conditions and antibiotic treatment, which has gradually become a great concern due to the proof of the role of this bacterium in carcinogenesis and its high prevalence in the world. Today, the treatment challenges of *H. pylori* requires special attention from researchers to provide a permanent and effective solution. Keywords: *Helicobacter-pylori*, Antibiotic-resistance, *H.pylori*-therapeutic-challenges, *H.pylori*-infection, *H.pylori*-treatment.

Determination of antimicrobial effect of thymol and carvacrole on multidrug-resistant *Escherichia coli* Strains

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نوع پذیرش: پوستر | کد مقاله: G-10362

Abstract: Background: Multidrug-resistant *Escherichia coli* is one of the most common and important pathogens causing hospital-acquired infections, which cause critical infections in humans. Typically, these infections occur in hospitalized patients or immunocompromised patients. Due to the increasing spread of *Escherichia coli* antibiotic resistance and the toxicity and side effects of existing drugs, more attention needs to be paid to more appropriate drugs with less toxicity and side effects. In this study, the antibacterial activity of *Zataria multiflora*'s active substance, Carvacrole and thymol, was evaluated. Materials and Methods: Essential oil was extracted from *Zataria multiflora* at full flowering stage by hydrodistillation and its constituents were analyzed by a combination of capillary GC and GC-MS. Antibacterial activity was measured against 10 multidrug-resistant *Escherichia coli* as well as six ATCC bacterial standards by disc diffusion, minimum inhibitory concentrations (MIC) and minimum bactericidal concentrations (MBC) using broth microdilution. Results: The main compounds of the essential oil of *Zataria multiflora* were thymol and carvacrol, representing 26,8% and 22,9% respectively. Disc diffusion results showed inhibition zones of 17-25 mm for the ATCC standards and 15- 22 mm for the 10 clinical isolates. MIC and MBC values were 0.04- 3.0 mg/ml for ATCC strains and 0.02 to 0.3 mg/ml for the clinical isolates. Conclusion: *Zataria multiflora* may have the potential to be used against multidrug resistant organisms such as clinical isolates of multidrug-resistant *Escherichia coli*. Keywords: *Escherichia coli*, *Zataria multiflora*, minimum bactericidal concentrations, minimum inhibitory concentrations

Determination of antimicrobial effect of essential oil of cinnamomum verum on carbapenem-resistant *Klebsiella pneumoniae*

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نوع پذیرش: پوستر | کد مقاله: G-12743

Abstract: Background: Carbapenem-resistant *Klebsiella pneumoniae* is one of the most common and important pathogens causing hospital infections and causing critical infections in humans. Typically, these infections occur in hospitalized patients or patients with other diseases of the immune system. Today, the increasing spread of antibiotic resistance in *Klebsiella pneumoniae* and the toxicity and side effects of the available drugs have caused more attention to be paid to more appropriate drugs with less toxic effects and side effects. In this study, the antibacterial activity of cinnamon's active substance, cinnamaldehyde, was evaluated. Materials and Methods: Essential oil was extracted from *cinnamomum verum* at full flowering stage by hydrodistillation and its constituents were analyzed by a combination of capillary GC and GC-MS. Antibacterial activity was measured against 10 Carbapenem-resistant *K. pneumoniae* as well as six ATCC bacterial standards by disc diffusion, minimum inhibitory concentrations (MIC) and minimum bactericidal concentrations (MBC) using broth microdilution Results: *Cinnamomum verum* essential oil consisting primarily of cinnamaldehyde (60-75%), cinnamyl acetate (1-5%), eugenol (1-10%). Disc diffusion results showed inhibition zones of 19-29 mm for the ATCC standards and 18- 32 mm for the 10 clinical isolates. MIC and MBC values were 0.015- 2.0 mg/ml for ATCC strains and 0.03 to 0.5 mg/ml for the clinical isolates. Conclusion: *Cinnamomum verum* may have the potential to be used against multidrug resistant organisms such as clinical isolates of Carbapenem-resistant *K. pneumoniae*. Keywords: *Klebsiella pneumoniae*, *cinnamomum verum*, minimum inhibitory concentrations, minimum bactericidal concentrations.

Drug Resistance in Patients with Urinary Tract Infection in Ghaemshahr city, Northern Iran

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نوع پذیرش: پوستر | کد مقاله: G-05649

Abstract: Drug Resistance in Patients with Urinary Tract Infection in Ghaemshahr city, Northern Iran Atefe Tavakoli¹, Shaghayegh Alipor¹, Parsa Dastvarz¹, Masoumeh Moslemi², Bahman Rahimi Esboei²* 1. Student research Committee, School of Medicine, Tonekabon branch, Islamic Azad University, Tonekabon, Iran. 2. Department of Molecular Biology and Medical Genetics, School of Medicine, Iran University of Medical Sciences, Tehran, Iran. 3. Department of Medical Parasitology, School of Medicine, Tonekabon branch, Islamic Azad University, Tonekabon, Iran. *Corresponding Author: Email address: Bahman5164@yahoo.com Full postal address: 4719115875 Phone number: +989112139542 Background: Urinary tract infections (UTI) are known as the most common healthcare acquired infection of women in the world. Escherichia coli (E. coli) is the pathogen that causes the vast majority of UTIs in most parts of the world. Approximately 150 million UTIs occurs every year worldwide. For the past years drug resistance in bacteria has become a global health problem and emerging threat due to mis-use of antibiotics. Hence, it is necessary to be aware of the changes in the spectrum of drug resistance to ensure appropriate treatment. Materials and Methods: In this cross sectional study, patients suspected with UTI infection were referred to the Urine Analysis (UA) test. The midstream urine was collected in a sterile tube. All samples were cultured in Blood Agar and Nutrient Agar and after 3 to 6 days, a smear was prepared for Geimsa staining. After assessment of the morphological aspects, differentiation cultures were done using TSI, SIM and etc., methods up to final diagnosis. Then antibiogram was applied to fine the rate of sensitivity using different kinds of Antibiotics. Results: During March 2020 to October 2022, from 362 patients with UTI, 273 (75.41%) patients were positive for E. coli infection. The Tetracycline and Nalidixic acid showed no anti-bacterial effects and Amikacin and Tobramycin showed the highest sensitivity. Conclusion: According to the results of current study, E. coli was the most important causes of UTI and the results of antibiogram test revealed that the uses of mixed antibiogram therapy have better effectiveness in comparison to the antibiotics alone. Keywords: Urinary tract infections (UTI), Escherichia coli (E. coli), Antibiogram, Tetracycline, Nalidixic

Evaluating synthesized recombinant proteins potent immunogenicity as human brucellosis CSV candidates

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نوع پذیرش: پوستر | کد مقاله: G-06239

Abstract: Background: Brucellosis is a reemerged zoonotic infectious disease and known as wave fever, Maltese fever, Mediterranean fever and etc. According to WHO, 500000 new cases of human brucellosis reported worldwide annually, and the most prevalent complication is DALY (Disability-Adjusted Life Years). Common ways to transmit infectious are contaminated meat and dairy products, needlestick in veterinarians and etc. Various vaccines for animal brucellosis have been made, but they have not been suitable for human. Today studies have been tended to explore types of vaccines such as CSV (Combined Subunit Vaccine) that protects human against brucellosis infection. In this regard, current review intends to compare and evaluate antigenicity and immunogenicity of CSV as a key way to control human brucellosis. Methods: By reviewing Iranian and foreign research articles published in journals, congresses and conferences until November 2022 in the field of designing and manufacturing human brucellosis candidate vaccines from four databases Google Scholar, Web of Sciences, PubMed and Scopus by searching keywords such as: Brucellosis, Combined Subunit Vaccine, rOmp, Bp26 and L7/L12, the necessary data were collected. Results: In brief, by comparison the results of brucellosis-CSV research articles showed that technology advancement and molecular techniques development related to vaccine design and manufacturing as well as a protective antigens selection by potent immunogenicity, led to design compounds which successfully stimulate immune system. Recombinant proteins as CSV complements were used mainly Omp group (10, 19, 25, 28 and 31), Bp26, L7/L12 and Virb12. Immunogenicity evaluating of CSV commonly determined and confirmed by iELISA method, which indicated increasing in IgG1/2 and a mixed Th1/Th2 serum titer in animal models and protected them against brucellosis infection. Conclusion: Therefore, as still vaccine plays a key and fundamental role in the prevention and control of human brucellosis, so developing in researches on about human brucellosis CSV field can promise a bright future for human brucellosis vaccines produce and subsequently human brucellosis reduction or eradication in world wild. Keywords: Brucellosis, Combined Subunit Vaccine, rOmp, Bp26, L7/L12

Investigation of drug resistance in patients with urinary tract infection

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نوع پذیرش: پوستر | کد مقاله: G-67408

Abstract: Background: Escherichia coli (E. coli), is a Gram-negative, facultative anaerobic, rod-shaped, coliform bacterium of the genus Escherichia that is commonly found in the lower intestine of warm-blooded organisms. E. coli is the most important pathogen that causes the vast majority of UTIs. Urinary tract infections (UTI) are known as the most common healthcare acquired infection of women in the world. The purpose of this study is to investigate the drug resistance of patients with urinary tract infection who referred to the health center and private clinics in Karaj city in 2014-2016. Materials and Methods: In this cross-sectional study, 200 samples of urine polluted with E. coli were collected and the drug resistance level was investigated using the antibiotics cefotaxime, ceftriaxone, gentamicin, ciprofloxacin, nalidixic acid, trimethoprim, cefazolin, and ampicillin. The results were analyzed by T-test and SPSS software. Result: The results of the antibiogram test showed that the highest resistance was against ampicillin, trimethoprim and cefazolin antibiotics and the lowest resistance was against nalidixic acid. Conclusion: In this study, E. coli was the most common bacteria isolated from UTI infection, and the antibiogram results showed that the resistance was different in different species. Keywords: E. coli, urinary tract infection, Antibiogram, Ampicillin

Investigation of frequency and determination of drug sensitivity of Gram-positive bacteria causing septicemia in In hospitalized patients of HAJAR Hospital, Shahrekord , Chaharmahal and Bakhtiari Province , 1400 .

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نوع پذیرش: پوستر | کد مقاله: G-06831

Abstract: Background and purpose: Blood infections are increasingly reported in the world , since Since they are important diseases, targeted antimicrobial treatment can reduce complications in patients with septicemia. In order to have a targeted treatment, it is necessary to accurately identify the bacteria and effective antibiotics for its treatment. Gram-positive bacteria are also one of the causes of this infection, research and investigation on these bacteria and identifying the most effective antibiotics for treatment and, as a result, reducing mortality are very important. Therefore, the purpose of this study is to investigate the frequency and determine drug sensitivity of Gram-positive bacteria causing septicemia in hospitalized patients of HAJAR Hospital, Shahrekord, Chaharmahal and Bakhtiari Province in 1400. Materials and methods: In this cross-sectional-retrospective study, all blood cultures referred to Hajar hospital laboratory from April to March 1400 were examined and studied. Blood cultures were cultured in standard Blood Agar and Chocolate Agar environments and bacterial growth was checked after 24 to 48 hours. Based on the type of bacteria grown, antibiotic sensitivity was evaluated on Mueller-Hinton's culture medium in the form of disk diffusion using commercial and standard disks. Finally, the findings were analyzed using descriptive statistics. Findings: The results of this study showed that out of 6376 blood cultures, 170 samples were positive (2.66%). Among them, 67 cases (39.41%) were infected with gram-positive bacteria. The antibiogram results showed the highest sensitivity to Linezolid (97.62%), rifampin (86.11%), amikacin (73.68%) and cefoxitin (73.08%), respectively. In this study, the most drug resistances were erythromycin (84.09%), ciprofloxacin (52.63%) and cefoxitin (25%). Conclusion: Conclusion: According to the results, most gram positive bacteria were Staphylococcus species. By analyzing antibiotics, it can be said that ciprofloxacin can still be used for septicemia caused by gram positives. Keywords: septicemia, gram positive bacteria, blood culture, drug sensitivity

A survey on the prevalence of biofilm related virulence genes: fimA, tosA and pilS in mammary pathogenic Escherichia coli (MPEC)

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نوع پذیرش: پوستر | کد مقاله: G-73120

Abstract: Background: Escherichia coli (E. coli) is one of the major causes of bovine mastitis with significant economic losses around the world. The emergence of hard-to-treat isolates of E. coli such as biofilm producing strains challenges the routine treatment strategies. So far, numerous biofilm associated genes have been introduced especially in diarrheagenic pathotypes of E. coli and some of the extraintestinal pathotypes of E. coli (ExPEC) like uropathogenic E. coli (UPEC). The aim of the present study was to investigate and determine the ability of biofilm production and the presence of biofilm related genes pilS, tosA and fimA in E. coli isolates causing clinical bovine mastitis. Materials and Methods: A total of 75 mastitis causing Escherichia coli were provided from the microbial collection of Faculty of Veterinary Medicine, Ferdowsi University of Mashhad. The ability of biofilm production was investigated by 96-well microtiter plate method. Moreover, presence of the genes were evaluated by PCR. Finally, results were statistically analyzed. Results: All the isolates were categorized into four groups in terms of biofilm production: 1) non-biofilm-forming strains, 2) weak producers, 3) moderate producers and 4) strong producers. Sixty-nine E. coli isolates (92%) were able to form biofilm in different degrees which is as follows: 26 weak biofilm-producer isolates (34.7%), 30 moderate biofilm-producer isolates (40%) and 13 strong biofilm-producer isolates (17.3%). Moreover, the only detected gene among the isolates was fimA (70/75; 93.3%). Statistical analysis showed a significant difference ($p = 0.039$) in distribution of fimA among the four groups of biofilm producers. Non-biofilm-forming strains were notably lack of fimA. Conclusion: The current study confirmed the presence of mastitis causing E. coli strains capable of biofilm formation. This, would be a concern in treatment procedures. Furthermore, absence of pilS and tosA in mammary pathogenic E. coli differentiate this pathotype from other ExPEC, UPEC in particular. Finally, it seems that other biofilm-forming mechanisms and genes rather than pilS and tosA are involved in MPEC. Keywords: Biofilm, MPEC, Mastitis, fimA

Use of immunochromatographic assay for rapid identification of TB

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نوع پذیرش: پوستر | کد مقاله: G-34852

Abstract: Use of immunochromatographic assay for rapid identification of TB Omid Moeini¹, Armit Hosseini¹, Mohammadmatin Nourikhani¹, Mahdi Nakhaee¹, Amir Gholamzad¹, Mehrdad Gholamzad² 1. Department of Laboratory Medicine, Faculty of Paramedical Sciences, Tehran Medical Sciences, Islamic Azad University, Tehran, Iran 2. Department of Microbiology and Immunology, Faculty of Medicine, Tehran Medical Sciences, Islamic Azad University, Tehran, Iran, Mgholamzad@iautmu.ac.ir *Corresponding Author: Department of Microbiology and Immunology, Faculty of Medicine, Tehran Medical Sciences, Islamic Azad University, Tehran, Iran, Mgholamzad@iautmu.ac.ir Background: Tuberculosis rapid immunochromatographic tests are a fast, easy and new test for the diagnosis of Mycobacterium TB, which is very efficient today. By giving a quick result, this test will help the physician to decide on the continuation of the treatment process. In this study, positive liquid samples of TB patients have tested. Materials and Methods: In this study, 159 samples that have positive liquid cultures are first checked with Rapid for negative or positive, and then these tests are checked with biochemical tests. Results: Of 159 positive liquid cultures, using the conventional method, TB is being identified in 119 (74.8%), Non-TB were found in 4 (2.5%), 14 (8.8%) cultures were contaminated and 22 (13.8%) cultures were found to be negative. Using the immunochromatographic assay, TB was detected in 118 (74.2%) liquid cultures, and 41 (25.8%) tests were negative. all tests have been passed the quality check. Conclusion: The immunochromatographic assay is a simple and rapid test which represents a suitable alternative to the conventional subculture method for the primary identification of Mycobacterium tuberculosis complex in liquid cultures of automated system. Keywords: Rapid Test, Immunochromatography Assay, TB

Antibacterial effects of chitosan-zinc oxide nanocomposite on *Streptococcus mutans* and *Actinomyces viscosus*

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نوع پذیرش: پوستر | کد مقاله: G-85120

Abstract: Background: Although today the prevalence of dental caries has decreased by adding fluoride, still many groups of society are suffering from tooth decay. This study was designed to investigate the antibacterial effect of chitosan-zinc oxide nanocomposite on *Streptococcus mutans* and *Actinomyces viscosus* as the main causes of tooth decay. Materials and Methods: In this study, the standard strain of *S. mutans* (ATCC 35668) and the standard strain of *A. viscosus* (PTCC 1202) were used. After the preparation of thymol-chitosan nanocomposite to determine the MIC and MBC of the nanocomposite and chlorhexidine as a control drug the Broth microdilution method was used. Thus serial dilutions of the drugs were mixed with bacteria to determine the minimum growth-inhibiting concentration by the serial dilution method. For descriptive statistics, the calculation of central and dispersion indices was used to describe the data. After measuring the normality of the data with the Shapiro-Wilk test, since the distribution of the data was normal, independent t-tests, ANOVA, Tukey's and Dunnett's post hoc tests were used, and P 0.05 was considered as the significance level. Results: The results of this study showed that the size of nanoparticles varies from 100 to 500 nm with an average of 275. Based on the findings, the lowest MIC for both bacteria belongs to nanocomposite chitosan-zinc oxide + chlorhexidine (3.33 µg/ml) and the highest amount was zinc oxide-chitosan nanocomposite (10.6 µg/ml for *S. mutans* and 13.3 µg/ml for *A. viscosus*). Similarly, the lowest MBC for both bacteria belongs to chlorhexidine-chitosan nanocomposite (4.66 µg/ml) and the highest amount was chitosan nanocomposite (13.3 µg/ml for *S. mutans* and 16.0 µg/ml for *A. viscosus*). Conclusion: The results of this study showed that zinc oxide-chitosan nanocomposite could be used in combination with chlorhexidine to reduce the incidence and severity of tooth decay and inhibit the bacteria that cause this widespread complication. Key words: Nanotechnology, Chitosan, Zinc, Zinc oxide, Caries, Bacteria

High prevalence of multidrug-resistant (MDR) and biofilm-producing strains of *Escherichia coli* recovered from clinical bovine mastitis

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نوع پذیرش: پوستر | کد مقاله: G-08246

Abstract: Background: Bovine mastitis is one of the most costly concerning in dairy industry which could be develop because of various infectious and non-infectious factors. Among them, mammary pathogenic *Escherichia coli* (MPEC) is the main causative agent of clinical type of mastitis in most part of the world. Bacterial features affect the pathogenesis as well as the treatment success. For example, the emergence of multidrug-resistant (MDR) and biofilm producing strains challenges the treatment strategies based on the antibiotic application. So far, more studies have been conducted on the rate of antimicrobial resistance and less on the ability of MPEC to produce biofilm and its relationship with antimicrobial resistance. The aim of the present study was to investigate and determine the antibiotic resistance, the ability of biofilm formation and possible relations in mastitis causing *E. coli*. Materials and Methods: A total of 75 *Escherichia coli* isolates recovered from clinical bovine mastitis were provided from the microbial collection of Faculty of Veterinary Medicine, Ferdowsi University of Mashhad. Antibiotic resistance against nine antibiotics was determined by agar-disk diffusion method. The antibiotics were the most prescribed agents in medicine and/or veterinary medicine which are as follows: amoxicillin (AMX), ceftiofur (CEF), chloramphenicol (C), enrofloxacin (NFX), erythromycin (E), gentamicin (GM), lincomycin (L), oxytetracycline (T) and trimethoprim-sulfamethoxazole (SXT). Moreover, the ability of biofilm formation were investigated using 96-well microtiter plate method. Finally, results were analyzed and possible relations among antibiotic resistance, MDR and biofilm formation were determined by chi-square test ($p < 0.05$ considered as significant). In cases of significant relations, Spearman's rank correlation was measured as well. All the calculations were performed in SPSS version 16.0. Results: The results determined the highest resistance against lincomycin (74/75; 98.7%) followed by erythromycin (67/75; 89.3%), and the lowest resistance against gentamicin (4/75; 5.3%). Furthermore, 78.7% (59/75) isolates were confirmed as MDR. Statistical analysis revealed significant associations among MDR and resistant to amoxicillin ($p = 0.000$), trimethoprim-sulfamethoxazole ($p = 0.003$) and oxytetracycline ($p = 0.000$). All of the strains showing resistance to these antibiotics were MDR. Moreover, resistance to amoxicillin ($\rho = 0.530$) and oxytetracycline ($\rho = 0.578$) showed a moderate and positive correlation with MDR, while Spearman's rho correlation coefficient for trimethoprim-sulfamethoxazole and MDR was weak ($\rho = 0.386$). In terms of biofilm production, it was found that 92% (97/75) of isolates were capable of producing biofilm. Furthermore, no significant relation was observed among the biofilm formation, antibiotic resistance and MDR. Conclusion: The current study confirmed the presence of strains with multiple resistance to antibiotics and the ability of biofilm production in *Escherichia coli* causing mastitis. Hence, there is a need to adopt appropriate treatment strategies to affect this microbial population more effectively. Keywords: Mastitis, MDR, Biofilm, AMR, *E. coli*.

The Influence of neonatal positioning on bacterial adhesion in endotracheal tube

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نوع پذیرش: پوستر | کد مقاله: G-83267

Abstract: Background: Recent data suggest that during mechanical ventilation, lateral patient position decreases the incidence of bacterial adhesion of ventilated neonates. The objective of this study was to evaluate the influence of lateral and supine position on bacterial colonization of endotracheal tube in neonates. Materials and Methods: We conducted a prospective, randomized, clinical trial with 31 intubated neonates; sixteen neonates were positioned supine, and fifteen were maintained in the lateral position. Tracheal aspirates were cultured in second and fifth days of mechanical ventilation. Data were analyzed with SPSS version 16. Results: In the second day of ventilation, positive cultures were recognized in 6.2% of supine group and 6.7% of lateral group. After 5 days, tracheal cultures were positive in 25% of supine group and 13.3% of lateral group that wasn't statistically significant ($P=0.9$ in second day and $P=0.9$ in the fifth day). The most common organisms isolated from tracheal aspirates were Gram-negative rods (Klebsiella). Conclusion: Since respiratory contamination is very common among ventilated neonates and the effect of lateral position on bacterial colonization of endotracheal tubes of intubated neonates wasn't established in our study, further studies are required to suggest ways to decrease bacterial colonization of intubated neonates. Keywords: Patient Positioning, Neonatal Sepsis, Bacterial Adhesion

Differential Identification of Non-Tuberculous Mycobacteria Using Gene Sequencing Analysis

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نوع پذیرش: پوستر | کد مقاله: G-23965

Abstract: Background: The role of non-tuberculous Mycobacteria (NTM) species in causing infections in human communities has become much more pronounced in recent years as compared to the past. Hence, hsp65 and ITS gene sequencing determination method were used in the present study to develop a valid method with high diagnostic value for the identification of clinical isolates of NTM in the Mashhad Tuberculosis Reference Laboratory. Materials and Methods: The required samples were collected in the period of April 2015 to March 2018. The patients with positive culture results, who had positive 16SrRNA-PCR and negative IS6110-PCR results were included in the study for further investigations and species identification. All the phenotypic species determination methods including analysis of the characterization of the colony, niacin, nitrate, catalase, aryl sulfatase, and tween 80 were performed for each of them. Subsequently, hsp65-PCR and ITS-PCR tests were done on the DNA of each sample. The PCR products were sent for sequencing determination. Results: Out of 556 clinical isolates of Mycobacterium were isolated from 4503 suspected tuberculosis patients, the 48 (8.6%) samples were included in the study as the suspected NTM. The results of hsp65-sequencing and ITS-sequencing showed that out of 48 tested samples, 30 (62.5%) *M. simiae*, 3 (6.25%) *M. abscessus*, 3 (6.25%) *M. fortuitum*, 2 (16.4%) *M. kansasii*, 2 (4.16%) *M. szulgai*, 1 (2.08%) *M. intracellulare*, and also 1 (2.08%) was diagnosed as *M. thermoresistibile*. Conclusion: All these findings showed that hsp65 and ITS genes can be used in identifying the most common species quickly and accurately in the country. The results also show a high prevalence of *M. simiae* in the northeast of the country. Keywords:

Seroepidemiology of Leptospirosis among healthy people in Zanjan, Northwest of Iran

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نوع پذیرش: پوستر | کد مقاله: G-61294

Abstract: Introduction: Leptospirosis is a zoonotic disease, especially in developing and tropical countries and is an important public health issue worldwide. This study aimed to investigate the seroprevalence of *Leptospira* in healthy people referred to Shahid Motahari Laboratory, Zanjan, Iran. Materials and methods: 181 healthy people referred to Shahid Motahari laboratory in Zanjan, Iran were included in the present study. Demographic information of people was collected based on a questionnaire and serum samples were prepared from each patient. Serum samples were kept at -20 °C until serology analysis. Anti-*Leptospira* IgG antibodies were measured in sera of participants by a commercially available enzyme immunoassay "NovaLisa *Leptospira* IgG ELISA" kit and the results were reported as positive, negative and equivocal. Results: Out of 181 serum samples, 43 (23.7%) samples were positive, 36 (19.9%) were equivocal and 102 (56.4%) were negative for anti-*Leptospira* IgG. The average age of the participants was 40.6 years old. No significant difference was shown between age and gender with anti-*Leptospira* IgG. There was no significant relationship between the IgG level and the rural residence of the participants. Moreover, no significant correlation was found between the amount of IgG and other characteristics of participants. Conclusion: According to high seroprevalence of *Leptospira* in healthy people, disease control and prevention policies are necessary in people with high risk of infection. Furthermore, comprehensive studies using Microscopic Agglutination Technique (MAT) are suggested for diagnosis of leptospirosis due to its unique diagnostic feature for seroepidemiology determining. Keywords:

Evaluation Of Carbapenem-Resistant Gram Negative Bacilli Colonization At The Intensive Care Unit Admission In Alzahra Hospital

زینب القاصی، © P, ¹سودابه رستمی، ²سید مهدی قاسمی، ³سعید عباسی⁴

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نوع پذیرش: پوستر | کد مقاله: G-42063

Abstract: Background: Colonization of carbapenem-resistant gram-negative bacilli (CR-GNBs) could as an important risk factor for the transmission of these nosocomial infections in the intensive care units (ICUs). The aims of this study were evaluation of frequency and determination of phenotypical and genotypic characterization of CR-GNBs colonization in patients being admitted in ICUs of Alzahra hospital, Isfahan, Iran. Materials and Methods: A total of 146 rectal swabs were collected and processed for isolation of CR-GNBs using selective, differential media and biochemical tests. Antimicrobial susceptibility test was performed by disc diffusion method for all these isolates according to CLSI guidelines. PCR test was carried out for detection of carbapenemase (blaNDM, blaSPM, blaOXA-48). Results: The frequency of colonized CR-GNBs in studied patients was 24.6%. Overall, 118 gram-negative bacilli isolates were identified, of which 36 isolates showed resistance to carbapenem. Meropenem was the most effective antimicrobial agent with 29.7% susceptibility. In addition, 88.1% of the isolates were trimethoprim-sulfamethoxazole resistant. Escherichia coli and Klebsiella pneumoniae were the most common colonizers. The most frequent detected carbapenemase were blaOXA-48, blaNDM and blaspm genes accordingly. Nine isolates of CR-GNBs co-harbored blaNDM and blaOXA-48. Also, two CR-GNBs isolates co-harbored blaSPM, blaNDM, and blaOXA-48. Conclusion: In our study, the colonization frequency of CR-GNBs was high and the emergence of carbapenemase genes among patients is alarming. Keywords:

Investigation of the Presence rate of efflux pump genes *adeI*, *adeJ* in clinical isolates of antibiotic resistant *Acinetobacter baumannii* by PCR Molecular method

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نوع پذیرش: پوستر | کد مقاله: G-81240

Abstract: Background: *Acinetobacter baumannii* is known as one of the most important causes of nosocomial infections all around the world. Efflux pumps are one of the main causes of providing resistance in this bacterium. This study was performed to evaluate the presence of pump efflux genes in clinical isolates of antibiotic-resistant *Acinetobacter baumannii* in Tehran hospitals. Materials and Methods: A total of 150 clinical isolates from Tehran's hospitals and *A.baumannii* isolates were identified by using biochemical methods in the laboratory. After biochemical tests, *Acinetobacter baumannii* have been confirmed by the presence of the blaOXA-51-like by the PCR molecular method. Antibiogram testing has been performed on 9 antibiotics in Muller Hinton agar medium according to CLSI disc diffusion method. After wards, the samples have been investigated in term of existing *adeI* and *adeJ* genes by Molecular PCR. Results: Examining the antibiotic resistance of the isolates showed that the level of resistance varies from 48% to 91% depending on the type of antibiotic. In this study, the isolates showed the highest resistance to tetracycline and the lowest resistance to gentamicin. Also, the isolates that were positive for the presence of *adeI* and *adeJ* genes showed the highest resistance to tetracycline, meropenem, and amikamycin, and the highest sensitivity to gentamicin and ciprofloxacin. and the isolates that were negative for the presence of *adeI* and *adeJ* genes showed the highest resistance to gentamicin and trimethoprim-sulfamethoxazole and the highest sensitivity to ceftazidime and imipenem. Conclusion: The conclusions of this study showed that although, the *adeIJ* genes in strains are related to antibiotic resistance, but the role of other factors should not be ignored in causing resistance. Keywords: *Acinetobacter baumannii*, Efflux pump, Antibiotic resistance, *adeJ* gene – *adeI* gene



Multilocus VNTR analysis-ompA Typing of Chlamydia trachomatis Isolates in Tehran, Iran

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نوع پذیرش: پوستر | کد مقاله: G-83296

Abstract: Background: Chlamydia trachomatis has emerged as an important causative agent of sexually transmitted infections in both males and females. This study is the first to describe the genetic diversity of C. trachomatis strains derived from patients with signs and symptoms of genitourinary infections admitted to Tehran health centers and hospitals using the high-resolution genotyping method, multilocus variable-number tandem-repeat analysis with ompA sequencing (MLVA)-ompA. Method: One hundred and sixty-seven urogenital specimens were collected from October 2019 to July 2020. Specimens were inoculated to cell culture and examined for the presence of C. trachomatis isolates by microscopic valuation. Out of 167 samples, 19 (11.3%) viable C. trachomatis organisms were isolated in cell culture. Eighteen isolates were successfully genotyped by MLVA-ompA analysis. Result: The most prevalent ompA genotypes were E, and the other genotypes were D, F and G, comprising 42.1%, 26.3%, 21% and 10.5% of isolates, respectively. Other genotypes were not detected from any of the samples. Out of the 18 fully genotyped isolates, 10 different MLVA-ompA genotypes were obtained. The most prevalent MLVA-ompA genotypes were 8.6.1-E (33.3%) and 8.5.2-D (16.6%). Genotype 8.6.1-E was common in both females and males. Conclusions: In conclusion, the MLVA-ompA method was more discriminatory than ompA typing alone and, therefore, a suitable complement to ompA. This method allowed clustering of the strains derived from patients to identify the dominant genotypes in the community and transmission patterns in sexual networks. Also, in this study, a high diversity of C. trachomatis strains was obtained in Tehran, which may be due to the low level of public health and awareness, and requires more studies in the future. Keywords: Chlamydia trachomatis; Genotyping; Cell culture; VNTR; MLVA-ompA

Prevalence of *Listeria monocytogenes* infection in women with spontaneous abortion, normal delivery, fertile and infertile

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نوع پذیرش: پوسنر | کد مقاله: G-40782

Abstract: Background: *Listeria monocytogenes* with a vast range of natural reservoirs is more known for being a food-borne pathogen. Human infections have shown an impact on pregnancy outcomes, so, this study survey the frequency of *L. monocytogenes* infection involving different groups of women. Methods: This study enrolled a total sample consisting of 109 women with spontaneous abortion, 109 women with normal delivery, 100 fertile women, and 99 infertile women aged 19–40 years and willing to participate in the study. The research tool in this study was a questionnaire and Polymerase chain reaction (PCR) test. Results: According to the results, the frequency of *L. monocytogenes* infection was 4/109 (3.66%) observed among women with spontaneous abortion, 2/109 (1.83%) among women with normal delivery, 3/100 (3%) among fertile women, and 0/99 (0%) among infertile women. Conclusion: There was no significant relationship between *Listeria monocytogenes* infection and pregnancy outcomes of spontaneous abortion and infertility. Keywords:

The Presence of Emerging and Re_emerging Pathogenic Microbial Agents in Dust Events

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نوع پذیرش: پوستر | کد مقاله: G-24903

Abstract: Background: Dust storms are one of the events that affect different regions of the world, including Africa, the Arabian Peninsula, and Central Asia. Exposure to dust particles is one of the events that can cause health problems. Remote transmission of microbial agents through dust particles is one of these effects. Methods: After searching the databases and removing irrelevant articles, we reviewed the articles. Results: In the reviewed studies, the presence of microbial agents in the atmosphere containing dust particles has been mentioned. Bacillus spp., Mycobacterium tuberculosis, Influenza virus, SARS-CoV-2 virus, Coccidioides spp. are among the cases mentioned. Studies have investigated the possible connection between the atmosphere containing dust particles and the increase in the number of people suffering from some infections, such as those suffering from the SARS-CoV-2 virus. Conclusion: More research is needed to evaluate the potential of survival and endangering human health by these microbial agents. This information can be effective in prevention and necessary solutions to deal with the possible effects of these infectious agents on the health of society. It is also recommended that more studies be conducted to investigate the synergistic effect of microbial agents in dust. Keywords: Dust, Particulate Matter, Climate Change, Emerging Disease

Antibiotic resistance, Ability of biofilm formation and colonization factors in Escherichia coli strains isolated from patients with urinary tract infection

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نوع پذیرش: پوستر | کد مقاله: G-73968

Abstract: Background: Urinary tract infection is the most common kidney and urinary tract disease in hospitalized and outpatients and one of the most bacterial infections in the world. E. coli is the most common cause of urinary tract infections. Biofilm production in E. coli increases the incidence of UTIs and makes treatment difficult due to the spread of multidrug resistance between them. This study was designed to investigate the pattern of antibiotic resistance and colonization genes in E. coli strains that make up biofilm. Materials and Methods: From January 2021 to April 2021, 105 Escherichia coli isolates were isolated from urine samples of patients with urinary tract infection referred to Razi Hospital in Rasht and confirmed by standard microbiological methods. Then, the antibiotic resistance of the strains was investigated by disk diffusion method and for phenotypic testing of biofilm formation was examined by 96-house microtiter plate method. Finally, for molecular tests, DNA of isolates was extracted by boiling method and the presence of colonization genes of these strains was examined by PCR method. Results: Our study showed that 52.4% of strains were ESBLs. The highest sensitivity to the antibiotics was for imipenem (97.1%) and meropenem (95.2%) and phosphomycin (91.4%) and the highest resistance was for cotrimoxazole (65.7%) and ciprofloxacin (62.9%) and ceftriaxone (40%). 29 strains (27.6%) formed strong biofilm, 60 strains (57.1%) formed moderate biofilm and 16 strains (15.2%) formed weak biofilm. In this study, the highest frequency of colonization genes in strong biofilm-forming strains were csgA with 93.1%, fyuA with 86.2% and pgaC with 65.5%, respectively. The highest frequency of colonization genes in moderate biofilm strains were fyuA with 90%, pgaC with 65% and csgA with 56.7%, respectively. And the highest frequency of colonization genes in weak biofilm strains were reported as fyuA with 87.5%, pgaC with 62.5% and csgA with 37.5%, respectively. Conclusion: Our study recommends the use of imipenem, meropenem, and phosphomycin antibiotics to treat urinary tract infections caused by Escherichia coli. Our study showed that the frequency pattern of colonization genes in Escherichia coli biofilm-producing strains (strong, moderate and weak) was different, while antibiotic resistance and prevalence of ESBLs producing strains in strong, moderate and weak biofilm-producing strains were not different. Keywords:

Investigation of azithromycin resistance in *Shigella* spp. isolated from children

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Background: Azithromycin (AZT) has widely been used for the treatment of shigellosis in children. Recent studies showed a high rate of decreased susceptibility to azithromycin due to different mechanisms of resistance in *Shigella* isolates. Accordingly, the purpose of this study was to investigate the role of azithromycin resistance mechanisms of *Shigella* isolates in Iran during a two-year period. In this study, we investigated the mechanisms of resistance among *Shigella* spp. that were isolated from children with shigellosis.

Materials and Methods: The minimum inhibitory concentration (MIC) of *Shigella* isolates to azithromycin was determined by the agar dilution method in the presence and absence of Phe-Arg- β -naphthylamide inhibitor. The presence of 12 macrolide resistance genes was investigated for all isolates by PCR for the first time in Tehran province in Iran.

Results: Among the 120 *Shigella* spp., only the *mph(A)* gene (49.2%) was detected and other macrolide resistance genes were absent. The phenotypic activity of efflux pump was observed in 1.9% of isolates which were associated with over expression of both *omp(A)* and *omp(W)* genes.

Conclusion: The high prevalence of the *mph(A)* gene among DSA isolates may indicate that azithromycin resistance has evolved as a result of antimicrobial selection pressures and inappropriate use of azithromycin.

Keywords: *Shigella*, Azithromycin; minimum inhibitory concentration (MIC); efflux pump inhibitor; Quantitative real-time PCR

Microbiological characterization of KPC-producing *Klebsiella pneumoniae* belonging to the international epidemic clone ST258 in Asia: a systematic review

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نوع پذیرش: پوستر | کد مقاله: G-29681

Abstract: Background: *Klebsiella pneumoniae* infection because of international epidemic clone ST258 constitutes a major health threat because of limiting efficient therapies. Hence, this study aimed to analyze the microbiological profiles of circulating of *K. pneumoniae* carbapenemase (KPC)-producing *K. pneumoniae* belonging to ST258 clone in Asia. Materials and Methods: A systematic search was prepared and reported through searching the Web of Science, PubMed, Scopus, Embase, and Google Scholar electronic data bases to find all available articles that are pertinent to our design from January 2000 to December 2019. Afterward, 10 publications meeting the inclusion criteria were included for data extraction and analysis. Results: The majority of included studies were from the eastern region including China, South Korea, Japan, Taiwan, and Hong Kong, and only one report from the western region was reported in Turkey. The earliest report was in 2010 from Korea and the late one in 2017 from China. All of those studies that performed a carbapenemase detection method indicated positive results. Except for one isolate, which containing blaKPC-3, all of the isolates harbor blaKPC-2. The minimum inhibitory concentration (MIC) of colistin against ST258 isolates was estimated ranging from 0.094 to 4mg/ml. The plasmid investigation showed a marked heterogeneity toward the studied isolates; however, IncFII type plasmids were the most prevalent plasmid. Conclusion: Our findings highlighted that despite the growing concern regarding the potential distribution of KPC-producing *K.pneumoniae* in Asia, strains belonged to the ST258 clone are not the main suspects. However, more clinical studies should be performed in the future to support our findings. Keywords:

Investigation of Dominant *Leptospira* Serovars in Sheep in Meshginshahr City, Iran

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نوع پذیرش: پوستر | کد مقاله: G-15602

Abstract: Background: Leptospirosis infection is an important zoonotic disease that some serovars of this disease can affect both humans and livestock. Also, due to its high prevalence in Iran, this disease can have a significant economic impact on livestock. All types of *Leptospira* spirochetes belonging to the *Leptospira* family are causative agents and are obligate aerobic and gram-negative. Mortality caused by disease in sheep flocks is usually around 20%. This study aimed to investigate the disease's serological infection in Meshginshahr city sheep, and the dominant strains of *Leptospira* were identified in this region. Materials and Methods: From May to September 2020, in total, 150 samples of female sheep and 50 male sheep in the age range of 1.5 to over 6 years were sampled. Venous blood samples were taken from all the studied sheep and then their serum was separated. In the present study, the MAT test proposed by WHO was performed to evaluate serum samples. The amount of agglutination in each sample was graded from +1 to +4, and only +4 was considered a positive sample, and the rest were doubtful and +1 was considered negative. Results: The predominant serovar in this study was *Leptospira Icterohaemorrhagiae*. Among all the collected samples, 22 cases were positive and 178 cases were negative, and the analysis by chi-score test showed a significant difference (P0.05). Conclusion: The results of the present study showed that there is *Leptospira* infection in the sheep population of MashginShahr city. Due to the role of rodents in the transmission of infection, the most important thing in disease control is to eliminate rodents, especially in livestock environments. This action reduces the incidence of leptospirosis in livestock and also the cases of the disease in humans. Keywords: Leptospirosis, Sheep, Iran

Examining the frequency and diversity of non-tuberculous mycobacteria in water and medical equipment by biochemical and molecular methods in Tehran hospitals

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نوع پذیرش: پوستر | کد مقاله: G-31867

Abstract: Background: There are two groups of mycobacteria in terms of pathogenicity, one group is pathogenic mycobacteria, which are capable of causing severe infections in humans and are associated with high mortality, and the other group are opportunistic species that are only pathogenic in people with weakened immune systems and The names of non-tuberculosis or atypical mycobacteria are known. Non-tuberculous bacteria are ubiquitous in nature and have high antibiotic resistance. The abundance and diversity of non-tuberculous mycobacteria in water and medical equipment of Tehran hospitals were investigated using phenotypic, molecular and genomic sequencing methods. Materials and Methods: The statistical population in this study was the water supply system and various departments of the army hospitals in Tehran city that use water. The sampling method in this project was non-probability and purpose-based. Water samples were prepared from different departments, including special care, surgery, infectious, gynecology, etc. A total of 198 water samples were collected. Membrane filters were incubated in Lowenstein-Jensen medium at 25°C and 37°C for 8 weeks. Results: NTM strains were divided into two groups based on growth rate. In general, 76 (40.4%) of the isolates were SGM and 112 (59.6%) of the isolates were RGM. Conclusion: The present study showed NTM strains can be an important component of hospital water sources and a possible source of hospital infections. Due to the high prevalence of NTM in the mentioned hospitals, it is better to follow the principles of hygiene and control, and the managers of these hospitals should be given recommendations regarding the principles of sterilization of devices such as HCD and hemodialysis. Keywords: Nontuberculous mycobacteria, Hospital drinking water, Iran

Seroprevalence of *Leptospira* infection in occupational risk groups in North Khorasan province, Iran

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نوع پذیرش: پوستر | کد مقاله: G-76931

Abstract: Background: Leptospirosis is an important zoonotic bacterial disease caused by *Leptospira* spp. Earlier studies from North Khorasan province (Iran) reported the presence of *Leptospira* in wild canines and rodents. To date, there is no data on the seroprevalence of leptospirosis among humans in this province. This study was performed to determine the prevalence of human leptospiral infection among people with different occupations. Materials and Methods: The study was conducted in urban and rural areas of the province. Among the serum samples collected from 278 subjects, 3 (1.1%) showed positive reaction with titer of 1:100 by the microscopic agglutination test (MAT). Results: Positive reactions were detected against *L. i. Canicola* and *L. i. icterohemorrhagic*. All of the seropositive samples derived from livestock farmers (n=3/106, 2.7%). Conclusion: The current study revealed that, though *Leptospira* infection is low in North Khorasan province, regular monitoring of the livestock and the farmers are important. Keywords: Leptospirosis, Microscopic agglutination test (MAT), livestock workers, North Khorasan province, Iran.

High prevalence and expression of antiseptic resistance genes among infectious t037/ST239 Methicillin Resistant Staphylococcus aureus (MRSA) strains in North Khorasan Province, Iran.

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نوع پذیرش: پوستر | کد مقاله: G-47613

Abstract: Background: Staphylococcus aureus is an important infectious agent and the majority of MRSA infections are nosocomial infections. To define the level and distribution of antiseptic resistance among infectious S. aureus strains we studied MRSA and methicillin-susceptible S. aureus (MSSA) isolates collected from different infection sites of patients. Materials and Methods: The prevalence and spread of antiseptic resistance among infectious S. aureus were determined. S. aureus isolates were investigated for susceptibility to antiseptic agents and detection of qacA/B and smr genes. Results: Among S. aureus isolates, 25 and 41 were MRSA and MSSA. The mean of MICs for Benzalkonium Chloride (BTC) among MRSA was statistically significantly higher than for MSSA (26 µg/ml versus 11.7 µg/ml, P=0.003) while there was no significant difference among MRSA and MSSA for Benzalkonium Chloride (BKC) and Chlorhexidine Digluconate (CHG). The qacA/B genes were carried in 68% of the MRSA and 58.2% of MSSA (P= 0.601), while smr was carried in 39% of MRSA and 29.3% of MSSA strains (P=1.000). MRSA strains with qacA/B and smr or qacA/B alone showed higher MICs than MRSA strains without these genes. In 15 out 25 cases, MRSA ST239 with spa types t037, t030 and t7688 was isolated from the infection site with 86.6% of them carrying a resistance gene (qacA/B or qacA/B + smr). Conclusion: The frequent presence of antiseptic resistance genes and a consequently elevated MIC against antiseptics among ST239 MRSA emphasizes the importance of mandatory monitoring MRSA for effective infection control. Keywords: Hospital infection, Methicillin Resistance S. aureus, Disinfection, Benzalkonium Chloride, Benzalkonium Chloride, Chlorhexidine Digluconate

Prevalence of multidrug-resistant *Acinetobacter baumannii* in patients hospitalized in the Intensive Care Unit in Iran: a systematic review

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نوع پذیرش: پوستر | کد مقاله: G-50986

Abstract: Introduction: *Acinetobacter baumannii* is one of the most important challenging opportunistic pathogens that has ability to develop resistance to a wide range of antibiotics and cause severe nosocomial infections, with a mortality rate of 43% in infected patients (1, 2). Multidrug-resistant *A. baumannii* (MDR) is one of the most common causes of ventilator-associated pneumonia. Multiple resistance has led to the overuse of colistin, which is the last treatment option for this bacterium (3). The increase in antibiotic resistance as well as the factors related to the pathogenicity and prevalence of this bacterium is very important (4). Controlling of nosocomial infections caused by multidrug-resistant Gram-negative bacteria is a serious problem (5). The prevalence of infection in intensive care unit patients worldwide is more than 50%, and gram-negative bacteria are the most common cause of multidrug-resistant ICU-acquired infections. MDR is one of the most common isolates in ICU patients, which increasingly leads to more complications in ICU patients and increased healthcare costs with limited treatment options (6). Methods: We systematically searched PubMed, Web of Science, and Google Scholar databases to investigate MDR and Iran. Selected articles were published between 2020 and 2022. These were duplicate articles were excluded from the study. Results: In the initial search, a number of forty articles were extracted, and after removing duplicates and evaluating the title and abstract, finally selected fifteen articles for analysis and were included in the study. The results of the studies showed that 70% to 100% were MDR, which is increasing over the years. *A. baumannii* resistance rate have been reported of clinical specimens to ciprofloxacin, imipenem, meropenem, doripenem, levofloxacin, cefotaxime, ceftazidime, cefepime, piperacillin, piperacillin/tazobactam and trimethoprim/sulfamethoxazole respectively 100, 75, 97, 96, 93, 93, 76, 92, 92, 89, 89, and 92 percent (7). The prevalence of this bacteria in respiratory samples has been reported as 50,4% (8). So *A. baumannii* is now considered a highly resistant pathogen to various types of antibiotics (5, 9-17). Conclusion: According to the results of this study there is a very high rate of resistance to most of the antimicrobial agents commonly prescribed for severe infections caused *A. baumannii*. Therefore, due to the rapid emergence of resistance even to colistin or tigecycline, monotherapy should be avoided. These results show the importance of providing antibiotics correctly in intensive care units and following antibiotic stewardship protocols as the only effective strategy to control antibiotic resistance in healthcare settings. It is also necessary to use careful infection control strategies. Keywords: *Acinetobacter baumannii*, multidrug-resistant bacteria, Intensive care unit

Frequency of *cbrA*, *cbrB*, *ndvB*, and *phoBR* genes in relation to biofilm formation in *Pseudomonas aeruginosa* clinical isolates

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نوع پذیرش: پوستر | کد مقاله: G-95276

Abstract: Background: After *Staphylococcus aureus* and *Escherichia coli*, *Pseudomonas aeruginosa* is the third cause of hospital-acquired infection (HAI). This bacteria's ability to colonize in different environments, especially in hospitals and biofilm formation, has added to its impact as an HAI. The molecular mechanism of biofilm formation is not well understood, but several genes contribute to this phenomenon. This study investigates the frequency of *cbrA*, *cbrB*, *phoBR*, and *ndvB* genes in biofilm-forming *P. aeruginosa* isolates. Methods: Fifty *P. aeruginosa* clinical isolates were collected from various sources such as urine, ulcer, blood, secretions, and trachea in Milad Hospital, Tehran, from 2017 to 2018. Biofilm formation in the isolates was assessed by the microtiter plate assay, and the frequency of *cbrA*, *cbrB*, *phoBR*, and *ndvB* genes was investigated by PCR. Results: Among the 50 isolates, 44% were strong biofilm former, 34% moderate biofilm former, 12% weak biofilm former, and 10% did not form biofilms. PCR revealed a frequency of 94% for the *cbrA* gene, 78% for *cbrB*, 96% for *ndvB*, and 48% for *phoBR*. The coexistence of all four genes was 68% in strong biofilm former isolates, 41% in moderate biofilm former isolates, 33% in weak biofilm former, and zero in the isolates that formed no biofilm. Conclusion: The high frequency of *ndvB* and *cbrA* genes and the coexistence of *ndvB* and *cbrB* suggest the contribution of these genes in the biofilm formation of *P. aeruginosa*.
Keywords: *Pseudomonas aeruginosa*, Biofilm, *cbrA*, *cbrB*, *phoBR*, *ndvB*



ATP-binding cassette protein in mycobacterium tuberculosis could be inhibited by selected anti-TB or herbal active ingredients

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Abstract: Multi-drug resistant Mycobacterium tuberculosis (MDR-TB) remains as a serious threat. Investigating new drugs using in-silico tools helps to shortening the route of research on tuberculosis (TB) treatment. Previously, we have shown that ATP-binding cassette proteins (ABCs) are over-expressed in MDR-TB isolates of TB patients. Hence, ABCs inhibition, that may have a role in extruding antibiotics from intracellular environment to the extracellular space, could be a potential method for enhancement and synergism of MDR-TB therapy.

Rifampin resistance among individuals with extrapulmonary tuberculosis: 4 years of experience from a reference laboratory

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نوع پذیرش: پوستر | کد مقاله: G-58721

Abstract: Background: Information is limited about the drug resistance patterns in extrapulmonary tuberculosis (EPTB) in Iran. This study aimed to determine the prevalence of EPTB and to investigate the drug-resistance pattern in Mycobacterium tuberculosis strains collected from extrapulmonary samples at the Tehran regional TB reference laboratory. Materials and Methods: Extrapulmonary specimens from individuals with suspected TB referred to the TB reference laboratories in five cities of Iran were collected. Both standard conventional methods (culture and direct smear microscopy) and Xpert MTB/RIF assay were used for the identification of mycobacteria. Drug susceptibility testing was done using Xpert MTB/RIF. The proportion method on Lowenstein–Jensen medium was performed for confirmation. Results: Between 2016 and 2020, a total of 12 050 clinical specimens from individuals with suspected TB were collected, of which 10 380 (86%) were pulmonary specimens and 1670 (14%) were extrapulmonary. Of the extrapulmonary specimens, 85 (5.0%) were positive for M. tuberculosis, and the remaining 1585 (95.0%) samples were negative by standard methods. Of 85 M. tuberculosis isolates, drug susceptibility testing was performed for 32 isolates, of which 1 (3.1%, 95% CI 0.0%–9.4%) was rifampin resistant and 31 (96.9%, 95% CI 90.1%–100%) were pan-susceptible. The rifampin-resistant isolate was also resistant to isoniazid, so was assigned as a multidrug-resistant TB. Conclusion: Our study indicated the frequency of drug-resistance among EPTB in Iran. Establishing rapid diagnostic methods for detection of drug-resistance in EPTB, performing drug susceptibility testing for all EPTB cases to provide effective treatment, and continuous monitoring of drug resistance, are suggested for prevention and control of drug resistance in EPTB in Iran. Keywords:

High prevalence of blaOXA-48 and High prevalence of blaOXA-48 and blaNDM producing carbapenem-resistant Klebsiella pneumoniae isolated from clinical samples in the Shahid Rajaei hospital in Tehran, Iran producing carbapenem-resistant Klebsiella pneumoniae

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نوع پذیرش: پوستر | کد مقاله: G-73421

Abstract: Background: Due to the increasing trend of antibiotic resistance, treating infections caused by Klebsiella pneumoniae has become challenging. Objectives: The present study aimed to investigate the prevalence of blaOXA-48 and blaNDM producing carbapenem-resistant K. pneumoniae isolated from clinical samples in the Shahid Rajaei hospital in Tehran, Iran. Methods: Various clinical samples were collected from 1186 patients admitted with open heart surgery in two wards (ICU and surgery) in Shahid Rajaei Heart Hospital in Tehran. K. pneumoniae isolates were identified by standard microbiologic tests. These isolates were tested for antibiotic susceptibility patterns using the disk diffusion and E-test methods. To detect the presence of carbapenemase, a modified carbapenem inactivation method (mCIM) was performed. Antibiotic resistance genes were detected using conventional polymerase chain reactions (PCR) by primers targeting blaOXA-48, blaSPM, blaIMP, blaVIM, and blaNDM genes. Results: A total of 131 clinical K. pneumoniae isolates were included, of which 45.8% (60/131) were considered carbapenem-resistant isolates. The highest resistance rate (100%) was against ceftriaxone, ceftazidime, cefazolin, and cefepime, whereas, the lowest resistance rate was toward tigecycline (3.3%). The carbapenemase-encoding blaOXA-48 and blaNDM-1 gene were detected in 96.7% and 66.7% of isolates, respectively. Among 58 blaOXA-48-positive K. pneumoniae isolates, eight different RAPD-PCR patterns were found at 80% similarity cut-off. A, B, C, D, E, F, G, and H include 20, 11, 7, 6, 6, 3, 2, and 2 members, respectively. Conclusions: The RAPD-PCR method reveals the clonal relationship between isolates and may help improve infection control procedures. Keywords: Klebsiella pneumoniae carbapenem-resistant, blaOXA-48, blaNDM, RAPD-PCR

The Prevalence of four fimbriae producing genes in *Escherichia coli* bacteria isolated from Urinary Tract Infections on Vali-e-Asr hospital in Arak

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نوع پذیرش: پوستر | کد مقاله: G-21453

Abstract: Background: After respiratory infections, urinary tract infections are the most common infectious disease in the world. The aim is the frequency assessment of four fimbriae producing genes in *Escherichia coli* isolates. Materials and Methods: One hundred bacterial isolates were isolated within three months. The middle urine sample was collected under sterile conditions and cultured in Blood Agar, Muller Hinton and EMB. The frequency of fimbria production genes *foc*, *afa*, *sfa*, *bmaE* in *E. coli* bacteria was evaluated. Also, the antibiotic sensitivity of the isolates to 10 common antibiotics was investigated and significance was evaluated at the level of 0.05. Results: The highest resistance was to ampicillin (82%) and the highest sensitivity to amikacin and tobramycin (100%). Using PCR method, the frequencies of *sfa*, *afa*, *foc* and *bmaE* genes were calculated as 32, 12, 52 and 26 percent, respectively. Urban areas two and five had the highest prevalence of these genes. Conclusion: The results indicate a high prevalence of the *foc* gene, which can be used in the preparation of mono or polyvalent vaccines. Also, there is a significant relationship between the presence of genes and variables such as age and place of residence, which can be used in the management of dealing with the mentioned bacteria and the preparation of local vaccines. Keywords: Fimbriae genes, *Escherichia coli*, Vaccine.

Investigating the genetic diversity of Escherichia coli bacteria isolated from urinary tract infections in Arak using RAPD-PCR method

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نوع پذیرش: پوستر | کد مقاله: G-73461

Abstract: Background: After pulmonary infections, urinary tract infections are the most common infectious diseases in the world, and the most important cause of bacterial infection is Escherichia coli. This research was conducted to investigate the relationship between uropathogenic E. coli isolates in Arak and their classification by RAPD-PCR molecular genotyping method. Methods: One hundred bacterial isolates were collected from Vali-E-Asr Hospital in Arak during 3 months and cultivated and kept in different common and specific environments. Specific identification of the isolates was done by biochemical and molecular methods of 16 srRNA. Ten universal decamer primers were used to prepare specific band patterns for each isolate/primer. ATCC 259222 bacteria were used as quality control in PCR and dendrogram drawing. Each reaction was repeated at least 3 times and SPSS 18, MVSP 3.0 and Band Leader 3 softwares were used. UPGMA and NJ cluster analysis with Jaccard and Nei & Li coefficients were used for phylogenetic grouping of isolates. Results: Only primer no. 1 for all isolates produced polymorph band and the highest band and also the highest average band belonged to primer number no. 1 by 7.3. At the similarity coefficient of 0.26, the first grouping was created and 100% similarity was not seen between any isolates. Genetic similarity was in the range of 0.26 to 0.74 and the lowest genetic similarity was between isolates 1 and 41 (0.26) and the highest similarity was between isolates 37 and 38 (0.78). Conclusion: A high genetic difference was seen between the isolates, which indicates that different sources can be the source of bacterial contamination of the urinary tract. RAPD-PCR phylogeny method is useful in determining the origin and source of contamination, grouping bacteria by cluster analysis and has high discrimination power, low cost, easy and fast application. Keywords: Escherichia coli, UPGMA, MVSP, Cluster analysis.

Molecular Epidemiology of Nontuberculous mycobacteria Isolated from Tuberculosis-Suspected Patients

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نوع پذیرش: پوستر | کد مقاله: G-54096

Abstract: Background: It is a growing problem around the world to deal with nontuberculous mycobacteria infection (NTM), but its clinical significance is still largely unknown. This study aims to investigate the epidemiology of NTM infections from various clinical samples and determine their clinical significance. From December 2020 to December 2021, 6,125 clinical samples were collected for this cross-sectional study. Materials and Methods: In addition to phenotypic detection, genotypic detection through multilocus sequence typing (hsp65, rpoB, and 16S rDNA genes) and sequencing was also conducted. Records of patients were consulted for clinical information, such as symptoms and radiological findings. Results: The NTM infection was detected in 62 (17.7%) out of 6,125 clinical samples that showed positive culture results for mycobacteria. Isolates of *Mycobacterium simiae* and *M. fortuitum* were the most frequent, followed by isolates of *M. kansasii* and *M. marinum*. We also isolated *M. chelonae*, *M. canariense*, and *M. jacuzzii*, which are rarely reported. Symptoms ($P=0.048$), radiographic findings ($P=0.013$), and gender ($P=0.039$) were associated with NTM isolates. *M. Fortuitum*, *M. simiae*, and *M. kansasii* presented with bronchiectasis, infiltration, and cavitory lesions most frequently, while cough was the most common symptom. Conclusion: In conclusion, *Mycobacterium simiae* and *M. fortuitum* were presented in seventeen and twelve NTM isolates from the collected samples. There is evidence that NTM infections in endemic settings may contribute to the dissemination of various diseases and the control of tuberculosis. In spite of this, further research is needed to evaluate the clinical significance of NTM isolates. Keywords: Nontuberculous mycobacteria, Clinical significance, Iran

Evaluation of cell-free extract *Limosilactobacillus fermentum* on Nonalcoholic steatohepatitis in vitro model through apoptosis pathway

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نوع پذیرش: پوستر | کد مقاله: G-94267

Abstract: Background: Non-alcoholic steatohepatitis (NASH) is one of the diseases in the spectrum of non-alcoholic fatty liver disease (NAFLD) caused by the accumulation of excess fat in the liver, chronic inflammation and cell death. The strain *Limosilactobacillus fermentum* was identified as an antimicrobial and antioxidant probiotic. In this study, the effect of *L. fermentum* on in vitro NASH model and the expression level of genes involved in apoptosis were investigated. Materials and Methods: the NASH model was induced on the HepG2 cell line using oleic acid and palmitic acid for 24 hours and confirmed by Oil red O staining. Then, the cell-free extract (CFE) of *L. fermentum* was extracted using the ultrasonic method and the cell line was treated with the extract for 48 hours. Total RNA was extracted using the kit and then cDNA was synthesised. Gene expression was verified by real-time PCR technique using the primers designed for the genes of interest. $2^{-\Delta\Delta CT}$ was used extensively used as a relative quantification strategy for data analysis. All statistical analyses were performed using Graphpad Prism 9 software. Data were expressed as mean \pm SEM of three biological replicates. P 0.05 was considered statistically significant. Results: after Oil red O staining, the absorption of lipid droplets by the vacuoles of the cells is clearly visible under the microscope and lipid droplets accumulation was observed in the NASH model. Treatment with CFE of *L. fermentum* dramatically decreased lipid droplets. Statistical analysis also showed that the group treated with CFE of *L. fermentum* significantly reduced the expression of genes involved in the intrinsic pathway of apoptosis, including caspase 3 and 9, compared with the control group receiving oil. Conclusion: based on the results which show a decrease in the expression of genes involved in the intrinsic pathway of apoptosis, *L. fermentum* may have a significant effect on ameliorating NASH disease by affecting of apoptosis pathways. Keywords: Non-alcoholic steatohepatitis, liver disorder, *Limosilactobacillus fermentum*, apoptosis.



Report of generalized sheep tuberculosis caused by *Mycobacterium bovis* in Sanandaj

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نوع پذیرش: پوستر | کد مقاله: G-26415

Abstract: Background: Cattle are known as the main host in bovine tuberculosis disease caused by *Mycobacterium bovis*, but the sheep is relatively resistant to this infection and therefore few cases of its disease occur in sheep. Only when cattle and sheep are in very close contact with each other and the abundance of mycobacterium in the environment is very high, sheep infected by this disease. Case Presentation: In the present study, a case of generalized tuberculosis in sheep in the slaughterhouse was reported. Disease diagnosis was done based on necropsy lesions (generalized tuberculous granuloma), Ziehl-Neelsen staining and PCR technique for *Mycobacterium bovis*. Conclusion: The present report shows that *Mycobacterium bovis* strains present in the region have the ability to be transmitted to sheep and cause disease with severe clinical symptoms. This report is very important particularly for mixed farming of cattle and sheep. Keywords:

Investigation of antibiotic resistance pattern and biofilm formation potential of *Escherichia coli* obtained from beef cattle in Ilam and Kurdistan provinces

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نوع پذیرش: پوستر | کد مقاله: G-76150

Abstract: Background: *Escherichia coli* bacterium is known as one of the microflora of the digestive system of humans and warm-blooded animals. However, some strains of this bacterium have the ability to cause various infections due to having different virulence factors. Accordingly, the present study aimed to identify antimicrobial resistant pattern and biofilm formation potential of *E. coli* obtain from beef cattle in Ilam and Kurdistan provinces. Methods: Beef samples were taken from neck, arms and thighs of 90 slaughtered cows (45 cows from Ilam and 45 cows from Kurdistan). Bacterial isolation was performed by culturing of samples on the selective and differential culture media and biochemical tests. The antibiotic susceptibilities and biofilm formation potential were done by Kirby Bauer's disk diffusion and microtiter plate (MtP) tests, respectively. The Spearman rank correlation test performed to study the correlation between antimicrobial susceptibility and biofilm formation and p values less than 0.05 were considered as a significant level. Results: Of 270 meat samples, 42 *E. coli* were isolated. In both provinces, samples taken from the thighs had significantly more *E. coli* bacteria than necks and arms. The highest resistance rate was reported to sulfamethoxazole and tetracycline (85.71%), followed by ampicillin (80.95%). Besides, all *E. coli* were sensitive to colistin. Based on MtP, 24 (57.14%), 12 (28.57%) and 6 (14.28%) isolates were categorized as strong, moderate and weak biofilm producer, respectively. The significant positive correlation (p 0.05) was found between biofilm formation and resistance to ampicillin, amoxicillin, amikacin, ciprofloxacin, gentamicin, tetracycline and ceftriaxone. Conclusion: High antibiotic resistance rates and strong biofilm formation ability of *E. coli* isolates obtained from red meat suggest the need for continuous surveillance in the food chain. Keywords:

The role of cefotaxime in antibiotic resistance in UTI

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نوع پذیرش: پوستر | کد مقاله: G-26510

Abstract: Background: *Klebsiella pneumoniae* is one of the most important cases of acquired infections and the second leading cause of urinary tract infections in the community and hospitals. The increasing emergence of multidrug resistance among hospital isolates of *Klebsiella pneumoniae* has limited treatment options for treating bacterial infections. The aim of this study was to determine the frequency of CTX gene in clinical isolates of *Klebsiella pneumoniae* causing urinary tract infection in Khorramabad. Materials and Methods: In a study conducted from June 2020 to August 2021, 100 isolates of *Klebsiella pneumoniae* isolated from urinary tract infection were collected from people who referred to the medical centers of Khorramabad city. The samples taken in the bacteriology laboratory were evaluated using biochemical methods and culture on EMB.TSI.BA.IMVIC media. Resistance was investigated by two phenotypic methods through disk diffusion and genotyping. Cefotaxime 30µg antibiotic disc was used for this purpose. Gene extraction was performed by boiling method. PCR was performed with specific primers and specific temperature program, Then the PCR products were loaded into the gel wells and the results were observed by electrophoresis. Results: Out of 100 samples taken, 57 cases were women, 39 cases were men and 4 cases were children under 12 years old., 30 samples (30%) showed resistance to cefotaxime. CTX-M resistance gene was observed in all cases that showed resistance to cefotaxime antibiotic by disk fusion method. Conclusion: The results and studies show that the CTX-M resistance gene is present in the community and this indicates the emergence of antibiotic resistance in the community, which is an important warning for the risk of resistance to various antibiotics and treatment in The future will be more difficult. Keywords: Cefotaxime, *Klebsiella pneumoniae*, UTI, Antibiotic resistance. Khorramabad

Frequency and antibiotic resistance patterns of isolated bacteria from blood culture of hospitalized patients in Khorramabad, Iran

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نوع پذیرش: پوستر | کد مقاله: G-53670

Abstract: Introduction: Blood infection (growth and proliferation of pathogenic microorganisms in the blood) is one of the most important issues in the medical community that can cause irreversible consequences if not properly diagnosed and treated promptly. Awareness of the diversity of bacterial agents of blood infection, determining the contamination of blood vessels as well as the study of antibiotic resistance of these bacteria is of great epidemiological importance and can be effective in choosing the initial antimicrobial treatment. Therefore, the aim of this study was to investigate the frequency and pattern of antibiotic resistance of bacterial strains in blood culture samples of patients of Shahid Rahimi Hospital in Khorramabad. Materials and Methods: This study was a cross-sectional study. First, through registration and archiving sources, samples sent for culture in the laboratory, patient code, demographic information, Gram staining, biochemical tests that were used to identify the bacteria and also the results of antibiotic sensitivity testing of each bacteria isolated from blood culture were recorded. Then, using the code, the name of patients, hospitalization date, clinical symptoms and treatment outcome were recorded in a checklist. Results: In the present study, there were 2591 total blood culture samples that 286 cases of them was positive, of which 247 positive samples after removing contaminated cases and uncompleted files were included in the study. The highest frequency of the studied blood culture samples was related to the emergency department (62%), ICU (23%) and the lowest frequency of the studied blood culture samples was related to the children's department (2.4%). From 247 positive blood culture samples were included in the study 70 (28%) Gram-negative bacilli and 177 (72%) Gram-positive cocci were reported. The highest frequency of Gram-negative bacteria was *Escherichia coli* 27 (38%) and the lowest was *Acinetobacter baumannii* 3 (4%). The highest frequency of Gram-positive bacteria was *Staphylococcus epidermidis* 96 (54%) and the lowest was micrococci was 9 (5%). From the Gram negative bacteria isolated from blood culture in this study the most resistant was *Acinetobacter baumannii* that was resistant (100%) to all of antibiotics (Cefoxitin, Cefepime, Ceftriaxone, Cefotaxime, Ciprofloxacin, Amikacin, Gentamycin, Tetracycline). From the Gram positive bacteria isolated from blood culture in this study the most resistant was Group D streptococci that was resistant to erythromycin antibiotics (92%). Conclusion: It seems that according to results of this study, the prevalence of antibiotic resistance in common microorganisms that causes septicemia is increasing compared to previous similar studies. Also, considering the importance of the emergence antibiotic resistance and changing the pattern of antibiotic sensitivity bacterial, antibiogram tests are necessary in the treatment of septicemia. Keywords: Blood infection, Blood culture Antibiotic susceptibility.

Evaluation of the emergence of *Acinetobacter baumannii* isolates containing VIM and SIM and drug resistant MDR genes isolated from surfaces and equipment of Tehran medical centers by PCR

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Abstract: Excessive and irregular use of antimicrobial substances in hospital and community are considered as the important retainer and retarder factors which lead to emergence, evolution and new resistance form of bacteria respect to antimicrobial materials. The purpose of this study is Identification of *Acinetobacter baumannii* isolates with VIM and SIM genes resistant to MDR drug separated from surfaces and medical care facilities in Tehran based on PCR method. Materials and Methods: In this descriptive- cross-sectional study which it was accomplished within 2 months, of 200 samples which had been sent to Hamkar Microbiology lab in west of Tehran, 40 *Acinetobacter baumannii* species were detected and isolated using by Biochemical tests and cultivations and also VIM and SIM genes were detected by PCR methods Results: The resistance of isolates were included 40 isolates (100%) respect to Imipenim and marpenim antibiotics and Lincomycine and ceftozoxime and Occiciline; 36 isolates (90%) ,Gentamicine 34 isolates (85.97%),Cyprofloxin; 39 isolates (98%),Cephtazidime;39 isolates (99%),Cephotaxime and cefoxime; 27 isolates, (69.4%) and Ampiciline and tetracycline; 28 isolates (70.2%) and 40 isolates (100%) were sensitive to Clestine and minimum absorbing average between Imipenim and marpenim antibiotics among 24 isolates (60.3%) was MIC \geq 64 ug/ml. frequency percentage of VIM and SIM genes in resistant isolates were included 7 isolates (19.4%) and 1 isolate (3.2%) respectively Conclusion: in this study, the importance of the emergence of *Acinetobacter baumannii* isolates resistant to drugs was studied and due to limited information systems and the potent of expression defects in secretive and mutation pumps in topoisomeres and diversity and prevalence of VIM and SIM genes and based on the results of this research, the resistant isolates can be prevented and controlled and also resistance pattern of phenotype and genotype respect to antimicrobial materials can be studied in the world and particularly in Iran and all researchers should consider it seriously. Keywords:

Demographic, Histological, and Clinical Factors on Patients Suffering from Peptic Ulcer Infected with *Helicobacter pylori*

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نوع پذیرش: پوستر | کد مقاله: G-29678

Abstract: Background: *Helicobacter pylori* (*H. pylori*) is a prominent factor causing peptic ulcers in adults and more than half of the world's population. The prevalence of this infection and histological and clinical characteristics are dependent on the different risk factors according to geographic region and demographic characteristics. In this study, the effect of demographic, histological, and clinical factors on peptic ulcers in patients with *H. pylori* infection was investigated. Materials and Methods: The current study was an analytical cross-sectional study. All patients who were referred to the endoscopy unit of Ayatollah Rouhani Hospital and Shahid Beheshti Hospital (Babol city, Iran) during 2006-2020 and whose gastric pathology samples were positive for *H. pylori* were included in the study. The two groups of patients with and without peptic ulcer disease were compared in terms of demographic, clinical, endoscopic, and histological features. Collected data were analyzed in SPSS v.24 software and Fisher's exact tests, and Pearson's correlation coefficient was performed ($p < 0.05$) (MUBABOL.HRI.REC.1399.245). Results: In assessing the severity of *H. pylori* infection, 162 (49.8%) patients had mild, 109 (33.5%) moderate and 54 (16.6%) severe infections. Finally, 325 patients were included in the study, of which 166 (51.1%) were male and 159 (48.9%) were female. The mean age of patients was 52.20 ± 14.54 years. 165 (50.80%) had a peptic ulcer and 160 (49.2%) had no peptic ulcer; 80 (24.6%) patients had a gastric ulcer and 102 (31.4%) had a duodenal ulcer. 47 (14.5%) patients smoked and 17 (5.2%) were alcohol users. 24 (7.17%) of patients with nausea and 24 (7.17%) of patients with dysphagia were examined endoscopically. Of patients with peptic ulcer, 66 (41.2%) were female and 94 (58.8%) were male. Of patients without peptic ulcer, 93 (56.3%) were female and 72 (43.7%) were male. Significant differences were found between females and 72 (43.7%) males ($p = 0.008$). No significant differences were found between other variables, between patients with peptic ulcer and those without peptic ulcer ($p > 0.05$). Conclusion: The results of this study showed a high frequency of peptic ulcer in patients with *Helicobacter pylori* infection and the Peptic ulcer was significantly more common in men than women. The above information can be used to guide internal medicine and gastroenterologists in approaching patients with *H. pylori*. Keywords: Risk factors, Peptic Ulcer, *Helicobacter pylori*

Prevalence and antibiotic resistance patterns of *Pseudomonas aeruginosa* in hospitalized patients with urinary tract infection (UTI)

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نوع پذیرش: پوستر | کد مقاله: G-17638

Abstract: Background: High antibiotic resistance in *Pseudomonas aeruginosa* has been a major concern in the past years. The World Health Organization (WHO) has stated that it is not possible to treat bacteria with existing drugs for several years. Therefore, finding an alternative to treatment is essential. Materials and Methods: This study was performed from 2019 to 2020 in the infectious ward of Labbafinejad Hospital in Tehran. The information of diagnostic tests and antibiogram was collected based on a questionnaire and reviewing the files of patients with urinary tract infections. In this study, 200 people were hospitalized with symptoms of urinary tract infection over a period of one year. A total of 356 urine cultures were performed. Of these 200 patients, 17 were infected with *Pseudomonas aeruginosa*. 25 antibiogram cultures were performed. Results: According to the results, the highest resistance to ceftriaxone, nitrofuranten and ceftazidime antibiotics (94.11%). And the best antibiotic effect for ciprofloxacin and imipenem (29.41%). Conclusion: Due to the high resistance of *P. aeruginosa* to existing drugs, it is necessary to find a new therapeutic approach, In order not to spread resistant strains, it is recommended that after obtaining antibiogram results, if you are allergic to other antibiotics, use them to continue treatment to prevent the emergence and spread of bacteria resistant to antibiotics, fluoroquinolones and carbapenem Prevent. Keywords: *Pseudomonas aeruginosa*, Multi drug resistanc (MDR), Urinary tract infection (UTI)

The Q fever and abortion status in dairy cow

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نوع پذیرش: پوستر | کد مقاله: G-07293

Abstract: Background: The role of Rickettsia as the cause of Q fever, Coxiella burnetti, is important as a zoonotic agent. The circulation of bacteria between different animal species and humans has been proven. Identifying the effective foci in the reproduction and spread of the disease in the livestock population is important. This disease is associated with clinical symptoms in most animal species. The aim of the current study is to investigate the prevalence of the disease and identify the related risk of abortion in dairy cows. Materials and Methods: A total of 84 dairy cows were selected in Zagros Milk and Meat Complex, Shahrekord, and the serum samples were prepared from their jugular vein. The samples were transferred to the microbiology laboratory of Ahvaz Veterinary Faculty to check the antibody titer against bacteria using a commercial special ELISA kit. Results: The results showed that 14.3% of the serum samples were positive in terms of antibody levels against Q fever. Half (50%) of the animals with a history of recent abortion were considered positive in terms of antibody level. Conclusion: This study showed that Q fever should be considered a zoonotic factor and a possible cause of abortion in dairy farms. Keywords: Coxiella Brunetti, Q fever, dairy cows, abortion

MTT assay in bio-mof (metal organic framework) on clinical and standard strains of Methicillin-resistant Staphylococcus aureus

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نوع پذیرش: پوستر | کد مقاله: G-89724

Abstract: Background: Methicillin-resistant Staphylococcus aureus (MRSA) is one of the most important causes of human infections. This bacterium has shown resistance to many antibiotics, especially beta-lactams. This increase in antibiotic resistance is considered a concern and should be controlled. The MRSA strain has the *mecA* gene, which encodes a protein called PBP2a and has a low affinity for binding to methicillin. Therefore, new strategies are needed to deal with MRSA-related infections. One of the recent efforts of researchers to overcome these challenges is the use of nanomaterials as innovative and promising alternatives to antimicrobial drugs. The present research has studied the life percentage of these nanostructures with the technique MTT assay. Materials and Methods: MRSA bacteria was confirmed by Genotyping and Phenotyping methods. The isolates and standard bacteria were cultured in Muller Hilton media and antibiotic discs were applied to the bacteria. *mecA* gene was confirmed by PCR in isolated MRSA. Cell Cytotoxicity assay in MRSA bacteria was performed by MTT assay (OD:570) and then the IC50% dose for each MRSA was determined Results: *mecA* gene Fragment was amplified in clinical and standard isolates and then the PCR product was run in agarose gel. (Fig1). List resistance and sensitive bacteria to antibiotic discs are shown in Table 1. However, all of clinical isolates are resisted to Gentamycin and Erythromycin and are sensitized Linezolid, Ciprofloxacin. Bio-MOF were tested to MRSA bacteria and besides standard strains. IC50% of Bio-MOF in MRSA bacteria and standard strains are shown in table 2. Taken together, mean all of clinical isolates have had lower IC50% than standard isolate to Bio-MOF and were statistically significant (two-tailed t.test, P.Value 0.0342, 95% confidence interval). Conclusion: There is a high antibacterial potential in metal-organic framework based nanomaterials (MOF), these materials are very environmentally friendly and are now widely used in the production of medical products. This compound has shown that can influence MRSA bacteria and block the bacteria amplification in low concentration. Keywords: Methicillin resistant Staphylococcus aureus, bio-MOF, MTT assay, Antibacterial

Investigating the rapid diagnostic value of fecal *Helicobacter* compared to the endoscopic method in diagnosing patients with gastric ulcer, indigestion and gastritis without ulcer.

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نوع پذیرش: پوستر | کد مقاله: G-46075

Abstract: Background: The isolation of *Helicobacter pylori* from clinical specimens by Marshall and Warren 15 years ago launched revolutions in gastroenterology and microbiology. Active *Helicobacter Pylori* (HP) infection can be diagnosed by invasive (biopsy based) or non-invasive methods, such as stool antigen testing. Materials and Methods: Thirty adults with dyspepsia referred for endoscopy provided a feces sample for testing and had biopsies taken. Patients were considered H pylori positive if invasive tests were positive. Fecal samples were collected from same patients and were tested for fecal antigen of H.Pylori rapid test. Results: The sensitivities and specificities of the Rojan Azma. H.pylori antigen kits (rapid immunochromatography method) when compared with Endoscopic based diagnosis were, 99.9 %, 98.1%, respectively. Conclusion: The rapid diagnostic test of fecal *Helicobacter* may be considered as an alternative to urea breath testing in the initial diagnosis of patients with dyspepsia who do not require immediate endoscopy. Fecal testing has the potential advantages of being simple to perform, relatively cheap, and samples can be submitted directly from primary care and performed with least available hardware and trained personal. Keywords: *Helicobacter pylori*, Fecal, Rapid test

Evaluation of antibacterial activity of silver nanoparticles and green tea extract on clinical isolates of Acinetobacter

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نوع پذیرش: پوستر | کد مقاله: G-89463

Abstract: Evaluation of antibacterial activity of silver nanoparticles and green tea extract on clinical isolates of Acinetobacter Mahla Nazarian¹, Nadia Kazemipour^{1*} ¹Department of Microbiology, Kerman Branch, Islamic Azad University, Kerman, Iran Contact information: Email: nadia_kazemi@yahoo.com Postal Address: Department of Microbiology, Kerman Branch, Islamic Azad University, Kerman, Iran; Phone: +983431321334, Fax: +983431320051 Background: Acinetobacter is a gram-negative opportunistic pathogen that has become resistant to many common antibiotics. Accordingly, the aim of this study was to investigate the pattern of antibiotic resistance of clinical isolates of Acinetobacter strains and also evaluation the effect of biosynthesized silver nanoparticles by aqueous extract of Camellia sinensis L. on bacterial isolates. Material and methods: In this descriptive laboratory study, 30 Acinetobacter isolates were obtained from the clinical laboratories in Kerman in the fall of 2021 and they were identified by biochemical methods. The Kirby-Bauer method was used to determine the resistance patterns of the isolates. Then, silver nanoparticles were biosynthesized from aqueous extract of Camellia sinensis L. after colorimetric and superficial plasmon resonance analysis by spectrophotometer, the effectiveness of biosynthesized silver nanoparticles on Acinetobacter isolates were investigated. The minimum inhibitory concentration of isolates was evaluated by biosynthesized silver nanoparticles and antibiotic gentamicin. Results: The results showed that 100% of the isolates were resistant to ceftazidime, ceftriaxone, oxacillin, 96.66% to imipenem, 90% to cefixime and cefotaxime, 86.66% to colistin and amikacin, 80% to ciprofloxacin and 70% to gentamicin. The bio-reduction of silver ions was determined by changing the color of the reaction solution from yellow to brown, and the surface plasmon resonance absorption band was 420 nm. The mean diameter of Inhibition zone created by biosynthesized silver nanoparticles at a concentration of 1 mg/ml was 14.6 mm and the minimum inhibitory concentration was determined at a concentration of 0.001 mg / ml. Conclusion: According to the results, silver nanoparticles prepared from green tea may show the good potential for controlling Acinetobacter infections after clinical tests. Keywords: Acinetobacter, Antibiotic resistance, Silver nanoparticles, Camellia sinensis L

Antibiotic Resistance and Biofilm Formation of *Pseudomonas aeruginosa*, a therapeutic challenge

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نوع پذیرش: پوستر | کد مقاله: G-85721

Abstract: Background: In this modern era, medicine is facing many alarming challenges. Among different challenges, antibiotics are gaining importance. *Pseudomonas aeruginosa* is a gram-negative bacterium that causes many diseases in different parts of the body. It is the most important cause of nosocomial infections in patients. *P. aeruginosa* is also recognized as an important cause of chronic infections due to its ability to form biofilms. Methods: Studies were collected using different keyword combinations: Biofilm, Antibiotic Resistance *Pseudomonas aeruginosa*, and nosocomial infections. The literature search strategy in this paper included searching PubMed, PMC, and Science Direct, Springer open, Google scholar and BioMed Central databases. Results: Significant changes were found in resistance of *P. aeruginosa* towards certain antibiotics of the β -lactam class. There was an increasing trend in the occurrence of resistance genes in β -lactamase-producing *P. aeruginosa*. Conclusions: Prior use of antibiotics and prior hospital or ICU stay was the most significant risk factors for acquisition of resistant *P. aeruginosa*. These findings provide guidance in identifying patients that may be at an elevated risk for a resistant infection and emphasize the importance of antimicrobial stewardship and infection control in hospitals. Keywords:

Molecular study of tigecycline resistance mechanisms in clinical isolates of *Acinetobacter baumannii*

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نوع پذیرش: پوستر | کد مقاله: G-98035

Abstract: Background: This study aimed to investigate the mechanisms of resistance to tigecycline and specify the sequence type (ST) of tigecycline-resistant *Acinetobacter baumannii* isolates in children. Methods: From February 2020 to March 2021, a total of 74 *A. baumannii* isolates were recovered from a children's hospital in Tehran, Iran. Antimicrobial susceptibility testing of the isolates was assessed for different classes of antibiotics and minimum inhibitory concentration (MIC) of tigecycline was determined by E-test. The expression of *adeB*, *adeG* and *adeJ* efflux pump genes were measured by quantitative real-time PCR (RT-PCR). Diversity of mutations in regulatory genes of RND efflux pumps (*adeRS*, *adeL* and *adeN*) and *trm* was specified by DNA sequencing in tigecycline-resistant isolates. Sequence types of tigecycline resistant were ascertained with Multilocus sequence typing (MLST) method. Results: A total of 68 (91.89%) isolates were determined to be MDR. Among 74 *A. baumannii* three isolates were resistant to tigecycline. Several substitutions were found in *adeRS*, *adeN* and *trm* but no mutation was found in *adeL*. On the other hand, *adeN* DNA sequence analysis revealed the presence of class 1 integron in two tigecycline resistant isolates. Nevertheless, overexpression in *adeB*, *adeG* and *adeJ* was observed in 1, 2 and 1 isolates respectively. These three tigecycline resistant isolates belonged to ST1720 and ST2285. This is the first study reporting on ST2285 in *A. baumannii* populations. Conclusions: we concluded that tigecycline resistance occurs as a result of various resistance mechanisms. Amino acid substitutions in regulatory system of RND efflux pumps and *trm* gene have important role in tigecycline resistance. Keywords:

Molecular Epidemiology of Panton-Valentine Leukocidin Harboring Hospital-Associated Methicillin-Resistant Staphylococcus aureus in Septicemic Children, Northeastern Iran, Bojnurd

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نوع پذیرش: پوستر | کد مقاله: G-38562

Abstract: Background: Methicillin-resistant Staphylococcus aureus (MRSA) is responsible for an increasing number of serious hospital- and community-acquired infections in adults and children. Sepsis caused by *S. aureus* is one of the major health problems associated with treatment failure in adults; however, its clinical outcomes, the rate of treatment failure, and its molecular epidemiology are poorly understood. The objective of this study was to evaluate the molecular epidemiology of Panton-Valentine Leukocidin (PVL) harboring MRSA strains isolated from children's blood culture in Bojnurd. Materials and Methods: Totally, 58 *S. aureus* strains were isolated from blood cultures in the major teaching hospital in Bojnurd. After the primary verification of Methicillin resistance by agar screening method, the isolated MRSA strains were confirmed with the detection of the *mecA* gene. *MecA*-positive strains evaluated for SCCmec, *agr*, and toxin profiles. Panton-valentine leucocidin- positive isolates were subjected to be evaluated for *spa* and sequence type (ST). Results: Our data indicated 53.4% (31) of isolates were MRSA. Twelve (38.7%) of these isolates had PVL gene that 25% (3) of them had *stx1* gene and 58.3% (7) had *etb* gene. One (3.2%), 64.5% (20), and 32.2% (10) of these isolates belonged to SCCmec I, III, and IV, respectively. Predominant ST and *spa* types among PVL positive isolates were ST6 and t304, respectively. Conclusion: We had an uncommon finding because PVL was routinely found in community-acquired MRSA, but in this study we found PVL harboring hospital-associated MRSA. A notable point about these isolates is that most of them belonged to Asian endemic clones. Keywords: Staphylococcus aureus, Methicillin, Panton-Valentine Leukocidin, Sepsis, Child

Morganella morganii Isolation from Patient Suffering from diabetic foot ulcer with Gangrene

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نوع پذیرش: پوستر | کد مقاله: G-08657

Abstract: Background: In rare cases, *Morganella morganii* is the cause of infection in diabetic patients with foot ulcers. In this study, two cases of diabetic foot ulcers were investigated, and *Morganella morganii* was isolated from their ulcers. Case Presentation: The first case was a 47-year-old woman with a complaint of diabetic foot ulcer. Osteomyelitis, kidney disorder, and gangrene were diagnosed. Wound cultures grew *Morganella morganii*. One month after the amputation, the patient suffered bleeding, infection and died. The second case was a 65-year-old woman with gangrene-diabetic foot ulcer. Osteomyelitis and kidney disorders were observed in the patient. A wound culture grew *Morganella morganii*. Angioplasty was performed and the patient was discharged (IR.MUBABOL.HRI.REC.1401.083). Conclusion: *Morganella morganii* was separated from a leg wound. The first patient died due to kidney failure, a weak immune system, and antibiotic resistance. Referral, diagnosis, and quick treatment of patients with diabetic foot ulcers are essential. Keywords: *Morganella morganii*, Diabetic foot ulcer, Gangrene

Evaluation of the presence of Metallo- β - Lactamases- related genes in clinical isolates of *Acinetobacter baumannii* with antibiotic resistance in Boroujerd

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نوع پذیرش: پوستر | کد مقاله: G-70618

Abstract: Introduction & Objective: The members of the genus *Acinetobacter* are Gram-negative cocobacilli that are frequently found in the environment but also in the hospital setting where they have been associated with outbreaks of nosocomial infections such as meningitis, endocarditis, skin and soft tissue infections, urinary tract infection, conjunctivitis, burn wound infection and bacteremia. This organism has been shown resistance to different antimicrobial agents. The aim of this study was to Evaluation of the presence of Metallo- β - Lactamases- related genes in clinical isolates of *Acinetobacter baumannii* with antibiotic resistance in Boroujerd. Methods: This study was performed on 46 *Acinetobacter baumannii* isolates from patients in Broujerd hospitals. Presence of *Acinetobacter baumannii* isolates were confirmed by biochemical tests. Drug susceptibility, presence of *vim*, *imp*, *ndm* and *spm* genes were determined using disk diffusion method and PCR methods, respectively. Results: The highest antibiotic resistance was against ceftazidime, imipenem and meropenem antibiotics and the lowest resistance was against levofloxacin and ampicillin antibiotics. The frequency of *imp* and *vim* genes was 3 (10%) and 2 (6.66%), respectively. Conclusion: Multiple antibiotic resistance in studied isolates the use of molecular techniques in the antibiogram test to select the most effective antibiotic treatment of infections and the importance of continued antibiotic surveillance that will provide succession in the efforts of infection control programs for the future. Keywords:

Isolation of *Pasteurella multocida* and bacteria with Pan-drug-resistant to antibiotics and causing nosocomial infection from a patient with multiple sclerosis

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نوع پذیرش: پوستر | کد مقاله: G-96708

Abstract: Background: *Pasteurella* species are one of the most common pathogenic bacteria common to domestic animals and they are seen more in people with weak immune system. The aim of this research is to investigate a case of a patient with multiple sclerosis in which *Pasteurella multocida* was isolated from his sputum sample. Case Presentation: The patient was a 28-year-old man with multiple sclerosis, who had complained of multiple coughs due to food stuck in his throat. The primary diagnosis was pneumonia and hydropneumothorax and complete collapse of the left lung. The patient's sputum culture after the first visit to the hospital was positive for *Pasteurella multocida*. *Pasteurella multocida* was not found in the second culture of the patient's sputum. In the subsequent cultures of the patient, *Acinetobacter*, *Klebsiella*, *Pseudomonas aeruginosa* and *Citrobacter* were found with extensive drug resistance to all antibiotics. In the secondary CT scan, mild pleural effusion on the left side, pneumothorax, and complete collapse with bronchiectasis was seen. Despite the treatments performed on the patient, the patient finally died of cardiac arrest and bradycardia (IR.MUBABOL.HRI.REC.1401.140). Conclusion: Infection with *Pasteurella multocida* was found in a patient with multiple sclerosis. Also, hospital-acquired infections with drug resistance caused by the weakness of the patient's system appeared in the patient who was hospitalized in the intensive care unit, and finally the patient died. It is necessary to reduce hospital infections along with practical and applicable plans. Keywords: *Pasteurella multocida*, Pan-drug-resistant, nosocomial infection multiple sclerosis

Investigating a Culture-based Isolation Method of Anaerobic Bacteria from the sputum of Cystic Fibrosis Patients

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نوع پذیرش: پوستر | کد مقاله: G-70843

Abstract: Background: Cystic fibrosis (CF), an inherited lung disease, is caused by a defect in the gene expressing the protein responsible for transporting chloride ions. In these patients, the accumulation of sputum in the pulmonary ducts causes hypoxia conditions and the growth of anaerobic bacterial pathogens (1). Direct sampling of sputum is challenging due to the use of special equipment. On the other hand, sampling using a swab probably leads to a small sampling volume, which is not enough to carry out some studies. The aim of this study was to determine the effectiveness of direct sputum sampling without using advanced equipment (cost-effective) and with enough sample volume, the conditions of transfer to the laboratory, and selective medium. Materials and Methods: 50 sputum samples were taken from the patients in a sterile sample collection container and immediately transferred to the thioglycollate broth (THO) culture medium. Both sputum and cultured (THO) samples were transported to the laboratory under anaerobic conditions using an anaerobic jar and gas pack type A. The sputum sample inoculated directly on four culture media, including brucella blood agar containing hemin and vitamin K1 (BA), brain heart infusion agar containing sheep blood, vancomycin, hemin, vitamin K1 (BHI), brucella blood agar containing laked sheep blood, kanamycin, vancomycin, hemin and vitamin K1 (LKV), brucella blood agar containing sheep blood, vancomycin and neomycin (VN) were cultured. The plates were incubated under anaerobic conditions at 37°C for 48 hours (2, 3). If no colony was observed in each plate, the THO medium was cultured once more in agar medium. The obtained pure colony was stored. The final concentration of used antibiotics kanamycin, neomycin, vancomycin (LKV), vancomycin (BHI), and vancomycin (VN) are 0/1 mg/ml, 100 µg/ml, 7/5 µg/ml, 7/5 µg/ml and 5 µg/ml respectively. BA culture medium was considered general culture medium and LKV, BHI, and VN culture mediums, respectively, to isolate Prevotella, Veillonella, and Fusobacterium bacteria. All the mentioned bacteria are obligate anaerobes. Then, obligate anaerobic testing of the isolates was carried out using the aerotolerance test. Results: A total of 172 bacterial strains were isolated from 50 sputum samples of patients. The number of strains isolated from the culture media on BA, LKV, BHI, and VN were 39, 15, 24, and 13, respectively. The result of the aerotolerance test also showed the lack of growth (obligate anaerobic bacteria) of 50 isolates exposed to oxygen. Obligate anaerobic strains isolated from BA, LKV, BHI, and VN cultures were 28, 4, 13, and 5, respectively. Conclusion: The results obtained from this study show the feasibility of the sputum sampling from CF patients without using a swab to isolate anaerobic bacteria. As expected, the general culture medium like BA has the ability to grow more strains than the selective culture mediums with antibiotics. Conversely, our results can indicate the variety of anaerobic bacteria present in the sputum of these patients, which probably requires more types of selective culture media for their isolation. Keywords: Anaerobic bacteria, Cystic fibrosis, Isolation, Culture-based.

Effects of the cell-free supernatant from a potential probiotic strain *Lactobacillus gasseri* ATCC 33323 on induction of apoptosis in HT-29 cell line

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نوع پذیرش: پوستر | کد مقاله: G-01482

Abstract: Background: Colorectal cancer (CRC) ranks third in cancer incidence and second in cancer-related death worldwide. There are many reports about the beneficial impact of bioactive components obtained from probiotics, prebiotics, and postbiotics on the prevention and treatment of colorectal cancer. The term postbiotics refers to a complex of biological micro- and macromolecules produced during the metabolic activity of a probiotic strain. In this study, we aim to investigate the effect of cell-free supernatant (CFS) derived from a potential probiotic strain *Lactobacillus gasseri* ATCC 33323 on apoptosis in a colorectal cancer cell line. Methods: *L. gasseri* was cultured on MRS broth for 50 h, and then centrifuged in 16000xg for 10 min. The pH of the supernatant increased to 7.5 with NaOH and was filtered using a 0.22-micron filter. The obtained CFS (10% v/v) was added to HT-29 cells, and after 24 h the mRNA expression level of MCL1, Bcl2, and Bax genes was measured by RT-qPCR. Results: *L. gasseri* strain ATCC 33323 significantly down-regulated the gene expression level of MCL1, and Bcl2 and up-regulated the expression level of Bax in HT-29 cells after 24 h of treatment. Conclusion: The potentially probiotic *L. gasseri* strain ATCC 33323 used in this study could possibly induce apoptosis in HT-29 cells. The bioactive components present in the CFS of this probiotic strain could be developed as efficient supplementation for prevention and treatment of colorectal cancer patients. Keywords: *Lactobacillus gasseri*; Postbiotics; Colorectal cancer; Apoptosis; HT-29 cells

Prevalence of Coagulase-Negative Staphylococcus (CoNS) isolated from patients in CCU and ICU of Sari Cardiovascular Hospital

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نوع پذیرش: پوستر | کد مقاله: G-62943

Abstract: Background: Coagulase negative staphylococcus (CoNS) are gram-positive cocci which are frequently found as normal flora on healthy human skin and mucus membranes. These organisms rarely cause disease, however, CoNS can cause infections in bloodstream and other tissues. Because of their ability to form biofilms on foreign material, most of these infections are hospital-acquired. CoNS have emerged as major pathogens in hospital settings with the increasing use of implanted medical equipment. Coagulase negative staphylococci responsible for nosocomial infections are almost always resistant multiple classes of antimicrobial agents, so preventing and developing antimicrobial agents will play important roles in limiting the prevalence of these infections. Methods: 148 CoNS-positive cultures were collected which 68 of them were isolated from patients in ICU and CCU. Samples collected were urine, endotracheal tube, blood, sputum and pleural fluid. Information of patients were collected and analyzed. Results: 68 positive cultures were isolated from patients admitted to ICU and CCU from July 2020 to March 2022. 52 CoNS-positive cultures were from urine samples. 51% of the patients were male and 49% were female. Conclusion: The emergence of CoNS as major pathogens in hospital settings and their increasing resistance to antimicrobial agents leads to new measures for prevention and development for new antimicrobial agents. Keywords: nosocomial infections, hospital infections, coagulase-negative staphylococcus

Investigation of molecular interaction of co-infection of *Pseudomonas aeruginosa* and *Staphylococcus aureus* in Cystic Fibrosis

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نوع پذیرش: پوستر | کد مقاله: G-32816

Abstract: Background: Cystic fibrosis (CF) is a genetic disorder that causes problems with breathing and digestion. The human pathogens *Pseudomonas aeruginosa* and *Staphylococcus aureus* are regularly co-isolated from CF patients. The purpose of this study is to investigate the reactions between *Staphylococcus* and *Pseudomonas* bacteria for survival and growth as well as the severity of pathogenicity in CF patients. Methods: Studies were collected using different keyword combinations: *S. aureus*, *P. aeruginosa*, co-infection, and CF. The literature search strategy in this paper included searching PubMed, PMC, and Science Direct, Springer open, Google scholar and BioMed Central databases. Results: Two pathogens co-colonize the same contamination specialties and shape a mixed-species biofilm, hence favoring their resistance to anti-microbials and resistant reaction. *P. aeruginosa* produces a number to toxins that are active against *S. aureus*. The vivo CF lung, *P. aeruginosa* may become less aggressive toward *S. aureus*. Overall, three major mechanisms of interaction between *P. aeruginosa* and *S. aureus* were observed: (i) the initial interactions in which *P. aeruginosa* express a number of virulence factors such as PYO, LasA, or rhamnolipids to outcompete *S. aureus*, (ii) adaptation of *S. aureus* to small colony variant (SCV) and L-forms through phenotypic and genetic modulations to ensure their survival and co-exist in the CF lungs with *P. aeruginosa*, (iii) adaptation of *P. aeruginosa* to the CF environment alters its QS networks and reduces its virulence factor production and promotes co-existence with *S. aureus*. Conclusion: These average interactions result in immoderate lung harm and accelerated antibiotic resistance in each of those pathogens. This overview summarized the records to be had to date concerning *P. aeruginosa* with *S. aureus* interactions in CF lung, but in addition, studied wants to be accomplished for whole know-how of the complicated micro-surroundings in the CF lung. Although this overview discusses the interactions of *P. aeruginosa* with *S. aureus* in CF lung, it's far noteworthy to say that *P. aeruginosa* with *S. aureus* additionally co-exists withinside the peritoneum of dialysis patients', diabetic foot wounds, catheters, and withinside the wounds and skin burn. Keywords:

Antimicrobial resistance patterns, virulence gene profiles, and molecular characteristics of *Salmonella enteritidis* and *Salmonella typhimurium* recovered from patients with gastroenteritis in three cities of Iran.

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نوع پذیرش: پوستر | کد مقاله: G-34187

Abstract: Background: We evaluated the distribution of virulence factors and mechanisms of antibiotic resistance in clinical isolates of *S. enteritidis* and *S. typhimurium* from three cities in Iran. Methods: From May 2018 to September 2021, 48 non-duplicate non-consecutive isolates of *S. enteritidis* and *S. typhimurium* were collected from hospitalized patients admitted to Iran's tertiary care hospitals. The isolates were cultured from gastrointestinal samples. Antibiotic susceptibility testing was performed by the disc diffusion and microdilution methods according to the Clinical and Laboratory Standards Institute (CLSI) guidelines. To identify the phenotypic β -lactamases, the phenotypic confirmatory disc diffusion method was used. PCR-sequencing was also used to look for extended spectrum β -lactamases (ESBLs) genes (*bla*TEM; *bla*SHV; *bla*CTX-M), carbapenemase genes (*bla*NDM), aminoglycosides (*strA*, *strB*, *aadA1*), tetracyclines (*tetA*, *tetB*), amphenicols (*floR*), sulfonamides (*sul1*, *sul2*), trimethoprim-sulfamethoxazole (*dfrA*) resistance genes, and integrons (classes 1 and 2). The presence of virulence associated genes such as *invA*, *stn*, *sopB*, *spvC*, *rck*, and *phoPQ* was examined by PCR-sequencing. The ability of biofilm formation was assessed with the crystal violet staining method. Results: Trimethoprim-sulfamethoxazole and imipenem were the most effective antimicrobial agents with 97% susceptibility. A high prevalence of resistance was shown in *S. enteritidis* to ciprofloxacin ($n = 20$, 71.43%) and nalidixic acid ($n = 19$, 67.86%) and in *S. typhimurium* to ceftazidime ($n = 9$, 45%). Overall, 3 (6.25%), 13 (27.08%), and 6 (12.5%) isolates were categorized as strong, moderate, and weak biofilm-producers, respectively. The isolates that formed the biofilm showed a higher percentage of resistance than the other isolates. Additionally, *bla*CTX-M, *bla*TEM, *bla*SHV, *sul1*, *sul2*, *tetA*, *tetB*, *floR*, *strA* and *strB* resistance genes were detected in 10 (20.8%), 5 (10.4%), 1 (2.08%), 7 (14.58%), 1 (2.08%), 3 (6.25%), 2 (4.1%), 1 (2.08%), 2 (4.1%), 1 (2.08%), 2 (4.1%), 1 (2.08%), 2 (4.1%), 1 (4.1%), 2 (4.1%) Furthermore, 7 (14.58%) of the cases had class I integron. All tested *S. enteritidis* strains had *invA* and *sopB*, and all *S. typhimurium* strains had *invA* and *phoPQ*. *spvC* was not detected in any of the isolates. Conclusions: The obtained results indicated that large-scale surveillance and effective infection control measures are also urgently needed to prevent the outbreak of diverse antibiotic-resistant isolates in the future. Keywords: Gastroenteritis, *S. enteritidis*, *S. typhimurium*, Antibiotic resistance genes, virulence factors

The effect of tetracycline on gene resistance (tet A) in *Klebsiella pneumoniae*.

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نوع پذیرش: پوستر | کد مقاله: G-71249

Abstract: Background: *Klebsiella pneumoniae* are the most common bacteria that cause infection of the disease system. Due to arbitrary and indiscriminate use of antibiotics and increasing resistance to antibiotics, the treatment of this disease is difficult. This study was conducted to determine the gene frequency (tet A) in *Klebsiella pneumoniae* clinical isolates. *Klebsiella pneumoniae* is one of the causes of urinary tract infection in Khorramabad. Materials and Methods: In a study conducted from June 2020 to August 2021, 100 isolates of *Klebsiella pneumoniae* isolated from urinary tract infection were collected from people who referred to the medical centers of Khorramabad city. The samples taken in the bacteriology laboratory were evaluated using biochemical methods and culture on EMB.TSI.BA.IMVIC media. Resistance was investigated by two phenotypic methods through disk diffusion and genotyping. Tetracycline 30µg antibiotic disc was used for this purpose. Gene extraction was performed by boiling method. PCR was performed with specific primers and specific temperature program, Then the PCR products were loaded into the gel wells and the results were observed by electrophoresis Results: Out of 100 samples taken, 57 were women, 39 were men and 4 were male. Children under 12 years old, 32 samples (32%) showed resistance to tetracycline. The resistance gene (tet A) was observed in all cases that showed resistance to tetracycline. Conclusion: Urinary tract infection is one of the most common acquired infections that affects millions of people in the world every year. One of the important causes of urinary tract infection is *Klebsiella pneumoniae*. Antibiotic resistance is one of the most serious public health problems. The results and investigations show that the TET-A resistance gene exists among people in the community. Keywords: *Klebsiella*, Tetracycline, Drug resistance, Khorramabad, Urinary tract infection

Prevalence of *Helicobacter felis* and *Helicobacter heilmannii* and Co-infection with *Helicobacter pylori* in Gastric Biopsy Specimens in Endoscopy Ward of Shahid Beheshti Hospital, Hamadan City, Iran

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نوع پذیرش: پوستر | کد مقاله: G-42836

Abstract: Background: *Helicobacter pylori* (*H. pylori*) has various strains associated with human infections. *H. pylori*, *H. heilmannii*, and *H. felis* are the most common strains in humans. *H. pylori* is associated with several human diseases such as chronic gastritis, peptic ulcer, mucous membrane lymphoma, and gastric adenocarcinoma. This study aimed to determine the prevalence rates of *H. felis* and *H. heilmannii* and the effect of co-infection with *H. pylori* in gastric biopsy specimens of patients. Materials and Methods: Totally, 80 gastric biopsy specimens were taken by a physician from the patients referred to Shahid Beheshti Hospital, Hamadan City, Iran. PCR test was used to confirm the presence of *H. pylori* in samples that had positive rapid urease tests. Moreover, the *ureB* gene and *ureA* and *ureB* genes were used for *H. heilmannii* and *H. felis*, respectively. Results: Of the study patients, 61.5% were females, and 38.5% were males with a mean age of 37.8 years. Of 80 biopsies, 50% were *H. pylori*-positive, 53.8% were *H. heilmannii*-positive, but no *H. felis* was identified in any sample. Results indicate that smoking, having a history of gastrointestinal diseases, and taking certain medications can be risk factors for *H. pylori*. Conclusion: Any agent contributing to gastric mucosal damage can enhance the susceptibility to bacterial contamination. Overall, the results indicate a low probability of interactions between *H. pylori*, *H. heilmannii*, and *H. felis*. Keywords: *Helicobacter pylori*, *Helicobacter heilmannii*, *Helicobacter felis*, Co-infection

Brucellosis in Humans with the Approach of Brucella Species Contamination in Unpasteurized Milk and Dairy Products from Hamadan, Iran

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نوع پذیرش: پوستر | کد مقاله: G-17093

Abstract: Background: As the most important human food source, milk and dairy products may lead to infectious diseases due to non-compliance with health standards. Brucellosis is one of the critical zoonotic diseases that affect the human population. Humans are usually infected by *Brucella* spp. via contaminated milk and dairy products and direct contact with infected animals. Materials and Methods: This study was conducted to determine the *Brucella* spp. contamination rate of milk and dairy products in the rural and urban areas in the city of Hamadan, west of Iran, in 2018-2019. In this descriptive-analytical study, 291 samples of nonboiling milk (227), fresh cheese (43), and cream (21) were collected from dairy products suppliers in the urban (No=103), rural areas (No=162), and industrial regions (No=26). We collected 72 samples from sheep and goats and 219 specimens from cattle. Samples were randomly selected from the target centers. Results: The overall contamination rate of collected samples with *Brucella* spp. found to be 4.1%. The milk and dairy products contamination in urban areas was 0.9%, rural 6.6%, and industrial regions 0%. Furthermore, the contamination rate varied from 9.7% to 2.5% for small ruminants and large ruminants, respectively, which was significant ($P=0.01$). Conclusion: Given the importance of dairy consumption in the human diet and higher contamination of milk and dairy products taken from cattle, sheep, and goats with *Brucella* species, it is recommended that control and prevention programs in sheep and goats must be taken more seriously. Keywords: *Brucella*, Contamination, Dairy products, Hamadan

An Approach to Using Immunogenic Extracellular Loops of Outer Membrane Proteins to Develop New Multi-Epitope Vaccines for *Acinetobacter baumannii*

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نوع پذیرش: پوستر | کد مقاله: G-93271

Abstract: Background: The development of an effective vaccine for *Acinetobacter baumannii* is urgently needed because of the increased resistance to antibiotics of the organism. Although attempts have been made to find effective vaccines for this bacterium, no approved vaccine against it is available. As outer membrane proteins (OMPs) are exposed to the surface, they make excellent targets for vaccines. Besides, OMPs contain a highly immunogenic extracellular loop. Hence, in this study, we designed a new multi-epitope vaccine for *A. baumannii* OMPs. Materials and Methods: It was found that sixty-five of the OMPs in 35 *A. baumannii* genomes deposited within the Vaxign database cover pathogenic and immunogenic linear B-cell epitopes, all of which are conserved, exposed, and immune-stimulating. A list of four linear B-cell epitopes that have the ability to elicit hyperimmune reactions has been developed based on defined criteria (allergenicity, antigenicity, and non-similarity to the host). In order to select the most optimal arrangement of these epitopes, epitope shuffling was performed. Results: Taking into account the complexity of multi-epitope vaccines, we proposed six different multi-epitope vaccines consisting of two naked arrangements, two loop-less C-lobe structures (LCL), and two FliC-based constructs. Based on the molecular docking results of an LCL-based multi-epitope vaccine, the best cellular docking scores and immune simulation results were found in his lab (Th1 cell population, IFN- γ , IL-12, IgM, IgG1, and IgG2 levels). Conclusion: It has been demonstrated that the study provides a valuable library of exposed epitopes consisting of 26 conserved, linear, and immunogenic B-cell epitopes (participating in 14 OMPs) and three optimized multi-epitope vaccines. In order to confirm whether the immunoreactivity of these vaccine candidates is as expected, further experimental studies will need to be conducted. Keywords: *Acinetobacter baumannii* Linear B-Cell epitope Epitope shuffling

Antibiotic resistance of Gram-negative bacteria isolated from urinary tract infections in pregnant women referring to the Central Laboratory of Rudbar-e-Jonub County, South of Kerman Province, Iran, 2022

مریم برخوردار مهنی - سمیه امیری ©¹

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نوع پذیرش: پوستر | کد مقاله: G-02987

Abstract: Antibiotic resistance of Gram-negative bacteria isolated from urinary tract infections in pregnant women Referring to the Central Laboratory of Rudbar-e-Jonub County, South of Kerman Province, Iran, 2022 Samia Amiri¹, Maryam Barkhori Mehni^{2*} 1. : Jiroft University of Medical Sciences, Jiroft, Iran 2. : Jiroft University of Medical Sciences, Jiroft, Iran Background: Recently, increasing in the antibiotic resistance of pathogenic bacteria is a big problem facing to the medical sciences especially about pregnant patients. To have sufficient information about the patterns of bacterial resistance to different antibiotics are very helpful for proper treatments. Materials and Methods: This research is a descriptive cross-sectional study in the laboratory over a period of six months and it was conducted on 50 pregnant women with UTI. Sampling was performed from the central laboratory of south Roodbar from pregnant women. Accordingly, Gram-negative bacteria were isolated and identified by using staining, biochemical tests and using differential and selective media. Antimicrobial susceptibility pattern of isolate related to gentamicin, vancomycin, tetracycline, ciprofloxacin, nitroforantoin, nalidixic acid-was evaluated using disk diffusion method and minimum inhibitory concentration was determined by agar dilution method. Results: In this study, 150 pregnant women were checked and 26.6% of them had UTI by gram-negative bacteria. This quantity of gram negative bacteria were divided as 50% Escherichia coli, 27.5% Klebsiella, 17.5% Enterobacter and 5% Proteus spp. Isolated gram-negative bacteria from pregnant women urine with UTI were sensitive to different antibiotics as gentamicin (97.5%), ciprofloxacin (85%), nitrofurantoin (82.5%), tetracycline (25.5%), Nalidyksyk acid (47.5%), amoxicillin (5%) and were sensitive to vancomycin (2.5%). Conclusion: The antibiotics gentamicin and ciprofloxacin as the most effective medication for the treatment of pregnant women with UTI were the majority. However, due to the results of the antibiogram in this research, antibiotic resistance of different bacteria should be understood in in different geographical areas and this is very essential in the treatment of pregnant patients. Keywords: Gram-negative bacteria, antibiotic-resistance, UTI, pregnant women

Antibiotic resistance of Gram-negative bacteria isolated from urinary tract infections in pregnant women referring to the Central Laboratory of Rudbar-e-Jonub County, South of Kerman Province, Iran, 2022

مریم برخوردار میهنی،¹ سمیه امیری داندوسکی² ©

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نوع پذیرش: پوستر | کد مقاله: G-06158

Abstract: Antibiotic resistance of Gram-negative bacteria isolated from urinary tract infections in pregnant women Referring to the Central Laboratory of Rudbar-e-Jonub County, South of Kerman Province, Iran, 2022 Maryam Barkhori Mehni,^{1*} Somayeh Amiri Dandusky² 1. : Jiroft University of Medical Sciences, Jiroft, Iran 2. : Jiroft University of Medical Sciences, Jiroft, Iran Background: Recently, increasing in the antibiotic resistance of pathogenic bacteria is a big problem facing to the medical sciences especially about pregnant patients. To have sufficient information about the patterns of bacterial resistance to different antibiotics are very helpful for proper treatments. Materials and Methods: This research is a descriptive cross-sectional study in the laboratory over a period of six months and it was conducted on 150 pregnant women with urinary infection. Sampling was performed from the central laboratory of south Roodbar from pregnant women. Accordingly, Gram-negative bacteria were isolated and identified by using staining, biochemical tests and using differential and selective media. Antimicrobial susceptibility pattern of isolate related to gentamicin, vancomycin, tetracycline, ciprofloxacin, nitrofurantoin, nalidixic acid-was evaluated using disk diffusion method and minimum inhibitory concentration was determined by agar dilution method. Results: In this study, 150 pregnant women were checked and 26.6% of them had urinary infection by gram-negative bacteria. This quantity of gram negative bacteria were divided as 50% Escherichia coli, 27.5% Klebsiella, 17.5% Enterobacter and 5% Proteus spp. Isolated gram-negative bacteria from pregnant women urine with urinary infection were sensitive to different antibiotics as gentamicin (97.5%), ciprofloxacin (85%) , nitrofurantoin (82.5%), tetracycline (25.5%), Nalidyksyk acid (47.5%), amoxicillin (5%) and were sensitive to vancomycin (2.5%). Conclusion: The antibiotics gentamicin and ciprofloxacin as the most effective medication for the treatment of pregnant women with urinary infection were the majority. However, due to the results of the antibiogram in this research, antibiotic resistance of different bacteria should be understood in in different geographical areas and this is very essential in the treatment of pregnant patients. Keywords: Gram-negative bacteria, antibiotic-resistance, pregnant women

Antimicrobial activity of Staphylococcus aureus isolated from raw milk of apparently healthy donkeys

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نوع پذیرش: پوستر | کد مقاله: G-45908

Abstract: Background: Antimicrobial resistance has become a worldwide threat to public health these days. Resistance in bacteria can occur in many ways. It approved the consumption of resistant bacteria in food originating from the animal and can transfer the resistant gene to normal bacterial flora. This especially could be more important in children. In recent years donkey milk has been used as a substitute for cow milk for infants because of its unique composition and similarity to human milk. Material and methods: in our study 26 donkey milk samples were collected from several towns in Yazd province. 6 Staphylococcus aureus isolates from donkey milk samples were confirmed by the biochemical tests and then tested for six antimicrobials include: penicillin, ampicillin, doxycycline, trimethoprim-sulfamethoxazole, ofloxacin, and furazolidone by disc diffusion method according to CLSI protocols. Results: Only 2 (33.33%) isolates had growth in the presentence of trimethoprim-sulfamethoxazole. others were completely sensitive to the antibiotic. Conclusions: Our study results show donkey milk can be a safe substitution for human milk. Because consumption of antimicrobial drugs is very rare in donkey milk in contrast to cow besides other advantages donkey milk has few resistant genes and won't cause antibiotic resistance in children and infants. Keywords:

Discovery of mucormycosis on mini-BAL samples of hospitalized pediatric with COVID-19, Mofid children's hospital from in coronavirus pandemic

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نوع پذیرش: پوستر | کد مقاله: G-67384

Abstract: Background: The coronavirus disease (COVID-19) has become a global problem due to global high prevalence and rapid transmission. Fungal infections could be detected in COVID-19 patients especially in ventilated patients. It is leading to increased morbidity and mortality. This study aimed to identify mucormycosis on mini-BAL samples obtained from hospitalized pediatric with COVID-19 in an Iranian children's hospital from April 2021 to February 2022. Materials and Methods: In this cross-sectional study, 100 children with confirmed COVID-19 enrolled. The demographic factors like age, gender, symptoms, previous history of COVID-19, and underlying disease were recorded for all patients. Fungal DNA was extracted from mini-BAL samples by special commercial kit. Nested PCR was performed with two sets of primers for mucormycosis. Results: Out of 100 infants with COVID-19, 12 were positive for mucormycosis. Among the 12 patients, fever, shortness of breath, cough, and decreased level of consciousness were reported in 11%, 13%, 16%, and 20%, respectively. The majority of cases suffered from heart diseases (40%), followed by underlying malignancy (33%). All positive cases had taken steroids and antibiotics, had significantly higher chest CT scan scores, and spent more time under a ventilator. Conclusion: The co-colonization of COVID-19 and mucormycosis was seen among 12% of children hospitalized in a COVID ICU. The clinicians should have a high degree of suspicion and a low threshold to begin treatment for aggressive diagnostic work-up when dealing with pediatric COVID-19. Keywords: mucormycosis, COVID-19, Pediatrics, Co-infection

Co-present of bacteremia by multi-drug resistant gram-negative bacteria and Covid-19 in children

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نوع پذیرش: پوستر | کد مقاله: G-98530

Abstract: Background: Multi-drug resistant (MDR) bacteria have been introduced as a mortality risk factor in children especially in hospitalized patients. All over the world, Covid-19 could complicate the treatment process, while bacterial and viral co-infection particularly in children is not well studied. This was a study on the antimicrobial patterns of gram-negative bacteria (GNB) isolated from blood samples of children with bacteremia and their correlation with Covid-19. Material and Methods: Blood culture of children which suspicious to bacteremia were prepared. The bacterial isolates were characterized based on standard microbiology laboratory, and MDR strains were detected based on CLSI 2021, and the p -value ≤ 0.05 was considered significant. The results of Covid-19 tests of the patients were recorded from the hospital's documents. Results: A total of 255 blood samples were collected from children with bacteremia, the frequency of bacterial isolates was like; Enterobacteriaceae spp. 43.5% (111/255), Pseudomonas spp. 33.7% (86/255), Acinetobacter spp. 21.6% (55/255), and Stenotrophomonas spp. 1.2% (3/255). Out of 255 GNB, 86.66% (221/255) of them were MDR, and the frequency of MDR strains was like; Enterobacteriaceae spp. 91.8% (102/111), Pseudomonas spp. 77.9% (67/86), Acinetobacter spp. 89% (49/55), and Stenotrophomonas spp. 100% (3/3). Out of 255 Children with GNB bacteremia, 25.1% (64/255) of them had confirmed the Covid-19 test, and 93.7% (60/64) of these patients had both MDR bacteremia and Covid-19. The correlation between MDR bacteremia and Covid-19 was significant (p value=0.002). The death rate was 43.33% (26/60) among these children. Conclusion: The high frequency of multi-drug-resistant GNB bacteremia in children was reported in this study with 86.6%, also the risk of superinfections and Covid-19 is notable in these patients and could lead to death. Keywords: Co-infection, bacteremia in children, Multi-drug resistance, Covid-19.

Bloodstream infections caused by antibiotic-resistant gram-positive bacteria in covid19 period from children's hospital in 2020&2021

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نوع پذیرش: پوستر | کد مقاله: G-46718

Abstract: Background: Antibiotic resistance is a serious problem for human health. Children are considered the most vulnerable group against these infectious agents due to their immune system status and special conditions. Determining the pattern of drug resistance can help a lot to improve the infection control process in the hospital and cause the correct administration of antibiotics. Therefore, we decided to collect and analyze the data of Mofid Children's Hospital in 2020 and 2021 to examine the pattern of antibiotic resistance of these strains, the frequency of bacterial isolates in clinical samples of patients and hospital wards that are most involved. Materials and Methods: In this cross-sectional descriptive study, during a period of covid 19, between 2020 and 2021 blood samples from different wards of Mofid Children Hospital were examined. Gram positive bacteria were detected by BACTEC. The necessary. Patterns of antibiotic resistance in isolated gram-positive bacteria (CLSI 2021), different wards of the hospital, frequency of bacteria in clinical samples taken from children, age, sex, were studied. Data were analyzed by SPSS software version 22. Results: We found 46 patients with Staphylococcus aureus bacteria, (45.7% boys). The most involved ward was transplantation (32.6%). Antibiotic resistance was above 80% in Oxacillin and Azithromycin and the lowest resistance was in Linezolid (4.3%). Coagulase-negative staphylococci samples were obtained from 228 patients, (56.6% boys). The most inpatient were from PICU (27.6%) and transplantation (9.18%). Oxacillin (90.1%) and Azithromycin (84.9%) had the highest resistance and Vancomycin (5.8%) and Linezolid (5%) had the lowest antibiotic resistance. Enterococci were isolated from 71 patients, including 66.2% of boys. The highest involved ward was transplantation (54.9%). The highest resistance was in Azithromycin (94.1%) and the lowest in Linezolid (10.1%) and Chloramphenicol (10%). Conclusion: The resistance of pathogens to current antibiotics is a growing global crisis. In order to achieve effective overcoming of resistance, strategies of struggle must be applied at the social, national and global levels. Keywords: Gram-positive - Sepsis - Blood culture - Pediatric sepsis - Drug resistance

The Aminoglycoside and Glycopeptide Resistance Pattern of Enterococcus faecalis and Enterococcus faecium Isolated from Healthy People's Feces and Hospital Environment

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نوع پذیرش: پوستر | کد مقاله: G-35189

Abstract: Background: The increased resistance of Enterococcus isolates to beta-lactams has led to the concurrent use of these antibiotics with aminoglycosides in recent years. Glycopeptides are also valuable antibiotics used for the treatment of infections caused by the strains resistant to other common antibiotics. This study aimed to evaluate the resistance pattern of Enterococcus faecalis and Enterococcus faecium isolated from the Mazandaran educational hospital environment and fecal samples of healthy hospital staffs and volunteers unrelated to hospitals. Materials and Methods: The fecal samples were diluted with PBS and the hospital surface samples were collected with wet swabs. Then, the samples were cultured on the M-Enterococcus agar medium. The isolates were identified with common biochemical and microbiological tests and confirmed by PCR. The antibiotic resistance against gentamicin, kanamycin, streptomycin, teicoplanin, and vancomycin was determined by the disc agar diffusion method. Results: Out of 145 isolates, 50 (34.5%), 50 (34.5%), and 45 (31%) were collected from the feces of staffs, non-staffs, and the hospital surfaces, respectively. In addition, 84 (57.9%) isolates were detected as E. faecalis and 61 (42.1%) were E. faecium. However, 141 (97.2%) and 133 (91.7%) isolates were susceptible to teicoplanin and vancomycin, respectively. On the other hand, 19 (13.1%), 110 (75.9%), 28 (19.31%), 4 (2.8%), and 5 (3.4%) isolates were resistant to gentamicin, kanamycin, streptomycin, teicoplanin, and vancomycin, respectively. Conclusion: This research showed that the rate of antibiotic resistance to aminoglycosides in the normal flora and hospital environment isolates is relatively reasonable. Although these drugs are used at the bedside for treating a broad range of infections, people usually consume less arbitrarily. Kanamycin was the only exception and requires further investigations. Keywords:

Genotyping of *Klebsiella pneumoniae* isolates recovered from patients admitted to Mousavi and Valiasr hospitals by (GTG)5-PCR method

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نوع پذیرش: پوستر | کد مقاله: G-74936

Abstract: Background: *Klebsiella pneumoniae* is not only a major hospital-acquired pathogen but also an important food-borne pathogen that can cause septicaemia, liver abscesses, and diarrhea in humans. The present study was aimed to determine the capability of (GTG) 5-PCR assay for molecular typing of *K. pneumoniae* strains isolated from patients with urinary tract infections. Methods: In this descriptive-sectional study, *K. pneumoniae* strains were collected from hospitalized patients with urinary tract infection in Mousavi and Valiasr Hospital, Zanjan, Iran. Isolates were identified by conventional microbiological tests. Bacterial DNA was extracted using boiling method and (GTG) 5-PCR assay was used for subtyping of the isolates. For clustering of isolates, dendrogram was generated according to the unweighted pair group method with arithmetic (UPGMA). Results: Overall, 105 *K. pneumoniae* isolates were isolated and subjected to the molecular typing study. The (GTG) 5-PCR assay was able to differentiate the *K. pneumoniae* strains into 28 clusters with the 80% similarity level Conclusion: The (GTG) 5-PCR assay enabled rapid molecular typing of *K. pneumoniae* strains. The strains of *K. pneumoniae* typed in this study would belong to different clones. Keywords:

The survey of Fluoroquinolone Resistance in Multidrug Resistant Clinical *Pseudomonas aeruginosa* Isolates

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نوع پذیرش: پوستر | کد مقاله: G-69187

Abstract: Background: *Pseudomonas aeruginosa* is an opportunistic pathogen, with high pathogenicity and high mortality in hospitalized and immunocompromised patients. The problem of multi-drug resistant (MDR) *P. aeruginosa* has created a worldwide healthcare crisis. Today *P. aeruginosa* nearly resistant to all current antimicrobial agents, especially to carbapenems and fluoroquinolones. *P. aeruginosa* possess fluoroquinolone resistance via the mutations in the quinolone resistance determining region (QRDR) topoisomerase II (GyrA and GyrB subunits) and topoisomerase IV (ParC and ParE subunits). In this study, we survey the rate of MDR and mutation in *gyrA* gene in clinical isolates of *P. aeruginosa*. Methods: In a descriptive study approved a total of 175 non-replicated *P. aeruginosa* isolates were collected from different specimens. MDR isolates detected by minimal inhibitory concentration (MIC) of Imipenem, Amikacin and Ciprofloxacin were performed by the E-test method. A PCR reaction for *gyrA* gene was performed for 30 isolates resistant to ciprofloxacin in the E-test method. For DNA sequencing, amplified products of *gyrA* gene underwent bidirectional Sanger sequencing using the ABI 3730 XL DNA analyzer. The *gyrA* sequences were aligned using the Clustal W v2.0 software. Results: From 175 different clinical isolates, 131 (74/8%) isolates were MDR by MIC method (90.3% resistance to Imipenem, 69.71% resistance to Amikacin and 97.2% resistance to Ciprofloxacin). Between multi drug resistance and specimen type a significant difference there were (urine P0/002, burn P0/000). Of 30 isolates which were sequenced for QRDR mutation (*gyrA* gene), 26(86.7%) isolates of FQ resistant had 1 or more active mutation in I *gyrA* sequence. All of the 26 resistant isolates possessed a mutation in substitution Ile87→Thr in *gyrA* gene, also in 4 burn isolates, there were a mutation in substitution Asn87→ Asp in *gyrA* gene. There is a significant difference between specimen type and MIC ciprofloxacin (urine P0/008, burn P0/034), also there were a significant difference between mutation in *gyrA* gene and MIC ciprofloxacin (P0/000). Conclusion: Taken together, the recent overuse of effective antipseudomonal antibiotics has led to increased resistance in clinical *P. aeruginosa* isolated. The present study showed that multidrug resistance is more common in the isolates obtained from urine and burn samples and a specific relationship among mutation in *gyrA* gene and MIC ciprofloxacin, which makes the treatment of these patients a challenge. Keywords: *Pseudomonas aeruginosa*, Fluoroquinolone Resistance, MDR, *gyrA*

Investigation of Bacterial Diversity in Schizophrenia Patients

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نوع پذیرش: پوستر | کد مقاله: G-46873

Abstract: Schizophrenia is among the leading causes of disability, morbidity, and mortality worldwide. The advent of sophisticated sequencing techniques has led to a growing interest in the potential role of gut microbiota in human health and disease. Advances in this area have transformed our understanding of a number of medical conditions and have generated a new perspective suggesting that gut microbiota might be involved in the development and maintenance of brain / mental health. Animal models have demonstrated strong though indirect evidence for a contributory role of intestinal microbiota in psychiatric symptomatology and have linked the microbiome with neuropsychiatric conditions. Aim of this study is to investigate microbial diversity in schizophrenia patients. The purpose of this study is to investigate the microbial diversity in schizophrenia patients and how environmental factors affect them. In one study, the gut microbiota was examined in relation to schizophrenia and other psychotic diseases. In comparison to non-psychiatric comparator groups, first-episode psychosis patients showed a changed taxonomic signature, with a considerably increased abundance of the families Lactobacillaceae, Halothiobacillaceae, Brucellaceae, and Micrococcineae, and a lower abundance of Veillonellaceae. Particularly among the taxa that were most significantly increased in patients, Lactobacillaceae were overrepresented. The microbiota of the oropharynx was examined in two investigations. In patients with schizophrenia, the diversity of oral microbes was reduced. Compared to non-psychiatric comparator participants, patients with schizophrenia exhibited larger relative proportions of Formicetes, but they had higher proportions of Bacteroidetes and Actinobacteria. There are numerous probable pathophysiological factors to schizophrenia, making it a diverse disease. The immune system is implicated in the pathophysiology and developmental course of many illnesses, according to a large body of research. The body's greatest immune system is located in the gut. Dysbiosis of the intestinal ecosystem may affect immune responses. As a result, chronic inflammation, oxidative stress, and other physiological dysfunctions that have been implicated in schizophrenia are proposed to be. Early microbiota colonization of the gut is essential for the best immune system development and function. Studies indicate that this condition is linked to a decline in microbial diversity and that global community disparities exist when compared to samples from non-psychiatric reference groups. Various microbial taxa have been linked in some studies to clinical illness traits, such as physical well-being, depressed and psychotic symptoms, and sleep. Increased intestinal inflammation and permeability may be one of the main ways that microbial dysbiosis affects systemic physiological functioning, according to studies. Keywords:



Isolation of enteroinvasive Escherichia coli (EIEC) from Imam Khomeini hospital, Tehran

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نوع پذیرش: پوستر | کد مقاله: G-01657

Abstract: Background: Despite being known; diarrheal diseases still cause the death of children in developing countries. Children at this age are sensitive to these diseases because their immune system is not fully developed. Materials and Methods: during December 2021 to August 2022, 88 sample collected and screened for present of Escherichia coli (E. coli). Among all sample, first screening shown that 45 isolate are E. coli. Molecular method was used to confirm these isolates, for this purpose uidA gene was used. Presence of ipaH genes in confirmed isolates indicates the presence of enteroinvasive E. coli. Results: Among all Escherichia coli isolates, 6 isolates had ipaH genes that were identified as enteroinvasive Escherichia coli. Conclusion: There are different types of Escherichia coli, each of which causes diarrhea in a different way. These bacteria can be transmitted to humans through contaminated food. One of the most important types of Escherichia coli that causes invasive disease in the intestine is EIEC. The identification of ipaH gene as one of the pathogenic plasmid genes in Escherichia coli, which causes attachment and invasion of epithelial cells, has a decisive role in distinguishing it from other bacteria. Keywords:

Linezolid resistance among multidrug-resistant Mycobacterium tuberculosis clinical isolates in Iran

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Abstract: Background: Management of multidrug-resistant (MDR) and extensively drug-resistant TB (XDR-TB) is still a main challenge from both a clinical and public health perspective. Over the last decade, MDR treatment success rates have remained static at around 50% so, the international tuberculosis community has recognized that new regimens and drugs with improved efficacy are urgently needed to enhance cure rates. Since 2006, WHO has recommended using linezolid (LNZ) in the treatment of MDR/XDR-TB and this drug now being included in many TB programs around the world. LNZ has exhibited an excellent anti-mycobacterial effect and is an effective third-line antibiotic for the treatment of the MDR- and XDR-TB patients, with favorable outcomes. Although LNZ resistance is rare, it has been reported in multiple countries. LNZ resistance is related to a mutation at nucleotide position 2061 in rrl (23S rRNA) LNZ peptidyl transferase center (PTC) binding site and the T460C mutation in rplC (L3 protein), primarily. But, there are limited data on the association between phenotypic and genotypic LNZ resistance in clinical isolates. So, we aimed to determine the prevalence of LNZ resistance and to identify the mutations associated with LNZ resistance among MDR-TB clinical isolates. Materials and Methods: Panels of 22 MDR isolates were obtained from Ahvaz Regional TB Laboratory, Southwest of Iran. All MDR isolates were determined by the Xpert MTB/RIF assay and proportion method for INH and RIF in this laboratory. The minimum inhibitory concentration (MIC) values of LNZ were determined using a range of concentrations, from 0.125 to 16 mg/L by broth microdilution method. All MDR-TB isolates were sequenced in the rrl and rplC genes conferring LNZ resistance. Obtained sequences were aligned together using ClustalW (<https://www.genome.jp/tools-bin/clustalw>) software to determine the consensus sequences. Consensus sequences were subjected to nBLAST analysis (<http://blast.ncbi.nlm.nih.gov>) and compared with Mycobacterium tuberculosis strain H37Rv. Results: Based on the critical concentration (0.5 mg/L) used for LNZ 3 isolates (13.6%) of the tested isolates were resistant that MIC concentration were 8 mg/L and more than 16 mg/L for 2 and 1 isolates, respectively. Eighteen isolates (87.4%) had the MICs range from 0.125 to 0.5 mg/L and were susceptible to LNZ. The genetic analysis of the MDR isolates illustrated just 1 of the 3 LNZ resistant MDR-isolates sequenced carried substitution mutations at nucleotide 421 (A/G) and 449 (T/A) in rplC gene resulting in amino acid exchange from valine to isoleucine at codon 141 and isoleucine to asparagine at codon 150, respectively. However, no resistance-related mutations were indicated in isolates with MICs below or at the critical concentration. None of the isolates harbored mutation in rrl



چهاردهمین گنگره بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



gene. Furthermore, there was no mutation in rplC and rrl genes among LNZ susceptible isolates. Conclusion: This research reveals that the prevalence of LNZ-resistant isolates is 13.6% among MDR-TB isolates and DST against LNZ may be useful in the management of complicated and drug-resistant cases. However, further studies on ribosomal and non-ribosomal mutations in LNZ resistant isolates as well as analysis of efflux pumps, could reveal possible mechanism of resistance in TB. Keywords:

آدرس دبیرخانه:

تهران، خیابان کارگر شمالی، رویروی مرکز قلب تهران،
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Investigating the effects of probiotic strain *Levilactobacillus brevis* IBRC-M10790 on activation of autophagy process in non-alcoholic steatohepatitis model using HepG2 cell line

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Background: Non-alcoholic steatohepatitis (NASH) is characterized by hepatic steatosis accompanied by inflammation, lobular and hepatocyte ballooning with and without fibrosis. Notwithstanding the rising prevalence and serious potential clinical consequences of NASH, there are currently no treatments licensed for this clinical indication. The current gold standard for the management of NASH relies on diet and lifestyle changes, although the discouraging results lead to the poor compliance of patients. In line with recent studies, probiotics can ameliorate the progression of NASH via modulation of hepatic steatosis as well as engulfing lipids accumulation in the liver through autophagy induction. Here, we aimed to investigate the effects of *Levilactobacillus brevis* IBRC-M10790 in activation of autophagy process in a NASH model induced in hepatocellular carcinoma cells (HepG2). **Methods:** *L. brevis* IBRC-M10790 was cultured on MRS agar under anaerobic condition. Cell-free supernatant (CFS) was obtained by centrifuging the bacterial culture at 13000 rpm for 15 min at 4°C. HepG2 cells were maintained in the DMEM medium until the cells reached 80% confluence. HepG2 cells were stimulated by adding oleic acid and palmitic acid to induce hepatic steatosis. The mRNA expression level of autophagy-associated genes including mTOR, LC3B, BECN1, ATG5, ATG12, and ATG16 was determined following treatment with CFS using RT-qPCR assay. **Results:** The induction of autophagy by *L. brevis* was demonstrated by increased levels of LC3B, BECN1, ATG5, ATG12, and ATG16 transcripts and reduced levels of mTOR gene expression. **Conclusion:** Our results suggest that CFS obtained from *L. brevis* IBRC-M10790 could induce autophagy in HepG2 cells. Further studies are needed to precisely characterize the beneficial compounds and metabolites released in the culture supernatant of this potential probiotic strain in order to use as supplements for the prevention and treatment of patients with NASH. **Keywords:** Fatty liver disease; NASH; Autophagy; *Levilactobacillus brevis*, CFS

A worldwide systematic review and meta-analysis of bacteria related to antibiotic-associated diarrhea in hospitalized patients

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نوع پذیرش: پوستر | کد مقاله: G-63205

Abstract: Background: Antibiotic-associated diarrhea (AAD) is a major hospital problem and a common adverse effect of antibiotic treatment. The aim of this study was to investigate the prevalence of the most important bacteria that cause AAD in hospitalized patients. Materials and Methods: PubMed, Web of Science and Scopus databases were searched using multiple relevant keywords and screening carried out based on inclusion/exclusion criteria from March 2001 to October 2021. The random-effects model was used to conduct the meta-analysis. Results: Of the 7,377 identified articles, 56 met the inclusion criteria. Pooling all studies, the prevalence of Clostridioides (Clostridium) difficile, Clostridium perfringens, Klebsiella oxytoca, and Staphylococcus aureus as AAD-related bacteria among hospitalized patients were 19.6%, 14.9%, 27%, and 5.2%, respectively. The prevalence of all four bacteria was higher in Europe compared to other continents. The highest resistance of C. difficile was estimated to ciprofloxacin and the lowest resistances were reported to chloramphenicol, vancomycin, and metronidazole. There was no or little data on antibiotic resistance of other bacteria. Conclusion: The results of this study emphasize the need for a surveillance program, as well as timely public and hospital health measures in order to control and treat AAD infections. Keywords: Antibiotic-associated diarrhea (AAD), Clostridioides (Clostridium) difficile, Clostridium perfringens, Klebsiella oxytoca, and Staphylococcus aureus.

Identification of urease positive bacteria other than *Helicobacter pylori* in endoscopy (stomach biopsy samples) of patients with gastritis.

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نوع پذیرش: پوستر | کد مقاله: G-15297

Abstract: Background: Gastritis is an inflammation of the mucous membrane of the stomach. The term gastritis should be used only in cases where inflammation of the gastric mucosa is confirmed histologically. Gastritis often occurs in the antrum. Sometimes it shows symptoms of gastroenteritis. For many years, it has been believed that *Helicobacter pylori* is the only urease-positive bacteria that causes ulcers and inflammation in the stomach, while today it is proved that other urease-positive bacteria other than *Helicobacter pylori* can exist in the stomach cavity. Considering the importance role of these bacteria lead to gastritis, the aim of this study is to investigate the prevalence of urease positive bacteria other than *Helicobacter pylori*, which present in the stomach of patients with gastritis. Materials and Methods: 165 biopsy samples from the stomach antrum of patients with gastritis referred to Sari hospitals were collected by a gastroenterologist. The biopsies were identified as positive RUT (rapid urease test) samples. The RUT positive samples were transferred to the microbiology laboratory by the transfer culture media of BHI. The positive biopsies in RUT were cultured on specific media. Then, the urease positive non-*Helicobacter pylori* colonies were analyzed by standard microbiological tests. Confirming the presence of *Helicobacter pylori* were detected by ELISA, Pathological tests, and fecal antigen tests. Results: Out of the 100 urease positive samples acquired from antrum using RUT kit, 77 samples were *Helicobacter pylori* according to the rapid urease test, pathology ELISA, and fecal antigen tests. 23 samples identified as non-*Helicobacter pylori* by microbiological tests. The results showed that the sensitivity of IgG test against pathology is 86% and its specificity is 100%. On the other hand, the sensitivity of IgA test against pathology is 41% and its specificity is 100%. Also, the sensitivity of the stool test against pathology is 87.5% and the specificity is 100. Among non-*Helicobacter pylori* bacteria, such as *Staphylococcus aureus*(4%), *Staphylococcus saprophyticus*(5%), *Staphylococcus epidermidis* (6%), *Streptococcus viridans* (3%), *Streptococcus pyogenes*(1%), *Neisseria sub flava*(1%), *Neisseria sicca*(2%), *Neisseria mucosa*(2%), *Klebsiella pneumoniae*(1%), *Escherichia coli*(1%), the *Staphylococcus epidermidis* was the most frequent. Conclusion: The results of these studies indicate that these bacteria can play an effective role in the occurrence of Keywords:

Antibiotic-Resistant rate of Klebsiella spp. Species Isolated from Patients Specimens

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نوع پذیرش: پوستر | کد مقاله: G-49786

Abstract: Introduction: Nosocomial outbreaks of multidrug-resistant Klebsiella species are caused by extended-spectrum beta-lactamase (ESBL) producer types. The incidence of resistant Klebsiella isolates has been steadily increasing. The resulting limitations in treatment options require new measures to manage multidrug-resistant Klebsiella. While prevalence determination of resistant Klebsiella against different antibiotics is a useful epidemiological tool for infection control, so we decided to investigate the antibiotic-resistant rate of Klebsiella spp. species that were isolated from patients' specimens. Methods: The information on resistant Klebsiella spp. species to antibiotics was gathered from the hospital information system, of Rouhani Hospital, Babol University of Medical Sciences in Babol (2020-2022). Klebsiella spp. species were identified by microbiological methods; also microbial susceptibility testing was performed by disk diffusion method according to clinical and laboratory standards institute (CLSI). SPSS 22 and Chi-square test were used (P-value less than 0.05) for data analysis, Results: Antibiotic resistance was as follows in different years; 2020; Piperacillin/Tazobactam (TZP) for 76 isolates (53.90%, Confidence interval (CI): 42.1-65.3), Ceftazidime (CAZ) for 85 isolates (76.5%; CI: 65.80-84.70), ceftriaxone (CRO) for 86 isolates (76.70%; CI: 6.10-84.90), meropenem (MEM) for 82 isolates (52.40%; CI: 41.10-63.40), amikacin (AMK) for 84 isolates (52.10%; CI: 40.10-62.20), ciprofloxacin (CIP) for 86 isolates (73.30%; CI: 62.50-82.00), sulfamethoxazole and trimethoprim (SXT) for 1 isolate (100%; CI: 5.50-100). 2021; TZP for 19 isolates (78.90%, CI: 53.90-93.00), CAZ for 34 isolates (88.20%; CI: 71.60-96.10), CRO for 38 isolates (92.10%; CI: 77.50-97.90), MEM for 43 isolates (72.10%; CI: 56.10-84.20), AMK for 44 isolates (50.00%; CI: 34.80-65.20), CIP for 44 isolates (81.80%; CI: 66.70-91.30), SXT for 19 isolates (78.90%; CI: 53.90-93.00) and nitrofurantoin (NIT) for 5 isolates (40.00%; CI: 7.30-83.00). 2022; TZP for 3 isolates (100%, CI: 31.10-100), CAZ for 62 isolates (79%; CI: 66.40-87.90), CRO for 81 isolates (76.80%; CI: 66.90-86.00), MEM for 39 isolates (64.10%; CI: 47.20-78.30), AMK for 69 isolates (56.50%; CI: 41.40-65.00), CIP for 66 isolates (80.30%; CI: 68.30-88.70), SXT for 79 isolates (75.90%; CI: 64.70-84.50), NIT for 28 isolates (53.60%; CI: 34.20-72.00). Conclusion: Antibiotic-resistant rate of Klebsiella spp was observed. Antibiotic-resistant rates are increasing over years. Keywords: Antibiotic Resistant, Klebsiella spp., Specimens

Gut microbiota in Ulcerative Colitis and Crohn's Disease: A Next Generation Based Study

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نوع پذیرش: پوستر | کد مقاله: G-64527

Abstract: Background: The microbial population varies at different stages of the disease in Inflammatory bowel disease (IBD) patients and may be associated with the severity of disease and therapy resistance in these patients. The association between IBD is not very well described but gut microbiota composition is mentioned as a risk factor. The present study aimed to characterize the differences of dominant gut microbiota among patients with IBD as compared to control groups. Materials and Methods: Here we characterized the normal human and IBD enteric microbiome by next generation sequencing (NGS) of the 16S rRNA amplification from fecal samples obtained from ulcerative colitis (UC) (n= 20) and Crohn's disease (CD) (n= 20) patients and controls (n= 0) (Samples collected from Tehran and Tabriz). All subjects are required to have been diagnosed with IBD (several stages) confirmed using standard clinical, endoscopic, and histological criteria. Bacterial microbiota determined by sequencing of the V4 region of the 16S rRNA gene (using Illumina MiSeq, 150-300b Paired-End, 30 Mb). Results: In terms of body mass index (BMI), cholesterol, triglyceride and fasting blood sugar, no significant association were found IBD patients (UC and CD) and healthy controls. The NGS results of IBD patients mainly representatives of several phyla including Proteobacteria, Bacteroidetes, and Firmicutes. Bacteroidetes and Firmicutes phyla were significantly high in IBD patients comparing to healthy subjects. The taxonomic richness and diversity of some viruses in IBD patients are more probable and these microorganisms can be used as biomarkers for disease diagnosis and management. Conclusion: This study performed gut microbiota IBD patients. This investigation indicated that IBD (UC and CD) patients have a different gut composition in comparison to healthy control, which could be associated with disease development. Keywords: Inflammatory bowel disease, Microbiome, Ulcerative colitis, Crohn's disease

Cinnamaldehyde against KPC enzyme producing *Enterobacter* spp. isolated from Hamadan and Tehran hospitals

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Abstract: Background: *Enterobacter* spp are among the most important opportunistic pathogens that cause serious hospital infections in immunocompromised people. The production of carbapenemases, especially KPC (*Klebsiella pneumoniae* carbapenemases) and the increase of multidrug resistant strains around the world is a challenge in the treatment and control of infection. Methods: In this cross-sectional study, 42 clinical isolates of *Enterobacter* were collected from patients referred to Hamadan teaching hospitals and Hospital in Tehran. Molecular detection was used to assess the minimum inhibitory concentrations (MIC) of the bioactive compound(s) and how they interacted with the ESBL producer. Finally, the statistical analysis of all data was done using SPSS software (Version 24) and chi-square test. Results: The results of antibiogram using disc diffusion method showed that the highest antibiotic resistance was ceftazidime (90%). Also, 28 isolates (66.6%) were MDR. 94.11% of isolates had positive MHT test and KPC gene was observed in 96.8% of isolates. MBC and MIC were 0.048 and 0.024, respectively. Conclusion: The KPC gene among isolates of *Enterobacter* spp increase is high and MDR strains is an important challenge in hospitals and medical centers because it causes failure in treatment and increase in mortality. The use of cinnamaldehyde can be used as a supplement in the treatment of intestinal infections along with antibiotics. Keywords:



Bdellovibrio bacteriovorus versus Bacterial Infections: Antibiofilm Strategy

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Abstract: Background: The predatory bacterium *Bdellovibrio bacteriovorus* can eliminate many Gram-negative bacterial strains both in the planktonic state and in biofilms, and consequently has gained attention as a potential antimicrobial and even probiotic agent. This bacterial predation is suggested to be an important balancing factor in different ecosystems including the human microbiota. It was also demonstrated that *B. bacteriovorus* has an impact on biofilm structures of Gram-positive bacteria. However, our knowledge of biofilm predation by *Bdellovibrio bacteriovorus* and its effect on biofilm structure is still incomplete. Materials and Methods: The bibliographic search was performed on PubMed, Scopus, and Web of Science databases on Dec 4, 2022. Search keywords including “*Bdellovibrio bacteriovorus*” AND “Biofilms” OR “antibiotic-resistant” OR “Gram-negative” OR “Gram-positive in all fields. Any languages or date restrictions were not applied. Identified studies were screened by title, abstract, and full text. Results: Previous studies have confirmed the predatory activity of *Bdellovibrio bacteriovorus* towards Gram-negative bacteria in biofilms, however, a higher level of endurance was observed in comparison to planktonic cells. Particularly, the effectiveness of *B. bacteriovorus* was investigated against significant antibiotic-resistant bacterial pathogens including species with biofilm-formation capability. In addition to killing the biofilm-forming prey, it was also demonstrated that *B. bacteriovorus* can inhibit biofilm formation and remove established biofilms. In a recent study, it was reported that biofilm removal could even be enhanced by using nanostructure-engineered *Bdellovibrio*. Moreover, studies have shown that *B. bacteriovorus* can reduce biofilms formed by Gram-positive bacterium, *Staphylococcus aureus*, by using an epibiotic-like predatory strategy to benefit from biofilm matrix nutrients. Conclusion: The findings of this review highlight the antimicrobial activity of *B. bacteriovorus* towards clinically significant Gram-negative pathogens and its ability to eradicate biofilms established by both Gram-negative and Gram-positive bacteria, due to the production of hydrolytic enzymes and direct cellular interactions. Furthermore, genetic and nanotechnology engineering and further analysis can be utilized to investigate the cellular interaction and tolerability of the predatory bacteria, which allows further validation of this potential biological control option. Keywords: *Bdellovibrio bacteriovorus*, Gram-negative, Biofilms



Nanoparticles versus Bacterial Infections: Antibiofilm Strategy

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نوع پذیرش: پوستر | کد مقاله: G-23486

Abstract: Background: One of the important elements in the formation of bacterial infections with multiple antibiotic resistance is biofilm. Recently, it has become clear that using nanotechnology to eliminate infections caused by bacterial biofilms has great promise. The purpose of the current review was to compile disparate data on NPs' strategies for treating illnesses caused by bacterial biofilms. It appears that more research is necessary to overcome the challenges posed by their kinetic and biocompatibility when producing NPs as antimicrobials or drug carriers. Materials and Methods: The bibliographic search was performed on PubMed, Scopus, and Web of Science databases on Dec 2, 2022. Search keywords including "Nanoparticles" AND "Biofilms" OR "antibiotic-resistant" OR "infections" OR "MBIC" in all fields. Any languages or date restrictions were not applied. Identified studies were screened by title, abstract, and full text. Results: One of the major results that may be attained by the immobilization of the antibiotic onto NPs is the removal of the barriers that impede the antibiotic's activity against bacteria. Antibiotics are stabilized by NPs and have their antibacterial efficacy increased, helping to prevent and treat infections. Conclusion: Studies show that the use of antibiotic nanocarrier systems has promising results in vitro and in vivo studies to eliminate bacterial biofilms. Keywords: Nanoparticles, Gram-negative, Biofilm

Determination of the Frequency of blaNDM-1 and blaIMP Genes in Carbapenem resistant *Acinetobacter baumannii* Isolated from

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نوع پذیرش: پوستر | کد مقاله: G-14502

Abstract: Background: *Acinetobacter baumannii* is one of the important agents that cause nosocomial infections. This bacteria has been designated as the top priority of the WHO critical pathogens list for research and the creation of new antibiotics due to its recent rapid progressive resistance to last-resort antibiotics like carbapenems. In *A. baumannii*, carbapenamase enzymes are recognized as the most common form of resistance. These Beta-lactamases, which progressively contribute to the formation of carbapenamase, include the genes blaNDM-1 and blaIMP. The purpose of this study was to count the number of blaNDM-1 and blaIMP genes found in isolates of *A. baumannii* obtained from the Imam Khomeini Hospital in Sarab, Iran, which produce carbapenamase. Materials and Methods: 65 isolates of *A. baumannii* were collected from patients at Imam Khomeyni Hospital in Sarab City in 2021 for this investigation. This bacteria was discovered using phenotypic techniques, and the presence of the blaOXA-51 gene was confirmed by PCR method. A test for antibiotic susceptibility (AST) was conducted using the Kirby-Bauer technique and CLSI recommendations. To find metallo-β-lactamases, a combined disk diffusion test (CDDT) was employed (MBL). By using the PCR technique, the frequency of the genes blaNDM-1 and blaIMP was also determined. Data were statistically analyzed using the SPSS program. Results: Results indicated that *A. baumannii* was resistant to Ceftazidime (97.3%), Ciprofloxacin, Imipenem (96%) and Gentamicin and Piperacillin-Tazobactam (96%) as well (91 percent). There was no sign of Colistin resistance. By CDDT, all 65 of the *A. baumannii* isolates yielded MBL. Additionally, it was discovered that 15.5 percent and 28 percent, respectively, of the isolates of the MBL-producing *A. baumannii* included the blaNDM-1 and blaIMP genes. Conclusion: In this investigation, we found that 99 percent of the isolates of *A. baumannii* were multi-drug resistant. It has been established that carbapenamase play a significant role in *A. baumannii*'s resistance to antibiotics, and among them, enzymes belonging to the blaNDM-1 and blaIMP genes have a significant and continuously growing contribution. Keywords: *Acinetobacter baumannii*; carbapenamase; blaNDM-1; blaIMP; burn

The antibiotic misuse as a bridge between dysbiosis and endocarditis: A systematic review

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نوع پذیرش: پوستر | کد مقاله: G-43286

Abstract: Background: Infective endocarditis (IE) is a fatal inflammation associated with significant morbidity and mortality. The microbiota plays an important role on the training and function of the host immune system against infections. Antibiotics can result in several negative consequences on the microbiota, from reduced diversity of species, alteration in metabolic activity, and the selection of antibiotic-resistant organisms. The aim of this study is to investigate the effect of antibiotics on microbiota leading to infective endocarditis. Materials and Methods: This review article was performed within articles published at PubMed, Science Direct, Google Scholar, SID, and Cochrane until December 2022. The keywords were antibiotics, dysbiosis, microbiota, and infective endocarditis. By searching this database; 58 articles were found, 27 of them by reading titles and abstracts were removed. 31 articles were selected under the inclusion criteria. Results: Finally, 31 articles were included in the study. Microbiota maintained intestinal homeostasis and protected the colonic epithelium from intestinal microbes by stimulating goblet cell secretion of mucin. Microbiome alterations induced by antibiotics affected health in the long term. Some antibiotics, including tetracycline and macrolides, killed healthy gut bacteria. Clarithromycin, metronidazole and omeprazole reduced Actinobacteria and Bifidobacterium. However, enterococci increased which caused 5%-20% of infective endocarditis (IE). The use of amoxicillin and erythromycin increased the antibiotic-resistant oral microbiota. A combination of colistin and amoxicillin induced antibiotic resistome and altered gut microbiota. By reducing microbiota, pathogenic bacteria such as streptococci and staphylococci entered the bloodstream and attacked the lining of heart valves and/or chambers which could lead to infective endocarditis. Conclusion: The overuse of antibiotics and the emergence of antibiotic-resistant bacterial strains is a global concern that may cause infective endocarditis by the reduction of microbiota. Keywords: Infective endocarditis, Dysbiosis, Antibiotics, microbiota

Investigation of Antibiotic Resistance Pattern and Carbapenemase Genotype of *Pseudomonas aeruginosa* in Clinical Strains obtained from Imam khomeyni Hospital in Sarab, Iran

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نوع پذیرش: پوستر | کد مقاله: G-40812

Abstract: Background and Aim: A range of illnesses are brought on by the opportunistic, non-fermenting bacteria known as *Pseudomonas aeruginosa*. Today, one of the issues facing the world's nations that can make it challenging for patients to receive specialised treatment is the spread of antibiotic-resistant bacteria. In this study, *Pseudomonas* bacteria from clinical samples isolated from patients referred to Imam Khomeyni Hospital in Sarab City in 2020–2021 were examined for patterns of antibiotic resistance and carbapenemase genotype. Methods: 72 strains of *Pseudomonas aeruginosa* were identified from various clinical specimens, including blood cultures, ICU parts, urine, wounds, and endotracheal tubes, in the current cross-sectional study. The 16sRNA gene was used to confirm the strains, and the Kirby Bauer disc diffusion test was used to assess the strains' microbiological susceptibility to aminoglycoside antibiotics, fluoroquinolones, and third-generation cephalosporins. E-test was used to determine the sensitivity to meropenem and colistin. Genes for carbapenemase such as IMP, VIM, and NDM were found. Results: The strains were most resistant to fluoroquinolones, piperacillin, and third-generation cephalosporins. The antibiotic piperacillin tazobactam was the most successful. There was 76 percent and 28 percent, respectively, resistance to meropenem and colistin. In 10, 12, and 13 different carbapenemase-producing bacteria, the genes IMP, VIM, and NDM, respectively, were found. Three genes were found to be co-expressed in five different strains. Conclusion: The study's simultaneous expression of 3 carbapenemase genes and the predominance of strains resistant to third-generation cephalosporins and carbapenem make it imperative to continuously monitor hospital strains and prescribe antibiotics judiciously. Keywords: *Pseudomonas aeruginosa*; Antibiotic resistance; Carbapenemase Genes

Assessment of Antimicrobial Resistance Profile of Gram-negative Bacteria Isolated from Blood Samples of Children with Bacteremia in Imam Khomeini Hospital in Sarab, Iran

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نوع پذیرش: پوستر | کد مقاله: G-92680

Abstract: Background: Antimicrobial resistance is now a major issue on a global scale. Despite being an evolutionary occurrence, it is spread through poor human actions. Since it was originally discovered in the 1940s, there has been a rise in concern due to their ability to reduce therapy options and spread resistance genes through other bacteria. In this investigation, gram-negative bacteria (GNB) isolated from blood samples of children with bacteremia at Imam Khomeini Hospital in Sarab, Iran, were the primary focus. Materials and Methods: We prepared blood samples of children with bacteremia and we used selective culture MacConkey and biochemical tests, fermentation of sugars, IMViC and urease activity as the standard protocols. Resistance isolates were determined against imipenem, meropenem, gentamycin, ceftazidime, levofloxacin, cefepime, aztreonam and tigecycline using disc diffusion method according to the latest updates of Clinical and laboratory standard institute (CLSI) 2021. Results: 130 GNB strains in all were taken from kids who were being treated for bacteremia in hospitals. Out of 130 GNB strains, 35.3 percent were *Pseudomonas* spp., 24.6 percent were *Acinetobacter* spp., and 49.2 percent were *Enterobacteriaceae* spp. The antimicrobial resistance frequency of *Enterobacteriaceae* spp., *Pseudomonas* spp. and *Acinetobacter* spp. were like: imipenem 37.2%, 73.5%, 87%, meropenem 43.4%, 91%, 90%, gentamycin 44%, 63.5%, 61.2%, ceftazidime 43.5%, 82%, 94.3%, Levofloxacin 40%, 22.5%, 39%, cefepime 41.35%, 71%, 90.5%, and aztreonam 36%, 57%, 91%, respectively. Conclusion: The results of this study showed *Enterobacteriaceae* spp. as most frequent GNB isolated from blood samples of children with bacteremia showed the most resistance activity against gentamycin. The high frequency of GNB bacteremia which are resistance to multiple antibiotics in children could put them in life threatening risks. Appropriate antimicrobial therapy for bloodstream infections is important in reducing morbidity and mortality in patients with bacterial bloodstream infections. Therefore, accurate microbiological diagnosis and their antimicrobial resistance profile can be crucial for prompt initiation of adequate treatment for bloodstream infections. Keywords: GNB; antimicrobial resistance; bacteremia, children

Phenotypic Detection of Metallo- β -Lactamase Producing Strains in Clinical Isolates of Gram Negative Bacteria

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نوع پذیرش: پوستر | کد مقاله: G-13820

Abstract: Background: Metallo-beta-lactamases (MBLs) are beta-lactamase enzymes produced by pathogenic bacteria and gradually found in Gram-negative organisms, mostly in *E. coli* species. Clinical infections with MBL-producing isolates are associated with higher morbidity and mortality. However, carbapenem resistance due to Metallo-beta-lactamases (MBLs) production has been gradually reported among clinical isolates of *E. coli*. Metallo- β -lactamases (MBLs) which hydrolyze the carbapenems (imipenem, meropenem, and ertapenem) and render them ineffective for treatment. In addition, MBLs are not susceptible to therapeutic β -lactamase inhibitors like sulbactam, tazobactam, or clavulanic acid. The emergence and uncontrolled spread of carbapenems in Gram-negative bacteria are under threat but normally carbapenems are used for the treatment of infections caused by β -lactam resistant bacteria including extended-spectrum enzymes producers. Methods: Regular investigation of the drug resistance among the clinical isolates will be helpful in formulation of the required policy to reduce the incidence of drug resistance among the bacteria and to start timely appropriate antimicrobial therapy. Although PCR-based genotyping remains as the golden standard for MBL detection and classification, its use is mainly restricted to research purposes. Diagnostic centers and laboratories still rely mostly on culture-based phenotypic test as a means for rapid detection of MBL activity. So far, many variations of phenotypic assays for MBLs detection have been reported. The standard methods are modified Hodge test (MHT), double-disc synergy test (DDST), combined disc diffusion test using imipenem and EDTA, and MBL E-test. Among the phenotypic methods, DDST methods are less sensitive compared to CDT for detecting MBL genes but earlier MHT were much sensitive than DDST. The modified Hodge test has been used extensively and is a phenotypic technique for detecting carbapenemase activity routinely used in clinical pathology laboratories. This test was recommended by the clinical and laboratory standards institute (CLSI, 2009). Results: The modified Hodge test is not specific for the detection of all carbapenemase enzymes, most significantly with isolates showing weak positive results and AmpC producers. Double-disc synergy testing has several versions; carbapenem with clavulanate, cloxacillin, EDTA or 2-mercaptopyruvic acid, and one which utilizes a double sided E-test. In combined disk test; imipenem versus imipenem with EDTA are used as a screening test for MBL producers. This method is efficient for detection of MBL with high carbapenemase resistance, but may be deficient for detecting MBL producers with low resistance to imipenem. Conclusion: Carbapenemase producing strains are resistant not only to carbapenems but to almost all beta-lactam antibiotics. Moreover, carbapenem resistance in Enterobacteriaceae is often associated with extended-spectrum beta-lactamase (ESBL) or with AmpC beta-lactamase production and porin loss. Polymyxins, tigecycline, and less frequently aminoglycoside antibiotics are the treatment options for carbapenemase producing bacteria based on in vitro susceptibility. Hence accurate and timely detection of these resistant mechanisms is very important in deciding the appropriate treatment. But detection of the resistant mechanisms is always a serious challenge to the clinical laboratories. Keywords: Metallo- β -Lactamase, Phenotypic detection, Gram negative bacteria

COVID-19 and Tuberculosis Coinfection: An Overview of Case Reports/Case Series and Meta-Analysis of Prevalence Studies

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نوع پذیرش: پوستر | کد مقاله: G-31825

Abstract: Background: Coinfection of coronavirus disease 2019 (COVID-19) with other respiratory pathogens is a serious concern that may make the diagnosis, treatment, and prognosis difficult for medical staff. Since COVID-19 and tuberculosis are both severe respiratory infections, their symptoms may overlap and even increase mortality in case of coinfection. The current study aimed to investigate the coinfection of tuberculosis and COVID-19 worldwide through a systematic review and meta-analysis. Materials and Methods: A systematic literature search based on the Systematic Reviews and Meta-Analyses" (PRISMA) was performed on September 28, 2021, for original research articles published in PubMed, Web of Science, and Embase databases from December 2019 to September 2021 using relevant keywords. Data analysis was performed using Stata 14 software. Results: Eighteen prevalence studies with 5,843 patients with COVID-19 and 101 patients with concurrent COVID-19 and Mycobacterium tuberculosis (M. tuberculosis) infection were selected for final evaluation. The prevalence of tuberculosis infection was 1.1% in patients with confirmed COVID-19. This coinfection among patients with COVID-19 was 3.6% in Africa, 1.5% in Asia, and 1.1% in America. 43 case reports and 14 case series were also selected. There were 89 adults (67 men and 22 women) with a mean age of 45.14 years who had concurrent infection with tuberculosis. Fever, cough, and weight loss were the most common clinical manifestations. A total of 20.83 % of evaluated patients died, whereas 65.62% recovered. Lopinavir/ritonavir was the most widely used antiviral drug for 10.41% of patients. Conclusion: Although the proportion of tuberculosis coinfection in COVID-19 patients is low, however, it is a critical issue, especially in high-risk individuals. Since we did not have access to all data worldwide, we could not report the exact rate of simultaneous tuberculosis in COVID-19 patients. Therefore, further studies in this field are strongly recommended. Keywords: COVID-19, Mycobacterium tuberculosis, Coinfection, Systematic review, Meta-analysis

Identification of microbial pathogens and antibiotic susceptibility pattern from respiratory secretions of patients with cystic fibrosis

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نوع پذیرش: پوستر | کد مقاله: G-41830

Abstract: Background: Chronic lung colonization with some pathogens is the major cause of morbidity and mortality among cystic fibrosis (CF) patients. Cystic fibrosis (CF) is an autosomal recessive genetic disease. Infections in these patients' genes are mostly caused by these bacteria: Staphylococcus aureus, Stenoterphomonas maltophilia, and particularly Pseudomonas aeruginosa and Candida. patients with cystic fibrosis are living much longer than in the past but still have chronic pulmonary infections and other medical complications related to their disease, including diabetes, intestinal obstruction, cirrhosis, hemoptysis, and pneumothorax. Materials and Methods: In this descriptive study, the population under investigation was 45 patients suffering from CF in Zahedan. Clinical specimens were taken by deep swabbing from the throat and data from every patient was recorded in a questionnaire. The specimens were cultured and isolated organisms were identified by biochemistry and using standard tests. The Kirby-Bauer disk diffusion method was used to determine the bacterial drug resistance pattern. Result: In this study, 57.8% and 42.2% were male and female respectively. P.aeruginosa was isolated from 12 patients(26.7%), S.aureus 15(33.3%), Candida 3(6.7%), A.baumannii 1(2.2%). Most of the patients used Inhaled tobramycin during therapy. Most isolates of P.aeruginosa (54.5%) showed resistance to Imipenem and Meropenem. Also, Most isolates of S. aureus (87.5%) were resistant to Erythromycin and Doxycycline. All of P.aeruginosa were sensitive to colistin, Aztreonam. Conclusion: This study showed that Pseudomonas aeruginosa strains have high resistance to Carbapenem and Cephalosporins. There was no special relationship between the age of patients and their gender with the pattern of antibiotic sensitivity. The result showed Inhaled Tobramycin is an effective drug could be for these patients. Also, according to the results sxt is an appropriate antibiotic for CF patients with S.aureus isolates who suffer from severe respiratory symptoms, especially in winter. Keywords: Cystic fibrosis, Antibiotic resistance

Prevalence and antimicrobial resistance of diarrheagenic Escherichia coli species associated with acute diarrhea among children under 10 years of age in the southeast, Iran

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نوع پذیرش: پوستر | کد مقاله: G-42617

Abstract: Background: Diarrheal disease is one of the driving causes of dreariness and mortality among children around the world, particularly in developing countries. Diarrheagenic Escherichia coli (DEC) is the major cause of gastroenteritis in children is related to tall resistance levels to antimicrobials. This study aimed to investigate the frequency, virulence markers, and antibiotic resistance patterns of diarrheagenic E. coli (DEC) isolated from adolescents in Zahedan, east of Iran. Method: In this cross-sectional study, 300 cases of E. coli from diarrheic stool samples of children under ten years old admitted to hospitals and central laboratories in Zahedan, during a 4-month period (July to October) were collected. After conducting standard biochemical tests and using polyvalent antisera, DEC pathotypes were diagnosed. The antibiotic-resistant pattern of these strains was conducted using 11 different antibiotics by using the standard agar disk diffusion method according to CLSI. Molecular identification of Escherichia coli diarrhea pathotypes was performed using multiplex-PCR and their specific primers. Finally, nucleotide sequencing was done. Results: Out of a total of 300 Escherichia coli samples, 89 cases (29.6%) of diarrhea-causing Escherichia coli (DEC) were isolated using polyvalent antisera. The most common isolate was EAEC so 26 strains (37.6%) had pcvd432 genes. In the next step, EPEC pathotype with 15 strains (21.7%) was identified as having eae gene. 11 strains (15.9%) had elt gene and 9 strains (13%) had est gene, so they belonged to ETEC pathotype. Also, 8 strains (11.5%) had iaH gene and belonged to EIEC patotype. The STEC patotype was not isolated from Escherichia coli isolated from children. In the study of antibiotic patterns, the highest rate of antibiotic resistance was related to ampicillin (94.8%), tetracycline (87.2%), and cotrimoxazole (70.5%). Also, the lowest levels of antibiotic resistance were related to imipenem (1%) and ciprofloxacin (8.9%), respectively. Conclusion: according to the distribution of DEC pathotype in children of Zahedan and increased antibiotic resistance of these pathotypes, antibiotics should be prescribed based on careful identification and antibiogram of this strain. Keywords: Escherichia coli, antibiotic resistance, Multiplex PCR

Phenotypic and genotypic characteristics of biofilm formation in *Acinetobacter baumannii* isolated from Children's Medical Center

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نوع پذیرش: پوستر | کد مقاله: G-68941

Abstract: Background: *Acinetobacter baumannii* strains have emerged as serious hospital pathogens due to the ability of biofilm formation and multiple antibiotic resistance. The susceptibility to antibiotics is significantly decreased in biofilm-associated pathogens. The current study aimed to survey the correlation of biofilm-formation ability, antibiotic resistance, and biofilm-associated genes of *A. baumannii* isolates collected from the Children's Medical Center, Tehran, Iran. Materials and Methods: Biofilm-formation ability of 70 *A. baumannii* isolates was assessed by microtiter plate 96-well. Antibiotic susceptibility testing was determined by disc diffusion method and microdilution broth method; the biofilm-associated genes were determined using PCR. Results: 22.9% of the clinical isolates were weak biofilm producers, while 32.9% and 37.1% of the isolates were moderate and strong biofilm formation abilities, respectively. Our findings showed that the non-MDR clinical strains provided a stronger biofilm formation. The prevalence of the genes encoding biofilm formation, *bap*, *blaPER-1*, *csuE*, *abaI*, and *ompA* was 22.85%, 24.3%, 100%, 100%, and 100%, respectively. Conclusions: Our results indicated that the correlation between antibiotic resistance and biofilm formation was not significant. The results of this study made a new insight into the antibiotic-resistant mechanism and biofilm formation in clinical pathogens of *A. baumannii* in our medical center. Keywords: Biofilms; *Acinetobacter baumannii*; Crystal violet; Anti-Bacterial Agents; Prevalence

Contamination of Water Sources of Karaj Hospitals with *Legionella pneumophila* and *Campylobacter jejuni*

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نوع پذیرش: پوستر | کد مقاله: G-16908

Abstract: Background: One of the most common routes of infection development in humans is contaminated water. *Legionella pneumophila* and *Campylobacter jejuni* are the important causes of community- and hospital-acquired pneumonia and gastroenteritis that are transmitted to humans via the inhalation of contaminated water droplets and consumption of contaminated water, respectively. Thus, continuous monitoring of the water supply systems for these pathogens has great importance in public health. Objective: This study aimed to evaluate the water contamination of Karaj hospitals with these two bacterial species. Materials and Methods: In this study, 62 water samples were obtained from different parts of the hospitals of Karaj from April to September 2019, including air conditioning systems, dialysis equipment, ventilation tanks, and different wards of a hospital such as infectious diseases, pediatrics, gastroenterology, dialysis, and intensive and neonatal intensive care units. The samples were collected in sterile containers and immediately transferred to the laboratory for further analysis. The culture on specific media, staining, and biochemical tests were performed to identify the *L. pneumophila* and *C. jejuni*. Results: Out of 62 water samples, 25.8% (16 samples) were positive for *L. pneumophila*; 68.75% were observed in hot water samples, and 31.25% were attributed to cold water samples. Among 62 samples, 4.84% (3 samples) were positive for *C. jejuni*, which were all detected in hot water samples. Conclusion: Considering that the methods of water refinery of municipal water have no high efficiency, the quality improvement of the water sources of hospitals seems to be necessary. Keywords:

The prevalence of ESBLs and biofilm formation in *Escherichia coli* isolated from urinary tract infection in Isfahan, Iran

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نوع پذیرش: پوستر | کد مقاله: G-70923

Abstract: Background: Uropathogenic *Escherichia coli* is a Gram-negative bacillus that is the most common cause of urinary tract infection. *E. coli* has the ability to produce biofilm as an important virulence factor. Due to the lack of sufficient information about ESBL resistance genes in this geographical area, this study aimed to investigate the prevalence of ESBLs in *E. coli* isolates to increase our knowledge about the role of these genes and biofilm formation in inducing resistance. Materials and Methods: 139 *E. coli* strains were isolated from urine samples. Antibiotic susceptibility testing was performed for the isolates by disk diffusion method. ESBL production was confirmed using double-disk synergy test. Molecular detection of ESBL genes was performed using PCR. Biofilm formation assay was performed by microtiter plate method. Results: The most effective antibiotic against this bacterium was nitrofurantoin. Multidrug resistance was observed in 119 (85.6%) isolates. ESBL phenotype was detected in 93 (66.9%) isolates. The PCR test results showed that blaCTX, blaVEB, and blaTEM were positive in 45 (32.4%), 87 (62.6%), and 10 (7.2%) isolates, respectively. The biofilm formation assay results revealed that 65 (46.8%), 58 (41.7%), 10 (7.2%), and six (4.3%) isolates were non-, weak, moderate, and strong biofilm producers, respectively. Conclusions: The high prevalence of ESBL genes is a public health concern in this region because they could be transmitted to other susceptible bacteria and induce resistance. This study showed that biofilm production could increase antibiotic resistance. Keywords: *Escherichia coli*, ESBLs, Biofilm formation, Antibiotic resistant



The prevalence of TB and MDR-TB in elderly (aged 50 years and above) tuberculosis patients in Tehran

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نوع پذیرش: پوستر | کد مقاله: G-36794

Abstract: Background: In Tehran, the prevalence of tuberculosis among the elderly is almost three times higher than that observed in the young. The purpose of this study conducted to evaluate the proportion of older tuberculosis patients (age 50 years and older), comparing the prevalence of MDR-TB in geriatric TB between two periods, and demographic description. Materials and Methods: A retrospective cohort study of elderly tuberculosis patients treated in the Tehran regional TB reference laboratory [TRTB-RL]. We used the chi-square test to compare the prevalence of MDR-TB in geriatric TB between; 2016 to 2017 and 2018 to 2019. Results: In Tehran, the prevalence of MDR-TB in old age tuberculosis was 4.6%. Between 2016–2017 and 2018–2019 among older people with TB, the prevalence of MDR-TB remained unchanged, consequently the chi-square statistic is 69.6982. The p-value is 0.00001. Accordingly, the result is significant at p .05. Conclusion: Older people living in Tehran participate in transmission chains, which shows that tuberculosis is not only due to the reactivation of the latent disease. The treatment results of elderly TB patients were relatively higher in 2018-2019 Keywords: prevalence, MDR, older, tuberculosis

Isolation and identification of ESBL producing Enterobacter in clinical specimens from Ali-ebn- abitaleb hospital, Zahedan, during 8 months

² عطیه حیدری پور، ² شهناز آرمین، ² فاطمه فلاح، © P, ¹ نازنین آهاری

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نوع پذیرش: پوستر | کد مقاله: G-62095

Abstract: Background: The increasing use of beta-lactam antibiotics since the beginning of the 1980s in the treatment of various bacterial infections has led to an increase in the emergence of resistance to them among of bacteria. So that today, one of the problems in treating nosocomial infections is caused by antibiotic-resistant Gram-negative bacteria such as Enterobacter species. The production of Extended-Spectrum beta- lactamase (ESBL) enzymes is one of the important mechanisms of antibiotic resistance in these bacteria. The purpose of this study is to investigate the frequency of Enterobacter species producing ESBL isolated from different clinical samples sent from two Ali Ibn Abi Talib Zahedan hospitals in a period of 8 months in Tehran. Materials and Methods: All positive cultures in the laboratory of Ali Ibn Abi Talib Hospital were identified as Enterobacter species within a period of 8 months enrolled in this study. The antibiotic susceptibility of bacteria was determined based on the CLSI, and ESBL- producing species were identified using the double disk method according to CLSI guide line. Results: In this cross-sectional study, 33 Enterobacter spp. were collected of which 30% were resistant to third generation cephalosporins and 27% of them had the ability to produce ESBL according to double-disk method. Conclusion: Considering that about one third of the Enterobacter spp. of Ali Ibn Abi Talib hospital in Zahedan were resistant to third generation cephalosporins and 27% of them also had the ability to produce ESBL. These results can be a warning for nosocomial infection control committee in that hospital to prevent and control spread of these antibiotic resistant bacteria because of the most of the ESBL producing genes located on the transferable genetic elements. Key words: Enterobacter spp extended-spectrum beta-lactamase, antibiotic resistance

The CFU of BCG vaccine and other related factors in tuberculin skin reaction

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نوع پذیرش: پوستر | کد مقاله: G-50479

Abstract: Abstract: The BCG vaccination at the birth seems to be an effective in prevention of Tuberculosis in our country. The aim of this present study was evaluation of CFU(colony Forming Unit) of BCG vaccination and other factors influencing the tuberculin skin reaction. Materials and methods: The inoculum of live BCG organisms in vaccinated infants was evaluated at birth and the correlation between the amount of CFU and PPD reaction was examined 3 months later. For this purpose, 854 newborn infants were included. PPD induration diameter was measured 72 hours after the tuberculin skin test. Results: Results have revealed that most of the vaccine samples contained more than 3 million live organisms. Vaccines showing more than 3×10^6 live organisms were associated with positive tuberculin skin test in more 93% of cases as compared with 69% positive induration of vaccines with less than 3×10^6 live organisms. Breast-fed infants showed more positive reaction to tuberculin skin test. Conclusion: The number of live organisms in vaccines can play an important role in the size of tuberculin skin reaction. Keywords: BCG vaccine, PPD, Tuberculin skin reaction, Children

Investigating the antimicrobial effects of different species of Scutellaria

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نوع پذیرش: پوستر | کد مقاله: G-52016

Abstract: Background: Today, various methods are used to treat microbial diseases. Treatment methods include the use of multiple antibiotics, radiation therapy, chemotherapy, and biological therapy. Due to the non-selective nature of most of these methods and drugs, a high percentage of healthy cells are destroyed along with infected cells. Process. Therefore, damage to healthy cells and recurrence of the disease are irreparable complications, disadvantages and limitations of these treatment methods. In recent years, due to the fear of the side effects of chemotherapy drugs, people prefer to use natural herbal products as traditional medicine for treatment. They give, All over the world, many microorganisms have caused different degrees of diseases. Chemical drugs that are used to treat various diseases have also reported side effects. Considering this importance, the purpose of this research is to investigate the antimicrobial effects of different species of Scutellaria species on different human microorganisms. Materials and Methods: This study is a systematic review study that was conducted by searching the websites and databases and herbal medicine journals with the keywords of antibacterial compounds, antiviral compounds, scutellaria species and their English equivalents without a time limit. and from all the articles found, 26 interventional articles were identified and used according to the purpose of the study. Results: Scutellaria plant from the mint family has antioxidant, anti-inflammatory, antiviral and antibacterial properties and is a rich source of natural phytochemical compounds such as flavonoids. The results of this study on different species of Scutellaria showed that the flavonoids baicalin, baicalein, apigenin and luteolin present in this genus are responsible for their antimicrobial effects. Discussion: Despite the fact that the antimicrobial properties of Scutellaria species have been shown, deciding whether the genus Scutellaria can be used as an antibacterial and antiviral agent in the clinic depends on many factors and requires There are more reviews. Keywords: Antimicrobial, Scutellaria species, microorganisms

Does *Prevotella copri* play a stimulating role in the development of autoimmune diseases?

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نوع پذیرش: پوستر | کد مقاله: G-54782

Abstract: Background: The gut microbiota affects the host's immune system and can be crucial in differentiating immune cells, considering that the major part of the immune system is located in the gastrointestinal tract. The loosening of enterocytes allows the microbial antigens to enter and activate the immune system via molecular mimicry. Therefore, it is alarming that changes in the gut microbiota can contribute to inflammatory and autoimmune diseases (AIDs) such as autoimmune neurological disorders, systemic lupus erythematosus, autoimmune dermatitis, inflammatory bowel disease, type 1 diabetes, and rheumatoid arthritis (RA). Human gut-colonizing species like *Prevotella copri*, *Ruminococcus gnavus*, and *Lactobacillus salivarius* are linked to the etiology of AIDs. In this study, we aim to review the role of *Prevotella copri* – one of the most common species in the human gut microbiome – in developing AIDs. Materials and Methods: In this review, we searched through the databases of Google Scholar, PubMed, EMBASE, and Scopus. Keywords such as “autoimmune diseases”, “Intestinal Microbiota”, “Gut Microbiota”, “*Prevotella copri*” and “Gastrointestinal Microbiome” were used to find the relevant papers that studied the role of *P. copri* in the context of AIDs. Results: *P. copri* has been positively and unfavourably linked to host health, especially through pro-inflammatory effects. Studies show that *P. copri* colonization of mice increased susceptibility to chemical colitis, and it is more abundant in the feces of ankylosing spondylitis patients (AS) and RA, especially patients with new-onset RA. *P. copri* can also produce antigens in RA patients that mimic synovial and ribosomal peptides. Conclusion: The gut microbiota is a large, intricate population with various potential functions. Numerous autoimmune diseases have been linked to changes in the gut microbiota's composition and functionality. One of the most critical intestinal bacteria is *P. copri*, and new studies have shown its role in the pathogenesis of RA. Keywords: *Prevotella copri*, Gastrointestinal Microbiome, Gut Microbiota, Intestinal Microbiota, autoimmune diseases.

Evaluation of nosocomial infections and determination of antibiotic resistance in Imam Khomeini and Mostafa Khomeini hospitals in Ilam

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نوع پذیرش: پوستر | کد مقاله: G-30792

Abstract: Background: Nosocomial infections also referred to as healthcare-associated infections (HAI), are infection(s) acquired during the process of receiving health care that was not present during the time of admission. Occurring within 48-72 hours of hospital admission. Knowledge about the common pathogens in every hospital ward can contribute to the effective control of infections and Reduce antibiotic resistance, Reduce mortality, Contribute to the health and economy of the community. Materials and Methods: This cross-sectional study was conducted in Imam Khomeini and Mostafa Khomeini Hospital in Ilam city. The basis of data collection was the forms of the Infection Control Committee and the laboratory, which are used in all hospitals in the country. To describe the data from frequency indicators, frequency percentage and cumulative frequency percentage. All analyzes were done in spss software version 19 and Excel 2010 was used to draw graphs. Results: The results obtained from Imam Khomeini Hospital in Ilam were reported as follows: 75% of the patients were from the ICU and most of the patients were infected in the first six months of the year. The next finding was that 73.7% of the samples were from body secretions. The most bacteria isolated from the samples was Citrobacter with 38.4%, followed by Escherichia coli with 38.4% and Klebsiella with 17.2%. The most antibiotic resistance reported was related to ceftriaxone (72 %), ceftazidime (71 %), Ciprofloxacin (56 %), ceftizoxime (56 %), gentamicin (49 %), and cefazolin (46 %). But the results of Mustafa Khomeini Hospital in Ilam city were reported as follows: Most of the patients (69.2 %) were infected or tested in the second 6 months of the year. The highest frequency of samples was related to urine culture (50 %). The highest frequency The bacteria were Staphylococcus aureus with 26.9%, E.coli with 23.1%, and Klebsiella with 19.2% respectively. Also, the highest reported resistance was Ciprofloxacin 54%, Amikacin 50%, Aztronam 46%, Ceftriaxone 42% respectively. Conclusion: The relative prevalence of infections in Imam Khomeini Hospital was as follow 16.2% urinary infection, 73.7% body secretions were reported. The relative prevalence of infections in Mustafa Khomeini Hospital was as follows: bronchial infection 26.9%, urinary infection 50%. Also, the most bacteria isolated from hospital infections were Citrobacter, Escherichia coli, and Staphylococcus aureus. The Multidrug resistance in different microorganisms of this study was high. The appearance of Citrobacter as a common bacteria with high antibiotic resistance in this study can be caused by a new change in the prevalence pattern of microorganisms in this hospital and is considered a serious warning. The relative prevalence of nosocomial infection in Imam Khomeini Hospital was 1.7%. Keywords: Bactria, nosocomial infections, antibiotic resistance.

Assessment of SCCmec types and aminoglycoside resistance profiles in coagulase negative staphylococci isolates of the infected patients

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نوع پذیرش: پوستر | کد مقاله: G-19865

Abstract: Background: Coagulase-negative staphylococci (CoNS) are the most important inhabitants of skin and mucous membranes of animals and humans. Methicillin resistance in CoNS (MR-CoNS) is mediated by the excess production of PBP2a, which is encoded by the *mecA* gene. Despite the increased resistance to these drugs, especially aminoglycosides, gentamicin and tobramycin are used to treat these staphylococcal infections either alone or in combination with beta-lactams or glycopeptides. We aimed to determine the susceptibility pattern to aminoglycosides and the prevalence of SCCmec types of CoNS isolates isolated from patients. Materials and Methods: This study, was performed on CoNS isolates (n=86) were collected from various clinical specimens obtained from the patients admitted to three teaching and treatment hospitals in Tabriz, Iran, between May, 2016, to March, 2017. The CoNS detection was based on the colony morphology, gram's staining, catalase test, resistance to bacitracin (0.04µg), coagulase and DNase activity and Sugar fermentation tests included mannitol, lactose, xylose, sucrose, trehalose, sorbitol and maltose fermentation for species identification. Antimicrobial susceptibility test was performed for cefoxitin (30µg), gentamicin (10 µg), amikacin (30 µg) and tobramycin (10 µg) by the disc diffusion method, according to the CLSI guidelines. The genomic DNA from CoNS isolates was extracted by the Cetyl Trimethyl Ammonium Bromide (CTAB) method. The frequency of *mecA* gene and SCCmec types in all CoNS isolates was evaluated by the polymerase chain reaction (PCR). Results: Of these, 86 isolates were obtained from hospitalized patients. The CoNS isolates included: *S. epidermidis* (n= 35), *S. haemolyticus* (n= 9), *S. hominis* (n= 14), *S. caprae* (n= 5), *S. schleiferi* (n= 2), *S. auricularis* (n= 8), *S. caseolyticus* (n= 2), *S. lugdunensis* (n= 2), *S. simulans* (n= 1) and *S. warneri* (n= 8). Almost 65% of the isolates showed resistance towards gentamicin, while 37.62% of them had resistance towards amikacin. The resistance to all three aminoglycoside antibiotics in methicillin resistance-CoNS (MR-CoNS) was more than that in methicillin susceptible-CoNS (MS-CoNS) (P 0.05). SCCmec types I, II, III, IV and V were encountered in 24.6 %, 0, 15.9 %, 1.4% and 2.9 %, respectively. Conclusion: the high frequency of resistance to aminoglycosides and cefoxitin as well as, prevailing SCCmec type I in the patients group requires attention. Keywords: Coagulase negative staphylococci, SCCmec, aminoglycoside resistance

Prevalence of macrolide resistance of *Mycoplasma pneumoniae* in children

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Abstract: Background: *Mycoplasma pneumoniae* is a common pathogen in community acquired pneumonia (CAP) in childhood. This species affects the respiratory system. Macrolide resistance in *Mycoplasma pneumoniae* species is increasing in the world. Therefore, the aim of this study is to review the prevalence of macrolide resistance of *Mycoplasma pneumoniae* in children. Materials and methods: We searched MEDLINE via PubMed, Scopus, Science Direct, Web of Science (ISI), Google Scholar (as English databases); Magiran, Iran Medex, Iran Doc, and SID (as Persian databases) during 1996 to September 2021 using the terms: *Mycoplasma pneumoniae* pneumonia (MPP), community acquired pneumonia (CAP), children, Macrolide resistance. Results: Prevalence of MPP occurs worldwide in the age range of 3 to 7 years. Recent epidemics have occurred in Korea. Although MPP is a mild and self-limiting disease, it can develop into a severe and fulminant disease. The prevalence of macrolide-resistant MPP is rapidly increasing, and has recently reached 80–90%, particularly in Asian countries. Macrolide-resistant *Mycoplasma pneumoniae* (MRMP) has a point mutation in the V domain of 23S rRNA, and most of the mutations are detected at positions 2063 and 2064 of the sequence. Conclusion: *Mycoplasma pneumoniae* strains show a good response to treatment with macrolides. Excessive use of macrolides may contribute to these mutations. MRMP can lead to clinically refractory pneumonia, shows no clinical or radiological response to macrolides, and can develop into severe and complicated pneumonia in children. Tetracyclines or quinolones can be alternatives for the treatment of MRMP. Key words: *Mycoplasma pneumoniae*, Macrolides resistance, children

Molecular detection of class I integron and its gene cassette to antibiotics in *Klebsiella oxytoca* strains

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نوع پذیرش: پوستر | کد مقاله: G-73450

Abstract: Introduction: Integrons are one of the mobile genetic elements that can carry resistance genes to various antibiotics. Meanwhile, the role of class I integron is important in creating and transmitting antibiotic resistance. The purpose of this study is to isolate Enterobacter strains, molecular investigation of class I integron and gene cassettes, and determination of antibiotic resistance and sensitivity. Methods: This study was conducted on 50 *Klebsiella oxytoca* samples isolated from clinical samples of patients. After sampling and culture on specific media and DNA extraction, the presence of class I integron gene and aadB cassette was done by PCR method. Antibiotic sensitivity and resistance test was also done by disk diffusion method. Results: After examining 50 strains, 14 samples were resistant to all antibiotics and 27 samples had multiple antibiotic resistance. The highest resistance was related to ceftizoxime and ticarcillin antibiotics, the lowest resistance was related to ofloxacin and amikacin antibiotics. Out of 50 samples of *Klebsiella oxytoca*, 25 samples had int1 gene and also out of 24 positive integron samples, 15 samples had aadB cassette. Conclusion: In this study, according to the significant statistics of the presence of class I integron and the gene cassette inserted in it in *Klebsiella oxytoca* isolates and its relationship with the pattern of multiple drug resistance, it can be concluded that these elements can play an important role in creating and transmission of antibiotic resistance. As a result, measures should be taken to prevent the emergence and spread of these antibiotic resistance elements. Keyword: class I integron, antibiotic resistance, *Klebsiella oxytoca*, gene cassette

Prevalence of multi-drug resistant *Escherichia coli* and Extended-Spectrum Beta-Lactamase Producing *Escherichia coli* Causing Bloodstream Infections in patients with leukemia

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Abstract: Background Extraintestinal pathogenic *Escherichia coli* (ExPEC) isolates are responsible for many bloodstream infections. Multidrug-resistant *Escherichia coli* (MDR *E. coli*) has become a major public health concern in many countries, causing failure in treatment with consequent huge health burden. *Escherichia coli* is the gram-negative organism most frequently isolated in adult patients with bacteraemia and in severe cases it may lead to death. Patients with malignancy are predisposed to developing BSI during their chemotherapy courses. Lots of evidence showed that the epidemiology of nosocomial infections in cancer patients changed over the past decades, with the reemergence of GNB as the predominant causative pathogens. Methods in a cross sectional study, 67 blood cultures were collected from leukemia patients suspected to have BSI from July 2021 to February 2022. The blood culture bottles were incubated aerobically at 35–37°C for 24 hours and then sub-cultured on routine microbiology culture media. The bacterial colonies were identified using microbiological tests. Antibiotic susceptibility tests were performed by Kirby-Bauer disc diffusion and broth microdilution methods. The phenotypic detection of ESBLs was carried out by the combination disc-diffusion test (CDDT). Results The results of antimicrobial susceptibility test showed that there was variation in resistance of *E. coli* isolates to the drugs used. *E. coli* isolates revealed high resistance (92%) to ampicillin, Amoxicillin /Clavulanic acid (88%) and Sulfamethoxazole-Trimethoprim(74.6%) , Tetracycline(67%), Nalidixic acid (64%), Cefixime(62.6%), ceftriaxone(61%), aztreonam (56.7%), ceftazidime (56.7%), cefepime (55.2%), ciprofloxacin(47.7%), Kanamycin(44.7%), levofloxacin (43.2%), gentamicin (31.3%), chloramphenicol(29.8%), Amikacin(14.9%), imipenem(5.9%), the Highest sensitivity was observed imipenem(92%), Amikacin(71.6%) and chloramphenicol (68%) followed by gentamicin(68.6%), levofloxacin(55.2%), Kanamycin(49%), ciprofloxacin(47.7%), cefepime(44.7%), aztreonam(43.2%), ceftazidime(38.8%), ceftriaxone(35.8%), Nalidixic acid(34.3%), Tetracycline(32%) Sulfamethoxazole-Trimethoprim(25.3%), ampicillin(7.4%), Amoxicillin /Clavulanic acid(2.9%). In total, 36(53.7%) isolates were found to be ESBL-producing strains. , 15 (22.3%) isolates were MDR, and 2(2.9%) was XDR. Conclusions Alarming rate of drug resistance among Bloodstream Infections in patients with leukemia and high rate of ESBL-producing *E. coli* was observed. It is extremely necessary to routinely investigate the drug resistance among all isolates and formulate strict antibiotics prescription policy in our country. Keywords: Leukemia, MDR, XDR , Extended spectrum beta-lactamase-producing, *Escherichia coli*

Molecular Analysis of β -lactamase Resistance Genes (blaGES, blaPER, blaVEB) in *Klebsiella pneumoniae* Strains Recovered from Clinical Sources

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Abstract: Background and Aims: *Klebsiella pneumoniae* is a facultative anaerobic Enterobacteriaceae that causes infections in hospitalized or otherwise immunocompromised patients. Currently, there is a continuous problem of antimicrobial resistance (AMR) in Gram-negative bacteria. *K. pneumoniae* developed different resistance mechanisms to several classes of antibiotics. The main mechanism complicated in β -lactam resistance is the production of β -lactamases. The enzymes are categorized into four classes according to amino acid structure. The genes for class A β -lactamases (blaVEB, blaPER, blaGES,) are broadly disseminated in organisms, often positioned on mobile genetic elements (MGEs) such as plasmids in Gram-negative bacteria. The current study aimed to determine the prevalence of class A β -lactamases encoding genes (blaVEB, blaPER, blaGES) among *Klebsiella pneumoniae* strains recovered from hospitalized patients. Materials and Methods: One-hundred different clinical samples were collected. Confirmation of *K. pneumoniae* isolates was done by polymerase chain reaction (PCR) for the existence of rpoB gene. Antimicrobial susceptibility testing was achieved by disk diffusion method in line with Clinical & Laboratory Standards Institute (CLSI 2018). Finally, the presence of three β -lactamase genes (blaVEB, blaPER, blaGES,) was detected by PCR. Results: Based on PCR results, rpoB gene was identified in all 100 *K. pneumoniae* isolates. Antibiogram demonstrated that highest rate of resistance was exhibited against ampicillin-sulbactam (90%) and the lowest rate of resistance was against tigecycline, (93%) and fosfomycin (100%). Of the 100 *K. pneumoniae*, 15 (15%), 10 (10%) and 2 (2%) isolates were PCR-positive for blaVEB, blaGES and blaPER β -lactamase genes, respectively. Conclusion: In this work, we emphasis on class A β -lactamases, as one of the most prevalent mediators of β -lactam resistance in Gram-negative pathogens. As regards *K. pneumoniae* is a nosocomial bacteria, the existence of β -lactamase encoding genes in clinical specimens even in low rates can be a dangerous alarm. The co-carriage of β -lactamase genes and other resistance elements on the same plasmid can lead to the emergence of multidrug-resistance phenotype. Keywords: *Klebsiella pneumoniae*, Nosocomial Infections, β -lactamases, Antimicrobial Resistance



Bacteriophages of Mycobacterium tuberculosis, their diversity, and potential therapeutic uses: A review

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Abstract: Tuberculosis (TB) caused by Mycobacterium tuberculosis (M. tuberculosis) is a highly infectious disease and worldwide health problem. Based on the WHO TB report, 9 million active TB cases are emerging, leading to 2 million deaths each year. The recent emergence of multidrug-resistant tuberculosis (MDR-TB) and extensively drug-resistant tuberculosis (XDR-TB) strains emphasizes the necessity to improve novel therapeutic plans. Among the various developing antibacterial approaches, phage therapy is thought to be a precise hopeful resolution. Mycobacteriophages are viruses that infect bacteria such as Mycobacterium spp., containing the M. tuberculosis complex. Phages and phage-derived proteins can act as promising antimicrobial agents. Also, phage cocktails can broaden the spectrum of lysis activity against bacteria. Recent researches have also shown the effective combination of antibiotics and phages to defeat the infective bacteria. There are limitations and concerns about phage therapy. For example, human immune response to phage therapy, transferring antibiotic resistance genes, emerging resistance to phages, and safety issues. So, in our present study, we introduced mycobacteriophages, their use as therapeutic agents, and their advantages and limitations as therapeutic applications. Keywords:

First report of optrA gene from clinical Linezolid-Resistant Enterococcus spp. in Iran and its prevalence in some hospitals in Isfahan

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Abstract: Introduction. There is concern over the emergence of linezolid-resistant Enterococcus species (LRE) as a result of transferrable resistance determinants. optrA, a novel plasmid-borne ABC transporter gene conferring resistance to both oxazolidinones and phenicols, has recently been identified in human and animal enterococci. This study aimed to detect the prevalence of optrA genes in clinical multiple drug resistance (MDR) Enterococcus isolates from hospitals at Isfahan University of Medical Sciences. Methods and Materials. At some teaching hospitals of Isfahan University of Medical Sciences, 175 enterococcal isolates were obtained from urine, blood, body fluids, wounds, and catheters for a descriptive study (cross sectional) the period May 2020 to December 2021. After identifying and confirming the isolated enterococci species by biochemical and genetic methods, an antibiogram and determination of the MDR isolates were performed according to Clinical and Laboratory Standards Institute Guidelines (CLSI-2022) instructions. Then, MDR Enterococcus strains were checked for the presence of the optrA gene using a polymerase chain reaction (PCR). In addition, the results were confirmed by sequencing the genome (from target range) of positive strains for the presence of optrA. All statistical analyses were conducted using SPSS v26 software. Significant results were defined as P 0.05. Results. In total, 175 clinical enterococcal isolates, 129 (73.7%), 34 (19.4%), and 12 (6.8%) isolates were identified as E. faecalis, E. faecium, and other species of Enterococcus, respectively. The prevalence of MDR Enterococcus spp. among 175 samples was 73.1%. The prevalence of the optrA gene among the total MDR isolates was 5.4% (7/128). Among the optrA Enterococcus isolates, 5 were E. faecium isolates and 2 were E. faecalis isolates. Resistance gene (optrA) were not significantly correlated with MDR isolates (p 0.05). Conclusion. This is the first report on the linezolid resistance gene optrA in Iran and its prevalence in clinical Enterococcus spp. isolates from hospitals at Isfahan University of Medical Sciences. According to our results, the optrA gene is present in 71.4% of linezolid-resistant enterococci, and the presence of optrA is significantly associated with linezolid resistance (P 0.05). Even one specimen expressing optrA should be considered alarming since genes for resistance can spread between clinical and non-clinical settings as well as species. Key Words. Enterococcus spp., optrA, linezolid-resistance

Antimicrobial Efficacy and Prevalence of Aureocin A53 among Staphylococcus aureus isolates

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نوع پذیرش: پوستر | کد مقاله: G-49617

Abstract: Background and Aim: Bacteriocins are defined as antimicrobial peptides or proteins with bactericidal activity against other bacteria. Aureocin A53 is an N-formylated antimicrobial peptide (AMP) produced by Staphylococcus aureus. Aureocin A53 has a broad spectrum of antibacterial activity against human and animal pathogens. The objective of this study was to detect and evaluate the wide range of antimicrobial activity of Aureocin A53 produced by the bacteriocinogenic Staphylococcus aureus. Methods: In this experimental study, 100 clinical isolates were selected from private diagnostic laboratories at Isfahan during the year 2021. They were cultured and incubated at 35°C for 18 - 24 hours. Antagonistic activity of isolates was tested by adopting agar plug method. Total DNA was extracted from clinical specimens and PCR was optimized using specific primers for the amplification of the complete sequence of some Aureocin A53 genes. Results: 100 isolates of Staphylococcus aureus were isolated from clinical samples. The concentrated supernatant containing aureocinA53 exhibited a strong bacteriolytic activity toward Staphylococcus aureus ATCC 25923. Additionally, aureocin A53 exhibited antagonistic activity against important including Methicillin-resistant Staphylococcus aureus (MRSA). Out of 100 isolates, 30 isolates had positive well assay samples. Based on the obtained results by the PCR analysis 3 isolates were positive for Aureocin A53 genes. Conclusions: The objective of the present study was to evaluate the inhibitory activity of Aureocin A53 against clinical strains of several Staphylococcus aureus. Further studies will provide valuable information on the characterization of this bacteriocin, and the investigation of its biosynthesis mechanism based on genetic information will be of great importance for future applications of this staphylococin. Key words: Staphylococcus aureus, Bacteriocin, Aureocin, Antimicrobial peptide

First report of poxtA and cfr genes related to linezolid resistance from human clinical Enterococcus spp. isolates in Iran

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Abstract: Background: Linezolid is often considered a last-resort treatment for severe infections caused by MRSA and VRE. As a result, linezolid-resistant enterococci pose a significant challenge to public and clinical health. The cfr gene, which encodes an rRNA methyltransferase, was first discovered in Staphylococcus sciuri's plasmid pSCFS1 and has since been found in a variety of bacteria. It gives resistance to phenicols, lincosamides, and oxazolidinones (PhLOPSA). Also, The ABC-F family protein poxtA has recently been shown to decrease susceptibility to phenicols, oxazolidinones, and tetracyclines. The goal of this study was to detect the emergence of linezolid resistance and the prevalence of cfr and poxtA genes in clinical Enterococcus isolates in Isfahan. Methods. In this descriptive study (cross-sectional), 175 non-duplicate enterococcal isolates were obtained from different clinical specimens at the Al-Zahra, Amin, and Khorshid hospital in Isfahan. After the biochemical confirmation of the strains, the PCR amplification of genes (ddl) was performed to determine the enterococci species. The antibiotic resistance profile of Enterococcus isolates was investigated based on CLSI 2022's instructions and analyzed using Whonet 2021 software. Then used a multiplex-PCR method to detect cfr and poxtA from whole genomic bacterial DNA. The confirmation of the gene detection process was done by genome sequencing. Statistical analyses were performed using SPSS version 26 software. A significance level of P 0.05 was used to define significant results. Results. Among our isolates, E. faecalis predominated 73.7%. As well, vancomycin and linezolid-resistant enterococci constitute 29.7% and 4.0%, respectively. The highest and lowest antibiotic resistance is for erythromycin (84.6%) and fosfomycin (0.6%), respectively. Nevertheless, MDR prevalence among E. faecium was 91.1%, 68.9% among E. faecalis. The prevalence of poxtA and cfr was 42.8% among linezolid-resistant enterococci and there is a significant relationship (P 0.05) between resistance to linezolid and the presence of each of these two genes. This study showed the simultaneous presence of all two genes (cfr and poxtA) in 28.5% of LREs. Conclusion. To the best of our knowledge, this is the first description of the prevalence of the linezolid resistance genes cfr and poxtA in human clinical Enterococcus spp. isolates in Iran. Accordingly, enterococci strains among Iranian patients are able to carry and spread the resistance genes such as optrA and cfr and subsequently causing resistance to linezolid which can be alarming. Key Words. Enterococcus spp., linezolid-resistance, poxtA, cfr

Prevalence of algD, pslD, pelF, Ppgl, and PAPI-1 genes involved in biofilm formation in clinical *Pseudomonas aeruginosa* strains

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Abstract: Background: Biofilm formation is one of the main virulence factors in *Pseudomonas aeruginosa* infections. This study aimed to investigate the presence of genes involved in biofilm formation in clinical *P. aeruginosa* isolates. Material and methods A cross-sectional study was conducted on 112 *P. aeruginosa* isolates. The biofilm formation assay was performed on all isolates. Antimicrobial resistance was determined by the disk diffusion method, and the presence of genes was detected by polymerase chain reaction. Isolates were typed with Rep-PCR. Results The results of biofilm formation demonstrated that 85 strains (75.9%) were biofilm producers and 27 strains (24.1%) were non-producers isolates. Antibiotic susceptibility pattern in biofilm-positive and biofilm-negative isolates obtained from hospitalized patients showed a high rate of antibiotic resistance to amoxicillin with 95.7% and 92.3%, respectively. Based on PCR amplification results, the frequency of genes involved in biofilm formation among all isolates was as follows: algD (78.6%), pelF (70.5%), pslD (36.6%), Ppgl (0%), and PAPI-1 (77.6%). Rep-PCR typing demonstrated that 112 *P. aeruginosa* isolates were classified into 57 types according to 70% cut-off. The predominant type was A which contained 15 isolates. Moreover, 7 isolates were clustered in genotype B, followed by C type (6), D (4), E (4), F (4), G (4), H (3), I (3), J (3 isolates), and other genotypes were shown in Figure 1. Also, 35 isolates were distributed in scattered patterns and showed single types. Conclusion Study results showed significant association between biofilm formation and resistance to antibiotics such as ceftazidime and meropenem. Analysis of Rep-PCR patterns indicated that the evaluated isolates were heterogeneous, relatively. Keywords: *Pseudomonas aeruginosa*, Biofilm formation, repetitive extragenic palindromic PCR, IRAN

Evaluation of antibacterial activity of five biocides and the synergistic effect of biocide/EDTA combinations on biofilm-producing and non-producing *Stenotrophomonas maltophilia* strains isolated from clinical specimens in Iran

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نوع پذیرش: پوستر | کد مقاله: G-30741

Abstract: Background: The overuse of biocides in healthcare-facilities poses risk for emergence and spread of antibiotic resistance among nosocomial pathogens. Hospital-acquired infections due to *S. maltophilia* have been increased in the recent years and with its various resistance mechanisms contribute to patient morbidity and mortality in hospitals. The current study aimed to evaluate the susceptibility of biofilm-producing and non-producing *S. maltophilia* clinical isolates to five commonly used hospital biocides, alone and in combination with EDTA to examine the synergistic effect of combining EDTA on the bactericidal activity of them by microbroth dilution method. As well as the frequency of efflux genes encoding resistance to biocides among isolates. Methods: This study included 97 *S. maltophilia* isolates. The susceptibility tests of five biocides were studied alone and in combination with EDTA against all *S. maltophilia* isolates by microbroth dilution method. Susceptibility of isolates to antibiotics was determined by disk diffusion method. Biofilm formation was determined by microtiter plate assay. Presence of *qacE*, *qacEΔ1*, *SugE1* genes was screened by PCR. Results: Based on minimum inhibitory and bactericidal concentrations of biocides sodium hypochlorite 5% (w/v) and ethyl alcohol 70% (v/v) were the strongest and weakest biocides against *S. maltophilia* isolates, respectively. The combination of EDTA with biocides significantly increased the effectiveness of the studied biocides. As well as among the isolates examined, 94 (95%) were able to produce biofilm. The frequency of *sugE1* resistance genes was found in 90.7% of our clinical *S. maltophilia* isolates. None of the isolates carried *qacE* and *qacEΔ1* gene. Conclusions: The current study recommended that using the mixture of biocides with EDTA can be effective in reducing nosocomial infections. Our results showed that the addition of EDTA significantly increased the efficacy of studied biocides and it is recommended to combine the usage of antiseptic and disinfectant with EDTA to increase potency and efficacy of them. Keywords: *Stenotrophomonas maltophilia*, Biocide-resistance, Antibiotic resistance, Nosocomial infection, Biofilm

Prevalence of nosocomial infections in Lordegan Shohada Hospital in 2017 to 2022

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نوع پذیرش: پوستر | کد مقاله: G-35902

Abstract: Background: A Health-care acquired infections (HAIs) or nosocomial infections (NIs) are a common problem in all countries of the world. The aim of this study Epidemiological evaluation of nosocomial infections in Lordegan Shohada Hospital from 2017 to 2020. Materials and Methods: This study was descriptive-analytical cross-sectional. Case finding was based on centers for disease control (CDC) definitions for nosocomial infection (NIs) and the nosocomial infection questionnaire of the Ministry of Health and Medical Treatment of Iran. Cases of NIs were confirmed based on clinical findings, tests and CXRay, and then registered in the Iranian Nosocomial Infections Surveillance (INIS). Results: Overall, 48343 patients were at risk for nosocomial infections during the study period, of these, 274 (0.6%) cases of nosocomial infections were detected, of which 132 (48%) were men and 142 (52%) were women. The most common type of nosocomial infection in this study was SSI (0.33%), PNEU (0.27%) and VAE (0.10). The highest rate of NIs was reported from ICUs (0.2). Conclusion: The prevalence of nosocomial infections in this center has been low compared to the global norm; this is not the reason that the prevalence of nosocomial infections is low, the most important reason for that is the irrational use of antibiotics and therefore the hiding of infection cases. The prevalence of microbial resistance is increasing, and this issue is worrying in the field of NIs control, and there is a need to think of a solution in the field of rational antibiotic prescription and thus preventing the occurrence of microbial resistance. Keywords: Incidence, Prevalence, Epidemiology, Nosocomial infections

Prevalence of binding genes in clinical isolates of *Acinetobacter baumannii* with multiple antibiotic resistance

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نوع پذیرش: پوستر | کد مقاله: G-35642

Abstract: Background: *Acinetobacter baumannii* is one of the most important multi drug - resistant species associated with nosocomial infections. Several factors involve in resistance to drug and its pathogenicity. Of these factors, OmpA and SmpA proteins plays a crucial role. The aim of this study was to prevalence of binding genes in clinical isolates of *Acinetobacter baumannii* with multiple antibiotic resistance. Methods: This study was performed on 46 *Acinetobacter baumannii* isolates from patients in Broujerd hospitals. Presence of *Acinetobacter baumannii* isolates were confirmed by biochemical tests. Drug susceptibility, presence of ompA and smpA genes were determined using disk diffusion method and PCR methods, respectively. Results: The highest antibiotic resistance was against ceftazidime (%74), imipenem (%50) and meropenem (%50) antibiotics and the lowest resistance was against levofloxacin (%21.74) and ampicillin (%17.39) antibiotics. The frequency of ompA and smpA genes was 16 (53.33%) and 23 (76.66%), respectively. Conclusion: Existence of multi drug resistance in most isolates as well as presence of ompA and smpA in all samples can cause bacterial virulence and drug resistance. Keywords:

Antiparasitic activity of pyocyanin pigment produced by *Pseudomonas aeruginosa* against *Leishmania major* in vitro

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نوع پذیرش: پوستر | کد مقاله: G-43695

Abstract: Background and Aim: Pyocyanin pigment is a blue redox compound with the metabolic activity that affects both eukaryotic and prokaryotic cells. Pyocyanin is produced only by the opportunistic pathogen *Pseudomonas aeruginosa*, which is a non-fermenting lactose gram-negative bacterium. The purpose of this study is to investigate the effects of pyocyanin pigment extracted from *Pseudomonas aeruginosa* on *Leishmania major* in vitro and also toxic effects on the PC12 cell line. Methods: To perform this test, *Pseudomonas aeruginosa* strain RTCC1474 was purchased from Razi Vaccine and Serum Research Institute, then pyocyanin pigment was extracted from this bacterium by using chloroform. The relative purity of the pigment was confirmed by thin-layer chromatography, spectrometry UV-Vis and FTIR. Finally, the effects of different concentrations of this pigment were investigated against *Leishmania major* and PC12 cell lines. Result: In this research, it was found that the lowest concentration of pigment (78 µg/ml) was able to reduce 50% of the *Leishmania major* parasite population in 24 hours and the concentration of 10000 µg/ml was able to eliminate 93.2% of the *Leishmania* parasite in 24 hours. The IC50 of pyocyanin on the *Leishmania* parasite was 66.68 µg/ml in 24 hours and 27.32 µg/ml in 48 hours. Also, the CC50 level of this pigment on the PC12 cell lines after 48 hours was 930 µg/ml and its SI index was 34.04. Statistical results were obtained with the use of GraphPad Prism version 9 software. Conclusion: According to the effects of pyocyanin pigment on bacteria, and fungi and its easy production process, and the results obtained, it was concluded that pyocyanin pigment significantly eliminates *Leishmania* and can be used as a drug for the definitive treatment of leishmaniasis. More complete studies should be done in vitro and in vivo on pyocyanin pigment and its effect on *Leishmania major*. Keywords: pyocyanin pigment, *Pseudomonas aeruginosa*, *Leishmania major*, Cell line, CC50

Effect of endophytic fungi isolated from Licorice (*Glycyrrhiza glabra*) on *Pseudallescheria boydii* in laboratory conditions

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Abstract: Background: Licorice (*Glycyrrhiza glabra* L) is one of the most important medicinal plants native to Iran, which is exported to a considerable extent every year. This plant has anti-inflammatory, antibacterial, antioxidant and expectorant properties and is effective in detoxification and liver protection. Licorice root is mentioned as medicine in most pharmacopoeias. The roots and rhizomes of this plant have been used medicinally in the pharmacopoeia of countries such as America for about 4000 years and have been registered in China and other countries. This plant is used in traditional Asian and European medicine to treat gastritis, respiratory infections, and in traditional Chinese medicine. It is also used to treat hepatitis, tumor growth, and heart diseases. Endophyte literally means inside the plant. Using the literal definition of endophyte broadly includes all plant hosts and their resident microorganisms. We consider endophytes as microorganisms that complete all or part of their life cycle by forming a colony inside the cells of the healthy tissues of the host plant, such as stems, roots and leaves. They live without any symptoms in the internal tissues of the plants. The symbiosis of endophytic fungi with plants and hosts is expressed as mutual symbiosis, because both the plant and the fungus benefit from this relationship. Methods: Samples were collected in the summer of 1401 from three different regions of Hamadan province. After surface disinfection, plant samples (including roots, stems and leaves) were placed in PDA culture medium. After that, endophytic fungi isolated from Licorice were used and their antagonistic effect on the human pathogenic fungus *Pseudallescheria boydii* (PFCC=462) obtained from Pasteur Institute carried out by cross-cultivation method on PDA culture medium. The experiment was conducted as a completely randomized block design with 5 treatments (4 endophytic fungi + control) and nine replications. Statistical analysis was done using SPSS 20.0 software and comparison of means with Duncan's test at 5% probability level. Results: The results showed that endophytic fungi had an effect on *Pseudallescheria boydii*, so that *Aspergillus niger* and *Fusarium oxysporum* showed the greatest and least effects on this fungus and the percentage of inhibition was 43.1% and 9.3%, respectively. Endophytic fungi *A. niger* like can be promising microorganism for the future as a biological control and antagonist on the pathogenic fungus *pseudallescheria boydii*. Keywords: Licorice, Endophytic fungi, *Pseudallescheria boydii*, antagonist

Helicobacter pylori virulence factors associated with gastric cancer, as an emerging infection

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نوع پذیرش: پوستر | کد مقاله: G-08465

Abstract: Background: Helicobacter pylori is a well-known Gram-negative bacteria, as a the most common bacterial infection in the world, cause of gastrointestinal diseases including gastric cancer, MALT lymphoma, and peptic ulcer; and non- gastrointestinal diseases. Based on the previous scientists' studies, more than 20 thousand strains have been isolated in laboratories, remarkably, only few strains have been established to be carcinogenic. Methods: In the present study, 16 articles including original and clinical trials about carcinogenic virulence factors of H.pylori were selected. These articles have been chosen via key words containing H, pylori, gastric cancer, virulence factors, and autophagy. Results: According to the results, three main virulence factor of H.pylori are cytotoxin associated gene A (CagA), vacuolating cytotoxin A (VacA), and α -subunit of urease (UreA). In order to initiate its action, H.pylori requires to enter the human host cell through connection of CagA specially EPIYA-D and EPIYA-C types to integrin beta1 (ITGB1) receptor. However, the procedure of entering is taking a place a slight interaction of CagA with the cell surface. So, bacterial adhesions such as BabA, SabA, AlpA/B, HopQ and OipA is important to attach the epithelial cell receptors like Lewis B and Lewis X. VacA have p33 and p55 subunits, and induce to develop the vesicles and vacuoles inside of cells. Anion-selective channels are the consequence of vacuole anastomosis, subsequently, more chloride ions to enter the cell thru these channels. Finally, it make a major ion changes, imbalance in the cell, and cause damages to the cell membrane which eventually leads to the osmotic swelling and cell damage. According to some studies, p33 subunit of VacA is also straight associated with mitochondrial dysfunction. Autophagy is a protection tool of human cells for residual cell homeostasis by limiting toxin inducing in contradiction of any invasive pathogen violence. VacA, CagA, HpGGT, and HP0175 are essential elements to induce autophagy in gastrointestinal epithelial cells through declining the amount of ATP which promotes the AMPK, a type of protein kinase which manages the energy status while opposite a critical situation and cell death. Conclusion: We found CagA, VacA, and UreA have their own specific types, each strain responsible to appear as a specific human disease. In future studies, the main virulence factors of bacteria may be identified and an effective vaccine to prevent gastric cancer may be invented. Keywords: Helicobacter pylori, virulence factors, gastric cancer

Effect of Endophytic bacteria isolated from *Nepeta crispa* on *Candida Glabrata* in laboratory conditions

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نوع پذیرش: پوستر | کد مقاله: G-29643

Abstract: Background: The Mofarah (*Nepeta crispa*) is from the Lamiaceae family, one of the native plants of Iran, which grows around Alvand Mountain in Hamadan province. This plant is used as an anti-bloating, anti-inflammatory and pain reliever. It is also used as a sedative, stomach tonic, and disinfectant to relieve respiratory and digestive disorders. Due to its medicinal properties as well as its aromatic smell, it is used in traditional uses as a flavoring agent in foods and drinks, especially in yogurt and buttermilk. Endophytic bacteria are non-pathogenic microorganisms living in plant tissues that increase plant metabolism, growth and resistance to pathogens and environmental stresses. By producing secondary metabolites, extracellular enzymes and other substances, endophytic microorganisms activate biochemical components and pathways of plant cells. These microorganisms are a new source of bio-chemically active compounds with potential to be used in medical, agricultural and industrial fields. This study was conducted with the aim of investigating the effect of bacterial endophytes isolated from *Nepeta Crispa* on the *Candida glabrata* in Hamadan province. Methods: Samples were collected in spring 1401 from three different regions of Hamadan province. After surface disinfection, plant samples (including roots, stems and leaves) were placed in nutrient agar culture medium. After that, the endophytic bacteria were isolated and their antagonistic effect on human pathogenic fungus (PFCC=52971) *Candida Glabrata* prepared from Pasteur Institute was performed by cross-cultivation method on yeast PDA medium. The experiment was conducted as a completely randomized block design with 3 treatments and one control. Statistical analysis was done using SPSS 20.0 software and comparison of means with Duncan's test at 5% probability level. Results: The result showed that endophytic bacteria had a significant effect on *Candida Glabrata*, so that *Bacillus subtilis* and *Providencia rettgeri* showed the greatest and least effect on this fungus, respectively, and the percentage of inhibition was 50% and 2.2%, respectively. Conclusion: *Bacillus Subtilis* endophytic bacteria can be a promising microorganism for the future as a biological control and antagonist on the pathogenic fungus *Candida Glabrata*.

Study of tetracycline and aminoglycoside resistance genes in *Escherichia coli* from cases of coli bacillosis in broiler flocks of Mazandaran province

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نوع پذیرش: پوستر | کد مقاله: G-08219

Abstract: Background: The infections caused by avian pathogenic *Escherichia coli* in birds are called (local or systemic) colibacillosis. The increase of antibiotic resistance is an important public health issue, and the creation and increase of antibiotic resistance is a complex issue that is caused by several interconnected factors. Since misuse helps spread antibiotic resistance among poultry farms and leads to the emergence of pathogens with multiple drug resistance, it is necessary to investigate antibiotic resistance genes. Materials and Methods: In this study, sterile swab samples were taken from the heart pericardium from 95 broiler chickens in industrial poultry farms in Mazandaran province, and 43 *E. coli* isolates were confirmed by biochemical and microbiological tests. The isolates were detected by PCR method in terms of tetA, aac(3)-IIa, Ant(3)-Ia resistance genes. Results: Of the 43 samples that were confirmed in biochemical tests, 35 samples contained the tetA gene, 24 samples contained the aac(3)-IIa gene, and 27 samples contained the Ant(3)-Ia gene. Conclusion: According to the results of the present study and the investigation of similar studies, the prevalence of resistance genes in the samples of colibacillosis in Mazandaran province is high. Keywords: *Escherichia coli*, broilers, resistance genes, Mazandaran province

Study of Fluorophenicol and Spectinomycin resistance genes in Escherichia coli from cases of coli bacillosis in broiler flocks of Mazandaran province

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نوع پذیرش: پوستر | کد مقاله: G-89531

Abstract: Background: Colibacillosis refers to any localized or systemic infection caused entirely or partly by avian pathogenic Escherichia coli (APEC). Every year, the Colibacillosis causes a lot of financial losses to the poultry industry in the world. The use of antibiotics for the treatment of infections and the use of growth supplements in the diet of broiler and egg-laying chickens has caused a lot of antibiotic resistance. Materials and Methods: In this study, 95 samples of industrial broiler chickens from Mazandaran broiler farms suffering from septicemia with pathological symptoms of pericarditis, perihepatitis, peritonitis and airsacculitis were collected. Samples were taken from the heart pericardium with a sterile swab. Finally, the isolates were detected by PCR method in terms of StCM and aadA2 resistance genes. Results: Of the 43 samples that were confirmed in biochemical tests, 41 samples contained the STCM gene and 41 samples contained the aadA2 gene. Conclusion: According to the results of the present study and the investigation of similar studies, the prevalence of resistance genes in the samples of colibacillosis in Mazandaran province is high. Keywords: Avian Escherichia coli, colibacillosis, Mazandaran province, broiler chicken

The impact of oral microbiota on the regulation of hypertension: A systematic review

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نوع پذیرش: پوستر | کد مقاله: G-57139

Abstract: Background: Hypertension is a chronic and frequent disorder, which can lead to cardiovascular disease, renal complications, and premature death worldwide. The interaction between the microbiota and human health is being recognized and oral microbiota directly affects dental caries and periodontal diseases. In this review, we discuss the impact of oral microbiota on the regulation of hypertension. Materials and Methods: This review article was performed within articles published at PubMed, Science Direct, Google Scholar, SID, and Cochrane until December 2022. The keywords were oral microbiota, hypertension, high blood pressure, and periodontitis. By searching these databases; 55 articles were found, 21 of them by Reading titles and abstracts were removed. 34 articles were selected under the inclusion criteria. Results: Finally, 34 articles were included in the study. Nitric oxide (NO) was fundamental to cardiovascular health and oral microbiota reduced dietary nitrate which was abundant in green leafy vegetables, such as beetroot and spinach to nitrite by the oral microbiota. Rothia species reduced salivary nitrate which could contribute to preventing oral diseases, as well as increasing systemic nitric oxide levels that could improve hypertension. The oral microbiota dysbiosis initiated periodontitis that significantly increased the risk of Atherosclerotic cardiovascular disease (ASCVD) and carotid artery calcification (CAC) in relation to apical and marginal periodontitis, subgingival dysbiotic bacterial species. Tannerella forsythia Treponema denticola and Porphyromonas gingivalis were responsible for severe clinical manifestation of periodontitis and its management could impact on the control of hypertension. The gut microbiota produced short-chain fatty acids (SCFAs) that could modulate blood pressure and vascular responses. Antihypertensive strategies targeting the microbiota, such as prebiotics, probiotics, and postbiotics (e.g., SCFAs), were considered for the treatment of hypertension. The overuse of antibiotics or antiseptic mouthwash especially chlorhexidine solution could eradicate oral microbiota which led to hypertension. Conclusion: It seems that the management of hypertension through the maintenance of the oral microbiota is a promising idea in hypertension and cardiovascular medicine. Keywords: Blood pressure; Hypertension; Oral microbiota; probiotics; periodontitis



Antibacterial resistance, a dangerous bell rings

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نوع پذیرش: پوستر | کد مقاله: G-15870

Abstract:

Antibacterial drugs have been used for decades in humans, animals, and even agriculture since antibiotic chemotherapy introduced. After that, antibiotic-resistance genes transferred between bacteria. Today antibacterial resistance became a global threat to human health. Understanding the molecular mechanisms used by bacteria to resist antimicrobial drugs is critical to detect the global pattern of resistance also for designing new drugs less susceptible to resistance development and novel strategies to combat resistance. On the other side evidence from different studies show that knowledge about antimicrobial resistance in the population is still scarce. It is necessary to educate people and the public to fight against resistance and decrease the consumption of drugs and resistance in society. Keywords:

Effect of *Allium jesdianum* herbal extract on wound healing

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نوع پذیرش: پوستر | کد مقاله: G-16548

Abstract: Background: The treatment of plant extracts as a use for chemicals in medicines and foods according to their placement in it. *Allium Jesdianum* plant, which belongs to the Lilaceae family, is a flowering plant native to Iran, which grows wild in the southwest and west of Iran at 1800-2600 altitude and 50 cm high in the Zagros mountains. This bulbous plant is traditionally used in the treatment of abdominal pain, rheumatism, vomiting, kidney stones, skin reducer, wound healing and cold consumption. The main part of the essential oil of this plant includes sulphide and terpenoid compounds. Antibacterial properties. In a recent study, the effect of the aqueous and methanolic extracts of the red bean plant on a number of pathogenic bacteria was investigated, considering the increase in the resistance of bacteria to antibiotics, the presence of antibacterial agents in plants. Methanolic and aqueous extracts of the plant. *Allium Jesdianum* was prepared in a recent interventional study. One of the important factors that affect the wound healing process is the microbial colonization of the wound. Therefore, a microbial infection may occur, which can lead to impaired wound healing. In the study of Kanso et al., which was related to acute wound healing. (2014) observed that the general absence of normal microbiota in MIC without microbes has a positive effect on the healing process of skin wounds. It was also previously believed that the inability to heal was associated with high microbial levels. In addition, clinical models in small and large animals showed that individual biofilms caused by *Staphylococcus aureus*, *Staphylococcus epidermidis* and *P. aeruginosa*, which directly lead to biofilm formation, delay wound re-epithelialization. Methods: According to the results, the main ingredients of the essential oil of the red bean plant are compounds such as pentacosane, hexadecanoic acid, di-2-propenyl tetrasulfide, dipropyl trisulfide, dimethyl trisulfide. Affected by *Enterococcus faecalis*. (P 0.05). As a result, the largest diameter of the halo of non-growth was seen in *Streptococcus pyogenes* and *Pseudomonas aeruginosa*. The aqueous extract of this plant was effective on all tested bacteria, except for *Enterococcus faecalis* (P(0.05)). In the methanolic extract, it was less effective than the aqueous extract (P(0.05)). Results: The extract of *Allium Jesdianum* plant contains organic sulfur compounds. These organosulfur compounds contain one or more sulfur atoms bonded to carbon, which is the basis of their biological activities, including antimicrobial, antioxidant, antitumor, and antiasthma activities. Conclusion: During this research, one of the advantages of using plant extracts instead of antibiotics is the lack of resistance of bacteria to these compounds. Also, the sulphide compounds of *Allium Jesdianum* plant extract have antibacterial properties, which, when used topically for wound healing, destroy the bacteria at the wound site and speed up its healing. More research should be done on this issue Keywords: *Allium Jesdianum*, Wound healing, Plant, Antibacterial, Herbal extract

Exploring the Bacterial Infections Effects on Spermatogenesis

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نوع پذیرش: پوستر | کد مقاله: G-69032

Abstract: Background: Bacterial contaminations play a troublesome and covered up part in male reproductive disappointment. Distinctive sorts of microbes are regularly able to meddled with regenerative work in both genders and lead to barrenness. In this consider, to advance assess the part of bacterial contaminations in male reproductive. Material and Method: We searched Medline, PubMed, Scopus and Google scholar databases to identify the potentially relevant studies on bacterial infections and their implications in male infertility. Results: All the microorganisms included in this article have negative impacts on the male reproductive function; be that as it may, there's plentiful prove to fault microscopic organisms such as Escherichia coli, Chlamydia trachomatis, Ureaplasma, Mycoplasma and Staphylococcus aureus for decreased richness and disintegration of sperm parameters. More studies are needed to clarify the molecular mechanisms by which different bacteria exert their detrimental effects on male reproductive system. Conclusion: Getting more knowledge into likely components, would altogether encourage the generation of modern, progressed, and compelling cures within the future. In see of all proof, we unequivocally recommend expanding mindfulness among individuals and considering screening programs for patients looking for richness both to dodge transmission and to progress ripeness results among them. Keyword: Spermatogenesis, Fertility, Bacterial Infection

Resistance (PMQR) genes and mutation in gyrA gene in clinical isolates of *Acinetobacter baumannii* isolated from Zahedan teaching hospitals

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نوع پذیرش: پوستر | کد مقاله: G-48379

Abstract: Background: *Acinetobacter baumannii* is an opportunistic pathogen and one of the most important micro-organisms causing nosocomial infections, especially in intensive care units. Quinolones and fluoroquinolones are important antibiotics in the treatment of infections caused by this organism but in recent years, the widespread use of these antibiotics has caused an increase in antibiotic resistance rate among the *Acinetobacter* strains. Mutations in the gyrA gene and the prevalence of plasmid-mediated quinolone resistance (PMQR) genes are among the most important mechanisms of resistance to quinolone and fluoroquinolones. Therefore, the aim of the present study was to determination of the frequency of (PMQR) genes and mutation in gyrA gene in clinical isolates of *Acinetobacter baumannii* isolated from teaching hospitals in Zahedan, the southeast Iran. Materials and methods: In this cross-sectional study, a total of 150 strains of *Acinetobacter* were collected from different clinical samples of patients referred to teaching hospitals in Zahedan during January to October 2020. Identification of *Acinetobacter baumannii* isolates was performed using conventional biochemical tests and finally amplification of the blaOXA-51 gene by polymerase chain reaction (PCR). Antibiotic resistance pattern was determined using agar disc diffusion method for seven antibiotics. The minimum inhibitory concentration (MIC) of ciprofloxacin was determined by E-test method (bioMérieux, France) on Mueller-Hinton agar medium following the CLSI guidelines. Bacterial genomes were extracted after which and the PMQR and gyrA genes in *A. baumannii* isolates were amplified by PCR using specific primers. Mutations in gyrA gene were detected by HinFI restriction fragment length polymorphism (RFLP) of PCR product. Results: According to the results of this study, the antibiotic resistance rates of clinical strains of *Acinetobacter baumannii* were as follow: Nalidixic acid and Ciprofloxacin (93.3%), Norfloxacin (92%), Gemifloxacin (90.6%), Gatifloxacin and Moxifloxacin (89.3%) and Levofloxacin (88%). About 93.3% of the studied strains had MIC \geq 4 μ g/ml for ciprofloxacin antibiotic. qnrA, qepA, qnrD, qnrB and aac (6')-Ib genes were detected in 74.6%, 66%, 56%, 24.6% and 6.6% of the strains respectively. However, qnrC and qnrS genes were not found in our strains. The frequency of mutation in gyrA gene was 88 percent. Conclusion: According to our study, the percentage of resistance to quinolone and fluoroquinolone antibiotics has increased which indicates an increase in the incidence of mutations in the gyrA gene and an increase in the prevalence of plasmid-mediated quinolone resistance (PMQR) genes in clinical isolates of *Acinetobacter baumannii*. Therefore, caution should be taken in the dosage of these antibiotics and antibiotic sensitivity should also be determined before its administration. Keyword:

Rise and spread of Carbapenemase-Producing *Klebsiella pneumoniae* as an emergent challenge in hospitals

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نوع پذیرش: پوستر | کد مقاله: G-94527

Abstract: Background: Bacterial infection is a well-established threat to human health, leading to excessive consumption of antibiotics, and subsequently, resistance of bacterial species to broad-spectrum antibiotics. *Klebsiella pneumoniae* is one of the main causative agents of nosocomial infections, especially in the intensive care units, and has demonstrated high resistance to carbapenems, due to production and release of carbapenemase enzyme. Due to the high risk and severe consequences of these infections, identification of resistance genes and other contributing factors are of utmost importance in their successful treatment and prevention. The aim of this study is to assess the phenotypic and genotypic resistance of *K. pneumoniae* to carbapenems, and investigate the frequency of this type of resistance in a general hospital in Tehran, Iran. Materials and methods: 120 *Klebsiella* strains were collected from different intensive care units (ICU) in the hospital, and underwent biochemical and microscopic identification tests. Afterwards, the Modified Hodge Test (MHT) was used for phenotypic identification of carbapenemase producing isolates, using meropenem disks. Carbapenem-resistant isolates were also subjected to a PCR test to identify the KPC gene that encodes carbapenemase. Results: MHT test results indicated that out of the 120 isolates, 98 (81.6%) and 22 (18.3%) isolates were resistant and sensitive to meropenem respectively. Moreover, the PCR test results indicated that among the resistant isolates, 80% harbored the KPC gene. Conclusion: The results indicate an increase in the prevalence of carbapenem-resistant *Klebsiella*, and their rapid spread among patients, in comparison with earlier reports. This might be considered as a contributing factor to the high mortality rates in the hospital's ICUs. This denotes the importance of antimicrobial resistance assessment as an integral part of treatment strategies in hospitals, to save lives and to prevent the spread of resistant strains. Keywords: Antibiotic Resistance, *Klebsiella pneumoniae*, Carbapenemase, KPC gene, Carbapenem

Distribution assessment of Extended-spectrum beta-lactamases (ESBL) producing clinical isolates of shigella

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نوع پذیرش: پوستر | کد مقاله: G-45786

Abstract: Background: Shigella is known as a major cause of diarrhea and around 70% of all its infections occur in children under the age of 5 years. One of the most concerning aspects of antibiotic resistance is the emergence and widespread distribution of resistance to β -lactam class drugs which is induced by the enzyme β -lactamase. Analyzing the distribution of β -lactamase is essential in optimal antibiotic administration and infection control. The current study evaluates the distribution of Extended-spectrum beta-lactamases (ESBL) producing clinical isolates of shigella in a single health center in Tehran, Iran. Materials and methods: Fifty isolates were identified as shigella using the standard biochemical tests. The production of ESBL was assessed based on the CLSI guideline using ceftazidime and cefotaxime antibiotic discs. In this method, the inhibition zone is evaluated once for the individual antibiotics and once accompanied with clavulanic acid and a $5 \leq$ increase in inhibition zone diameter in the presence of clavulanic acid was considered as proof of ESBL production. Results: Based on the test results, 50 percent (25/50 isolates) were confirmed to be ESBL producing strains. Conclusion: The emergence of ESBL enzymes in shigella strains and isolates can be considered as a global health risk for both developed and developing countries. As β -lactam class drugs are one of the most used antibiotics in Iran, information about the distribution of ESBL strains is vital in effective infection treatment and control. Keywords: Shigella, Extended-spectrum beta-lactamases, Antibiotic resistance, beta-lactamase

Probiotics and treatment of Helicobacter pylori

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نوع پذیرش: پوستر | کد مقاله: G-83562

Abstract: Background: Probiotics, including bacteria and yeast, are live microorganisms that have demonstrated beneficial effects on human health. Recently, probiotic bacteria (Microbiota) are constantly being studied and their applications are also being considered in promising adjuvant treatments for various intestinal diseases. Helicobacter pylori is a Gram-negative, spiralshaped, microaerophilic and neutrophil bacterium that has been associated with gastrointestinal diseases in humans and can lead to chronic gastrointestinal diseases such as dyspepsia, peptic ulcers, gastric adenocarcinoma and MALT lymphoma. Today, the discussion of the positive effect of probiotics in improving the symptoms of gastrointestinal diseases (GID), especially H. pylori infection, has become very hot topic. This narrative, non-systematic review provides an update on the new approaches in the treatment of H. pylori by consuming probiotics. Materials and Methods: We performed an online search on PubMed and Google Scholar and other Web of Science with the keywords: Helicobacter-pylori, Probiotics, gastrointestinal-diseases-treatment, Microbiota, H.pylori-treatment and summarized the recommended and clinically tested probiotics, epidemiology, new treatment challenges in H.pylori infection by consuming probiotics. Results: We retrieved 89 published papers about H. pylori infection and Probiotics from January, 2020 to June, 2022. We found that the most commonly recommended treatment regimen is standard triple therapy (STT), which contains three lines of antibiotics, but in recent years, probiotics and placebos have also been prescribed alongside them. Administration of probiotics such as Lactobacillus plantarum (9.3% success rate), Lactobacillus acidophilus (6.2% success rate), Lactobacillus bulgaricus (5.8% success rate), Lactobacillus gasseri (1.2% success rate), Bifidobacterium longum (2.1% success rate) and Saccharomyces boulardi fungi (11% success rate) and the combination of all (32.5% success rate) in various clinical works has led to reduction of inflammations, acceleration of treatment, positive response to treatment and reduction of antibiotic side effects. However, several studies have shown that probiotics alone are not a suitable solution for the treatment of gastrointestinal infections, especially H. pylori infection, but they reduce the complications caused by the treatment and increase adherence to the treatment regimen, which is a step it will be important in the control and treatment of H. pylori infection. Conclusion: H. pylori is a bacterium with more than 20 pathogenic tools and solutions to resist environmental conditions and antibiotic treatment, which has gradually become a great concern due to the proof of the role of this bacterium in carcinogenesis and its high prevalence in the world. Although the treatment of H. pylori with the use of probiotics does not increase the eradication rate of H. pylori, it reduces the complications caused by the treatment and increases adherence to the treatment regimen. Keywords: Helicobacter-pylori, Helicobacter-pylori-infection, Probiotics, gastrointestinal-diseases-treatment, H.pylori-treatment, Microbiota. Keywords:

Association between Colorectal Cancer and Fusobacterium nucleatum and Bacteroides fragilis Bacteria in Iranian Patients: A Preliminary Study

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نوع پذیرش: پوستر | کد مقاله: G-09245

Abstract: Background: Recent studies have proposed that commensal bacteria might be involved in the development and progression of gastrointestinal disorders such as colorectal cancer (CRC). Therefore, in this study, the relative abundance of Fusobacterium nucleatum, Bacteroides fragilis, Streptococcus bovis/galloyticus, and Enteropathogenic Escherichia coli (EPEC) in CRC tissues, and their association with clinicopathologic characteristics of CRC was investigated in Iranian patients. Moreover, the role of these bacteria in the CRC-associated mutations including PIK3CA, KRAS, and BRAF was studied. Method: To these ends, the noted bacteria were quantified in paired tumors and normal tissue specimens of 30 CRC patients, by TaqMan quantitative Real-Time Polymerase Chain Reaction (qPCR). Next, possible correlations between clinicopathologic factors and mutations in PIK3CA, KRAS, and BRAF genes were analyzed. Results: In studied samples, B. fragilis was the most abundant bacteria that was detected in 66% and 60% of paired tumor and normal samples, respectively. Furthermore, 15% of the B. fragilis-positive patients were infected with Enterotoxigenic B. fragilis (ETBF) in both adenocarcinoma and matched adjacent normal samples. F. nucleatum was also identified in 23% of tumors and 13% of adjacent normal tissue samples. Moreover, the relative abundance of these bacteria determined by $2^{-\Delta CT}$ was significantly higher in CRC samples than in adjacent normal mucosa ($p = 0.05$). On the other hand, our findings indicated that S. galloyticus and EPEC, compared to adjacent normal mucosa, were not prevalent in CRC tissues. Finally, our results revealed a correlation between F. nucleatum-positive patients and the KRAS mutation ($p = 0.02$), while analyses did not show any association between bacteria and mutation in PIK3CA and BRAF genes. Conclusion: The present study is the first report on the analysis of different bacteria in CRC tissue samples of Iranian patients. Our findings revealed that F. nucleatum and B. fragilis might be linked to CRC. However, any link between gut microbiome dysbiosis and CRC remains unknown. Keywords:

Molecular Analysis of Dominant Paranasal Sinus Bacteria in Patients with and without Chronic Rhinosinusitis

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نوع پذیرش: پوستر | کد مقاله: G-52146

Abstract: Background: Recent studies have established the possible role of microbiota in developing various diseases. In this regard, attention has shifted to the evaluation of microbiota changes in the paranasal sinuses and its relationship to chronic rhinosinusitis (CRS), especially CRS with nasal polyposis (CRSwNP). This study aimed to examine the bacterial communities of the sphenoidal sinus in Iranian patients with and without CRS. Materials and Methods: The investigation included 36 subjects, including 18 patients with CRSwNP who underwent Functional Endoscopic Sinus Surgery (FESS) and 18 non-CRS patients who underwent Endoscopic Endonasal Approach (EEA) for pituitary adenoma. The surgeries were performed under general anesthesia, and the sphenoidal sinus was sampled using sterile rayon-tipped swabs coated with a sheet. TaqMan quantitative real-time polymerase chain reaction (qPCR) method (the 16S rDNA gene from bacteria) was used for detection of bacterial communities in different samples. Results: *Staphylococcus haemolyticus* and *Pseudomonas aeruginosa* were significantly more prevalent in CRS patients than non-CRS patients (P -value ≤ 0.05). However, no significant difference in the frequency of *Corynebacterium* spp. and *Staphylococcus aureus* was observed between the two groups, and no *Streptococcus pneumoniae* or *Haemophilus influenzae* species were isolated from any of the samples. Conclusion: The current study's findings indicated a significant difference in the frequency of certain bacterial species in patients with CRS versus non-CRS patients. By establishing a link between microbial burden and CRS, it is possible to develop effective treatments or even prevent disorders in this body area. Keywords:

Detection of resistance to rifampicin and isoniazid in Mycobacterium Tuberculosis isolates by High Resolution Melting (HRM) Real-Time PCR

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نوع پذیرش: پوستر | کد مقاله: G-34108

Abstract: Background: Drug resistance to isoniazid (INH) and rifampin (RIF) as two main drugs of the first line of tuberculosis (TB) treatment in Mycobacterium tuberculosis (Mtb) isolates is increasing due to the excessive use of these drugs. Isoniazid resistance is mainly caused by mutations in the catalase-peroxidase (katG) gene and the mabA-inhA gene regulatory regions, and mutations in the rpoB gene are responsible for RIF resistance. Detection of Mtb drug-resistant isolates by conventional methods is time-consuming. Thus, developing rapid molecular techniques seems vital for detecting drug resistance and preventing the spread of drug-resistant bacteria. Therefore, this study was carried out to evaluate antibiotic susceptibility to RIF and INH in Mtb isolates using High-Resolution Melting Analysis (HRMA). Materials and Methods: 20 rifampin and isoniazid-resistant Mtb isolates were evaluated by standard proportional method from 431 tuberculosis patients who were referred to the Northeast Tuberculosis Reference Laboratory in Mashhad from 2016 to 2018. All drug-resistant Mtb clinical isolates were screened for genetic mutations in rpoB, katG, and promoter region of the inhA gene using PCR and real-time PCR amplification. Then, the presence of mutations in these genes was investigated by the HRMA method Results: HRMA assay identified katG gene mutations and the mabA-inhA promoter region in 15 of 18 isoniazid-resistant samples, and rpoB gene mutations were successfully evaluated in 11 out of 13 RIF-resistant samples. The sensitivity and specificity of the HRMA method were 83.3% and 91% for isoniazid and 84.6% and 85.1% for rifampin, respectively. In this study, 100% of rifampin-resistant samples had mutations in the rifampin resistance determining region (RRDR). Also, 88.8% of isoniazid-resistant samples had mutations in the katG gene and the mabA-inhA promoter region Conclusion: The results of this study showed that HRM assay is a rapid, accurate, and cost-effective method possessing high sensitivity and specificity for determining antibiotic resistance among Mtb clinical isolates, screening of their associated mutations, and preventing the emergence of possible MDR strains. Keywords: Mycobacterium tuberculosis, Drug resistance, HRMA, Isoniazid, Rifampin

Comparison of indirect ELISA and AGP test for the diagnosis of influenza virus H5N1

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نوع پذیرش: پوستر | کد مقاله: G-12496

Abstract: Background: Always a diagnostic technique that is more simple, fast and cost-effective, is preferred for strong clinical monitoring as well as disease diagnosis. Indirect ELISA technique was used in this study is a method that has these features to detect subtypes H5N1. Conventional methods such as agar gel immunodiffusion (AGP) test have problems such as sensitivity and specificity. Moreover, conventional isolation methods for the detection of avian influenza virus are intensive work and time consuming. The most extensive serological methods for detection of antibodies are diffusion in agar gel or AGP and hemagglutinin inhibition (HI) test. The aim of this study was investigating and comparing Indirect ELISA and AGP methods for the diagnosis of H5N1 influenza virus in term of both efficiency and accuracy. Materials and Methods: In this Experimental study, 27 Female Balb/c mice were randomly divided into 3 groups (control, T1 and T2 groups). T1 and T2 groups were infected by subcutaneously injection of H5N1 virus antigen, followed by two booster injections with a 15 days interval. Then blood drawing and serum isolation were performed. Different dilutions of isolated serum were prepared, and then titration of produced polyclonal antibody was determined by indirect ELISA and AGP. Results: The results showed that in low serum dilutions, AGP test was not able to detect viral antigens, while those same low concentrations were identified by ELISA test in high sensitivity. The antibodies produced in serum of immunized mice were significantly high which indicated by Elisa, while results showed by AGP. Comparing immunized mice with control mice demonstrated a significant difference in the amount of produced antibody (P 0.05). Furthermore, the time required to gain outcome in all tests of AGP was much more than that for the ELISA test. Conclusion: It is arising from results that the indirect ELISA test is a much faster and even more accurate test comparing to AGP. The main disadvantage of AGP test is less sensitivity and requiring a long time for the formation of a precipitate. Thus, ELISA can be a reliable test for fast detection of infection which is required in epidemic virus infections such H5N1. Keywords: Indirect ELISA, AGP, H5N1.



چهاردهمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Activity of meropenem-vaborbactam against different beta-lactamase producing *Klebsiella pneumoniae* and *Escherichia coli* isolates in Iran

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نوع پذیرش: پوستر | کد مقاله: G-49305

Abstract: Background: We evaluated the activity of meropenem-vaborbactam against beta-lactamase producing *Klebsiella pneumoniae* and *Escherichia coli*. Materials and Methods: The methods applied in this study are: Antibiotic susceptibility testing, double disk synergy test, modified Hodge test, detection of ESBL, AmpC, carbapenemase genes by PCR, MLST analysis. Results: Our results showed that among *E. coli* and *K. pneumoniae* isolates, 41.1% and 40% of strains produced ESBL, respectively. Additionally, the prevalence of *K. pneumoniae* and *E. coli* producing AmpC was 4% and 45.5%, respectively. 64.2% of *K. pneumoniae* strains and one *E. coli* isolate produced carbapenemase. Conclusion: Based on the phenotypic results of this study, vaborbactam was an effective inhibitor on the third-generation cephalosporins-resistant isolates ($p < 0.0001$). Meropenem-vaborbactam combination had the highest efficacy on KPC producing strains, and it had limited activity on isolates producing OXA-48, whereas no effect was observed on NDM-1 producing isolates. Our study provided valuable information regarding the vaborbactam inhibitory effect on β -lactamase-producing strains. Keywords: Vaborbactam, KPC, ESBL, *K. pneumoniae*, *E. coli*

Microbiological Surveillance of peritoneal dialysis-associated peritonitis and their antimicrobial susceptibility testing profiles: A two-year study in Mashhad, Iran

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نوع پذیرش: بوستر | کد مقاله: G-79356

Abstract: Background: Peritonitis is a common and serious complication in patients on continuous ambulatory peritoneal dialysis (CAPD) and is one of the most important reasons for their treatment failure. Culture-negative peritonitis is a major problem in PD patients that makes their treatment challenging. Bacterial agents are the most common causative agents associated with peritonitis. The aim of this study was to improve the detection of organisms associated-peritonitis in PD patients and evaluation of their antimicrobial susceptibility testing profiles by using the International Society for Peritoneal Dialysis (ISPD) guidelines. Materials and Methods: The present study was performed cross-sectionally for two years (October 2018 to September 2020). A total of 63 samples of peritoneal fluid related to 44 patients with suspected peritonitis were collected. All patients were admitted to the peritoneal dialysis centers of Ghaem and Imam Reza hospitals in Mashhad. For all these samples, cell count, centrifugation, culture (aerobic, anaerobic, and mycobacterial), and Preparation of smear were performed. Then all isolated organisms were identified according to ISPD guidelines by using standard microbiological, biochemical, and molecular methods. Finally, for all positive samples, the antibiotic susceptibility testing was performed by the Kirby Bauer method, according to CLSI (Clinical and Laboratory Standards Institute). Staphylococcus spp. isolates were also evaluated for methicillin resistance. Also, the culture results of the present study were compared with the routine laboratory results. Results: During the study period, one hundred and twenty-four patients used peritoneal dialysis, and thirty-six episodes of peritonitis identified in forty-four patients (among them, 8 cases were had refractory peritonitis). The age of patients was ≥ 12 years and the mean age of PD patients with peritonitis was 46.1 ± 12.6 years, of them, 55% of peritonitis cases were female. According to the results of this study, the majority of peritonitis in PD patients was related to gram-positive cocci such as coagulase-negative staphylococci (57.14%), Staphylococcus aureus (14.28%), Corynebacterium Spp. (2.85%) and alpha-hemolytic streptococci in the viridians group (2.85%). Other less common peritonitis-causing organisms included gram-negative bacilli (Pseudomonas, Escherichia, Enterobacter) (11.4%), Mycobacterium tuberculosis (2.85%), and Candida spp. (5.71%). Nontuberculous mycobacteria (NTMs) as well as obligated anaerobic bacteria were not isolated as a cause of peritonitis. In addition, the rate of methicillin resistance in Staphylococcus isolates was 32%. Furthermore, the results obtained from this study, were compared to those obtained by routine culture identification and susceptibility testing results. There were differences in results of seven samples, and successfully, we were able to isolate and identify the causative agent (Mycobacterium tuberculosis, Corynebacterium aquaticum, Staphylococcus aureus, Staphylococcus epidermidis (2 cases), Streptococcus salivarius and Streptococcus viridans), while the routine laboratory had reported negative. Conclusion: It seems that the major cause of PD-related peritonitis organisms remained Gram-positive cocci. Diagnosis of mycobacterial peritonitis is also very important and requires prompt and appropriate treatment to prevent catheter removal and conversion to permanent hemodialysis. Keywords: Peritoneal dialysis, Peritonitis, Nontuberculous mycobacteria/NTMs, Diagnosis.

Study of antibiotic resistance of Enterobacteriaceae in Mazandaran in 1400-1401.

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نوع پذیرش: پوستر | کد مقاله: G-59067

Abstract: Background: Antibiotic resistances are common in hospitals and society, and the treatment of hospital infections is a big challenge for specialists and patients. Among the problems caused by these types, we can mention septicemia, pneumonia, and bacteremia. In this study, we investigated the antibiotic resistance pattern of Enterobacteriaceae species in one of the hospitals of Mazandaran province. Materials and Methods: From October 1400 to July 1401, samples were obtained from CCU, ICU, emergency, surgery and outpatient departments. The samples were isolated from urine, blood, tracheal tube, wound, sternum, pericardium, pleural, valve and sputum. TSI, McConkey, Urea and IMVIC differential biochemical tests were used to isolate Enterobacteriaceae species. Mueller Hinton agar culture plate (manufactured by Merck company) was used for antibiogram. Antibiotic discs were purchased from Iran PAD TAN TEB company. Antibiogram was done by Kirby-Bauer disc diffusion according to CLSI guidelines. Results: During 10 months 177 samples were obtained, of which 117 were female and 60 were male. The species of Enterobacteriaceae were: E. coli (N=91/51.4%), Klebsiella (N=39/22%), Citrobacter (N=25/14.1%), Enterobacter (N=22/12.4%). Antibiogram results are in the table below. Table: antibiogram results

Organism	Antibiotic	E. coli	Klebsiella	Citrobacter	Enterobacter	S	I	R	S	I	R	S	I	R	CP	50%						
1%	48%	25%	2%	73%	56%	15%	29%	54%	11%	35%	F/M	93%	---	7%	18%	10%	72%	63%	14%	23%	41%	15%
44%	AN	75%	12%	13%	49%	11%	40%	66%	11%	23%	79%	7%	14%	CAZ	30%	---	63%	15%	5%	8%	38%	6%
56%	35%	20%	45%	CFM	30%	3%	67%	22%	---	78%	31%	9%	60%	33%	13%	54%	CRO	35%	1%	64%	18%	2%
80%	29%	15%	56%	55%	14%	31%	GM	74%	7%	19%	21%	9%	70%	42%	14%	44%	64%	---	36%	IPM	24%	6%
70%	15%	---	85%	16%	4%	80%	37%	16%	47%	SXT	35%	4%	61%	24%	---	76%	42%	---	58%	58%	---	42%

ciprofloxacin (CP); nitrofurantoin (F/M); Ceftriaxone (CRO); gentamicin (GM); imipenem (IMP); trimethoprim-sulfamethoxazole (SXT). Our findings showed that imipenem antibiotic had the most resistance and amikacin had the least resistance between the Enterobacteriaceae family. Conclusion: Due to the spread of emerging diseases such as covid and the increase in the use of antibiotics as recommended by specialists or self-treatment, there is a possibility of creating more antibiotic resistance in the future. Enterobacteriaceae family causes hospital infections and may cause the death of patients, therefore, more attention and care should be taken in the treatment of this type of bacteria. Keywords: Enterobacteriaceae, Antibiotics Resistance, Disk diffusion

Investigation of antibiotic susceptibility of Staphylococcus spp. in Sari in 1400-1401.

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نوع پذیرش: پوستر | کد مقاله: G-16384

Abstract: Background: Currently, one of the most important causes of death in the world is the development of antibiotic resistance. Staphylococcus aureus is one of the important cause of infection. This bacterium does not usually pathogen, but if it enters the tissues or blood stream, it can cause an infection. Treatment of drug-resistant S. aureus is one of the challenges of specialists in treating infections. Staphylococcus epidermidis is a coagulase-negative staphylococcus (CNS), which is very important in causing catheter and implant infections. Due to the resistances created in staphylococci and the need to choose the right treatment, in this study we investigated the antibiotic resistances Staphylococcus spp. Materials and Methods From bahman 1400 to aban 1401, 62 samples were obtained from surgery, CCU, ICU, emergency, and outpatient departments. In order to identify Staphylococcus species, biochemical tests related to gram positives were performed. The seven antibiotics used in this study are as follow: vancomycin, erythromycin penicillin, ampicillin, novobiocin, oxacillin and cefoxitin. Antibiotic discs were purchased from Iran PAD TAN TEB company. Mueller Hinton agar culture plate (manufactured by Merck company) was used for antibiotic susceptibility test. Antibiogram was done by kirby bauer disc diffusion according to CLSI Guidances. Results After 10 months of sampling, a total of 62 Staphylococcus samples were collected, of which 41 samples were related to S. aureus and 21 samples were related to cuagolase negative staphylococci(CNS). Most of the S. aureus were obtained from women (58.5%) and most of the CNS isolated from men (57.1%). Antibiogram results are given in the table below. Table: antibiogram results

Organism	Antibiotic	S (%)	I + R (%)	S (%)	I + R (%)
S. aureus N=41(66.1%)	vancomycin	100	0	90	10
CNS N=21(33.9%)	erythromycin	0	100	0	100
	penicillin	0	100	0	100
	ampicillin	8	92	14	86
	novobiocin	100	0	100	0
	oxacillin	53	47	35	65
	cefoxitin	69	31	53	47

Conclusion According to the findings of our study, the best antibiotics to eliminate staphylococcus species in laboratory conditions are novobicin and vancomycin. Due to antibiotic resistance, specialists should be more careful and attentive in prescribing antibiotics

Keywords: Staphylococcus, Antibiotics Resistance, Disk diffusion

Frequency of *Helicobacter pylori* Stool Antigen and Anti-*H. pylori* IgM and IgA Antibodies in Gastritis Suspected Patients in Sari, during 2021-2022

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Background: *Helicobacter pylori* is a gram negative microaerophilic bacilli with a global prevalence. *H. pylori* can cause some intestinal diseases like chronic gastritis, peptic ulcer, duodenal ulcer and gastric cancer. The aim of the study was to evaluate the *Helicobacter pylori* stool antigen concentration and also serum concentration of anti-*H. pylori* IgM and IgA antibodies in gastritis suspected patients.

Materials and Methods: In a cross-sectional study, 2892 specimens (blood=1071, stool=1821) were collected from suspected patients and concentration of *Helicobacter pylori* stool antigen and serum concentration of anti-*H. pylori* IgM and IgA were determined by Enzyme-linked immunosorbent assay (ELISA). Participants were categorized based on their age group, gender, serum anti-*H. pylori* IgM and IgA and *Helicobacter pylori* stool antigen.

Results: The total of 2892 gastritis suspected patients (1753 females and 1139 males) with age-baseline of 41.89 years were included in this study. According to the data analysis, relative frequency of *Helicobacter pylori* stool antigen, anti-*H. pylori* IgM and IgA positive samples in considered population was 25.1%, 7.1%, 24.05%, respectively. There was no significance difference between female and male in frequency of positive results in each test (stool antigen test; female: 25.02%, male: 25.22%, anti-*H. pylori* IgM; female: 7.46%, male: 6.75%, anti-*H. pylori* IgA; female: 25.82%, male: 21.88%).

Conclusions: Regarding to importance of *Helicobacter pylori* infection and its ability in causing dysfunctions and disease such as gastritis, peptic ulcer and gastric cancer, it seems screening for this infection is necessary. In our population, there was not significance difference between female and male and also different ages in frequency of positive results, so screening for anti-*H. pylori* IgM and IgA and stool antigen is recommended for all genders and age groups.

Keywords: *Helicobacter pylori*, Stool antigen test, Serum IgM, Serum IgA, Gastritis



چهاردهمین کنفرانس بین المللی آزمایشگاه و باالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Prevalence of ESBL-Producing Enterobacter Species Resistant to Carbapenems in Iran

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نوع پذیرش: پوستر | کد مقاله: G-57148

Abstract: Background: Carbapenems are the last-line therapy for multidrug-resistant (MDR) infections caused by Enterobacterales, including those caused by Enterobacter species. However, the recent emergence of carbapenem-resistant (CR) and extended-spectrum β -lactamase (ESBL)-producing Enterobacteriaceae pathogens, which are resistant to nearly all antibiotics, has raised concerns among international healthcare organizations. Hence, because there is no comprehensive data in Iran, the current study aimed to evaluate the prevalence of antibiotic resistance among Enterobacter species, especially CR and ESBL-producing strains, in Iran. Materials and Methods: • e literature search was performed up to June 21, 2021, in national and international databases using MeSH extracted keywords, i.e., Enterobacter, antibiotic resistance, carbapenem, ESBL, and Iran. Study selection was done based on the predefined inclusion and exclusion criteria, and data analysis was carried out using the Comprehensive Meta-Analysis (CMA) software. Results: • e pooled prevalence of Enterobacter species resistant to various antibiotics is as follows: imipenem 16.6%, meropenem 16.2%, aztreonam 40.9%, cipro-oxacin 35.3%, nor-oxacin 31%, levo-oxacin 48%, gentamicin 42.1%, amikacin 30.3%, tobramycin 37.2%, tetracycline 50.1%, chloramphenicol 25.7%, trimethoprim/sulfamethoxazole 52%, nalidixic acid 49.1%, nitrofurantoin 43%, ceftriaxone 49.3%, ceftazidime 47.9%, ceftazidime/avibactam 52.4%, cefotaxime 52.7%, ceftazidime 47.9%, cefepime 43.6%, and ceftizoxime 45.5%. • e prevalence rates of MDR and ESBL-producing Enterobacter species in Iran were 63.1% and 32.8%, respectively. Conclusion: In accordance with the warning of international organizations, our results revealed a high prevalence of ESBL-producing Enterobacter species in Iran, which is probably associated with the high prevalence of Enterobacter species resistant to most of the assessed antibiotics, especially MDR strains. However, the resistance rate to carbapenems was relatively low, and these drugs can still be considered as drugs of choice for the treatment of Enterobacter infections in Iran. Nevertheless, continuous monitoring of drug resistance along with antibiotic therapy based on the local data and evaluation of the therapeutic efficacy of new antibiotics or combination therapeutic strategies, such as ceftazidime/avibactam, meropenem/vaborbactam, plazomicin, and eravacycline, is recommended. Keywords:



چهاردهمین کنفرانس بین المللی آزمایشگاه و باالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Evaluating the effectiveness of Chlorhexidine on Gram-positive and Gram-negative bacteria in Iran: a systematic review

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نوع پذیرش: پوستر | کد مقاله: G-50248

Abstract: Background: Chlorhexidine is a highly effective, broad-spectrum antimicrobial agent available as a mouthwash, gel, spray, root canal rinse, and periodontal chips. Different results of the effectiveness of this substance have been reported in the studies, hence the aim of this survey is a systematic review of the studies conducted on the minimum inhibitory concentration (MIC) of chlorhexidine on Gram-positive and Gram-negative bacteria isolated in health care centers in Iran. Materials and Methods: The data of this systemic review study were searched from international database including EMBASE, Scopus, PubMed/Medline and Cochrane library using appropriate English keywords until October 2022 and after filtering based on inclusion and exclusion criteria, 12 articles entered our study. Results: Out of a total 12 articles, 7 studies were conducted on Gram-positive bacteria, 4 studies were conducted on Gram-negative bacteria and 1 study was assessed on both groups. Most studies have been done on *Staphylococcus aureus* and *Pseudomonas aeruginosa*. The lowest and admissible MIC was 0.5 µg/mL and on the flip side the highest was 625 µg/mL. Conclusion: Based on our analysis, antibacterial activity of chlorhexidine against Gram-negative and positive bacteria was discouraging. However, further clinical studies are necessitated to provide clinical evidence to support these observations. Keywords:

The microbiota as an optional treatment to prevent the negative consequences of smoking: A systematic review

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نوع پذیرش: پوستر | کد مقاله: G-92108

Abstract: Background: Cigarette smoking is a preventable cause of mortality. Tobacco smoke increases the risk of many diseases linked to the oral cavity, inflammation pathway, gastrointestinal, cardiovascular system, and cancer. Microbiota interacts with the immune system and plays a crucial role in preserving human physiological homeostasis. In this review, we discuss microbiota as an optional treatment to prevent the negative consequences of smoking. Materials and Methods: This review article was performed within articles published at PubMed, Science Direct, Google Scholar, and Cochrane until January 2023. The keywords were microbiota, gut microbiome, and cigarette smoking. By searching these databases; 58 articles were found, and 11 of them by reading titles and abstracts were removed. 40 articles were selected under the inclusion criteria. Results: Finally, 40 articles included in this study. Smoking raised potentially pathogenic species while decreasing some beneficial flora. For instance, the abundance of oral microbiota such as Bacteroidetes (constitutes 25% of all gut microbiota), Proteobacteria (at phylum), Streptococcus sanguinis, Streptococcus, Actinobacillus, and Haemophilus (at species) reduced in the smoker, while Moryella, Bulleidia, Moraxella, Rothia dentocariosa, Prevotella melaninogenica, and Bulleidia moorei were increased. In the airway, enrichment of some harmful species like Veillonella, Megasphaera, Streptococcus pneumoniae, Haemophilus influenzae, Moraxella catarrhalis, Fusobacterium, and Streptococcus pyogenes was observed in a smoker rather than a nonsmoker. In addition, compared to non-smokers, smokers had a reduction in vaginal Lactobacillus spp. Cigarettes could affect the oral microbiome by suppressing the immune response, hypoxia, and biofilm development. Also, the enzyme activity related to amino acid production and metabolism of amino sugars and nucleotide sugar was accelerated by smoking. The lung microbiome varies in number and taxa as a result of tobacco smoke's suppression of innate immune systems, which triggers unfavorable inflammatory reactions. Dysbiosis in the gut microbiome would be associated with toxic compounds such as nicotine, volatile organic compounds (such as benzene), acetaldehyde, polycyclic aromatic hydrocarbons, heavy metals, and toxic gases. Decreased insulin and leptin levels through glucose-lipid metabolic disorders were seen in smokers. Smoking cigarettes would disrupt the balance of bile acids and cholesterol metabolism, alter the diversity of the gut microbiota, and lead to hepatic metabolic dysfunction. Glycerophospholipids were one of the metabolites that had mediated shifts in bacterial taxa. Some research demonstrated that smokers' vaginal secretions contain benzopyrene diol epoxide (BPDE), which could boost the induction of bacteriophages in Lactobacillus and put women at risk for bacterial vaginosis. Steering probiotics through a diet rich in prebiotics and probiotics could be a strategy to confer a health benefit for smokers. Lactobacillus plantarum as a dietary supplement could be helpful in protecting against cardiovascular disease. Fecal microbiota transplant (FMT) was another option that would alter the smoker's gut bacteria profile. Conclusion: Decrease bacterial diversity and microbial consortia alterations in smokers may account for smoking-related disease. It seems that modulation of the microbiota may become a potential therapeutic option for preventing smoking's ramifications. However, further research needs to be done on this topic. Keywords: Oral microbiota, Gut microbiome, Cigarette smoking, Probiotics

Antimicrobial and antioxidant potential of silver-modified ZnO nanoparticles synthesized by the eco-friendly method using *Launaea acanthodes* extract

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نوع پذیرش: پوستر | کد مقاله: G-53680

Abstract: Background: Today, the emergence of pathogenic and antibiotic-resistant bacteria has become one of the major health problems worldwide. In the present study, the synthesis of silver-modified ZnO nanoparticles (ZnO-Ag) using *Launaea acanthodes* (*L. acanthodes*) extract (ZnO-Ag@LA) was investigated and its antibacterial and antioxidant properties were investigated. Methods and Materials: The structure and properties of the ZnO-Ag@LA were investigated by X-ray diffraction (XRD), dynamic light scattering (DLS) and Fourier-transform infrared spectroscopy (FT-IR). Broth microdilution method was used to evaluate the antibacterial properties of the ZnO-Ag@LA. Also, the antioxidant properties of nanoparticles were measured by DPPH method. Results: XRD test results showed that the nanoparticles were well formed and ZnO-Ag@LA was pure. DLS analysis also showed that ZnO-Ag@LA have a hydrodynamic diameter of about 60 to 80 nm. The results of FT-IR analysis also showed that the functional groups in *L. acanthodes* extract are responsible for the formation of ZnO-Ag@LA. The antibacterial results showed that the ZnO-Ag@LA have strong antibacterial properties against *Escherichia coli* (MIC = 235 µg / ml) and *Staphylococcus aureus* (MIC = 470 µg / ml). The antioxidant properties of nanoparticles also showed that the ZnO-Ag@LA have good antioxidant properties. Conclusion: Overall, the present study was able to provide a promising, environmentally friendly and easy way to synthesize substances with antibacterial and antioxidant properties. Keywords:



چهارمین کنفرانس بین المللی آزمایشگاه و بائین

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Prevalence and characterization of toxin profiles of *Clostridium perfringens* isolates from infants and children in Iran

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نوع پذیرش: پوستر | کد مقاله: G-53768

Abstract: Background: *Clostridium perfringens* is a bacterial pathogen of humans and livestock, which can produce several toxins causing histotoxic diseases and gastrointestinal illnesses when are present inside the gut. Here, we investigated the prevalence and toxin profiles of *C. perfringens* isolates from Iranian infants and children with gastrointestinal symptoms. Materials and Methods: A total of 185 fresh stool specimens were collected from hospitalized and outpatient infants and children aged from 2 days to 16 years who referred to Bahrami Children's Hospital. Samples were cultured on egg yolk agar supplemented with 10% sheep blood and neomycin (0.008 mg/200 ml), and incubated at 37°C for 48 h under an anaerobic atmosphere (85% N₂, 10% CO₂ and 5% H₂) generated by Anoxomat® Gas Exchange System. The presence of toxin genes including *cpa*, *cpb*, *cpb2*, *etx*, *iap*, *cpe* and *netB* was examined by PCR. Results: Overall, *C. perfringens* was isolated from 32.4% (60/185) of the diarrheal subjects. Higher rate of colonization (53%) was observed among infants aged 1-3 years. All isolates carried *cpa* gene encoding alpha toxin typed as toxinotype A, and only 10% (6/60) were *cpe*-positive typed as toxinotype F. No isolates carried the other toxin genes over-mentioned. Conclusion: This study demonstrates that the majority of *C. perfringens* isolates from feces of Iranian infants and children were classified as toxinotype A, and a relatively low number of the isolates were classified as toxinotype F. The high prevalence of *C. perfringens* isolates among diarrheal infants and children suggests the clinical importance of this bacterial pathogen as an etiologic agent in this susceptible age group in Iran. Keywords: *Clostridium perfringens*, toxin profile, infants, children, diarrhea

Inhibitory effect of pyocyanin pigment of *Pseudomonas aeruginosa* on *Candida albicans* in vitro

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نوع پذیرش: پوستر | کد مقاله: G-30197

Abstract:

C of skin and mucosal infections. Antibiotic treatments for this funguandida albicans as an opportunistic pathogen can cause a wide ranges have several side effects that cause drug resistance. In this study, the inhibitory effect of pyocyanin pigment extracted from *Pseudomonas aeruginosa* on the growth of *Candida albicans* was investigated. In this experimental study, pyocyanin peptide was extracted from *Pseudomonas* and its effect on *Candida albicans* by minimum inhibitory concentration and minimum fungicidal concentration to evaluate the antifungal effects of this substance on *Candida albicans* in the laboratory. By studying different concentrations of pyocyanin pigment, it was shown that *Candida albicans* did not grow at concentrations of 40000-20000-10000-5000ug/ml and in the wells after these concentrations, growth of *Candida* strain was observed. Based on the results of this study, a certain concentration of pyocyanin can have an inhibitory effect on the growth of *Candida albicans* and prevent its growth; therefore, further experiments are needed to investigate the composition of this substance and its wider use in therapeutic cases. Keywords:

Detection of blaVIM gene in Pseudomonas aeruginosa strains isolated from hospitalized patients

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نوع پذیرش: پوستر | کد مقاله: G-93705

Abstract: Background: Pseudomonas aeruginosa is one of the main pathogens of hospital infections. Treatment of infections caused by Pseudomonas aeruginosa has caused many problems for patients due to the high resistance. Reports worldwide emphasize beta-lactam resistance in recent years. This research was conducted with the aim of determining the pattern of drug resistance and identifying the metallobeta-lactamase blaVIM gene of Pseudomonas aeruginosa. Materials and Methods: In this study, 130 bacterial isolates were collected from hospitalized patients during 10 months. For all metallobeta-lactamase producing strains, the antibiotic resistance pattern was performed using disk diffusion method, according to the CLSI protocol. CDDT method (imipenem-imipenem+EDTA) was used to detect metallobeta-lactamase and PCR methods were used to identify metallobeta-lactamase gene blaVIM. Results: Out of 130 isolates of Pseudomonas aeruginosa, 98 isolates were resistant to imipenem. Using the CDDT method, 61 isolates were detected with metallobeta-lactamase, of which 27 isolates contained the blaVIM gene. Conclusion: The results of this study showed that a large percentage of Pseudomonas aeruginosa strains produce metallobeta-lactamase. Therefore, according to the research, it is necessary to identify strains containing metallobeta-lactamase for better control and treatment of patients. Keywords: Pseudomonas aeruginosa, VIM gene, antibiotic resistance



چهاردهمین گنگره بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Antimicrobial resistance and COVID-19

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نوع پذیرش: پوستر | کد مقاله: G-29538

Abstract: Background Antimicrobial resistance (AMR) is a similar cross-cutting challenge that has received international attention since 2015 and has already been identified as a global public health priority for 2020. The Coronavirus Disease 2019 (COVID-19) pandemic helps explain the potential long-term effects of AMR. In this review, we discuss the relationship between antimicrobial resistance and COVID-19. Material and Methods: This review article was performed within articles published at PubMed, Science Direct and Google Scholar, until January 2023. The keywords were Antimicrobial resistance, COVID-19, and Infection prevention control (IPC). By searching these databases; 82 articles were found, 67 of them by Reading titles and abstracts were removed. 15 articles were selected under the inclusion criteria. Result: Finally, 15 Articles included in this study. To help the AMR research community it should be understood the mechanisms of SARS-CoV-2 transmission, its interactions with other diseases, policy responses to COVID-19 worldwide, behaviors related to COVID-19 interventions, and the direct and indirect effects of COVID. The occurrence of AMR in a population was determined by three factors: Origin, transmission and burden of infection at the population level. The emergence of antimicrobial resistance could be driven by selective pressure on human, animal or environmental microbial populations. COVID-19 pandemic was a reminder of the importance of adherence to infection prevention control (IPC) measures to ensure the safety of hospitalized patients. Most of the IPC measured essential to contain the spread of SARS-CoV-2 also helped to reduce the spread of antibiotic-resistant bacteria. Conclusion It appears that reducing the usage of existing antibiotics to treat severe COVID-19 can slow AMR. Understanding how COVID-19 is impacting AMR trends, and what to expect if these trends remain the same or worsen, is the next step in combating AMR. Keywords Antimicrobial resistance (AMR), COVID-19, Infection prevention control (IPC)

Effects of azithromycin (AZT) and extracellular vesicles derived from mesenchymal stem cells (MSC-EVs) injection on the bacterial clearance in a mouse model of sepsis

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نوع پذیرش: پوستر | کد مقاله: G-41863

Abstract: Background: Studies showed that azithromycin (AZT) have the ability to reduce the colony forming units (CFU) of certain bacteria, despite its effects on the bacterial clearance is not as extensively as the broad spectrum antibiotics. However, since extracellular vesicles derived from mesenchymal stem cells (MSC-EVs) are not antibiotics in nature but have immunomodulatory activities, it is intriguing to investigate the effects of concomitant administration of these two agents in a mouse cecal ligation and puncture (CLP) model of sepsis. Materials and Methods: C57BL/6 female mice were randomly divided into the sham group, the cecal ligation and puncture (CLP) group, the AZT group, the MSC-EVs group, and the AZT+MSC-EVs group. The CLP group underwent abdominal surgery and received sterile saline via intravenous injection (i.v.), the AZT group received 100 mg/kg AZT via intraperitoneal injection (i.p.), the MSC-EVs group received 200 mg/kg of MSC-EVs via i.v. injection, and the AZT+MSC-EVs group received i.p. injection of 100 mg/kg of AZT and a tail vein injection of 200 mg/kg of MSC-EVs. After 24 hours, mice were euthanized by exsanguination under anesthesia. One milliliter (ml) of cold sterile saline was injected into the peritoneal cavity of mice with a insulin syringe and the peritoneal lavage was collected. Peritoneal lavage of each mice were cultured on trypticase soy agar (TSA) in a totally sterile conditions. The plates were put into a microbial incubator with 37 degree centigrade temperature for 24 hours. After 24 hours, the plates were investigated. Results: All treatment groups including AZT group, MSC-EVs group, and AZT+MSC-EVs group, showed significant reduction in the colony forming units per ml (CFU/ml) of bacteria. Conclusion: The co-administration of AZT and MSC-EVs with the dose of 100 mg/kg and 200 mg/kg, respectively, can be effective in the clearance of bacteria which is probably due to the influence of AZT as an antibiotic. Keywords: Extracellular Vesicles, Exosomes, Mesenchymal stem cells, Sepsis, CFU



چهاردهمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Examining the anti-bacterial, anti-viral, anti-fungal and anti-parasitic effect of species of scutellaria

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نوع پذیرش: پوستر | کد مقاله: G-52736

Abstract: Background: Indiscriminate use of antibiotics has led to the creation of multi-drug resistant pathogens that cause various infectious diseases. Currently, medicinal plants are considered as an important source of new treatments against multi-drug resistant pathogens. Plant extracts and their secondary metabolites are known to have significant potential to combat infectious diseases. The purpose of this study is to investigate the antimicrobial effect of different species of Scutellaria plant. Methods: The methods of selecting references for this review by searching the websites and banks of Pubmed, Iranmed, Scopus, Google scholar and Cochrane with the keywords of the compounds "scutellaria", "antibacterial", "antifungal", "antiviral" and their English equivalents have been done without a time limit, and all the found articles that were recognized according to the purpose of the study were used. Results: The results of this study showed the antimicrobial properties of Scutellaria species. Plant extracts of Scutellaria species and their secondary metabolites such as quinones, alkaloids, lectins, polypeptides, flavonoids, terpenoids and tannins have significant potential to combat infectious diseases caused by bacteria, viruses, parasites and fungi. Without any known side effects. Discussion: The results of this study showed the importance and therapeutic potential of Scutellaria species. But more detailed studies may be useful to discover more compounds responsible for this activity. Due to the increase in resistance to antimicrobials and the slow pace of new discoveries, the fight against infectious diseases has become more difficult today. Studies on plant extracts or compounds are important to discover new sources as antimicrobial agents. The results of the research show that the essential oils have been investigated in only a few species of Scutellaria, which is very limited. I hope that more activities will be done in this regard. Keywords: Antimicrobial, Scutellaria species



چهاردهمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Extended Spectrum β -lactamase Production in Uropathogenic Escherichia coli

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نوع پذیرش: پوستر | کد مقاله: G-96804

Abstract: Background: The increasing use of beta-lactam antimicrobials in the treatment of bacterial infections has led to an increase in resistance against them. One of the problems in the treatment of nosocomial infections is enzyme resistance to extended-spectrum beta-lactamases (ESBL) among clinical isolates, especially Escherichia coli. The present study was conducted with the aim of investigating the antimicrobial patterns of uropathogenic Escherichia coli. Materials and Methods: In this research, 100 strains of Escherichia coli were confirmed by biochemical tests. In the next step, a sensitivity test was performed for 5 selected antibiotics. Then, ESBL-producing strains were identified using the combined disk method. Results: The results of the phenotypic tests showed that 39 (39%) of the 100 Escherichia coli strains were ESBL producing strains. Conclusion: The present study shows that Escherichia coli strains producing beta-lactam are increasing. In order to prescribe the right medicine and prevent their increasing resistance, it is necessary to adequately identify these strains. Keywords: ESBL; imipenem; UPEC; MDR



چهاردهمین گنگره بین المللی آزمایشگاه و باالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Antibiotics in Klebsiella pneumoniae strains

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نوع پذیرش: پوسنر | کد مقاله: G-89435

Abstract: Background: Integrons are one of the mobile genetic elements that can carry resistance genes to different antibiotics. Meanwhile, the role of class I integron is important in creating and transmitting antibiotic resistance. The purpose of this study is to isolate Escherichia coli strains, molecular investigation of class I integron and gene cassettes and determine antibiotic resistance and sensitivity. Materials and Methods: This study was conducted on 100 samples of Klebsiella pneumoniae isolated from Khorramabad hospitals. After sampling and culture on specific media and DNA extraction, the presence of class I integron gene and aadB cassette was done by PCR method. Antibiotic sensitivity and resistance test was also done by disk diffusion method. Results: After examining 100 strains, 60 samples were resistant to all antibiotics and 78 samples had multiple antibiotic resistance. The highest resistance was related to ticarcillin and cefepime antibiotics, the lowest resistance was related to gentamicin and amikacin antibiotics. Out of 100 samples of Klebsiella pneumoniae, 48 samples had int1 gene and also out of 34 positive integron samples, 23 samples had aadB cassette. Conclusion: isolates and its relationship with the pattern of multiple drug resistance, it can be concluded that these elements can play an important role in the creation and transmission of antibiotic resistance. Keywords: Class I integron, antibiotic resistance, Klebsiella pneumoniae, gene cassette

آدرس دبیرخانه:

تهران، خیابان کارگر شمالی، روبروی مرکز قلب تهران،
کوچه دانش ثانی، بعد از تقاطع صالحی، پلاک ۱۵، واحد ۲

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Association between Serum Liver Enzymes and Metabolic Syndrome in Patients with Prediabetes and Type 2 Diabetes in population from Hoveyzeh cohort study: A case-control study in Iran

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نوع پذیرش: پوستر | کد مقاله: G-30928

Abstract: Background: Prediabetes and type 2 diabetes (T2DM) are common metabolic syndrome (MetS) manifestations. Although there are no clear biological explanations for the relationships between liver indicators and glucose metabolism, one possible mechanism is that MetS and T2DM increase the risk of liver damage, increasing liver enzyme levels. Therefore, the aim of this study was to investigate the association between MetS and alanine aminotransferase (ALT), aspartate aminotransferase (AST), and γ -glutamyltransferase (GGT) in pre-diabetic and T2DM patients in the Persian cohort compared to a control group. Materials and Methods: In this cross-sectional study, 2,259 pre-diabetes, 1,664 T2DM and 5,840 controls (age 35-70 years) who were selected from the Hoveyzeh cohort center were examined. Body mass index (BMI), blood pressure (BP), fasting blood glucose (FBG), and liver enzymes: GGT, ALT, and AST were determined using the standard protocols. MetS subjects were also identified based on the National Cholesterol Education Program guidelines. Results: Prediabetes and T2DM were closely correlated with MetS, and liver enzymes (ALT, GGT, ALT/AST). MetS increases the risk of T2DM by 12.45 [95% CI: 10.88-14.24] fold, while an increase in ALT/AST ratio increases the risk of T2DM by 3.68 [95% CI: 3.159-4.154] fold. ROC curve analysis also revealed the diagnostic roles of GGT, ALT, AST, and the ALT/AST ratio among pre-diabetics, diabetics, and the control group. In correlation analysis, GGT and ALT were positively associated with FBG, BMI, and BP. Conclusions: Our results indicated a significant increase in liver enzymes and MetS status in both pre-diabetic and T2DM subjects, with the differences being more pronounced in diabetic individuals. Consequently, these variables may be considered as diagnostic factors for the early detection of diabetes. However, more research is needed to confirm these results. Keywords:

Effect of metformin on Covid-19 severity in type 2 diabetic patients with a focus on laboratory results

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Background: In the terrifying pandemic caused by SARS-CoV-2, diabetic patients exhibit more severe outcomes, and mortality rates are high among them. Based on recent studies, metformin as the most prescribed drug for T2DM treatment may improve severe outcomes in diabetic patients infected with SARS-CoV-2. On the other hand, abnormal laboratory findings can help to differentiate between the severe and non-severe form of Covid-19. According to the mentioned issues, the effect of metformin on severity of Covid-19 was investigated in T2DM patients with SARS-CoV-2 infection. **Materials and Methods:** The study included 84 individuals diagnosed with COVID-19, 54 patients were diabetic and

divided into two groups according to their anti-diabetic drugs: patients who were treated only with metformin and patients who treated with other anti-diabetic drugs. Other participants were non-diabetic and diagnosed with Covid-19. Biochemical parameters were measured by routine laboratory methods before, during and after SARS-CoV-2 infection. **Results:** During infection, FBS, creatinine, ALT, AST, Ferritin and LDH were significantly lower in metformin-users than non-users (*P-value*: 0.02, 0.01, 0.03, 0.04, 0.0009, and 0.01 respectively). Also, after recovery, there were statistically significant differences between metformin users and non-users with respect to most of the study parameters, except FBS, BUN, and ALP (*P-value*: 0.51, 0.28, and 0.35 respectively). Interestingly, LDH increased during infection in all subgroups (*P-value*: 0.006 for metformin users, 0.0009 for non-users, and 0.04 for people without T2DM). There was also a significant decrease in LDH level after recovery in metformin consumers and healthy people (*P-value*: 0.03 and 0.016 respectively). In metformin users and individuals without T2DM, ferritin levels were higher than before infection (*P-value*: 0.009, 0.008 respectively) and decreased after recovery (*P-value*: 0.03, 0.006 respectively). **Conclusion:** The current study revealed that metformin may be associated with improved Covid-19 outcomes in patients with T2DM. Nevertheless, more research with larger sample size is required to prove the protective effect of metformin against SARS-CoV-2 infection. **Keywords:** Covid-19, T2DM, Metformin



چهاردهمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Association between Serum Liver Enzymes and lipid profile in Patients with Prediabetes and Type 2 Diabetes in population from Hoveyzeh cohort study: A case-control study in Iran

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نوع پذیرش: پوستر | کد مقاله: G-37524

Abstract: Background: Dyslipidemia is significant risk factors for type 2 diabetes (T2DM). on the other hand, some studies have linked serum concentrations of liver enzymes, such as alanine aminotransferase (ALT), aspartate aminotransferase (AST), and γ -glutamyltransferase (GGT), to T2DM, and dyslipidemia. Therefore, the aim of this study was to investigate the relationship between liver enzymes and lipid profiles in pre-diabetic and T2DM patients in the Iranian group compared to the control group. Materials and Methods: In this cross-sectional study, 2,259 pre-diabetes, 1,664 T2DM and 5,840 controls (age 35-70 years) who were selected from the Hoveyzeh cohort center were examined. Fasting blood glucose (FBG), total cholesterol (TC), high-density lipoprotein cholesterol (HDL-C), triglyceride (TG), and liver enzymes: GGT, ALT, and AST were determined using the standard protocols. Results: Prediabetes and T2DM patients had significantly higher FBG, TC, TG, ALT and GGT, while HDL-C was significantly lower in these patients. ROC curve analysis also revealed the diagnostic roles of GGT, ALT, and the ALT/AST ratio among pre-diabetics, diabetics, and the control group. Elevated ALT/AST ratio increases the risk of T2DM by 3.68 [95% CI: 3.159-4.154] fold. In correlation analysis, GGT and ALT were positively associated with FBG, TC, and TG and negatively associated with HDL-c. Conclusions: Our results indicated that the higher levels of ALT, GGT and lipid profile may be considered as diagnostic factors for the early detection of diabetes. However, further studies are needed to confirm the significance of these findings. Keywords: Liver enzymes, lipid profile, T2DM, Hoveyzeh, Persian cohort.



چهاردهمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Rutin exerts anti-inflammatory and nephroprotective effects against paraquat-induced renal injury in male rats

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نوع پذیرش: پوستر | کد مقاله: G-72108

Abstract: Background: Paraquat refers to one of the key herbicides, intoxication with which causing renal damage. Rutin is a flavonoid with antioxidant properties. The present study was aimed at investigating the effect of paraquat on serum parameters of kidney function included Cr (creatinine) and Urea as well as IL-1 β gene expression in rats with paraquat-induced nephrotoxicity. Materials and Methods: The current study randomly divided 32 male Wistar rats weighing 200-250 g into four groups. The first group was the control; the second just received paraquat at a dose of 50 mg per kilogram of body weight; the third group just received rutin at a dose of 100 mg per kilogram of body weight; and the fourth group received rutin at a dose of 100 mg per kilogram of body weight besides paraquat at a dose of 50 mg per kilogram of body weight. The level of Cr (creatinine) and Urea, as well as the IL-1 β gene expression level were checked 14 days after the test. Results: According to the results, oral administration of paraquat for 14 days resulted in a significant increase. Conclusion: Keywords:

Effect of Humulus lupulus on serum biochemical parameters in carbon tetrachloride-induced acute renal injury in rats

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نوع پذیرش: پوستر | کد مقاله: G-20386

Abstract: Background: Renal diseases are one of the most common health problem in the world. In recent years, herbal medicines have the potential to treat a wide range of diseases. The purpose of this research is to investigate the protective effects of Humulus lupulus (hop) extract on renal damage caused by carbon tetrachloride (CCl₄). Materials and Methods: In this study, 24 male Wistar rats were randomly divided into 4 groups (n=6). Group 1: (normal control group) received normal saline (0.5 mL/kg) for 14 days. Group 2: (damage control group) received 0.5 ml of normal saline for 14 days and 1 mL/kg of CCl₄ (50% v/v in olive oil) intraperitoneally on the 14th day. Group 3: (100 mg of the hop extract daily and 1 mL/kg of CCl₄ (50% v/v in olive oil) intraperitoneally on the 14th day. Group 4: (200 mg of the hop extract daily and 1 mL/kg of CCl₄ (50% v/v in olive oil) intraperitoneally on the 14th day. Forty-eight hours after the CCl₄ injection, rats were anesthetized and blood was taken from their heart tissue. Then, the biochemical tests were performed and the results were analyzed using SPSS software. Results: The administration of CCl₄ increased the levels of urea, uric acid, and creatinine (P<0.05). Pretreatment with Humulus lupulus extracts, led to considerable improvements in these values as compared to those of the injury control group (P<0.05). Conclusion: The results suggest that use of hop extracts can protect the kidneys from damage caused by carbon tetrachloride and may be used as a potential drug to minimize acute renal injuries caused by environmental toxins. Keywords:



چهاردهمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Curcumin synergistically enhances the anti-cancer effects of Etoposide on MCF7 and MDA-MB-231 breast cancer cell lines

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نوع پذیرش: پوستر | کد مقاله: G-62459

Abstract: Background: Common chemotherapeutic drugs possess great problems, including less effects due to chemo-resistance and adverse effects on body organs; hence, combination with natural compounds has emerged as a potential procedure to encounter cancer. Curcumin is a natural polyphenol possessing various abilities against cancer, such as apoptosis induction and cell cycle arrest. Here we investigated curcumin and etoposide, singly and in combination, on apoptosis induction in breast cancer cell lines. Materials and Methods: Cur and ETO- treated cell proliferation was determined through MTT viability assay. The drugs' impacts on cancer cell apoptosis was investigated using Annexin V flow cytometry and caspase-3 and -9 activity assays. Bax and Bcl-2 gene expression were determined through qRT-PCR. The levels of p53 protein were determined utilizing western blotting. A not-significantly effective dose of ETO was selected through MTT assay, and was utilized in combination with 75 μ M of curcumin. Results: Curcumin potentiated the activities of ETO on cancer cell' apoptotic death, through higher caspase activities. Also, the combination of Cur and ETO showed higher influence on the reduction of Bcl-2 gene and the promotion of Bax expression. Furthermore, the protein levels of the tumor suppressor p53 was elevated through treatment with the combination of Cur and ETO, compared to ETO and Cur alone. Conclusion: Curcumin is able to potentiate the impacts of etoposide on breast cancer cells apoptotic death. Therefore, we introduce the aforementioned mixture as a potential treatment for breast cancer. Keywords:

Capparis spinosa and Quercetin interact synergistically to reduce diet-induced nonalcoholic steatohepatitis and fibrosis in the rat model by suppressing TGF- β /Smad3 signaling pathways

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نوع پذیرش: پوستر | کد مقاله: G-16032

Abstract: Background: Liver diseases such as non-alcoholic fatty liver disease (NAFLD) and non-alcoholic steatohepatitis (NASH), have emerged as concerns and important public health issues worldwide. Here, we aim to investigate how quercetin (QC), Capparis spinosa (CS), a combination of QC and CS, and Saroglitazar (SARO), a double peroxisome proliferator-activated receptor (PPAR) α/γ ligand, affected NASH in an animal model. Materials and Methods: NASH was induced in Wistar male rats by administering a high-fat diet (HFD) for 42 days. Four groups of HFD rats received QC, CS, a combination of QC and CS, and SARO. We measured the masses of both the liver and the body. In addition, the expression level of genes involved in the biosynthesis and β -oxidation of fatty acids as well as inflammatory and profibrotic genes were evaluated. Results: The combined group (CS+QC) exhibits significantly adjusted liver weight, gained body mass gain, and liver TG than the other groups. The combined group (CS+QC) corrected alanine transaminase (ALT), aspartate transaminase (AST), low-density lipoprotein-cholesterol (LDL-C), and high-density lipoprotein-cholesterol (HDL-C) values more effectively than Saroglitazar and quercetin. The combined group significantly reduced transforming growth factor beta (TGF- β) and inflammatory expression genes, which are connected to fibrosis, steatosis, lesions, and inflammation factors in the liver. In addition, there was a significant reduction in p-Smad2/3 and p-Smad3 protein expression in the combined CS and QC groups. Conclusion: Our results showed that the combined group reduced fibrosis, steatosis, and signs of necrosis caused by inflammation in the HFD-NASH more than CS and QC groups alone. Keywords:

Association of Omentin rs2274907 and FTO rs9939609 gene polymorphisms with insulin resistance in Iranian individuals with newly diagnosed type 2 diabetes

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نوع پذیرش: پوستر | کد مقاله: G-40721

Abstract: Background: Insulin resistance (IR) and fat accumulation in visceral adipose tissue are key players in developing type 2 diabetes (T2D). Several adipose tissue derived-gene polymorphisms are related to higher body mass index (BMI), insulin resistance and T2D. The association of omentin rs2274907 (Val109Asp) and fat-mass and obesity-associated (FTO) rs9939609 gene polymorphisms with overweight/obesity and T2D is controversial. The aim of this study was to determine the association between omentin Val109Asp and FTO rs9939609 polymorphisms and insulin resistance in newly-diagnosed T2D patients. Materials and Methods: The case-control study included 83 newly-diagnosed T2D patients and 85 healthy matched controls, aged 20–80years. Fasting blood glucose and insulin levels were measured by the enzymatic method and enzymelinked-immunosorbent assay, respectively. Insulin resistance was calculated using the homeostasis model assessment (HOMA) index. Genotyping was examined using the polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP). Results: There are significant differences between both omentin Val109Asp and FTO rs9939609 polymorphisms and studied individuals ($P=0.011$ and $P=0.0001$, respectively). Both genetic polymorphisms of omentin Val109Asp and FTO rs9939609 (T/A) are significantly related to higher HOMA index ($P=0.030$ and $P=0.046$, respectively). However, omentin Val109Asp polymorphism was only related to individuals who were overweight/obese. Additionally, both omentin Val109Asp and FTO rs9939609 polymorphisms were significantly positively correlated to familial history of diabetes ($P=0.046$ and $P=0.024$, respectively). Conclusion: Omentin V109D and FTO rs9939609 genetic variations may change insulin metabolism and have key roles in developing T2D through insulin resistance. Thus, the evaluation of these polymorphic regions may be helpful for predicting type 2 diabetes. Keywords: Type 2 diabetes, Insulin resistance, Omentin, Fat mass-and obesity associated (FTO), Gene polymorphism



چهاردهمین کنفرانس بین المللی آزمایشگاه و باالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



the enhancement of HepG2 cell line apoptosis

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نوع پذیرش: پوستر | کد مقاله: G-39610

Abstract: Background: HCC is the most common type of liver cancer worldwide. The current remedies for cancer, including chemo- and radiation-therapy, both lead to severe issues for patients' organs, sometimes causing death. ETO as a widely used chemo-drug possesses the same problems. For years, combinational therapy is considered as a potential adjustor for common treatments, alleviating their side effects. Quercetin, as a phytochemical has been studied for its various potentials against cancer. In this study, we explore whether synergy happens between Que and ETO on the apoptosis of Hep-G2 Hepatocellular carcinoma cells. Materials and Methods: Through MTT assay the impacts of the drugs was assessed on cell growth. The apoptotic death rates of treated cells were examined through Annexin/PI double staining and caspase-9 and -3 activities. The relative expression of Bax and Bcl-2 genes were obtained using qRT-PCR. Through western blotting, the levels of p53 protein were determined. Results: Both Que and ETO reduce the cell viability, and increase the apoptotic rates, caspases activities, Bax gene expression, and the p53 protein levels of Hep-G2 cells. The combination of Que and ETO show clear synergy in terms of cell growth and cell apoptosis. Quercetin significantly enhances the influences of ETO on the caspases activities, Bax and Bcl-2 genes expression and p53 protein levels. Conclusion: Our results proved that Quercetin exhibits synergy when co-treated with ETO, on Hep-G2 cells. Based on this, we conclude that further studies on the aforementioned combination could lead to a potential anti-cancer compound against HCC. Keywords:

Exosomes ameliorates liver fibrosis by inhibiting the Smad3C through up regulating the miR-126

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نوع پذیرش: پوستر | کد مقاله: G-34702

Abstract: Background: Activated hepatic stellate cells (HSC) by the TGF- β signaling pathway, are likely to worsen liver fibrosis, later-stage of NASH. Along with the HSC activation, the extracellular matrix (ECM) proteins, namely collagen- I α , and α -SMA will also overexpress. MicroRNA-126a, HSC activation Modulator, affect Smad2/3 phosphorylation. The aim of the study is the influence of exosomes on miRNAs involved in the liver fibrosis progression, including miR-126a in the HSC-T6 cell line. Materials and Methods: In the current study, the effects of LPS-stimulated mesenchymal cell exosomes on miR-126a expression and smad3c phosphorylation in the HSC-T6 cell line are inspected. Firstly, the HSC-T6 cells were cultivated in DMEM with FBS (10%). Secondly, the separation of MSCs-derived exosomes was performed, using exocib kit. Finally, the expression levels of each collagen- I α , α -SMA, and miR-126a gene were scrutinized through real-time PCR. Western blotting was executed in order to examine phosphorylation levels of smad3c protein. Results: TGF β 1 treatment increased P-Smad2/3 phosphorylation, α -SMA, and Collagen1 α . miR-126a expression, however, was down-regulated by TGF β 1. Treatment with exosomes caused a considerable decrease in p-Smad2/3 phosphorylation levels, α -SMA, and Collagen1 α gene expression, while it up-regulated miR-126a expression. Conclusion: Owing to our observations, it was MSCs-derived exosomes that decreased the expression levels of genes associated with hepatic fibrosis such as collagen- I α , and α -SMA. In addition, exosomes impede smad3c phosphorylation via increasing miR-126a expression, resulting in averting liver fibrosis progression. Therefore, exosomes should be valued as an advantageous treatment strategy. Keywords:

Long non-coding RNAs as potential biomarkers for oral squamous cell carcinoma diagnosis

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نوع پذیرش: پوستر | کد مقاله: G-93182

Abstract: Background and aim: Oral squamous cell carcinoma (OSCC) is the sixed most incident cancer with high tendency to metastasize. Unfortunately, in advanced stages, patients have a low 5-year overall survival rate approximately below 50%. Surgery, chemotherapy, and radiotherapy are the routine options for the treatment of OSCC; however, early diagnosis based on non-invasive biomarkers such as long non-coding RNAs (lncRNAs) can improve patient's survival. In this review, we present an overview about the potential of lncRNAs to ascertain OSCC patients. Method: In this study, we searched Google Scholar, PubMed, and Scopus databases, and included original article, systematic review, and meta-analysis investigations. Results: lncRNAs are a novel group of non-coding RNAs consisted of more than 200 nucleotides. lncRNAs have contributed to different fields of cancer biology including proliferation, migration, invasion, apoptosis and etc. Many results have reported that lncRNAs dysregulation are associated with different types of cancer particularly OSCC. lncRNA JPX was upregulated in OSCC cells, and its expression was correlated with cell proliferation, migration and invasion. JPX complemented with miR-944, and thereby enhanced CDH2 gene expression as a cell-cell adhesion molecule. Another study demonstrated that over-expression of MALAT1 lncRNA increased cisplatin resistance accompanied by apoptosis inhibition via activation of PI3K/AKT/m-TOR signaling pathway. While its knockdown provoked apoptosis and induced cisplatin sensitivity in OSCC cells. Moreover, GAS5 lncRNA was identified as a tumor suppressor which inhibits proliferation, invasion, and epithelial-mesenchymal transition in OSCC through targeting miR-21/PTEN axis. These results indicating that lncRNAs can function either as oncogene or tumor suppressor in OSCC progression. Taken together, the assessment of lncRNAs expression pattern in body fluid of OSCC patients can be an alternative option for the diagnosis of patients who are in early stages. Conclusion: lncRNAs can be potential therapeutic targets and also as useful biomarkers for early diagnosis of OSCC patients. Keywords: long non-coding RNA, oral squamous cell carcinoma, diagnosis, biomarker

Human salivary microRNAs profile for the early detection of oral squamous cell carcinoma

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Background and aim: Oral squamous cell carcinoma (OSCC) is one of the worst types of cancers with high mortality. Despite recent advances in therapeutic approaches, the overall 5-year survival rate has remained unchanged. While at early stages the survival rate is approximately 89%, at late stages it decreases to 39%. Discovering the non-invasive biomarkers can help to distinguish OSCC patients in early stages. MicroRNAs (miRNAs) are small non-coding RNAs which regulate gene expression. We aimed to review the association of human salivary microRNAs profile for the early detection of OSCC. **Method:** Original articles, Systematic review, and meta-analysis investigations are included by searching related articles published in Google Scholar, PubMed, and Scopus databases. **Results:** MiRNAs can regulate target mRNA expression through binding to its 3' untranslated region, which leading to direct destruction or translational inhibition. Thousands of miRNAs are present in saliva, and a panel of salivary miRNAs can be used for OSCC detection. Recently, salivary diagnostics has attracted scientists and clinicians since the method of sample collection for disease is non-invasive, accurate, and cost-effective. Salivary miRNAs may provide an alternative and better strategy in the diagnosis of OSCC, and also to monitor and investigate more easily its evolution and therapeutic response. Several miRNAs, including miR-29b, miR-21, miR-155, and miR-92b have been reported to regulate OSCC proliferation, migration, and invasion. Furthermore, miR-504 over-expression in OSCC cells resulted in the repression of cell cycle-associated proteins such as cyclin D1 and E2F1, as well as enhanced P21 expression as an inhibitor of cell proliferation. Additionally, one study demonstrated that salivary exosomal miR-24-3p triggers the proliferation of OSCC cells *in vitro* and *in vivo* via the suppression of PER1 tumor suppressor gene. So, miRNAs can act as either oncogene or tumor suppressor in OSCC development, and finding the miRNAs involved in the initiation and development of OSCC can shed more light about the regulatory mechanisms of OSCC pathogenesis. **Conclusion:** Targeting salivary miRNAs could be a useful therapeutic approach, and identifying the precise mechanisms of miRNAs in the pathogenesis of OSCC, can pave the way to find better therapeutic and management strategies. **Keywords:** oral squamous cell carcinoma, miRNA, saliva, early diagnosis, biomarker

Influence of novel formulation of the *Artemisia annua* aqueous extract on some of the hepatic function indicators during second-degree burns of mice

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نوع پذیرش: پوستر | کد مقاله: G-58201

Abstract: Background and Objective: Hepatic integrity and function are essential for the postburn response. *Artemisia annua* is a well-known medicinal plant with considerable anti-inflammatory, antioxidant and hepatoprotective properties. The current study aimed to evaluate the effects of copper nanoparticles (CuNPs) loaded with *Artemisia annua* aqueous extract on the hepatic function indicators including ALT, AST, ALP, GGT and total protein in second degree burns in male mice. Materials and Methods: The green synthesis of CuNPs have established by using aqueous extract of *Artemisia annua*. 60 adult male mice were used. After induction of anesthesia, 2nd degree burns were induced, then the mice were randomly divided into control, Eucerin, and experimental groups that the CuNPs ointment (0.2%), CuNPs *Artemisia* ointment (0.2%) and the *Artemisia* extract ointment (5%) were administered twice a day for 21 days. Blood samples were collected before burning induction and on day 3, and serums were used to evaluate hepatic injury. Data were presented as mean± DS and statistical analysis was performed by one-way analysis of variance (ANOVA), followed by Tukey's multiple comparison test ($p < 0.05$). Results: Induction of 2nd degree burn significantly increased serum level of AST, ALT and ALP were in the control & Eucerin groups while ($P > 0.05$), Treatment with CuNPs and *Artemisia* ointment resulted in a significant decrease in AST, ALT and ALP level ($P < 0.05$). Meanwhile a non-significant decrease in total protein levels ($P > 0.05$) was seen. There was no significant difference in GGT levels between the different groups ($p > 0.05$). Conclusion: Green synthesized copper nanoparticles using *Artemisia annua* may improve hepatic function which may be due to the antioxidant properties, however, histopathological and molecular studies are necessary. Keywords: *Artemisia annua*, Liver indicators, Hepatoprotective.



چهارمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Association between night sleep duration and lipid profile in individuals referring to PERSIAN cohort center of Sabzevar

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نوع پذیرش: پوستر | کد مقاله: G-84125

Abstract: Background: Lack of sleep is associated with numerous diseases and health disorders including increased risk of obesity and metabolic disorders, increased risk of cardiovascular disease and lipid profile disorders. This cross-sectional study was performed to determine the relationship between overnight sleep and blood lipid levels in patients referred to the cohort center of Sabzevar University of Medical Sciences. Materials and Methods: This cross-sectional study was performed on all patients referred to the Persian cohort center of Sabzevar University of Medical Sciences. The required information of the study including: age, sex, number of hours of sleep per night and lipid profile including: cholesterol, LDL, HDL and triglyceride and history of diabetes, blood pressure and smoking and alcohol consumption were extracted from the participants' files. Data were entered into SPSS-22 software and statistically analyzed. Results: The results of this study showed that I observed no significant correlation between bedtime hours and body mass index, triglyceride, cholesterol, HDL and LDL. On the other hand, the results of the present study showed that in the age group of 46 to 55 years, the amount of HDL increased with decreasing night time sleep and in the age group over 65 years, with increasing nighttime sleep, the level of LDL increased. Also, no significant difference was observed between the middle of the night sleep in the study population in terms of history of diabetes, blood pressure, smoking and alcohol. Conclusion: In our study, the relationship between night sleep and blood lipid levels was not significant. Further prospective studies are recommended. Keywords:



چهاردهمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Matrigel enhances differentiation of human adipose tissue-derived stem cells into dopaminergic neuron

فروزان آب سالان ©¹ P

دانشکده پزشکی دانشگاه علوم پزشکی آبادان

نوع پذیرش: پوستر | کد مقاله: G-82436

Abstract: Background: Therapy based stem cells have offered a novel therapeutic approach for the improvement of neurodegenerative diseases, especially Parkinson. Hence, developing a well-established culture model with appropriate stem cells is extremely crucial in regenerative engineering to provide efficient targeted cells. Human adult mesenchymal stem cells derived from adipose tissue (hADSCs) have emerged as a promising source of stem cells due to their unique potentials of self-renewal and differentiation into other stem cells. The purpose of this study was to investigate the differentiation capacity of hADSCs into dopaminergic and neuron-like cells in the 3D culture plate (Matrigel). Methods and materials: hADSCs were obtained from adipose tissues of patients and then characterized morphologically with flowcytometry. Isolated cells were harvested to perform differentiation on Matrigel and tissue culture plate (TCP) supplemented with induction factors. The survival rate of cells during neural induction was monitored by MTT. The expression of specific cell markers was analyzed by QRT-PCR and immunocytochemistry on days 2, 8 and 14. The level of released dopamine was measured using HPLC technique. Results: Matrigel had a positive effect on maintaining cell growth compared to those on TCP. Moreover, the number of TH and MAII positive cells is substantially higher in Matrigel than in TCP. Sox2 and Nestin had a prominent expression in hADSCs within the first days of differentiation. The gene expression of neural markers such as TH, Nurr1, LMX1A and DAT was detected and increased after day 8. Moreover, the dopamine released in the cell harvested on Matrigel was greater than those seeded on TCP. Conclusions: Overall, hADSCs could generate dopaminergic cells, which suggest its strong capability to serve as a tool for Parkinson disease model in the regenerative medicine. Keywords:

Drosophila melanogaster testis structure can be affected by *Crocus sativus* stamen hydro-alcoholic extract

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نوع پذیرش: پوستر | کد مقاله: G-19807

Abstract: Background: Infertility is a major and multinational problem worldwide that is increasing in both developed and developing countries. Due to the high costs of today's treatment methods and the lack of definite results, many couples are looking for comprehensive treatment methods using traditional herbal medicines. In this research, the effects of hydro-alcoholic extract of *Crocus sativus* Stamen with contain essential compound like as vitamin E, Pyranone, Linoleic acid, Linolenic acid, on the developmental and physiological changes of the testes structure of *Drosophila* were investigated. Materials and Methods: Investigating the developmental structure of the *Drosophila* testis performed by using the method of placing 2 pairs parent in per vials containing culture medium and then measurement of length, area and cell number of testes of offsprings 0-1 day old which passes developmental stage in culture medium (n=7). The same experiment performed using the culture medium containing hydro-alcoholic extract of saffron flower stamen with concentrations (0.05, 0.1 and 0.2 gr/lit) (n=7 for each concentration). for the investigation of physiological effect of the extract on the testis structure, we placed 0-1 day old offsprings, inside the culture medium containing 0.2 gr/lit hydro-alcoholic extract saffron flower stamen for 36 hours and then similar measurement performed for their testis, and compared with the same parameters in control group (n=7). Results: In the developmental experiments, the groups treated with flower stamen extract showed a significant increase in the size of their traits, so that the number of cells and the area of the testes at 0.2 g/lit showed the greatest difference in increasing the amount compared to the control group (P 0.05). Also, testis length (mm) in 0.1 and 0.2 gr/lit showed a significant increase compared to the control group (P0.05). Also, in the study of the physiological effects of flower stamen extract on the testes of fruit flies, all 3 traits of length, area and the number of cells at a concentration of 0.2 gr/lit showed a significant increase compared to the control group (p 0.05). Conclusion: It seems that saffron flower stamen extract maybe can increase reproduction by reducing free oxygen activity and with its antioxidant activity, because of components Pyranone, Linoleic acid, Linolenic acid and Vitamin E in *Crocus sativus* stamen, therefore can be studied pre-clinically as a useful and natural compound for Improve reproduction and for treatment infertility issues. Keywords: *Drosophila melanogaster*, Testis, *Crocus sativus* stamen, reproduction



چهاردهمین گنگره بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Evaluation of Long non-coding RNA- LINC00299 in breast tumor tissues of Iranian Women

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نوع پذیرش: پوستر | کد مقاله: G-93465

Abstract: Background: Breast cancer (BC) is the most prevalent cancer in females and the second reason of cancer-related mortality in females in the world. Many polymorphisms have been linked to cancer in genome-wide association experiments, and they are linked to long non-coding RNAs (lncRNAs). LncRNAs, which have 200 nucleotides in their transcripts, affect many biological processes, including differentiation, migration, apoptosis, cell cycle, and cell proliferation. This study aimed to investigate the expression and significance of lncRNA-LINC00299 (long intergenic non-coding00299) in breast cancer. Materials and Methods: Breast cancer samples were obtained from Iran National Tumor bank. Total RNA was extracted from each sample and then treated with DNase. Q-PCR was used to detect the mRNA expression of lncRNA- LINC00299 in breast cancer and adjacent normal tissues as respective controls. Results: Real-time PCR data analysis also showed that the expression of LINC00299 gene in breast tumor tissue was increased by 2.3 times, which is statistically significant (P0.0380). Examining the relationship between LINC00299 gene expression and various clinicopathological parameters of breast cancer tissues showed that there was a significant increase in LINC00299 gene expression in estrogen receptor positive tumors compared to estrogen receptor negative tumors (P 0.05). However, there was no significant correlation between LINC00299 expression and other clinicopathological parameters (P >0.05). Conclusion: Since the expression of lncRNA- LINC00299 gene is increased in tumor breast tissues compared to normal tissues, this gene can be considered a suitable biomarker for breast cancer. Keywords: Breast Cancer, Long non-coding RNA, Gene expression, LINC00299

Laboratory Based Methods; Which one for Routine Biomonitoring of Blood Lead Level Determination?

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نوع پذیرش: پوستر | کد مقاله: G-76548

Abstract: Background. Lead or plumb (Pb) is a major toxicant that has threatened human health for years. There is no safe level of exposure and deposition of a small amount of Pb in the human body has a negative impact on an individual's health. In the present study we report internal quality control assessment and precision of the method used for blood Pb determination by GFAAS. Method & Materials. Varian SpectrAA-220 with partition tube and deuterium background correction was used for the analysis. The evaluation quality control blood material was Seronorm trace element & heavy metals whole blood (levels I & II). Results. The "lowest method limit of detection" was 0.74 $\mu\text{g/dL}$, and based on the regression analysis the lowest quantification concentration was 3.00 $\mu\text{g/dL}$ (%CV = 4.6). In addition, obtained (short term precision) %CV for Seronorm (I) & Seronorm (II) was 7.3% & 5.4% respectively. Conclusion. We conclude that prevention of lead exposure should remain the primary goal of health care providers, public health professionals, and employers for both adults and pediatrics. In addition, the choice between laboratory based technologies for biomonitoring of blood lead level depends on factors such as sample type, analytical requirements, accuracy, precision, operator's expertise, budget and etc. Furthermore, routine confirming of the presence of lead even in low concentrations (3.00 $\mu\text{g/dL}$) by GFAAS is a reference reliable analytical method. Lastly, regarding GFAAS, it is suggested that laboratories measuring blood lead level be assure of the analytical performances in order to improve intralaboratory short term precision that eventually depending on the condition and tube type will helps to improve long term precision as well. Keywords:

Therapeutic Effects of Resveratrol on Cancer

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نوع پذیرش: پوستر | کد مقاله: G-23450

Abstract: Background: Cancer, also known as malignant tumor, is a major public health problem around the world, not only brings unutterable pains to patients, but also leads to heavy economic burden to the families and society. Resveratrol (3, 5, 4'-trihydroxystilbene) is a phytoalexin contained in a variety of plants. Resveratrol is found in various plants, including grapes, and is used in traditional Chinese medicine. In traditional medicine, resveratrol has long been used as an herbal remedy. In modern medicine, resveratrol is of great interest as a "multitargeting agent" because of its anti-oxidant, anti-inflammatory, anti-obesity, anti-diabetic, anti-bacterial, anti-carcinogenic, cardio-protective, and immunomodulating properties. Methods: In the current study, keywords including Resveratrol, Therapeutic, and Cancer were reviewed from the list of Mesh and other credible websites including PubMed, Science Direct and Google Scholar and the data was organized. The searches comprised all published paper from 2000 to 2022. All of full text was considered and the papers manifested as only abstract was excluded. The full papers selected that specific effect on cancers only. Totally 50 papers were selected and studied in this review. Results: Articles show in the MCF-7 breast cancer cell line treated with 10-5 M resveratrol, the reduction of the Bcl-2/Bax ratio through enhancement of p53-dependent transcriptional activity at least partially contributes to resveratrol's pro-apoptotic activity. Resveratrol exerts a broad spectrum of molecular effects associated with the control of cancer development. These include the reduction of glucose uptake and lactate synthesis, and consequent caloric restriction that inhibits proliferation and metastasis, and induces apoptosis. Resveratrol inhibits cell proliferation and overcomes chemoresistance by inhibiting the nuclear factor-kappa B (NF-κB) and signal transducer and activator of transcription 3 (STAT-3) pathways and down-regulating the genes involved in cell survival. Many researches showed resveratrol downregulates the expression of β-catenin and blocks β-catenin nuclear translocation through perturbation of the long non-coding RNA MALAT1. Also, it lowers the expressions of IKK-induced TNF-β, leading to the inhibition of cancer cell proliferation through deactivation of NF-κB. Some scientists concluded that resveratrol suppresses the phosphorylation of Src-STAT3 and induces apoptosis of cancer cells. One article demonstrated that resveratrol induced nuclear accumulation of COX-2 and facilitates p53-dependent apoptosis in human breast cancer cells. Other articles demonstrated that resveratrol can inhibit tumor angiogenesis in breast cancer xenografts. Also, resveratrol impaired VEGF expression through downregulation of HIF-1α, which may reduce angiogenesis during hepatocarcinogenesis. More directly, resveratrol can play an efficient role in anti-angiogenesis by affecting the growth of capillary endothelial cells in vitro and new blood vessels growth in vivo. Conclusion: Previous studies have shown that resveratrol has numerous pharmaceutical properties, including anti-tumorigenic capabilities against a number of different tumor cell types, including breast, prostate and esophageal cancer cells. The available literature suggests that in cancer, resveratrol acts through multiple mechanisms, including proapoptotic, anti-proliferative, anti-inflammatory, and anti-angiogenesis mechanisms. Keywords: Resveratrol, Therapeutic, Cancer

miRNAs as a Biomarker in Alzheimer's Disease

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نوع پذیرش: پوستر | کد مقاله: G-26130

Abstract: Background: Alzheimer's disease (AD) is a multifactorial, age-related neurological disease characterized by complex pathophysiological dynamics taking place at multiple biological levels, including molecular, genetic, epigenetic, cellular and large-scale brain networks. Alterations in microRNA (miRNA) signaling have been implicated in the epigenetics and molecular genetics of all neurobiological processes associated with Alzheimer's disease pathophysiology. miRNAs are conserved small non-coding RNAs and modulate gene expression negatively at the post-transcriptional level. Approximately 70% of the currently identified miRNAs are expressed in the brain. Therefore, miRNAs may serve a potential role in monitoring neurodegenerative processes, and specific miRNAs may correlate with certain neurodegenerative diseases. Methods: In the current study, keywords including miRNAs, Biomarker, and Alzheimer's Disease were reviewed from the list of Mesh and other credible websites including PubMed, Science Direct and Google Scholar and the data was organized. The searches comprised all published paper from 2000 to 2022. All of full text was considered and the papers manifested as only abstract was excluded. The full papers selected that specific effect on Alzheimer's Disease only. Totally 50 papers were selected and studied in this review. Results: Articles revealing that miR-9, miR-125b and miR-128 were elevated in AD hippocampus compared with normal controls. Another research examined the possible role of miRNAs serum as another alternative biomarkers for AD, revealing that serum miR-125b may be used as a noninvasive biomarker for AD. Also, another study indicated that just five miRNAs – miRNA-9, miRNA-34a, miRNA-125b, miRNA-146a, and miRNA-155 – are significantly abundant in AD neocortical brain tissues as well as the extracellular fluid and cerebrospinal fluid and each miRNA was found to interactively contribute to the AD pathophysiology. Scientists suggested that Alzheimer's patients show increased level of miRNAs in the blood and cerebrospinal fluid, miRNAs are considered promising non-invasive candidates for AD diagnosis and prognosis. Downregulated expressions of miR-29a/b-1, miR-29c, and miR-339-5p have been reported to upregulate the expression of BACE1 in AD brain, thereby increasing Amyloid- β production. Also, the expression of miR-15/107 in cerebral cortical gray matter is correlated with amyloid plaque density. One study suggested that miR-146, miR-106, miR-9, miR-29, miR-107, miR-181, miR-128, miR-125b, miR-210 and miR-34 are among those miRNAs that have been identified to be dysregulated in AD and, hence, these may serve as potential diagnostic biomarkers for AD, as will be discussed herein. Conclusion: Expression profiling of small non-coding RNAs, miRNAs, has shown diagnostic potential in Alzheimer's disease, and has come a long way in the past two decades. Hence, circulating miRNAs have been proposed as one of the most promising biomarkers for AD as well as other neurodegenerative diseases. Keywords: miRNAs, Biomarker, Alzheimer's Disease

The prominent role of exosomes in the development of oral squamous cell carcinoma

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Abstract: Background and aim: Oral squamous cell carcinoma (OSCC) is the sixth most frequent malignancy in the world. This neoplasm involves lips, tongue, buccal mucosa, floor of mouth, gums, pharyngeal regions and salivary glands. Although the procedures of OSCC treatment have been improved recently, but this disease has a poor prognosis and low overall survival rate yet. Identifying novel diagnostic biomarkers for early detection is very vital. Exosomes play essential roles in cell-cell communication and OSCC invasion into the lymph structures by transferring cargo between cells. Our aim in this review is to summarize the crucial role of exosomes in the progression of OSCC. Method: In this study databases such as Google Scholar, PubMed, and Scopus were searched, and ultimately related research articles, systematic review, and meta-analysis investigations were included. Results: It is estimated that more of 90% of all head and neck neoplasms are OSCC. OSCC is commonly diagnosed in the late stages of the disease and can invade into the lymph nodes, and therefore is prevalent lethal malignancy in the world. The poor prognosis of this disease is due to two main reasons: 1- The high rate of recurrence 2- Frequent metastasis in distant areas by exosomes. Exosomes are lipid bilayer nanoparticles that transport many types of biomolecules such as lipids, proteins, mRNA, and non-coding RNAs (ncRNAs) including microRNAs (miRNAs), long non-coding RNAs (lncRNAs) and circular RNAs (circRNAs) which deliver them to the recipient cells. Exosomes have pleiotropic activity such as tumor development, invasion and use in the clinical setting as promising tools for early diagnosis and the monitoring of patient's response to treatment. The cargo of exosomes especially ncRNAs by modifying posttranscriptional gene regulation, play an important role in human cancers. These molecules can serve as oncogene or tumor suppressor that correlated with growth, invasion, drug resistance and advanced tumor stages of OSCC through various signaling pathways. It was shown that exosomal miRNAs such as miR-21 and miR-24-3p having higher levels in the serum of OSCC patients and can be utilized as diagnostic biomarkers. Another investigation revealed that exosomal-mediated transferring of APCDD1L-AS1 lncRNA into OSCC cells can stimulate chemoresistance. Likewise, exosomal circRNA circGDI2 has tumor-suppressive role in OSCC and its upregulation inhibited OSCC growth. In general, discovering the regulatory



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mechanisms of ncRNAs transferred by exosomes can help us better understand OSCC pathogenesis. On the other hand, delivering the inhibitory ncRNAs by exosomes into OSCC cells can be considered as a novel therapeutic option. Conclusion: Exosomes perform critical roles during initiation, progression and metastasis of OSCC through transmitting ncRNAs including miRNAs, lncRNAs, and circRNAs. Therefore, changing the contents of exosomes can play an effective role in the treatment of OSCC. Keywords: oral squamous cell carcinoma, exosomes, non-coding RNAs, biomarker, tumorigenesis



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The effect of Covid-19 vaccination on women's reproductive health

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نوع پذیرش: پوستر | کد مقاله: G-92015

Abstract: Background: After a lot of attention was paid to the possible side effects of covid-19 vaccination in various aspects and considering menstrual disorders as a common complaint after receiving the covid19 vaccine from women, In order to estimate the relationship between vaccination and menstrual disorders, we investigated vaccinated women of reproductive age. Methods: In order to conduct this study, a questionnaire was prepared that helped to identify menstrual disorders. The participants, a statistical population of 100 premenopausal women who received the vaccine, were asked to answer the questionnaire carefully. Results: Due to the great influence of the menstrual cycle, menstrual disorders are common among women in general. By conducting this study, we observed a significant increase in menstrual disorders after vaccination, which includes increased properties, irregular properties, severe with a large amount of the pain is less Conclusion: This study shows the effect of vaccination on menstrual disorders and the quality of women's health. Keywords: menstrual disorders- covid19 vaccine-menstrual cycle

Effect of *Ferula macrocolea* essential oil on serum level of liver and kidney enzymes as well as hematological parameters in BALB/C mice

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نوع پذیرش: پوستر | کد مقاله: G-57231

Abstract: Background: Today, plants and their derived compounds play an important role in medicine and treatment of diseases. Therefore, due to the increasing use of herbal compounds, each herbal product should be evaluated in terms of toxicological studies before being used as a pharmaceutical form. This study was conducted in order to investigate the subacute toxicity of *Ferula macrocolea* essential oil on hepatorenal functions and hematological parameters in BALB/C mice. Materials and Methods: Subacute toxicity was investigated by examining the serum level of liver and kidney enzymes as well as blood parameters followed by the oral treatment of mice with *F. macrocolea* essential oil for 14 days (0.1, 0.2, 0.4 and 0.6 ml/kg). Results: The results of acute toxicity studies after a single dose of *F. macrocolea* essential oil of 1.24 ml/kg was administered intraperitoneally to mice and the mice were monitored for 14 days. The median lethal dose of this compound was determined to be 1.79 ml/kg. Considering that the study of acute toxicity in this study was done with a dose of 1.28 ml/kg, no cases of animal death were observed, and also in the study of subacute toxicity with doses (0.1, 0.2, 0.4 and 0.6 ml/kg) had no toxic effect on vital organs such as liver and kidney as well as blood parameters. Conclusion: Finally, according to the results of the study, none of the blood parameters and the histological characteristics of the studied organs have changed with the consumption of *F. macrocolea* essential oil, so it has no significant toxicity and it can be used for the possible effect on various diseases in future studies. Keywords: *Ferula*, toxicity, acute and subacute toxicity, LD50



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Anticancer effects of Geraniol on breast cancer cell line (MCF-7)

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نوع پذیرش: پوستر | کد مقاله: G-48752

Abstract: Background: Cancer is a complex genetic disease that is a major public health problem worldwide. Natural products due to their wide range of biological activities and fewer undesirable side effects, have been used as alternative treatments for cancers. In this study we investigated anti-cancer effects of Geraniol against human breast carcinoma cell line MCF-7. Materials and Methods: This study was performed by an in vitro assay. The anti-cancer effects of Geraniol at different concentrations on MCF-7 breast cancer cells were evaluated by MTT assay. Data were analyzed using one-way variance test Results: The evaluation of the toxicity effect of Geraniol using MTT assay showed that geraniol significantly inhibited the growth of human breast cancer cell MCF- in a dose- and time- dependent manner. Calculated IC50 value for MCF-7 cells was 25 μ M. Conclusions: The result of our study confirms that Geraniol has cytotoxic effects on breast cancer cells and can induce anti-cancer effects. Keywords: breast cancer, cytotoxicity, geraniol, MCF-7.

Impact of caloric restriction and quercetin on oxidative stress markers in aged rats

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نوع پذیرش: پوستر | کد مقاله: G-21437

Abstract: Background: Aging is caused by the progressive accumulation of various changes in the body, which is associated with an increase in oxidative stress and related diseases. Free radicals are directly responsible for the damage and defects during aging. In this study, we have aimed to evaluate the potential of caloric restriction (CR) and quercetin (QUER) in reducing the destructive effects of aging in male wistar rats. Materials and Methods: Two age groups of rats (8 and 20 weeks) were included in the study and subdivided to normal diet (ND), ND with QUER (15 mg Kg⁻¹, IP), ND with CR, and ND with QUER and CR groups. Activities of catalase (CAT), paraoxonase (PON1), liver enzymes and lipid profile, and the expression of Sirt1 and NQO1 genes were analyzed. Result: The liver enzymes and lipid profile in the 20-week-old rats were higher than those in 8-week-old rats, and the administration of QUER and CR returned these values to the normal range. The PON1 activity of older rats was lower than that of younger. The use of both QUER and CR increased CAT and PON1 activity in 8 and 20-week-old rats. In both age groups, the simultaneous use of QUER and CR significantly reduced total cholesterol, triacylglycerol, and liver enzymes, while increasing HDL-C (P 0.05). CR alone and in combination with QUER significantly raised the expression level of the NQO1 and Sirt1 genes. Conclusion: Collectively, it can be concluded that QUER and CR together decrease the destructive effects of aging by increasing the level of NQO1 and related antioxidant enzymes. These results incline us to utilize CR and flavonoids in our life style to counteract the age related accumulation of oxidative macromolecular damage and benefit from their anti-aging potential. Keywords: Aging, Caloric restriction, Quercetin, Catalase, Paraoxonase, NQO1

Are Angiotensin-Like Protein 3 and 4 the worthwhile factors for predicting the risk of type-2 diabetes and metabolic syndrome?

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نوع پذیرش: پوستر | کد مقاله: G-46370

Abstract: Background: ANGPTLs (Angiotensin-like proteins) 3 and 4 of the ANGPTL protein family play an important role in the development of type 2 diabetes. These glycoproteins affect the modulation of glucose and lipid metabolism. They inhibit lipoprotein lipase (LPL) activity and provoke lipolysis. This study was aimed to investigate the serum levels of ANGPTL3 and 4 proteins in the serum of type 2 diabetic subjects with metabolic syndrome in comparison to the healthy control group. Materials and Methods: Three groups of individuals were included in this study; Group I: 47 patients with type 2 diabetes and metabolic syndrome; Group II: 25 patients with type 2 diabetes and without metabolic syndrome; Group III: 40 non-diabetic healthy people without metabolic syndrome as a control group. After collection of 5 ml fasting blood samples, serum concentrations of Fasting blood sugar (FBS), cholesterol, triglyceride (TG), HDL-C (High-density lipoprotein-Cholesterol) and LDL-C (Low-density lipoprotein-Cholesterol) were measured by the enzymatic method; blood pressure, height and weight with standimeters; and ANGPTL3 and 4 by the enzyme-linked immunosorbent assay (ELISA). Results: The serum ANGPTL 3 level was significantly different among the groups ($p=0.000$). In patients with type 2 diabetes and metabolic syndrome, ANGPTL 3 and 4 levels were lower than the control group. Conclusion: Altogether, our findings suggest that the decreased levels of ANGPTL 3 and 4 may be a causative factor for type 2 diabetes. Keywords:



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Examination of vitamin D level and sodium intake in patients of Ahmadnejad hospital in Katalam city in Mazandaran province during 2021- 2022

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نوع پذیرش: پوستر | کد مقاله: G-69538

Abstract: Background: Since vitamin D receptors and vitamin D activating enzyme are located on all white blood cells, vitamin D can modulate immune responses and vitamin D deficiency is associated with frequent infections. The ESR test can be a complementary test in the diagnosis of inflammatory diseases, so that the greater the blood cell sedimentation interval, it means that the inflammatory response of the immune system has been extensive. Materials and Methods: In this cross-sectional descriptive study of 2315 people (2276 vitD + 39ESR), blood samples were obtained from patients who referred to the laboratory, serum was separated from the samples, and vitamin D was done using the vitD3 test, and sodium determination was done using the ESR test. The test results were analyzed using student T-test and SPSS statistical test Results: Among the 2315 referred patients, there were 902 male and 1413 female. 1389 patients were over 40 years old and 926 patients were under 40 years old. Out of all the vitamin D tests, 15 people had low vitamin D levels and 2256 patients had average or normal vitamin D levels. 5 patients had low vitamin D and among all the ESR tests performed, 7 patients were positive and 32 patients were negative. Conclusion: Vitamin D is one of the most important diseases that intervene in the regulation of the immune system, and sodium determination is one of the important and cheap tests to predict all types of infections in a non-specific manner. Key words: Infectious diseases, ESR, vitamin D, ESR

Nanoliposome-loaded thymol increases apoptosis and decreases EGFR gene expression in the SW1116 cell line derived from colorectal cancer

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نوع پذیرش: پوستر | کد مقاله: G-07489

Abstract: Background: Colorectal cancer is the third most common cancer in the world and the fourth leading cause of cancer death. Different factors such as environmental and genetic factors and lifestyle affect it. Plant compounds can be effective in the treatment of various cancers due to the presence of phenolic, alkaloid, and antioxidant compounds. Thymol is a natural monoterpene phenol found in some plants and shows several biological effects. The aim of this study was to investigate the effect of thymol-containing nanoliposome in SW1116 cell lines derived from colorectal cancer. Materials and Methods: SW1116 cells were treated with different doses of thymol and liposome-loaded thymol. The extent of inhibition of cell proliferation was evaluated by MTT assay. The rate of cell apoptosis was checked using flow cytometry. EGFR gene expression was measured using a Real-Time PCR technique Results: The results of the MTT test showed that thymol and thymol loaded with nanoliposomes decrease the proliferation of SW1116 cells. The IC₅₀ of thymol and thymol loaded with nanoliposome for the SW1116 cell line were 8.5 and 6.2 µg/ml, respectively. Thymol loaded in nanoliposome inhibited proliferation significantly (P=0.0001) compared to thymol alone. The staining results in the flow cytometry test showed an increase in the percentage of apoptotic cells, especially in thymol loaded with nanoliposomes in the treated cells. Real Time PCR results also showed that both thymol and loaded thymol decreased the expression of EGFR genes in the cell line. But this gene expression reduction effect was more significant in thymol loaded with nanoliposome (P=0.001). Conclusion: The results of this research show that thymol and thymol loaded with nano-liposome can be effective in the treatment of colorectal cancer and by inducing apoptosis, inhibiting cell proliferation and reducing EGFR gene expression, it causes the death of cancer cells. Keywords: thymol, nanoliposome, SW1116, cancer



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Evaluation of serum vitamin D and its relationship with blood lipid pattern in patients

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نوع پذیرش: پوستر | کد مقاله: G-93065

Abstract: Background: According to the proposed mechanisms, vitamin D can reduce the absorption of fats and increase the synthesis of bile acids from cholesterol, affecting serum levels of fat profiles including triglycerides and total cholesterol. Materials and Methods: In this observational study, 156 patients referred to the laboratories of Azad University hospitals were selected and reviewed by available means; Subjects were then assessed for serum vitamin D levels, and the required demographic information, such as age and gender, was entered into a checklist containing the variables studied. Then the level of vitamin D and its relationship with triglycerides, total cholesterol, LDL and HDL were examined. Results: Based on the results of this study, 41% of study participants were male and 59% female and also the mean age of patients was 43.79 years. The mean serum level of 25-hydroxyvitamin D was 40.31 ± 20.79 ng / ml. The percentage was 6-41; also, serum level of 25-hydroxyvitamin D was more than 60 ng / ml in 12.2% of subjects. According to the results of one-way analysis of variance, the mean LDL decreases significantly with increasing serum level of 25 hydroxyl D vitamin. Conclusion: The results of this study showed that there is no significant relationship between serum levels of hydroxyl D vitamin and triglycerides and total cholesterol, while the LDL level of individuals decreases with increasing serum levels of hydroxyl D vitamin. Keywords: Vitamin D, Blood lipids, Total cholesterol.

Circular RNAs: the new regulatory molecules in gastric cancer

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نوع پذیرش: پوستر | کد مقاله: G-89735

Abstract: Background: Gastric cancer (GC) is the fifth most prevalent cancer and the third most common reason of cancer death in the world. Diagnosis in advanced stages, limitations in treatment methods and high metastasis cause poor prognosis and low overall survival in GC patients. Circular RNAs (circRNAs), a class of noncoding RNAs, have a covalently closed loop structure without free ends. CircRNAs are involved in the pathogenesis of various diseases such as GC; however, their functions are not well known. This review describes principal aspects of circRNAs including synthesis, attributes, function and then focuses on their relationship with GC. Method: In this review, we searched original article, systematic review, and meta-analysis articles from PubMed, Google Scholar and Scopus databases. Results: The most circRNAs are derived from protein-coding genes. CircRNAs are synthesized from pre-mRNAs in an alternative splicing process entitled “back splicing”, in which 3' end of upstream exon joined to 5' end of downstream exon. Exonic circRNA (ecircRNA), circular intronic RNA (ciRNA), and exon-intron circRNA (EIcircRNA) are the three main types of circRNAs. CircRNAs exhibit biological characteristics such as stability, conserved sequence, and tissue specificity. It was previously thought that circRNAs are produced as a result of splicing errors, but in several studies, it was shown that circRNAs are widely expressed in many tissues and are conserved in species. Several functions have been reported for circRNAs. MicroRNAs (miRNAs) sponge is one of the most important functions of circRNAs. CircRNAs are considered as upstream regulators of miRNAs that targeted them by miRNA response element (MRE) sequence and consequently prevent their inhibitory effect on the target mRNAs. Additionally, CircRNAs can act as a scaffold for proteins and boost enzymatic reaction. Some of classical RNA binding proteins are bound to circRNAs. Studies have been revealed that circRNAs can play a role in gene expression regulation. Interestingly some of circRNAs code proteins. CircRNAs are involved in the different processes of GC development such as proliferation, invasion, metastasis, and drug resistance. CircRNAs can play oncogenic role and thereby promote GC progression. On the other hand, some circRNAs are tumor-suppressor and inhibit tumor growth. Tumor-suppressor circRNAs have a protective effect and their expression decreases in GC. CircHIPK3 enhances the proliferation of GC cells by sponging miR-637 and abolishes its inhibitory effect on AKT. circREPS2 has been reported as an anti-metastatic circRNA that targets miR-558 and regulates RUNX3/b-catenin signaling. There is an urgent need to find biomarkers for the early diagnosis and monitoring the prognosis of GC patients. CircRNAs are stable than linear RNAs and express aberrantly in body fluids and tumor tissues, and also there is a relationship between their expression and clinicopathological features of GC. Thus, circRNAs can be promising biomarkers for diagnosis and prognosis of GC patients. Conclusion: Despite the growing researches in the last years, the performance of circRNAs is not fully understand yet. A better understanding of circRNAs mechanism helps to further identify GC pathogenesis. They can be considered as new therapeutic targets and diagnostic biomarkers. Keywords: Stomach Neoplasms, Circular RNA, biomarker, diagnosis,

Urinary metabolites, non-invasive biomarkers to study and diagnose irritable bowel syndrome

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نوع پذیرش: پوستر | کد مقاله: G-04397

Abstract: Background: Irritable bowel syndrome (IBS) is a common functional gastrointestinal disorder (FGID), characterized by chronic abdominal pain, cramping, bloating, and altered bowel habits. IBS is reported to affect about 12% of the world population with a remarkable health burden in terms of decreased health-associated quality of life. Despite the high prevalence and chronic nature of IBS, its underlying pathophysiology is not fully understood, and a multifactorial etiology is attributed to this FGID. Recent investigations have demonstrated that neuroendocrine changes, mucosal immune activation, microbiome alterations, and metabolic defects during the pathogenesis of IBS may result in the formation of particular metabolites that can be excreted through the urine. Thus, metabolomics analysis of urine specimens from IBS patients can provide new insights into pathophysiology and diagnosis of IBS. Herein, we aim to systematically review the urine metabolomic profile linked with IBS. Methods: In the current study, MEDLINE@/PubMed database, as well as the Embase was searched to achieve related publications. In this regard, “irritable bowel syndrome” OR “IBS”, “urine”, “metabolomics” OR “metabolome”, “biomarker”, and “diagnosis” were used as MeSH keywords. Furthermore, an advanced search strategy was employed using (“irritable bowel syndrome” OR “IBS”) AND “urine” AND (“metabolomics” OR “metabolome”), (“irritable bowel syndrome” OR “IBS”) AND (“metabolomics” OR “metabolome”) AND “biomarker”, (“irritable bowel syndrome” OR “IBS”) AND “urine” AND (“metabolomics” OR “metabolome”) AND “diagnosis”). For a more efficient search, inclusion and exclusion criteria were considered as follows: All related controlled clinical trials, in vitro evaluations, and in vivo studies were included, whereas Meta-analyses were excluded. Results: Through scanning multiple publications, we realized that liquid chromatography tandem mass spectrometry (LC-MS/MS), gas-chromatography mass spectrometry (GC-MS), and Nuclear magnetic resonance (NMR) were the principal techniques used to identify and quantify urinary metabolites. In the following, we noticed that IBS patients had a unique urinary metabolic profile, which could separate them from patients with other FGIDs such as ulcerative colitis. Key metabolites in this context were a subset of amino acids and organic acids, including histidine, proline, lysine, glutamine, glutamate, phenylalanine, citrulline, lactic acid, Sumiki's acid, oxoglutaric acid, adipic acid, o-hydroxyphenylacetic acid, and 3-Hydroxyisovaleric acid. IBS patients could also be differentiated from healthy subjects by their urinary metabolic fingerprints. These IBS-specific urinary metabolites included a series of hydroxy-lysine metabolites (i.e. O-glycosylgalactosyl-hydroxylysine, O-galactosyl-hydroxylysine, and lysine), mannopyranosyl-tryptophan, imidazole propionate, glutamine, serine, ornithine, dimethylglycine, and dimethylguanosine, as collagen degradation and intestinal mucosal turn-over products. Moreover, phosphatidyl choline acyl-alkyl C38:6, p-hydroxybenzoic acid, 2-methylsuccinic acid, palmitic acid, hippuric acid, hydroxyphenylacetic acid, ornithine, and dopamine were the urinary metabolites decreased in IBS patients compared to healthy controls. Conclusion: Considering the type of excreted metabolites, the ambiguous pathogenic aspects of IBS could be disclosed. For instance, excretion of collagen degradation and intestinal mucosal turn-over products reflects a mild inflammation through the disease. Also, the presence of dopamine literally shows the involvement of neuroendocrine changes. On the other hand, all these metabolic fingerprints provide novel insights into IBS diagnosis to be partially independent of Rome criteria. Keywords: Irritable bowel syndrome, Metabolomics, Urine, Biomarker, Diagnosis

Green Synthesis of Silver Nanoparticles using Juglans regia Extract and its anti-bacterial and anti-cancer effect through expression of SRD5A2, HSD3B1, HSD3B2 genes in PC3 and DU145 prostate cancer cell lines

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نوع پذیرش: پوستر | کد مقاله: G-50231

Abstract: Background: The green synthesis of silver nanoparticles has been the focus of many researchers in recent years. Silver nanoparticles are used as anti-microbial and anti-cancer agents and, in this study, we intend to evaluate the antimicrobial and anticancer effect of silver nanoparticles synthesized with Jaglans regia leaf extract by evaluating the expression of HSD3B1, HSD3B2 and SRD5A2 genes in PC3 and DU145 cell lines. Method: First, the ethanolic extract of Jaglans regia was prepared and added to 2 mM silver nitrate solution. After discoloration of the extract, the physical and chemical properties of the reaction product were investigated by spectrophotometric, DLS, FTIR, SEM and TEM Methods. The antimicrobial properties of the synthesized nanoparticles were evaluated using MIC and MBC tests at 20, 35, 50, 65, 80 nM concentrations. Cytotoxicity was assessed by MTT assay on PC3 and DU145 cell lines. Apoptosis and cell cycle inhibition were assessed by flow cytometry. Gene expression was tested by Real Time PCR. Results and Discussion: The spherical morphology and size of 40 ± 15 nm, silver nanoparticles were confirmed by TEM and SEM images. FTIR proved covalent bonds and silver nanoparticle formation. MIC and MBC experiments showed that silver nanoparticles on Pseudomonas aeruginosa (gram-negative representative) at 35 nM MIC and at 50 nM MBC and on Staphylococcus (gram-positive representative) at 65 nM MIC and at 80 nM MBC They have desirable antimicrobial properties. The anti-cancer properties of silver nanoparticles were demonstrated on cell lines using MTT assay and IC 50 was observed in PC3 class, 20 nM and in DU145 class, 10 nM. Decreased gene expression was demonstrated by Real Time PCR. In PC3 cell line, the expression of SRD5A2 genes was 2/5 times higher than control, HSD3B1 was 1/25 times higher than control group and HSD3B2 was 1/20 times higher than control. In DU145 cell line, the expression of HSD3B1 gene was 1/40 times higher than the control and HSD3B2 gene was 1/2 times higher than the control group. Conclusion: Jaglans regia extract is able to reduce Ag ions to silver nanoparticles. Silver nanoparticles synthesized from Jaglans regia extract have acceptable antimicrobial and anticancer properties. Keywords:

Circular RNAs roles in the occurrence, progression, and even treatment of prostate tumor cells

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نوع پذیرش: پوستر | کد مقاله: G-65347

Abstract: Introduction: Prostate cancer (PC) is one of the non-cutaneous cancers commonly prevalent among males. Recent experimental techniques are performed inadequately for PC diagnosis; therefore, developed diagnostic biomarkers must be innovated. One of the critical factors that play an essential role in this issue is microRNAs (miRNAs), which are small fragments of RNA that affect the expression of proteins, translationally, modulate vital signaling pathways at the cellular level, and contribute to cancer pathogenesis and execute tumorigenic influences through dysregulation. The RNA molecules are circular and stable with a closed covalently structure. Circular RNAs (circRNAs) play an incomparable role in the incidence and progression of prostate cancers and can even be therapeutic for these tumor cells. Therefore, this study was performed due to the investigation of circRNAs important role in prostate cancer. Methods: All data were assembled through diverse valid scientific resources, such as PubMed, Google Scholar, and science direct, using terms including "circRNA," "Prostate cancer," "signaling pathway," "biomarker," "diagnosis," and "treatment." The collected data were eventually evaluated. Results: In this study, circRNA expression, performance, and operations that are related to cell proliferation and metastasis were assessed. The results revealed that circRNAs up-regulation could have a critical role as oncogenes. On the other hand, in several examinations, the down-regulation of circRNAs depicted their tumor-repressing function. Moreover, in most investigations, circRNAs have been realized to sponge miRNAs that negatively regulate the function or expression of the downstream miRNAs. In addition, circRNAs have been shown to have a connection with regulatory proteins. The latter-mentioned relationship eventually regulates signal transduction, either a tumor repressor or an oncogenic one. Furthermore, circRNAs identification in a straightforward, brisk, and definitive way reveal their potential roles as a reliable detectable biomarker for prognosis as well as the diagnosis in human body fluids in PC patients. Conclusion: To conclude, recent studies have shown that circRNAs, a particular RNA with a circular structure, are of great significance for PC diagnosis, treatment, and prognosis. Detection accuracy, in-depth mechanisms exploration, clinical diagnosis and transformation of therapy, and other aspects need to be investigated more. Ultimately, the roles that circRNAs play in PCs are worthy of further exploration. Keywords: CircRNAs, Prostate Cancer, Biomarker, miRNAs, Small RNAs

Investigation of the potential effect of alpha-pinene on the miR-21 and EMT marker (N-cadherin) in hepatocellular carcinoma cells (HepG2).

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نوع پذیرش: پوستر | کد مقاله: G-93480

Abstract: Background: Several studies have reported that alpha-pinene, as a natural compound, has a number of properties, one of which is its ability to inhibit the growth of cancerous cells. Some studies in recent years indicate that alpha-pinene can prevent the invasion of malignant cells in some cancers, despite the lack of studies on its effect on cell invasion. During epithelial-mesenchymal transition (EMT), cancer cells lose their epithelial characteristics, so they can migrate to adjacent tissues. It is believed that microRNA-21 (miR-21) is indirectly involved in the EMT process, which in turn leads to the migration and invasion of tumor cells into the surrounding tissues. Therefore this study aimed to investigate the effect of alpha-pinene on the expression of miR-21 and N-cadherin in HepG2 cells. Methods: In the current study, the human hepatocellular carcinoma cell line HepG2 was treated with different concentrations of alpha-pinene for 24 hours. The expression levels of mir-21 and N-cadherin were determined by RT-qPCR. Results: Alpha-pinene significantly downregulated miR-21 and N-cadherin in different treatment groups compared to the control group. Conclusion: Based on the results of this study, it is likely that alpha-pinene plays a critical role in inhibiting the migration and invasion of HCC cells by downregulating miR-21 and N-cadherin. So, we concluded that alpha-pinene could be helpful in preventing the proliferation of cancer cells. Keywords: Hepatocellular Carcinoma, Alpha-pinene, Epithelial-Mesenchymal Transition, MicroRNA, N-cadherin.



چهارمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Investigation of the potential effect of alpha-pinene on the miR-106b and EMT marker (E-cadherin) in hepatocellular carcinoma cells (HepG2).

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نوع پذیرش: پوستر | کد مقاله: G-91270

Abstract: Investigation of the potential effect of alpha-pinene on the miR-106b and EMT marker (E-cadherin) in hepatocellular carcinoma cells (HepG2). Ghasem Farhadi Jalil Babadi¹, Parisa Khanicheragh³, Mohammad Yazdi¹, Mahdi Alaei¹, Mojgan Azadpour^{1*} 1 Razi Herbal Medicines Research Center, School of Medicine, Lorestan University of Medical Sciences, Khorramabad, Iran 2 Department of Biological Sciences and Biotechnology, Faculty of Science, University of Kurdistan, Sanandaj, Iran 3 Department of Biochemistry and Clinical Laboratories, Faculty of Medicine, Tabriz University of Medical Sciences, Tabriz, Iran *Author for correspondence: Mojgan Azadpour, Ph.D. Razi Herbal Medicines Research Center, School of Medicine, Lorestan University of Medical Sciences, Khorramabad, Iran. Email: mojganazadpour@yahoo.com **Abstract Background:** As a natural compound, alpha-pinene is reported to have a number of properties, including its ability to inhibit the growth of cancerous cells. Recent studies suggest that alpha-pinene can prevent the invasion of malignant cells in some cancers. During epithelial-mesenchymal transition (EMT), cancer cells lose their epithelial characteristics and migrate to adjacent tissues. There's evidence that microRNA-106b (miR-106b) indirectly contributes to EMT, which leads to tumor cells migrating and invading other tissues. Therefore this study aimed to investigate the effect of alpha-pinene on the expression of miR-106b and E-cadherin in HepG2 cells. **Methods:** The human hepatocellular carcinoma cell line HepG2 was treated for 24 hours with different concentrations of alpha-pinene in the present study. The expression levels of miR-106b and E-cadherin were determined by RT-qPCR. **Results:** Alpha-pinene significantly downregulated miR-106b in different treatment groups compared to the control group. Furthermore, at different alpha-pinene concentrations, E-cadherin gene expression was significantly increased. **Conclusion:** By downregulating miR-106b and increasing E-cadherin expression, alpha-pinene inhibits HCC migration and invasion. So, we concluded that alpha-pinene could be helpful in preventing the proliferation of cancer cells. **Keywords:** Hepatocellular Carcinoma, Alpha-pinene, Epithelial-Mesenchymal Transition, MicroRNA, E-cadherin.



چهاردهمین گنگره بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Investigation of the potential effect of alpha-pinene on the miR-21 and EMT marker (Vimentin) in hepatocellular carcinoma cells (HepG2).

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نوع پذیرش: پوستر | کد مقاله: G-92580

Abstract: Background: According to several studies, alpha-pinene has a number of properties, including inhibiting cancer cell growth. Some studies in recent years indicate that alpha-pinene can prevent the invasion of malignant cells in some cancers, despite the lack of studies on its effect on cell invasion. As cancer cells undergo epithelial-mesenchymal transition (EMT), they lose their epithelial characteristics and migrate to adjacent tissues. MicroRNA-21 (miR-21) may play an indirect role in the EMT process, which ultimately results in tumor cells migrating and invading surrounding tissues. Therefore this study aimed to investigate the effect of alpha-pinene on the expression of miR-21 and Vimentin in HepG2 cells. Methods: In the current study, the human hepatocellular carcinoma cell line HepG2 was treated with different concentrations of alpha-pinene for 24 hours. The expression levels of mir-21 and Vimentin were determined by RT-qPCR. Results: Alpha-pinene significantly downregulated miR-21 and Vimentin in different treatment groups compared to the control group. Conclusion: Based on the results of this study, it is likely that alpha-pinene plays a critical role in inhibiting the migration and invasion of HCC cells by downregulating miR-21 and Vimentin. So, we concluded that alpha-pinene could be helpful in preventing the proliferation of cancer cells. Keywords: Hepatocellular Carcinoma, Alpha-pinene, Epithelial-Mesenchymal Transition, MicroRNA, Vimentin.



چهاردهمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Investigating new methods in cancer diagnosis and treatment and cancer gene therapy based on nanoparticles (a systematic review)

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نوع پذیرش: پوستر | کد مقاله: G-45267

Abstract: Background: Despite many advances in cancer treatment, cancer is still one of the leading causes of death worldwide. Cancer treatments have progressed significantly, current cancer treatments include surgical intervention, radiation therapy, and the use of chemotherapy drugs. Therefore, in the fight against cancer, screening, and early diagnosis provide important information for timely cancer treatment and are very important for improving the quality of life of patients. Intratumoral heterogeneity of cancer cells is the main obstacle to effective cancer treatment. Therefore, researchers are looking for ways to kill cancer cells. Today, the emergence of new diagnostic technologies can help improve the treatment of various cancers. Cancer nanotechnology is a new branch in biology that makes a connection between nanotechnology and clinical cancer research, and it has been considered worldwide for cancer treatment. The purpose of this study is to investigate new methods in cancer diagnosis and treatment and cancer gene therapy based on nanoparticles. Methods: This study is a systematic review study that was conducted in 1401. By using the keywords of Cancer, gene therapy, nanoparticles, treatment in reliable databases including PubMed, Scopus, Cochrane, Web Of Science, Embase, and Google scholar search engine without a time limit. To ensure the completeness of the search results, the sources of the articles were checked and after removing the duplicate titles from the endnote software and checking the titles and abstracts, the related articles were checked using JBi tools, after checking the quality of the articles, the findings in the checklist the target was entered. Results: A total of 42 articles were reviewed and finally, 14 articles were selected that were related to the purpose of the study. According to the investigations, the results of some studies show that nanotechnology in cancer medicine has emerged as a promising approach to defeating cancer and has shown good progress in the field of drug development and delivery. Through early detection, prevention, and personalized therapy using nanoparticles and quantum dots, cancer nanotechnology offers a unique technology against cancer that can identify a cancer cell and target it to deliver cargo to treat that cancer cell. Nanotechnology has steadily expanded into the domains of cancer chemotherapy, radiotherapy, diagnostics, and imaging, showing the capacity of each to enhance and advance patient care, and has greatly contributed to cancer drug delivery. Conventional cancer treatment methods have side effects and diagnostic methods are time-consuming and expensive. The functionalization of these nanoparticles with various biological molecules, such as antibodies, helps them to deliver an early detection of cancer cells through their plasmonic resonance properties. Conclusion: The obtained results show that many advances have been made in the field of cancer diagnosis and treatment, and cancer nanotechnology has been able to highlight different approaches in the progress of cancer treatment and appears as a promising approach to defeating cancer. Keywords: cancer, gene therapy, nanoparticle, treatment



چهاردهمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Correlation of adiponectin index with infertility and abortion in Iranian women with polycystic ovary syndrome

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نوع پذیرش: پوستر | کد مقاله: G-07123

Abstract: Background: Polycystic ovary syndrome (PCOS) is one of the most common endocrine disorders that affect metabolism and reproductivity. Adiponectin is known as an agent with anti-inflammatory, anti-atherogenic, cardioprotective, and insulin-sensitizing properties. Some studies suggested the clinical applications of adiponectin for predicting metabolic diseases and identifying their underlying metabolic complications, such as IR in PCOS women. This study aimed to assess the association of adiponectin index with infertility and abortion in Iranian women with PCOS. Materials and Methods: A data set of 144 women with PCOS (including 57 infertile patients and 87 patients with a history of recurrent abortion) and 51 healthy control was enrolled in this study. Biochemical parameters were measured and adiponectin index was calculated using the following formula: adiponectin/fasting blood glucose*fasting insulin. Results: Our results showed that with every 0.001 unit increase in adiponectin index, the chance of PCOS-infertile decreases by 12%. Also, each 0.001 unit increase in adiponectin index could decrease the chance of abortion by 9% in PCOS women. Conclusion: In this study, we showed that the adiponectin index is correlated with a decreased risk of infertility and abortion in PCOS patients. Keywords:

The Effect of Wet Cupping (Al-hijamah) and Limonene on Oxidative Stress and Biochemical Parameters in Diabetic Rats

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نوع پذیرش: پوستر | کد مقاله: G-84026

Abstract: Background: According to the international diabetes federation, 629 million adults will suffer from diabetes by 2045. Wet cupping therapy is a combination of bleeding and dry cupping and has been used in traditional medicine as a complementary therapy for diabetes. Limonene was shown to have both antioxidant and antidiabetic activity but its potential alongside other treatments has not been thoroughly explored. Although wet-cupping therapy is widely used under different conditions, its potential in the treatment of diabetes is not well-examined. Materials and Methods: Male Wistar rats were then injected with alloxan and nicotinamide to induce diabetes. After cupping, the rats' serum nitric oxide, creatinine, SGPT, SGOT, cholesterol, triglyceride, glucose, GPX, urea, and HDL levels were determined. The glutathione, catalase, glutathione peroxidase, malondialdehyde, and protein level of the serum, renal, and liver were then measured. Results: The results showed a significant differences in serum glucose levels among the diabetic rats receiving wet cupping and limonene, in serum glutathione levels in diabetic rats receiving limonene or limonene and wet cupping compared to the diabetic rats, in liver GSH levels in control rats receiving limonene and wet cupping, in the liver GPX activity in control rats receiving limonene, and in liver catalase activity in control rats receiving limonene and wet cupping compared to control group. There was no significant change in serum NO, protein, creatinine, SGPT, SGOT, cholesterol, triglyceride MDA, urea, catalase, HDL, renal GSH, MDA, catalase, liver protein, and MDA Level. Conclusion: The findings of the present study suggested that a combination of limonene and wet cupping therapy could be presented as an agent to lower elevated blood glucose levels in diabetic rats. Further clinical studies are required to confirm the findings. Keywords: Wet Cupping Limonene Oxidative Stress Diabetes

Total antioxidant capacity in human seminal plasma of infertile men and their relationship with sperm parameters

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نوع پذیرش: پوستر | کد مقاله: G-80321

Abstract: Background: Oxidative stress plays a key role in the pathogenesis of male infertility. But, the adverse effects of oxidative biomarkers on sperm quality remain unclear. This study aimed to investigate the levels of TAC (total antioxidant capacity) in seminal plasma and their relationship with sperm parameters. Materials and Methods: The study subjects included 77 individuals with the age ranging between 24 to 35 years old. The subjects were classified into two groups; control group including 40 fertile and 37 infertile patients. The semen samples were collected into sterile container and Routine semen analysis was performed within 1 hour. After semen analysis, samples were centrifuged at 4,000 g for 10 minutes and stored at 20°C for measurement of the TAC biomarker. This biomarker was evaluated using the ferric reducing ability of plasma (FRAP) method. Results: In this study, the mean TAC in the seminal plasma was significantly lower for infertile men than for men in the control group ($1,697.11 \pm 708.18$ and $2,015.50 \pm 670.95$ $\mu\text{M/L}$, $p=0.046$) in addition we found a Positive correlations between TAC and sperm count ($p=0.043$, $r=0.232$) and between TAC and normal sperm morphology ($p=0.025$, $r=0.255$). Conclusion: In conclusion, Decreased levels of TAC cause infertility in men and TAC levels is lower in the seminal plasma of idiopathic infertile men than in that of healthy fertile men. Keywords:



چهاردهمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Recent Advances in Developing Portable Sensing assays for Sensitive Cancer Biomarker Determination

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نوع پذیرش: پوستر | کد مقاله: G-75608

Abstract: Recently, as technology has advanced, electrochemical portable assays provide accurate, dependable, and sensitive approaches to various biomarkers and analytes. Portable biosensors and bio-electronic systems have been employed effectively in different areas including medicine, pharmacology, environment monitoring, and food quality management. Some of the available techniques for cancer biomarkers detection are included enzyme-linked immunosorbent assay (ELISA), radioimmune assays (RIA), Polymerase Chain Reaction (PCR), chemiluminescence immunoassay (CLIA), western blotting, flow immunoassay (LFIA), and later Fluro-enzymatic immunoassay. Nevertheless, because of the drawbacks such as high costs, limited sensitivity, time consumption, and constraints, an appropriate replacement for such approaches is needed. Portable biosensors can be utilized to overcome these restrictions and improve detection functionality. The trace determination of the most cancer biomarkers in body fluids by mobile health (mHealth) equipment requires high bio-affinity sensors that depend on the applied “bioreceptors”. The technologies should be sensitive and selective without incorrect false positive and false negatives results. Also, they should be able to detect cancer-specific biomarkers in a non-invasive or minimum invasive manner. Portable point-of-care (POCT) sensing devices have shown their wide range of applications, ranging from the monitoring of health systems to the diagnostic and treatment of most cancers. Portable-based biosensors are small, cost effective, sensitive, and online detection equipment provides real-time determination of biological agents. Nanomaterial-based compounds, microfluidic systems, and the wireless networking skills are significantly required for design and development of mobile based biosensing assays. The aim of this review is to discuss the new progress of mHealth bio-affinity technology from laboratory testing to mobile POCT tools and electronic portable assays for the detection of cancer biomarkers. This review discusses the latest advancements in portable sensing assays which are highly sensitive to cancer biomarkers. Initially, the technique and definition of several created portable biosensing assays will be described shortly. Afterward, the usage of various biosensing and portable sensing approaches to measure various types of cancer biomarkers will be described. Ultimately, existing restrictions, remedies, and future changes will be offered for improvements to such portable tests. Keywords:



Improvement of Streptozotocin-Induced Diabetic Wound Healing Using Zinex Ointment

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نوع پذیرش: پوستر | کد مقاله: G-84573

Abstract: Background: Diabetes mellitus is a metabolic disease that causes vascular damages due to the excessive accumulation of glucose and poor wound healing in diabetic patients is a serious public health challenge. Various investigations have been performed in different compounds application to increase the rates of diabetic wound closure and healing. The present study aimed to evaluate the effects of Zinex ointment to increase the rate of wound closure and the re-epithelialization process in diabetic rats. Methods: This study was performed on 56 Balb/C mice. For diabetes induction, the animals were fed by a high-fat diet for 2 weeks and followed by a single dose of STZ (30 mg/kg) injection intraperitoneally. For similarity to the human diabetic wound model, the excisional wound splinting method through a biopsy punch was hired. Glucose and insulin levels were measured by a glucometer and an ELISA kit, respectively. Histopathological examinations were also performed by H&E and Mason trichrome staining methods. Results: Macroscopic observations indicated the increase in wound closure rate in the Zinex group compared to other groups. Histopathological data also showed a significant decrease of inflammation and increased collagen synthesis in the Zinex treatment group compared to the silver sulfadiazine and control groups. Conclusion: The Zinex ointment could improve the rate of closure and re-epithelialization in diabetic rat wounds through inflammation reduction and collagen synthesis acceleration. Keywords: Diabetes mellitus, Re-epithelialization, Streptozotocin, Wound healing, Zinex



چهارمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Evaluation of activity and concentration of paraoxonase 3 enzyme in Parkinson's patients

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نوع پذیرش: پوستر | کد مقاله: G-92316

Abstract: Background: Paraoxonase enzyme consists of three families 1, 2 and 3. And all this family of enzymes play a role in inflammatory and antioxidant reactions and protect cells against antioxidants. Therefore, in recent years, more studies have been conducted on them in relation to many diseases, including inflammatory and neurodegenerative diseases. According to these findings and previous studies, considering that oxidants play an important role in promoting Parkinson's disease and these paraoxonase enzymes play an important role as antioxidants, as a result, we decided to investigate the activity and level of paraoxonase 3 enzymes in Parkinson's disease. Materials and Methods: In this study, we selected 75 people with Parkinson's disease and 75 healthy people who were free of any kind of neurological and metabolic disease. Serum levels of PON3 were determined using commercially available ELISA kit. Activity of PON3 determinate by spectrophotometry. Data are expressed as mean \pm standard deviation for continuous variables, and frequencies and percentages for categorical ones. For continuous variables, the existence of a normal distribution was ascertained by the Kolmogorov-Smirnov test. Moreover t test used for comparing quantitative factors. Results: According to our study, the level of paraoxonase 3 enzyme error in parkinsonian patients was higher than the control group, but it was not statistically significant, but compared to the activity of this enzyme, the level of activity of this enzyme in the control group was higher than the control group, and it was statistically significant (P 0.001). Conclusion: According to our study and the information obtained from this study, it can be concluded that the activity level of paraoxonase 3 enzyme decreases in Parkinson's patients and this enzyme does not play its antioxidant role against oxidants in Parkinson's patients. As a result, people become prone to Parkinson's disease, which, of course, requires more studies in this field. Keywords: Parkinson's disease, paraoxonase 3, antioxidant.



چهاردهمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Utilizing Artificial Intelligence for Improved Cancer Detection

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نوع پذیرش: پوستر | کد مقاله: G-13248

Abstract: Background: Timely diagnosis of cancer is one of the most important steps in curing cancer, if not the most important. Unfortunately, due to the many variegated types of disease and also the specific condition of each patient which determines if they can receive/respond to the treatment or not, the diagnosis of cancer remains a challenge for the medical team. Implementing Artificial Intelligence which has proven itself over these recent years may be the Holy Grail for prompt diagnosis of cancer that results in decreased mortality rate and cost of the treatments. Methods: An AI system for the detection of breast cancer that uses Deep learning convolution neural networks to detect calcification and soft tissue lesions from mammograms and then rates their level of malignancy. The results were compared with the normal diagnosis of 101 radiologists. It must be mentioned that radiologists had access to the previous mammograms of the patients but AI did its analysis only based on the current data they had. Results: The overall performance of the AI according to the statistics was slightly better than the mean performance of the radiologists. AI had a better performance than 62 of the 101 radiologists and a better sensitivity than 57.9% of the radiologists. Although the top radiologists always performed better than the AI. The performance and sensitivity of AI were closely comparable to the average performance and sensitivity of the radiologist. Conclusion: With the fast advancements of artificial intelligence algorithms in all areas of human life, their major role in the near future of the medical world is undeniable. Implementation of AI will shorten the diagnosis time of the disease, and lower the cost of treatment both for the patient and the national health system while decreasing the mortality rate. With more resources and focus on the use of AI in the medical area, we could certainly enter a new era of medicine. Keywords:



چهاردهمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Dual role of TGF- β in early pregnancy: clues from tumor progression

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نوع پذیرش: پوستر | کد مقاله: G-62845

Abstract: Background: TGF- β signaling in the endometrium is active during the implantation period and has a pivotal role in regulating endometrial receptivity and embryo implantation. During embryo implantation, both apoptosis and proliferation of endometrial cells happen at the same time and it seems TGF- β is the factor that controls both of these processes. As shown in cancer cells, in special conditions this cytokine can have a dual effect and switch the action from apoptosis to proliferation. Materials and Methods: Owing to the similarity between embryo implantation and cancer development and also unusual pattern of proliferation and remodeling in the uterus, in this review we suggest the existence of such a switching (switch the action from apoptosis to proliferation) in endometrium during the early pregnancy. In this review, we explained the potential mechanisms that can determine whether the TGF- β causes apoptosis or proliferation including differences in the function of the TGF- β isoforms, differences in the distribution of the TGF- β receptors on the surface of target cells, variety in the levels of TGF- β and severity of its signaling, production of factors by the target cell that can antagonize TGF- β -induced apoptosis. Moreover, we provide evidence that steroid hormones, as well as embryo itself, are the potential factors that control the role switching of TGF- β . Results: We suggest this hypothesis that TGF- β may induce either cell proliferation or apoptosis based on the cell condition through the various mechanisms. Conclusion: TGF- β has a dual effect in tumor progression and can switch the cell fate from apoptosis to proliferation, and possibly plays a similar role in endometrium during the early pregnancy. Keywords:

Evaluation of the cytotoxicity and antioxidant effects of South Khorasan jujube honey and its comparison with commercial honey in MCF-7 cell line.

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نوع پذیرش: پوستر | کد مقاله: G-17459

Abstract: Background: Breast cancer is one of the most important causes of death among women in the world. Honey is one of the natural compounds. So far, many studies in vivo and invitro have been conducted regarding the anti-cancer properties of honey. In this study, we investigated the cytotoxicity and antioxidant effect of Jujube honey (JH) on MCF-7 and compared its effects with Commercial honey (CH). Materials and Methods: First, we measured the amount of total phenolic compounds (TPC) of jujube and commercial honey using a Folin-Ciocalteu reagent (Kavosh Arian Azma Co., Iran). 1×10^4 MCF-7 cells were seeded in a 96-well plate in RPMI-1640 then incubated at 37°C and 5% CO₂ for 24 hours. Then cells were treated with different concentrations of JH and CH (0-10%) for 24 hours. Then, by MTT test, the cytotoxic effects of honeys were evaluated. After determination IC₅₀, 2×10^5 cells, were seeded in a 6-well plate in RPMI-1640 then incubated at 37°C and 5% CO₂ for 24 hours, then cells were treated with concentrations lower than IC₅₀, after 24 hours, cells were treated with 2,7-Dichlorofluorescein diacetat (DCF-DA) (10 μM in RPMI) for 45 minutes at 37 °C and 5% CO₂. After trypsinizing and washing the cells twice with PBS, the amount of intracellular ROS was measured by flow cytometry (CyFlowCube 6, SysmexPartec, Germany). Result: The results obtained from the MTT assay showed that JH (IC₅₀= 3.5%) had higher cytotoxicity than CH (IC₅₀= 8%) in MCF-7 cell line. 2,7-Dichlorofluorescein diacetat was used to monitor the ROS level into the cell by flow cytometry technique. The results showed that both JH and CH decreased intracellular ROS level in MCF-7 cell line, but this decrease in JH has been more than CH. The amount of intracellular ROS in the control, CH (1%) and JH (1%) were 97%, 89% and 77% respectively. Conclusion: The difference between honeys is due to the difference in flower source, geographical origin, storage method and honey collection season. These factors affect the amount and type of chemical compounds in honey. Our results show that JH has higher phenolic compounds and antioxidant properties than commercial honey, both JH and CH prevent the growth of cancer cells, but JH exerts its effect at a lower IC₅₀ than CH. Keywords: Honey, cytotoxicity, breast cancer, antioxidant.

Experimentally-induced polycystic ovarian syndrome elevated inflammatory cytokine release and expression of TLR-2 and TLR-4

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نوع پذیرش: پوستر | کد مقاله: G-15239

Abstract: Background: Polycystic ovarian syndrome (PCOS), is the most prevalent endocrine-related disease in women at the reproductive age. Recent studies have reported a chronic low-grade inflammation in PCOS women. However, the molecular mechanism(s) of mentioned inflammation remains uncertain. In this study we aimed to show the role of inflammatory cytokine and in particular TNF- α and the most relevant inflammatory genes role in the PCOS. Materials and Methods: PCOS was induced in female mice (22-days old) with DHEA (60 mg/kg/day, IP) in PCOS group (n=6) and control group received 0.1 ml/mouse/day sesame oil for twenty eight consecutive days. Both blood sampling and tissue collection from animals were conducted a day after the last treatment. Serum level of TNF- α as an inflammatory cytokine was measured by R&D systems kit (614 McKinely place NE Minneapolis, MN 55413, USA) according to the manufacture's instruction. Quantitative-PCR analyses were conducted on the ovarian tissue to explore the expression level of two main inflammatory genes of TLR-2 and TLR-4. Results: our results indicate that the DHEA-induced PCOS in mice resulted in a significant elevation of TNF- α concentration compared to the control group. At the same time, qPCR analyses revealed 1.4-fold upregulation of both inflammatory encoding genes of TLR-2 and TLR-4, when calculated based on the house keeping gene of GAPDH and also following adjusting with the expression of mentioned genes in the control group. Conclusion: our results suggest that the DHEA-induced PCOS produce an inflammatory condition, which characterized by elevation of TNF- α and up-regulation of TLR-2 and TLR-4. Keywords:

Therapeutic effect of Trace elements (Micronutrients) on Multiple myeloma and cancer progression

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نوع پذیرش: پوستر | کد مقاله: G-31962

Abstract: Background: In the human body, trace elements and micronutrients, play a vital role in growth, health and Immune system function. Estimating the serum levels of trace elements in hematologic malignancy patients can determine the severity of the tumor. The micronutrients are Iron, Manganese, Copper, Iodine, Zinc, Cobalt, Fluoride, and Selenium. Multiple myeloma (MM) is a hematopoietic malignancy and is characterized by plasma cell clonal expansion in bone marrow. The average survival in patients with new treatment regimens and the use of myeloablative chemotherapy with autologous stem cell transplantation (ASCT) is more than 6 years. Despite the advances in treatment methods, myeloma remains largely incurable. In addition to conventional medicine, treatment is moving toward less expensive noninvasive alternatives. One of the alternative treatments are use of dietary supplements. Materials and Methods: Authors searched English published articles in local and international journals over the period 2000 to 2022 using several databases including Scopus, PubMed, Scholar, and Science Direct. Then, the relevant articles were revised. During this period, different articles have been published, but we tried to choose and review articles that introduced effective data. Results: In this review we focused on three trace elements including iron, zinc and selenium in 3 main topics included the immune system, oxidative and anti-oxidative factors, and cell cycle, which include proliferation and apoptosis. The immune system has a strong dependency to Zinc, Iron and Selenium availability and escaping from immune system is very important for cancer development and malignancies. Increased levels of TNF- α in myeloma patients are associated with the aggressiveness of the disease. Zinc deprivation leads to the expression of the TNF α gene. One of the factors that play a role in the pathogenesis of cancer and increasing the risk of carcinogenesis is oxidative stress. Zinc with reducing oxidative stresses and increasing antioxidative markers eventually reduces the risk of developing multiple myeloma, such as NOX1, NOX2, SOD1, SOD2, NRF2. ROS are formed upon iron exposure, thus causing cell death and impairing MM cell proliferation and Proteasome inhibitor Bortezomib in combination with iron is more effectively interferes with MM cell survival and disease progression than individual agent therapies. Selenium-containing heterocyclic compounds inhibit the proliferation of human multiple myeloma cells. Cell proliferation and cell death ratios are mechanisms which protect tissues from generating tumors. Also trace elements can inhibit proliferation and induce cell apoptosis in cancerous cells in a dose-dependent manner. Conclusion: In modern medicine, the use of some trace minerals in combination with approved drugs for some diseases can increase the speed of recovery of patients. The research results shows that trace elements can be used as a not only preventive but also therapeutic tool, especially in reducing inflammation in hematological cancers such as multiple myeloma, but depending on the dose used, minerals such as zinc, iron and selenium can have opposite effects. We hope that the prospect of correct use of trace element supplements in the future could be promising for the treatment of diseases. Keywords:



چهاردهمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Improving the results of newborn thyroid screening using TSH measurement and algorithms to improve technical and human errors

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نوع پذیرش: پوستر | کد مقاله: G-71965

Abstract: Background: One of the most prevalent endocrine diseases associated with mental impairment and developmental retardation in newborns is neonatal hypothyroidism. Neonatal thyroid screening programs are used in several countries to quickly identify and treat hypothyroidism. This study's main goal was to enhance thyroid screening programs utilizing primary blood TSH or backup TSH assessments because some individuals are overlooked owing to procedural and administrative mistakes. Materials and Methods: 9,118 infants were assessed using the methodology. Additionally, the sampling strategy and laboratory results were enhanced by the application of quality control techniques. Results: Our method discovered three neonates that were missed by existing algorithms utilizing the cutoff point of more than 20 mU/l for blood TSH. Conclusion: The systems based on the primary blood TSH/backup TSH measurements improve the thyroid screening findings, according to the results. Keywords: Neonatal hypothyroidism, thyroid screening, TSH measurements, technical errors



چهاردهمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



The crosstalk between miRNAs and the PI3K/AKT signaling pathway in breast cancer

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نوع پذیرش: پوستر | کد مقاله: G-87520

Abstract: Background: Breast cancer as one of the most frequently diagnosed tumors, causes the second highest rate of mortality in women worldwide. Breast cancer tumorigenesis is a complicated process involving the upregulation of oncogenes or downregulation of tumor suppressor genes. Recent studies demonstrated that some MicroRNAs (miRNAs) as oncogenic factors are upregulated and promote tumor growth and metastasis by inducing the oncogenic signalings such as PI3K/Akt, Ras/Raf/Mek/Erk, and Wnt/ β -catenin pathways. In this study, we review the role of regulatory miRNAs in PI3K/AKT signaling in the pathogenesis of breast cancer. Materials and Methods: We conducted literature searches with Google Scholar and PubMed using the keywords including breast cancer, microRNA, PI3K/AKT signaling pathway from 2010 to 2022. Results: miRNAs can affect many important cellular processes including cell proliferation, apoptosis, invasion, and metastasis by regulating the expression of their related mRNAs. It has been shown that the oncogenic or tumor suppressive effects of miRNAs on breast cancer tumorigenesis may be mediated by regulating the activity of PI3K/Akt signaling pathway. Conclusion: The current data suggest that miRNAs can regulate the tumorigenesis of breast cancer through targeting PI3K/AKT pathway and can be used as prognostic or diagnostic biomarkers for breast cancer therapy. Therefore, pharmaceutical interventions targeting miRNAs of the PI3K/AKT signaling pathway may provide a promising therapeutic strategy for the treatment of breast cancer. Keywords: PI3K/AKT signaling, MicroRNA, Breast cancer

Anti-inflammatory function of Apo lipoprotein B-depleted plasma is impaired in nonalcoholic fatty liver disease

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نوع پذیرش: پوستر | کد مقاله: G-03942

Abstract: Background: Non-alcoholic fatty liver disease (NAFLD) is associated with an increased risk of cardiovascular events. HDL exerts various protective functions on the cardiovascular system including anti-inflammatory activity by suppressing adhesion molecules expression in inflammation-induced endothelial cells. This study was designed to search if the anti-inflammatory capacity of Apo lipoprotein B-depleted plasma (apoB-depleted plasma) is altered in NAFLD patients. Materials and Methods: A total of 83 subjects including 42 NAFLD and 41 control subjects were included in this cross-sectional study. Anti-inflammatory function of HDL was determined as the ability of apoB-depleted plasma to inhibit tumor necrosis factor- α (TNF- α)-induced expression of adhesion molecules in human umbilical vein endothelial cells (HUVECs). Results: Incubation of inflammation-stimulated HUVECs with the NAFLD patients' apo-B depleted plasma led to higher levels of expression of adhesion molecules compared to the control subjects' plasma samples, reflecting an impaired anti-inflammatory capacity of apo- B depleted plasma in the NAFLD patients. Impaired anti-inflammatory capacity of apo-B depleted plasma was correlated with fatty liver and obesity indices. After adjustment with obesity indices, the association of anti-inflammatory capacity of apo B-depleted plasma with NAFLD remained significant. Conclusion: Impaired anti-inflammatory activity of apoB-depleted plasma was independently associated with NAFLD. Keywords:

The interplay between miRNAs and Wnt/ β -catenin signaling pathway in colorectal cancer: from tumorigenesis to metastasis

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نوع پذیرش: پوستر | کد مقاله: G-58902

Abstract: Background: Colorectal cancer (CRC) is the third most common malignancy worldwide with over 700,000 attributable deaths per annum. Despite recent progress in improving diagnostic and therapeutic strategies, the overall survival rate remains low and patients suffered from adverse clinical outcomes and poor prognosis. It has been shown that CRC carcinogenesis is a multistep process that involves genetic alterations in oncogenes or tumor-suppressor genes resulting in the activation of various cellular signaling pathways such as Wnt/ β -catenin signaling pathway. Increasing evidence indicates that microRNAs (miRNAs) exert oncogenic effects in CRC tumorigenesis by upregulating the Wnt/ β -catenin signaling pathway. This review summarizes the current knowledge on the regulatory role of miRNAs on Wnt/ β catenin signaling in the pathogenesis of CRC. Materials and Methods: Our research was based on Google Scholar and PubMed databases by related keywords and MeSH terms including: colon cancer, colorectal cancer, tumorigenesis, microRNAs, and Wnt/ β -catenin signaling pathway from 2010 to 2022. Results: Molecular data indicate that the oncogenic miRNAs can promote tumor cell proliferation, migration, invasion and metastasis by upregulating the Wnt signaling-related proteins including β -catenin, cyclin D1 and c-myc. Interestingly, the tumor suppressive miRNAs inhibit tumor malignant features of CRC via repressing the Wnt/ β -catenin signaling pathway. Conclusion: These findings support the hypothesis that modulation of miRNAs profile is a key mechanism in anti-tumor properties of Wnt/ β -catenin pharmacological inhibitors in cellular or clinical models. Therefore, pharmaceutical interventions targeting the Wnt/ β -catenin signaling regulatory miRNAs may provide a promising therapeutic strategy for the treatment of CRC. Keywords: Wnt/ β -catenin signaling pathway, miRNA, Colorectal cancer, colon cancer and tumorigenesis



چهاردهمین گنگره بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



The effect of supplementation of omega-3 on serum levels of antioxidant status in patients with bipolar disease

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نوع پذیرش: پوستر | کد مقاله: G-89104

Abstract: Background: Antioxidants are involved in the membrane-associated pathologies in the central nervous system and play major roles in the prevention of the progression of neuropsychiatric disorders, such as bipolar disorder (BD). Omega-3 fatty acid supplementation helps to prevent lipid peroxidation and improve antioxidant status. Aims: This study aimed to investigate the effect of supplementation of omega-3 on serum levels of antioxidant status in patients with bipolar disease. Methods: In this study, 28 men and women with BD received an omega-3 fatty acid supplement (2 gr/daily) while other patients (n=28) received edible paraffin oil (2 gr/daily) for 60 days. The activities of superoxide dismutase (SOD), catalase (CAT), and total antioxidant capacity (TAC) were evaluated in pre-intervention and post-intervention. The study was registered at the Iranian Registry of Clinical Trials IRCT (IRCT20211220053469N2; www.irct.ir). Results: The results showed that omega-3 supplementation increased the activities of SOD (12.94 ± 3.84 U/mL vs 17.72 ± 3.59 U/mL) and CAT (5.08 ± 1.61 nmol/min/mL vs 6.43 ± 1.33 nmol/min/mL) in post-intervention compared with pre-intervention ($P=0.001$). Our findings also showed that omega-3 supplementation increased the activities of SOD (17.72 ± 3.59 U/mL vs 13.79 ± 3.12 U/mL) and CAT (6.43 ± 1.33 nmol/min/mL vs 4.89 ± 1.45 nmol/min/mL) compared with the control group in post-intervention ($P=0.001$). Our findings showed that omega-3 supplementation did not have significant effects on the serum concentration of TAC compared with pre-intervention ($P=0.373$) and control group ($P=0.604$). Conclusion: In conclusion, omega-3 supplementation increases the activities of SOD and CAT and can decrease disease progression via increasing antioxidant status. Keywords: Antioxidant capacity, Bipolar disease, Catalase, Omega-3

Comparison effect of kaolinite, talc nanocomposite chitosan-capped inorganic/organic hybrid on full-thickness infected wound healing

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نوع پذیرش: پوستر | کد مقاله: G-13062

Abstract: Background: Damage of skin could be triggered by trauma, chronic wounds, and surgical procedures. Certain bacteria infect wound areas, such as *Staphylococcus aureus*, and *Pseudomonas aeruginosa*. Infection in wounds increases the volume of exudates, prevents the formation of granulation tissue, and delays the wound healing process. Some natural rocks have been traditionally used for the treatment of wounds. Perlite is a generic name for an amorphous volcanic alumina silicate rock and has been utilized as a carrier for bacterial inoculants. We aimed to synthesize a nanocomposites (NCPs) prepared from kaolinite NCPs and talc, perlite, and chitosan; however, reducing and capping agents were needed to immobilize kaolinite NCPs and Talc on perlite. Phytochemical compounds of the plant extract were reported as appropriate choices for reducing metal ions and stabilization and production of nanoparticles. This study was conducted to compare the effects of a novel topical wound dressing based on an ointment containing kaolinite NCPs/perlite and talc/perlite nanocomposites and its chitosan-capped derivative on the wounds infected in mouse models. Materials and Methods: In order to investigate the effects of NCPs on wound healing process, a concentration (2% w/w) of Perl, kaolinite/Perl, talc/perl, kaolinite NCPs /Perl/Chit and talc/Perl/Chit powder was added into a base ointment. To induce the infected wounds, the mice were initially anaesthetized as reported previously. A circular full-thickness skin wound (7 mm²) was created by surgical biopsy punch and infected by an aliquot 5 × 10⁷ MRSA [6]. The healthy BALB/c male mice (n = 90) were divided into five groups (n = 18), each of which included 18 mice, 24 h after inoculation of the bacteria. The mice were treated on a daily basis with 0.5 g ointments containing (I) Perl, (II) kaolinite NCPs /Perl, (III) kaolinite NCPs /Perl/Chit, (IV) talc/Perl/Chit (V) mupirocin® ointment (Mup, and (VI) control mice as negative control. The wound area was measured with a graph sheet as reported by previous studies on days 3, 7, and 14. Moreover, the bacteriological examination of granulation tissue was performed as reported previously on days 3, 7, and 14. The data were reported as CFU/g of granulation tissue Results: The results revealed that kaolinite NCPs /Perl/Chit and talc/Perl/Chit were mesoporous and spherical in a range of 13–15 nm, respectively. Topical administration of kaolinite NCPs /Perl/Chit and talc/Perl/Chit ointments accelerated wound healing by reducing bacteria colonization, collagen biosynthesis, and re-epithelialization. Conclusion: kaolinite NCPs /Perl/Chit and Ag/Tlc/ Csn are suggested to be taken into consideration as a medical combination for improving infected wound healing and as a promising agent for clinical administration.

Covid19 and liver enzymes.

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نوع پذیرش: پوستر | کد مقاله: G-31854

Abstract: Background: Liver enzymes have key roles in the liver metabolisms, catalyzing the biochemical reactions and detoxifying toxins, drugs and other xenobiotics. The activity of liver enzymes changes in liver disorders. These changes may help us in prognosis and diagnosis some liver diseases. Covid19 is a viral infectious disease that infects host cells by binding to the ACE2 receptor. This receptor is also express in hepatocytes suggesting that liver injury may be caused by direct viral invasion. Immune mediated injury caused by severe inflammatory reaction after covid19 infection can also cause liver injury (cytokine storm). Materials and Methods: In this study, liver enzymes including AST, ALT, ALP, LDH and Alpha 1 antitrypsin(AAT) as a protease inhibitor playing an important role in protecting lung tissue were investigated in 31 hospitalized patients with positive PCR test for covid19 and 31 healthy individuals(as controls). AAT measured by nephelometric method, which is based on the reaction between a specific antibody and an antigen. ALP and LDH measured by photometric method based on color measurement. AST and ALT measured by kinetic method based on measurement of produced NADH. Result: Serum AAT (178.9 ± 41.4 mg/dl) vs (129.4 ± 13.9), AST (38.9 ± 22.1 U/L) vs (23.7 ± 6.2), ALT (32.06 ± 11.7 U/L) vs (17.9 ± 6.2) and LDH (578.1 ± 206.2 U/L) vs (269.5 ± 69.6) in covid19 patients show a significant increasing as compared to healthy controls P (0.05). But serum ALP (170.9 ± 50.6 U/L) vs (145.7 ± 40.7) doesn't exhibit a significant increasing. Conclusion: It has been concluded in these patients the liver enzymes should be analyzed and checked parallel to other laboratory tests and the physicians must pay attention to administration for treatment. Keywords:

Investigating metabolic syndrome indicators in morbidly obese patients referred to Ghadir Mother and Child Hospital in Shiraz, before and after bariatric surgery

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نوع پذیرش: پوستر | کد مقاله: G-72548

Abstract: Background: Obesity is one of greatest challenges for healthiness. Obesity has negative effects on physical, psychological and social healthiness. Surgery procedures can have positive effects in decreasing obesity. This study was conducted to survey metabolic syndrome indicators in morbid obese patients referring to Ghadir mother and child hospital of Shiraz, before and after bariatric surgery. Materials and Methods: The target populations were including all the morbid obese patients referring to Ghadir mother and child hospital of Shiraz during 2018-2022 years and 165 patients were studied. The data were collected for waist circumference, Low-density lipoprotein (LDL), triglycerides (TG), blood glucose and blood pressure. The data were investigated for normality and since they were normal, we used parameteric test of paired-T by using SPSS software. Results: The results showed that bariatric surgery methods could have a significant effect on all the investigated variables in metabolic syndrome (P0.001). The results of this study showed that bariatric surgery significantly reduced waist circumference (P0.001), fasting glucose (P0.001), triglycerides (P0.001), LDL (P0.001) and blood pressure (P0.001). Conclusion: In conclusion, the results showed that surgery procedures had positive effects in decreasing syndrome metabolic signs in morbid obese patients referring to Ghadir mother and child hospital of Shiraz. Keywords:



Anti-tumor mechanism of Rigosertib in K-Ras mutant colorectal cancer cells

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نوع پذیرش: پوستر | کد مقاله: G-47362

Abstract: Background: Colorectal cancer (CRC) is a major cause of cancer-related mortality worldwide with over 700,000 attributable deaths per annum. The therapeutic potency of Rigosertib (RGS) in the treatment of myelodysplastic syndrome has been investigated previously, but little is known about its mechanisms of action. Materials and Methods: The present study aimed to investigate the anti-cancer mechanism of RGS in CRC cell lines including Caco2, HT-29, SW-480, and CT-29. The cytotoxic effects of RGS on CRC cells were assessed by MTT assay. The regulatory effects of RGS on the expression of P21 were investigated by Real-Time PCR and western blotting. To further investigate the tumor suppressive mechanism of RGS, the cell cycle progression was analyzed by flow cytometry method in different CRC cells. Results: RGS inhibited cell viability, cell proliferation, and cell cycle progression in a cell-type specific manner, and that was dependent on the presence of mutations in KRAS, or its down-stream effectors. Conclusion: Our findings support the anti-cancer effects of RGS as a potent RAS signaling inhibitor in CRC cells. Further studies are required to investigate the tumor suppressive mechanism of RGS, which may provide a new option for CRC treatment. Keywords: Colorectal cancer, Rigosertib, p21



چهاردهمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Interplay of miRNAs and PI3K/AKT/mTOR signaling in Hepatocellular carcinoma

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نوع پذیرش: پوستر | کد مقاله: G-61342

Abstract: Background: Hepatocellular carcinoma (HCC) is the third leading cause of cancer death with over 600,000 deaths annually worldwide. Despite recent advances in diagnostic and therapeutic strategies, the 5-year survival rate remains below 30% in HCC patients with recurrent or metastatic tumors. Thus, understanding the mechanisms underlying HCC is essential for developing novel therapeutic strategies. Molecular data indicated that the HCC pathogenesis involves multiple genetic and epigenetic changes resulting in uncontrolled activation of multiple oncogenic signaling pathways, including phosphoinositide 3-kinase (PI3K) and canonical Wnt signaling route. Aberrant activation of the oncogenic PI3K signaling by regulatory microRNAs (miRNAs) has been shown to be related to clinicopathological features of HCC. The present review summarizes the major findings about the regulatory role of miRNAs in the PI3K/AKT/mTOR pathway in the pathogenesis of HCC. Materials and Methods: We performed literature searches with PubMed and Google Scholar using the keywords and MeSH terms including Hepatocellular carcinoma, microRNA, and PI3K/AKT/mTOR pathway from 2010 to 2022. Results: Emerging data revealed that miRNAs have prominent implications for regulating cellular proliferation, differentiation, apoptosis, and metabolism through targeting the PI3K signaling related proteins including AKT, PTEN, and mTOR. Furthermore, the tumor suppressive miRNAs were shown to inhibit the progressive features of HCC by repressing the PI3K/AKT/mTOR signaling pathway. Conclusion: The recognition of the crucial role of miRNAs in hepatocarcinogenesis represents a promising area to identify novel anticancer therapeutics for HCC. Therefore, downregulation of oncogenic miRNAs is a key mechanism in the antitumor properties of pharmacological PI3K/AKT inhibitors in cellular or clinical models of HCC. Keywords: Hepatocellular carcinoma, microRNA, PI3K/AKT/mTOR pathway



چهاردهمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Role of regulatory non-coding RNAs on Wnt/ β -catenin signaling pathway in tumorigenesis of urinary tract cancers

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نوع پذیرش: پوستر | کد مقاله: G-41673

Abstract: Background: Urinary tract (UT) cancers are among the most common dangerous tumors that can be located in different parts of the urinary system such as kidney, bladder, prostate, and urethra. Non-coding RNAs (ncRNAs) are emerging as important regulators in various pathological conditions including tumorigenesis, metastasis, and drug resistance in human cancers. It has been shown that ncRNAs accelerate tumor growth and progression by regulating various signaling pathways including Wnt/ β -catenin. This review summarizes the current knowledge on the regulatory role of ncRNAs on Wnt/ β -catenin signaling in tumorigenesis and metastasis of UT cancers. Materials and Methods: Our study was based on PubMed and Google scholar databases by related key words such as: ncRNA, miRNA, lncRNA, Wnt/ β -catenin, urinary tract cancers from 2015 to 2022. Results: LncRNAs and miRNAs play crucial roles in UT cancer migration, invasion, and metastasis by regulating the expression of various genes and proteins at transcriptional and post-transcriptional levels. To investigate the regulatory mechanism of miRNAs/lncRNAs on UT cancers, it has been shown that the effects of these ncRNAs on tumorigenesis of kidney, bladder, and prostate cancers may be mediated by regulating the activity of the Wnt/ β -catenin signaling pathway. Conclusion: Considering the complex interplay between lncRNAs and miRNAs in UT cancers, it has been suggested that downregulation of oncogenic, or restoration of tumor suppressor ncRNAs may repress the malignant features of UT cancers. Keywords: ncRNA, Wnt/ β -catenin, Urinary tract cancer

Radiation injuries treatment

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نوع پذیرش: پوستر | کد مقاله: G-12649

Abstract: Radiation injuries are infrequent, so the medical services meet few cases with radiation injuries. These injuries mostly appear without specific signs and symptoms in early stages, while molecular changes leading to tissue damages start early post radiation. Experience from management of Chernobyl radiation accident casualties and others show that designing the accurate plan for treatment is mandatory in few days post radiation in a situation with many uncertainties. In these conditions laboratory tests will solve the problem. Acute radiation sickness (ARS) is a combination of clinical signs and symptoms occurring in stages over a period of hours to weeks due to a significant partial-body or whole body exposure 1 Gy, as injury to various tissues and organs is expressed. ARS with moderate severity (whole body exposure greater than 2 Gy) needs basically reversed isolation and cytokine therapy for treatment. Cytogenetic biodosimetry shows us the precise hematopoietic radiation injury and we can move on a clear path. Cutaneous radiation syndrome (CRS) proposed to describe an inflammatory reaction of the skin with a particular cytokine profile, observed after radiation exposure. Following exposure to high doses it is not only the skin which is involved, but also the subcutaneous tissue, and even muscles and bones. For superficial lesions of distal extremities, treatment is limited to excision with conservative surgery. In cases of profound and large necrosis, the lesion should be excised and wound bed covered with a good quality, full-thickness skin graft. In case of painful deep ulcerations and necrosis, the classical techniques of plastic surgery should be applied (ulcerectomy, necrectomy, wound closure by rotation flap, amputation). New approach in treatment of sever CRS support by dosimetry guided surgery and mesenchymal stem cell therapy. Early stages of CRS show minimal sign and symptoms including redness, tingling and pruritis disproportionate to the actual severity of the injury. some advanced imaging techniques such as thermography, high frequency ultrasound or blood perfusion imaging show the extent and depth of the lesion. These clarification needs for accurate treatment planning. Internal contamination is the deposition of radioactive material inside the body. Despite some irritant materials such as fluorine compounds of uranium, most radionuclide incorporations have not any specific sign or symptoms in early stages, so treatment must initiate based on accident and patient history, and then confirmed by body counters or bioassay lab techniques. The most usual methods for treatment are chelation therapy, isotopic dilution, metabolic blocking, mobilizing agents, reduction of GI uptake and mechanical (BP lavage). Keywords:

Comparison of concentration, activity, and genotype of alpha-1-antitrypsin protein in patients with liver cirrhosis and healthy people

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نوع پذیرش: پوستر | کد مقاله: G-02618

Abstract: Background: Cirrhosis of the liver is the end stage of chronic liver disease. The most important causes of cirrhosis are alcohol consumption, viral hepatitis, and alpha-1-antitrypsin (A1AT) deficiency. Alpha-1-antitrypsin is an important serine protease inhibitor in humans, encoded by the SERPINA1 gene, and synthesized in liver cells. Liver diseases associated with A1AT deficiency are caused by intracellular accumulation of mutated A1AT protein in hepatocytes. The present study was aimed to investigate the concentration, activity, and genotype of A1AT protein in patients with liver cirrhosis compared to healthy individuals. Methods: The present cross-sectional study was conducted on 25 patients with cirrhosis who referred to the Taleghani Hospital in Tehran, Iran, and 25 healthy control individuals who were matched for age, and gender to the patients. Cellulose acetate electrophoresis was used for A1AT concentration, trypsin inhibitory capacity (TIC) method was used to determine activity, and the PCR-RFLP method was used for genotyping to determine the Z and S deficiency alleles. Independent two-sample t-test and chi-square test were used to analyze data. Results: The mean of serum concentration ($P=0.003$) and TIC levels ($P0.001$) were significantly lower in patients with liver cirrhosis compared to healthy individuals. Genotype in both study groups was MM allele. Conclusion: The lower concentration and activity of A1AT protein in patients with liver cirrhosis can be considered potential prognostic and diagnostic biomarkers in patients with cirrhosis. Keywords: Serine protease, Liver cirrhosis, Alpha-1-antitrypsin gen

Prevalence of Glucose-6-phosphate Dehydrogenase (G6PD) Deficiency in Gerash City

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نوع پذیرش: پوستر | کد مقاله: G-30428

Abstract: Background: Glucose-6-phosphate dehydrogenase (G6PD) deficiency is an X-linked disorder that is one of the most common monogenic diseases in humans. This genetic disorder has different clinical manifestations, which include icteric newborn, hemolysis, and acute icteric following exposure to pharmaceuticals and chemical substances. The aim of this study was to determine the prevalence of G6PD deficiency in infants born in Gerash city. Materials and Methods: This descriptive cross-sectional study was carried out from 2018 to 2022. Blood sample of newborns that referred to Mohammad-Rsololla health center, were taken from heel prick and then the level of G6PD was evaluated using the fluorescent spot test. Results: In the present study, a total of 2564 newborns were included. G6PD deficiency was detected in 9.24 % (N=237) newborns. 193 (14.5%) of the males and 44 (3.56%) of females' neonates were G6PD deficient. Conclusion: As our results showed, the G6PD deficiency in the present study was more than four times higher in male than female newborns. Given the relatively high prevalence of G6PD deficiency in this study, continuous screening for G6PD enzyme activity in all newborns is recommended. Keywords: G6pd Deficiency, Neonatal screening, Gerash city

The effect of jujube honey of South Khorasan on Cyclin d1 gene expression in MCF-7 cell line

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نوع پذیرش: پوستر | کد مقاله: G-58924

Abstract: Background: The most common form of cancer among women is breast cancer. Previous research has shown that deregulation of the cell cycle can take place in cancer at various stages. The best-studied cell cycle protein is cyclin D1, a 34 kDa protein that marks the transition from G1 to S-phase and is a well-known human oncogene in the context of breast cancer. The CCND1 gene codes the cyclin D1 protein. Targeting cyclin D1 is therefore thought of as an alternate method of cancer therapy. In this study, we investigated the effect of Jujube honey from South Khorasan on cyclin D1 gene expression in the MCF-7 cell line. Materials and Methods: 1×10^4 MCF-7 cells were seeded in a 96-well plate in RPMI-1640 and incubated at 37°C with 5% CO₂ for 24 hours. Then cells were treated with different concentrations of Jujube honey (0–10%) for 24 hours. The cytotoxic effects of honey were then assessed using the MTT test. After the determination of IC₅₀, 1×10^6 cells were seeded in a 6-well plate, and after 24 hours, the cells were treated with a concentration of honey (a concentration lower than IC₅₀) for 24 hours under the conditions of 37 °C and 5% CO₂. Then, the culture medium was removed, the cells were washed with PBS, the cells were trypsinized, and cellular RNA was extracted using the Pars Tous kit. 1000 ng of extracted RNA were converted into cDNA by reverse transcription reaction. For this purpose, we used the Pars Tous cDNA synthesis kit. After designing the primer (B2M: as an internal control and CCND1 gene producing cyclin D1 protein), the Pars Tous company master mix kit was used to perform real-time PCR test. Finally, the obtained data were analyzed by the $\Delta\Delta C_t$ method and the relative amounts of mRNA related to the CCND1 gene in the treatment group compared to the control group were calculated through the $2^{-\Delta\Delta C_t}$ formula. Result: MTT results showed that the IC₅₀ of jujube honey is 3.5% , and real-time PCR results also showed that the treatment of the MCF-7 cell line with Jujube honey compared to the control caused a decrease in CCND1 gene expression. Conclusion: According to our results, jujube honey can deeply inhibit the growth and proliferation of MCF7 cells by targeting cyclin D1. Keywords: breast cancer, honey, cyclin D1.



چهاردهمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



The Effects of Asthma on the Oxidative Stress Factors in Children with Pneumonia

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نوع پذیرش: پوستر | کد مقاله: G-70426

Abstract: Background: Pulmonary vascular stress oxidative has been implicated in adverse clinical outcomes of community-acquired pneumonia (CAP). Although chronic lung problems such as asthma may affect the consequences of pneumonia, the exact mechanism of this effect remains unclear. The present study aimed to assess the effects of asthma on the oxidative stress biomarkers in children pneumonia. Materials and Methods: A cross-sectional study designed with a total of 75 children including both severe CAP and asthma (as group I), severe CAP alone (as group II), and healthy children (as group III) was conducted. Fasting blood samples were taken to the assay of serum malondialdehyde (MDA) and total antioxidant capacity (TAC). Results: We observed TAC levels in groups I and II (0.997 ± 0.22 and 1.23 ± 0.21 mmol/l, respectively) were significantly lower compared with group III (1.46 ± 0.19 mmol/l, P value = 0.000). It was significantly higher in group II than in group I (P value = 0.000). Also, we observed MDA level in groups I ($6.94 \pm 1.61 \mu\text{mol/l}$) and II were significantly higher compared with group III ($1.89 \pm 0.27 \mu\text{mol/l}$; P value = 0.000) Conclusion: Asthma can increase oxidative stress of pneumonia in children. Keywords: Community-Acquired Pneumonia, Asthma, Oxidative stress



چهاردهمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Prevalence of Phenylketonuria in Gerash City

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نوع پذیرش: پوستر | کد مقاله: G-98057

Abstract: Background: Phenylketonuria (PKU), which is characterized by insufficiency of phenylalanine hydroxylase enzyme activity, is an autosomal recessive disorder of phenylalanine (Phe) metabolism. In this patient, the high blood Phe concentrations pass through the blood-brain barrier and cause brain damage and severe intellectual disability if left untreated. The aim of this study was to determine the prevalence of PKU in infants born in Gerash city. Materials and Methods: A cross-sectional study was performed on 2564 infants referred to the Mohammad-Rsololla health center from March 2018 to April 2022, Blood samples were taken from a heel prick and then PKU test was done by the Fluorometric method. Results: Of 2564 (1232 female and 1332 male) newborns screened for PKU, we cannot detect any phenylketonuria in newborn. Conclusion: As our results showed, it seems the prevalence of phenylketonuria in our region is low. A more extensive study with more samples is recommended to find accurate information about the prevalence of PKU. Keywords: Phenylketonuria (PKU), Neonatal screening, Gerash city



چهاردهمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Investigating new methods in cancer diagnosis and treatment and cancer gene therapy based on nanoparticles (a systematic review)

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نوع پذیرش: پوستر | کد مقاله: G-45267

Abstract: Background: Despite many advances in cancer treatment, cancer is still one of the leading causes of death worldwide. Cancer treatments have progressed significantly, current cancer treatments include surgical intervention, radiation therapy, and the use of chemotherapy drugs. Therefore, in the fight against cancer, screening, and early diagnosis provide important information for timely cancer treatment and are very important for improving the quality of life of patients. Intratumoral heterogeneity of cancer cells is the main obstacle to effective cancer treatment. Therefore, researchers are looking for ways to kill cancer cells. Today, the emergence of new diagnostic technologies can help improve the treatment of various cancers. Cancer nanotechnology is a new branch in biology that makes a connection between nanotechnology and clinical cancer research, and it has been considered worldwide for cancer treatment. The purpose of this study is to investigate new methods in cancer diagnosis and treatment and cancer gene therapy based on nanoparticles. Methods: This study is a systematic review study that was conducted in 1401. By using the keywords of Cancer, gene therapy, nanoparticles, treatment in reliable databases including PubMed, Scopus, Cochrane, Web Of Science, Embase, and Google scholar search engine without a time limit. To ensure the completeness of the search results, the sources of the articles were checked and after removing the duplicate titles from the endnote software and checking the titles and abstracts, the related articles were checked using JBi tools, after checking the quality of the articles, the findings in the checklist the target was entered. Results: A total of 42 articles were reviewed and finally, 14 articles were selected that were related to the purpose of the study. According to the investigations, the results of some studies show that nanotechnology in cancer medicine has emerged as a promising approach to defeating cancer and has shown good progress in the field of drug development and delivery. Through early detection, prevention, and personalized therapy using nanoparticles and quantum dots, cancer nanotechnology offers a unique technology against cancer that can identify a cancer cell and target it to deliver cargo to treat that cancer cell. Nanotechnology has steadily expanded into the domains of cancer chemotherapy, radiotherapy, diagnostics, and imaging, showing the capacity of each to enhance and advance patient care, and has greatly contributed to cancer drug delivery. Conventional cancer treatment methods have side effects and diagnostic methods are time-consuming and expensive. The functionalization of these nanoparticles with various biological molecules, such as antibodies, helps them to deliver an early detection of cancer cells through their plasmonic resonance properties. Conclusion: The obtained results show that many advances have been made in the field of cancer diagnosis and treatment, and cancer nanotechnology has been able to highlight different approaches in the progress of cancer treatment and appears as a promising approach to defeating cancer. Keywords: cancer, gene therapy, nanoparticle, treatment

Relationships between the serum fat-soluble vitamins, circulating proprotein convertase subtilisin/kexin type 9, and lipid profile in overweight population

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نوع پذیرش: پوستر | کد مقاله: G-85910

Abstract: Background: people who haThe lipid profile plays a major role in coronary artery stenosis. The aim of this study is to investigate the relationship between vitamins (A, E and D), circulating proprotein convertase subtilisin/kexin type 9 (PCSK9) and lipid profile in the overweight population. Methods: The research included 120 overweight participants. ELISA technique was used to measure serum PCSK9 and vitamin D levels. HPLC method was used to measure the serum vitamin A and vitamin E levels. The lipid profile was measured by routine laboratory tests. Results: The serum PCSK9 values correlated considerably to total cholesterol ($r=0.23$, $P=0.009$) and LDL-C ($r=0.17$, $P=0.05$) values. The serum vitamin E values correlated considerably to PCSK9 ($r=0.233$, $P=0.01$), vitamin A ($r=0.47$, $P=0.0001$), VLDL-C ($r=0.30$, $P=0.002$), total triglyceride ($r=0.61$, $P=0.0001$), total cholesterol ($r=0.309$, $P=0.001$), values. However, there were not communication between the levels of circulating A and D vitamins, the total cholesterol serum, sdLDL-C and LDL-C values. Conclusion: The results of study indicated that there is a partial correlation between serum vitamin E and LDL-C levels associated to PCSK9. Vitamin E supplements can be recommended for overweight people who have higher LDL-C levelsve higher LDL-C levels.

CK18, FGF-21 and M2BPGi can be used as a non-invasive panel to diagnose non-alcoholic fatty liver disease

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نوع پذیرش: پوستر | کد مقاله: G-45038

Abstract: Background: Early diagnosis of Non-alcoholic fatty liver disease (NAFLD) can help to treat it. The use of non-invasive markers such as Cytokeratin 18 (CK18), fibroblast growth factor 21 (FGF-21) and Mac-2 binding protein glycosylated isomer (M2BPGi) can be useful to early diagnosis of NAFLD. CK18 is a cytoskeletal protein and the main intermediate filament family member expressed in the liver. FGF-21 a liver-secret hormone, has recently been shown to possess beneficial effects on lipid metabolism and hepatic steatosis. M2BPGi is a hematological biomarker that predicts high-grade fibrosis and cirrhosis. Therefore, this study was conducted to investigate the biomarker potential of CK18, FGF-21, and M2BPGi in NAFLD patients. Materials and Methods: This case-control study included 50 healthy subjects and 50 patients with NAFLD. Blood were collected from the participants and centrifuged. Then its serum was separated and frozen at -80 until the parameters were analyzed. We evaluated serum levels of CK18, FGF-21, and M2BPGi by ELISA. Also, we used Student's t-test and receiver operating characteristic (ROC) analysis to evaluate the data. Results: Serum concentrations of CK18, FGF-21, and M2BPGi were significantly higher in patients with NAFLD, compared with the healthy subjects (P .001). Also, the results showed that CK18, FGF-21, and M2BPGi has good specificity and sensitivity for diagnosing NAFLD. Conclusion: Based on the obtained results, CK18, FGF-21, and M2BPGi can be used as a biomarker for NAFLD diagnosis. Although more studies are needed. Keywords:

Effect of Citronellol on the Alleviation of Acute Kidney Injury and Oxidative Damage Induced by Gentamicin in Experimental Nephrotoxic Rats

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نوع پذیرش: پوستر | کد مقاله: G-21674

Abstract: Background: Gentamicin leads to the production of free radicals and renal impairment. Monoterpenes like citronellol, are compounds that have antioxidant properties. Antioxidants can play a crucial role in preserving the oxidant-antioxidant balance. Hence, the present study investigated the effects of citronellol on acute kidney injury (AKI) and renal function recovery following gentamicin administration in rats. Materials and Methods: 36 male Wistar rats were randomly divided into 6 equal groups; healthy control, gentamicin, DMSO carriers, citronellol 50, citronellol 100, citronellol 200. After 12 days of treatment, the animals were anesthetized with ketamine and xylazine. Serum and kidney samples were taken for gene expression and histological experiments. Results: Gentamicin-induced nephrotoxicity caused an increased in expression of TNF- α and IL-6 genes and glomerular damage. On the other hand, citronellol decreased the expression of TNF- α and IL-6 genes, furthermore, improvement in histological alterations was displayed in three groups receiving citronellol compared with the gentamicin group. Conclusion: Citronellol as an antioxidant and anti-inflammatory agent, decreased the expression of pro-inflammatory cytokines such as TNF- α and IL-6 genes. Moreover, it reduced the damages of glomerulus and curved tubes near the kidney, hence, it can improve kidney function by preserving kidney nephrons. Keywords: Citronellol; Gentamicin; Acute Kidney Injury; Pro-inflammatory cytokines

Hydroalcoholic extract of *Scrophularia striata* has a protective effect on thioacetamide-induced liver cirrhosis by reducing oxidative stress and suppressing the expression of TIMP 1, TLR-4, and MFN2 genes.

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نوع پذیرش: پوستر | کد مقاله: G-89521

Abstract: Background: Liver cirrhosis is one of the most important causes of death from liver diseases. Nowadays, the use of herbal medicines has increased due to its availability, less side effects and cheapness for the treatment of liver diseases. The present study was conducted to examine antidiabetic effects of *Scrophularia striata* (*S. striata*) ethanolic extract and evaluate its effects on oxidative stress markers and the expression of metalloproteinase 1 (TIMP 1), toll-like receptor-4 (TLR-4), and Mitofusin (MFN2) genes in the thioacetamide-induced liver cirrhosis rats. Materials and methods: 24 male rats were selected by simple random sampling. Rats were randomly assigned to 4 groups: Group I (control), group II (TAA injected rats), group III (TAA injected rats + 100 mg/kg.bw of *S. striata*) and group IV (TAA injected rats + 200 mg/kg.bw of *S. striata*). Liver cirrhosis was induced in rats by a 300 mg/kg.bw thioacetamide administration twice with an interval of 24 hours. Results: After 8 weeks of treatment by *S. striata* at doses of 100 and 200 mg/kg.bw, biochemical factors and oxidative stress markers (SOD, TAC, GPX, CAT and MDA) were measured using spectrophotometric methods. Gene expression of TIMP 1, TLR-4, and MFN2 were analyzed using real-time PCR. ANOVA and Bonferroni post hoc test analysis were applied to evaluate the data. The results showed the *S. striata* extract significantly decrease the ALT, AST and ALP, liver expression levels of TIMP 1, TLR-4, and MFN2 genes and improve oxidative stress markers (SOD, TAC, GPX, CAT and MDA) in the liver tissues when compared to control group. Also, it was found that the beneficial effects of the *S. striata* were dose-dependent. Conclusion: In conclusion, Moreover, *S. striata* by reducing the expression of TIMP 1, TLR-4, and MFN2 genes and improving oxidative stress might be used as adjuvant treatment for liver cirrhosis. Keywords:



Protective Role of Citronellol on Antioxidant Enzymes Following Gentamicin Administration in Nephrotoxic Rats

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نوع پذیرش: پوستر | کد مقاله: G-81705

Abstract: Background: Gentamicin is an antibiotic that leads to nephrotoxicity by producing of free radicals in renal tissue. Citronellol, a monoterpene, has antioxidant and anti-inflammatory activities. Antioxidants can have an effective role in preserving the oxidant-antioxidant balance. Hence, this study evaluated the role of citronellol on antioxidant enzymes following gentamicin administration in experimental nephrotoxic rats. Materials and Methods: 36 male Wistar rats were randomly divided into 6 equal groups; healthy control, gentamicin, DMSO carriers, citronellol 50, citronellol 100, citronellol 200. The animals were anesthetized by ketamine and xylazine after 12 days of treatment. Serum and kidney samples were taken for biochemical and gene expression assessments. Results: Treatment with citronellol decreased the levels of urine protein, creatinine and kidney malondialdehyde (MDA). Citronellol 50 and 100 increased the levels of serum glutathione (GSH) and kidney glutathione peroxidase (GPX), furthermore, citronellol 200 increased the level of serum nitric oxide (NO) and the expression of catalase (CAT) gene. The expression of GPX gene increased in all treatment groups. The levels of serum urea and kidney CAT showed no significant differences between treatment groups and gentamicin group. Conclusion: Citronellol with its antioxidant properties can reduce kidney damage caused by nephrotoxicity following gentamicin consumption, hence, it can improve kidney function by preserving kidney nephrons. Keywords: Gentamicin; Citronellol; Antioxidant enzymes; Rat



چهارمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Effect of Jujube Honey as a Wound Healer on Human Dermal Fibroblast Compared to Commercial honey

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نوع پذیرش: پوستر | کد مقاله: G-84052

Abstract: Abstract Aim: The objective of this study was to compare the effect of Jujube honey (JH) and commercial honey (CH) on viability and wound healing in human dermal fibroblast (HDF) based on total phenolic content, antioxidant capacity, and diastase activity of two honey. Methods: A honey health assessment was done based on honey's total phenolic content, antioxidant capacity, and diastase activity (h-PAD) scoring. In this way, the total phenolic content, antioxidant capacity, and diastase activity of JH and CH were measured. Cultured HDFs were exposed to various doses of JH and CH, and the viability of the exposed HDFs was assessed. The rate of cell wound closure was then investigated. Result: The total phenolic content of JH was $606.4 \pm 0.11 \mu\text{g}$ Gallic acid equivalent per mg, while CH honey had a value of 112.1 ± 0.095 . Total antioxidant activity of JH was compared to that of CH. In JH and CH, it was $203.58 \pm 10.5 \mu\text{M/L}$ and $4.66 \pm 10.5 \mu\text{M/L}$, respectively. According to the results, JH had a high h-PAD score, whereas CH had a low h-PAD score. A nontoxic concentration of JH and CH was determined for further experiments. The migration test findings revealed that JH increased the ability of HDFs to move and wound healing as compared to the CH and control groups. Conclusions: The honey samples efficiently affected the proliferation and viability of HDFs. Moreover, high h-PAD scoring (JH) can enhance migration and wound closure in HDFs more than low h-PAD scoring (CH). Keywords: Honey, Human dermal fibroblast, Wound healing



چهاردهمین کنفرانس بین المللی آزمایشگاه و باالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Examining the Normality of Aspartate Transaminase in Patients Suffering from Coronavirus Disease 2019, Who Received Remdesivir

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نوع پذیرش: پوستر | کد مقاله: G-79684

Abstract: Introduction: Remdesivir is used for therapy of severe coronavirus disease 2019 (COVID-19) caused by severe acute respiratory syndrome (SARS) coronavirus 2 (CoV-2). Also, aspartate transaminase (AST) is an enzyme from the group of transferase that is mainly found in the liver. Research has shown that remdesivir can affect liver enzymes and cause disruption in their production. This study aimed to examine the rate of the normality of AST in patients with COVID-19, who received remdesivir. Methods: In this descriptive-cross sectional study, 204 patients suffering from COVID-19 were detected by Real-time polymerase chain reaction (PCR). Information about them was extracted from hospital information systems (HIS) (17 Shahrivar Hospital, Babol University of Medical Sciences, Iran, 2021). Descriptive statistics and frequency table drawing were used to analyze the data. A T-test was used to check the relationship between variables (P-value less than 0.05). Results: The prevalence of men and women was 103 (50.49%) and 101 (49.50%), respectively. Results showed that 149 (73.03%) patients showed a normal level of AST. Also and 55 (26.96%) patients did not AST normal level. There was no significant difference between the normal level of AST and genus ($p=0.078$). Conclusion: Most patients who received remdesivir had a normal level of AST. But prescribing remdesivir for patients with COVID-19 must be performed with more consciousness. Keywords: Aspartate Transaminase, Patients, Coronavirus Disease 2019, Remdesivir

Using Random Forest algorithm to identify colorectal cancer metastasis-related biomarkers

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نوع پذیرش: پوستر | کد مقاله: G-47159

Abstract: Background: Metastasis has always been the main reason for cancer-related death. Relatively 20% of colorectal cancer (CRC) patients are diagnosed with metastasis, and there are currently no treatments that specifically target these metastases, nor are there any ways for early identification of metastasis. Artificial intelligence has recently been widely used in medical science studies and has shown great potential. Random Forest is a popular machine-learning algorithm that is commonly used in cancer studies. In this study, we applied the Random Forest algorithm to identify essential genes engaged in colorectal cancer metastasis process. Materials and Methods: GSE51244 gene expression profile in the GEO database was analyzed using the limma package in R. genes with $|\log_{2}FC| \geq 1$ and adj. p-value 0.05 were selected as the primary gene set for further analysis. Gene ontology enrichment analysis was performed using the David database to figure out specific pathways related to primary genes. Subsequently, the RF algorithm was applied to select the best features among these genes. Additionally, we used Artificial Neural Network (ANN) algorithm in SPSS to evaluate the accuracy of selected genes in discriminating metastatic samples from non-metastatic ones. At last, we used RT-qPCR on 16 low-stage, 24 high-stage colorectal cancer samples and six liver metastasis samples to validate our in-silico findings. Results: Gene expression profile analysis using limma package revealed 536 DEGs comparing metastatic and non-metastatic samples. Gene ontology analysis using DAVID showed pathways related to these genes are complement and coagulation cascade, chemical carcinogenesis, and PPAR signaling pathway, which their relation to cancer metastasis is investigated in several studies. After applying RF algorithms, 36 genes were selected as the best features. Then we used these genes to build an ANN model in SPSS. The AUC of this model was 0.833, which shows the high accuracy of this model. Moreover, ANN was used to estimate the accuracy of every single gene in distinguishing metastatic samples, demonstrating that WNT5a has the highest accuracy among the selected genes. RT-qPCR showed no significant differences between high-stage and low-stage samples, but its expression was significantly lower in liver metastases compared to primary tumors. Conclusion: In conclusion, the results of our study demonstrated that the Random Forest algorithm could identify gene-related colorectal cancer metastasis with high accuracy (AUC=0.83). The genes discovered in this work can be further examined and looked into as potential biomarkers for colorectal cancer metastasis and be used for therapeutic and diagnostic purposes. Experimental validation indicated that WNT5a expression is lower in metastatic samples than in non-metastatic ones, confirming our findings. WNT5a can be considered as a biomarker for the prognosis of metastatic CRC. Keywords: Metastasis, Colorectal Cancer, Artificial Intelligence, Random Forest, Prognosis

Relationship between ABO Blood Groups and COVID-19 Severity in Hospitalized Patients

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نوع پذیرش: پوستر | کد مقاله: G-86392

Abstract: Background: The coronavirus disease 2019 (COVID-19) pandemic caused by SARS-COV-2, emerged in 2019 and then, turned into a health system burden. Numerous studies were carried out investigating the correlation between COVID-19 susceptibility and ABO and Rh blood groups and indicated that the blood group A-containing individuals were more susceptible. In contrast, the people with group O seemed to have less susceptibility. Therefore, we aimed to evaluate the relationship ABO and Rh blood group distribution with COVID-19 illness. Keywords: COVID-19, ABO blood groups, Age, Gender Materials and Methods: A total of 1006 (821 PCR-positive and 185 PCR-negative) participants were enrolled in our study from July to March 2021 who were admitted to the infectious diseases ward of Taleghani hospital, Urmia, Iran. Patients under 18 years old and with a history of pulmonary diseases were excluded from the study. RT-PCR technique was used to detect COVID-19 in all the participants. Also, ABO and Rh blood types were determined using commercial kits. Results: Patients with blood group A had the highest (41.4%) percentage of positive PCR test results. While, any significant differences were not observed between gender and the distribution of blood types in COVID-19-positive patients. There was not a significant difference in the distribution of the blood groups in COVID-19-positive participants based on age groups (≤ 60 and 60 years old). Conclusion: The blood group A may be associated with a higher risk for COVID-19 illness in the patients admitted to the hospital. Keywords:

Blockage of Wnt/ β -catenin Signaling Pathway in Colorectal Cancer Resistant Cells by Nitazoxanide Effects on Peptidylarginine Deiminases Expression

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نوع پذیرش: پوستر | کد مقاله: G-84097

Abstract: Background: Multidrug resistance (MDR) is the major cause of unsuccessful cancer treatment in which drugs cannot be effective against cancer. Therefore, it is necessary to identify the critical mechanisms of MDR developing and targeting those via novel compounds. Accordingly, the current study was performed to investigate for the first time the combination effect and molecular mechanism of nitazoxanide (NTZ) and oxaliplatin (OXP) on LS174T/OXP-resistant cells. Methods: The effect of NTZ on OXP cytotoxicity in LS174T and LS174T/OXP cell lines was evaluated by MTT assay. Then, the changes in the expression level of MDR1, MRP1, CTNNB1, peptidylarginine deiminase (PAD)2, and PAD4 genes and proteins were evaluated by RT-qPCR and western blotting methods, respectively. Lastly, the apoptosis assay was performed by flow cytometer. Results: OXP resistant and sensitive cells were identified based on the IC50 values (11567 nM vs. 1745 nM, p0.05 for 24 h treatment; and 5161 nM vs. 882 nM, p0.05 for 48 h incubation). The combination of NTZ and OXP for 48 h led to a reduction in IC50 values in resistant cells (2154 nM, p0.05). The effect of NTZ plus OXP significantly decreased the expression of MDR1 (p0.001), MRP1 (p0.05), and CTNNB1 (p0.001), while PAD2 and PAD4 expression was significantly increased (p0.001). This combination therapy enhanced the percentage of the sub-G1 population (apoptosed) compared to other groups. Conclusion: The results showed that NTZ leads to notable upregulation of PAD2 and PAD4, which can disrupt the Wnt/ β -catenin signaling pathway, and reversed the MDR by reducing MDR1 and MRP1 expression. Keywords:

Effect of silymarin supplementation on the lipid profile changes in 1,2 dimethylhydrazine-induced mice colon cancer

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نوع پذیرش: پوستر | کد مقاله: G-74509

Abstract: Background: Colorectal cancer (CRC) is considered the third most common cancer and the second leading cause of cancer death globally. The effects of dietary fats in the pathogenesis of CRC were reported; especially cholesterol in the diet was shown to be co-carcinogenic in animal models of CRC. Silymarin (SMN), a flavonoid extracted from *Silybum marianum*, is well-known for its hepatoprotective, anti-inflammatory, and anti-cancer properties. Also, several studies have reported about its ability to reduce low-density lipoprotein (LDL) and total cholesterol (TC) in hyperlipidemic rats. Therefore, we aimed to evaluate the effect of SMN-supplemented, modified diet on lipid profile changes in mouse colon cancer. Materials and Methods: Twenty-four male BALB/c mice (25-30 g) were allocated into three groups (control, DMH, SMN-DMH) with eight mice per group. CRC was induced through intraperitoneal injection of DMH at the dose of 20 mg/kg b.w. weekly for ten consecutive weeks. The mice in the SMN-DMH group were fed with a modified diet containing 2500 ppm SMN that is prepared freshly every day for eight weeks after CRC induction (11-18 w). At the end of the 18th week, the mice were euthanized via cardiac blood puncture. Then, the serum samples were taken immediately and stored at -21 °C for further biochemical evaluations. Lipid profile indices (LDL, HDL, triglyceride (TG), and TC) were measured in the serum samples using a biochemistry autoanalyzer system. Results: Treatment with DMH resulted in markedly higher levels of LDL and TG compared to the control group. SMN supplementation reduced these parameters significantly (P<0.05). Furthermore, DMH increased TC levels and decreased HDL levels significantly compared to the control mice. Although treatment with SMN could regulate HDL and TC levels, no significant changes were observed in comparison with the DMH group. Conclusion: SMN-enriched diet could improve the impaired lipid profile caused by mouse CRC. Thus, it may exert an improving effect on the disturbed lipid profile of CRC patients in clinical practice. Keywords: Silymarin, colorectal cancer, 1, 2 dimethylhydrazine, lipid profile



چهارمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Measurement of Vitamin D in Patients Admitted to Intensive care unit during the Outbreak of Coronavirus

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نوع پذیرش: پوستر | کد مقاله: G-38910

Abstract: Introduction: Vitamin D is a group of vitamins, which increase the absorption of calcium, phosphate, and magnesium in the intestine, and help the growth and strength of bones. In diseases related to respiratory viruses, vitamin D has a role in preventing disease as well as limiting disease severity. Also, immune response activity is dependent on adequate levels of vitamin D, considering the outbreak of coronavirus and the need for patients to have a strong immune system, this research was conducted to measure the vitamin D level in patients suspected of suffering from the coronavirus infection hospitalized in the intensive care unit (ICU) ward. Methods: In this descriptive study, 78 patients that were admitted to the ICU and suspected of coronavirus infection were considered. Patients, Information was extracted from hospital information systems (HIS) (Rouhani Hospital, Babol University of Medical Sciences, Iran, 2020). Vitamin D levels were measured by kit. Descriptive statistics, frequency table, and T-test were used to check the relationship between variables (P-value less than 0.05). Results: Results showed that 27 (34.61%) and 51 (65.38%) patients were women and men, respectively. Vitamin D levels were measured as follows; severe deficiency (20 ng/ml) in 34 (43.58%) patients, deficiency (20-29 ng/ml) in 27 (34.61%) patients, sufficient (30-100 ng/ml) 17 (21.79%) patients. There was no significant difference between the normal level of Vitamin D and genus (P-value higher than 0.05). Conclusion: Results showed that the patient's prevalence with severe deficiency and deficiency level of Vitamin D was more than the patient with a sufficient level of Vitamin D. So a treatment using Vitamin D is necessary for patients suffering from coronavirus infection, especially patients who are admitted in ICU. Keywords: Vitamin D, Patients, Intensive care unit, Coronavirus



چهاردهمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Investigating the relationship between antioxidant factors and missed abortions in Asalian hospital in Khorramab

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نوع پذیرش: پوستر | کد مقاله: G-26308

Abstract: Background: Abortion is defined as the spontaneous termination of a pregnancy at a stage in the pregnancy in which the fetus or fetus is unable to live independently. The essential substances needed for embryonic growth and development are provided through the placenta and from the mother. Therefore, examining the contents and differences in the levels of trace elements in the mother and fetus's body is important for a detailed analysis of how the fetus develops in the womb and the factors that affect their growth. During a normal pregnancy there is a balance between oxidative factors and the antioxidant system. Significant increase in the level of oxidative stress factors with the emergence of a stage of abortion that is an advanced and irreversible stage. Lack of some antioxidant activities associated with trace elements (zinc, copper, selenium and manganese) can cause Poor pregnancy outcomes such as fetal intrauterine growth restriction, preeclampsia and increased risk of chronic diseases in adulthood. Asalian was in Khorramabad

Investigating the effectiveness and side effects of rectal misoprostol compared to vaginal misoprostol in patients with forgotten abortion candidates in Asali Hospital

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نوع پذیرش: پوستر | کد مقاله: G-57832

Abstract: Background: Abortion refers to the termination of pregnancy before the 20th week of pregnancy of birth weighing less than 500g. about 10-15% of pregnancies lead to miscarriage, 80% of which occur in the first trimester. Missed abortion is an ultrasound diagnosis that is an empty pregnancy sac or fetus without cardiac activity that must be confirmed by re-ultrasound. there are several methods for extracting and discharging fertilization products in forgotten abortion. The main issue is to provide a method that is effective and low -cost and has minimal side effects. Misoprostol is used in midwifery to induce labor, prepare the cervix, and induce abortion. unlike other prostaglandins, misoprostol selectively affects the uterus and cervix and has no adverse effects on the bronchi and blood vessels. This study has performed a comparative study between rectal and vaginal misoprostol in women with abortion -induced pregnancies, considering the numerous cases of abortion clients in asali hospital. Materials and Methods: This randomized clinical trial was performed in 2016 on 60 pregnant women with a gestation age of 6 to 14 weeks admitted to asli hospital in Khorramabad. The vaginal placement was performed. In both groups, 600 µg misoprostol made in iran was given, which was repeated once very 24 hours in three doses. When no excretion was present within 72 hours, the patients would be discharged and followed up on an outpatient basis Results: In the present study, 60 patients were studied, of whom 30(50%) received rectal misoprostol and 30(50%) received vaginal misoprostol. Demographic indicators in the two groups were not statistically significant. The mean age was 28.93 years in the rectal group and 32.43 years in the vaginal group, which was statistically significant ($p= 0.031$). in the rectal group, the dose of misoprostol in 25 patiens(83.3%) was one dose(600 micrograms). 10 patients(33.3%) received two doses(1200 micrograms), and one patient (3.3%) received three doses of misoprostol. The average dose in the vaginal group was 840 micrograms. There was no significant difference between the twongroups based on the independent t-test ($p=0.066$).in the rectal group, on average , 12.07 hours after misoprostol administration, the products of pregnancy were excreted , and the rate was 19.18 hours in the vaginal group, showing a significant difference between the two groups based on the mann-whitney test($p=0.005$). in the ultrasound after the removal of products, nine patients (30%) in the rectal group had remmants of pregnancy products and needed curettage, so the success rate of abortion in the rectal method was 70% , while in the vaginal group, 8(26.7%) had remmants of pregnancy products. The success rate of abortion in this group was 73.3%, showing no significant differences between the two groups according to the chi-square test($p=1.00$). there were no significant differences between the two groups in complications such as fever , mausea, vomiting, diarrhea, heavy bleeding, severe pain, ulterine rupture, and sepsis Conclusion: Misoprostol is effective in both rectal and vaginal methods for medical abortion in the first trimester of pregnancy in people without a history of cesarean section. Keywords:



Iron Chelator or Iron Supplement Consumption in COVID-19? The Role of Iron with Severity Infection

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نوع پذیرش: پوستر | کد مقاله: G-73928

Abstract: Iron is a trace element that is used to replicate the virus and has a role in the vital functions of the body and the host's innate immune system. The mechanism of iron in COVID-19 severity is still not well understood. The aim of this study was to evaluate the association of the iron with COVID-19 severity. A case-control study was performed on 147 patients with a positive PCR test result and 39 normal individuals admitted to the Persian Gulf Martyrs Hospital in Bushehr, Iran. The iron profiles and related tests were measured along with hematological analytes. Hemoglobin (Hb), Fe, and saturated transferrin decreased in all the groups compared to the controls, but ferritin increased in the patient groups. After adjusting for age and sex, we found that increased ferritin levels augmented the odds ratio (OR) of the disease in the moderate (OR = 2.95, P = 0.007), severe (OR = 6.1, P 0.001), and critical groups (OR = 8.34, P 0.001). The decreased levels of Fe reduced the OR of the disease in the mild (OR = 0.96, P 0.001), moderate (OR = 0.96, P 0.001), severe (OR = 0.95, P 0.001), and critical (OR = 0.98, P = 0.001) groups. Fe (AUC = 85.95, cutoff 75.5 µg/dL, P 0.001) and ferritin (AUC = 84.45, cutoff 157.5 ng/dL, P 0.001) have higher AUC for disease prognosis, but only ferritin (AUC = 74.89, cutoff 261.5 ng/dL, P 0.001) has higher AUC for disease severity assays. It could be concluded that the use of iron chelators to reduce iron intake can be considered a therapeutic goal. In addition, measuring Fe and ferritin is beneficial for the diagnosis of the disease and determining its severity. Keywords:

Relationship Type of Plasma Free Fatty Acids with Insulin Resistance Indices and Oxidative Stress: A Case-Control Study

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نوع پذیرش: پوستر | کد مقاله: G-63098

Abstract: Background: Diabetes is the main metabolic disorder and it is developing both in the world and in Iran. Free Fatty Acids (FFAs) are vital for energy homeostasis and pathogenesis of a variety of diseases, including diabetes. As a result, we presumed and investigated the types of FFAs and their links to Insulin Resistance (IR) indices and Oxidative Stress (OS). Methods: A case-control study was conducted on 44 diabetics, 44 prediabetics with IFG, and 44 individuals in the control group. A gas chromatography flame ionization detector was used to estimate FFAs, which were then classified based on length and saturation. Total Antioxidant Capacity (TAC), malondialdehyde (MDA) level, paraoxonase-1 (PON-1), superoxide dismutase-3 (SOD-3), and catalase (CAT) activity were measured. Demographic data, biochemical markers, and HOMA-IR were also assessed. Result: In both case groups, HOMA-IR was higher, but PON-1 and TAC were reduced. Also, MDA and $\omega 6$ fatty acids had risen in diabetes in comparison with controls and prediabetes. LCFFA, SFFFA, USFFFA, and total FFA levels were higher in the cases compared to the controls, and they had a direct relationship with HOMA-IR, BMI, FBS, HbA1C, and MDA, as well as an inverse relationship with antioxidant parameters. Furthermore, adjusting these fatty acids significantly increased disease development. SCFFFA and $\omega 3/6$ fatty acids had a negative correlation with HOMA-IR, FBS, and insulin, and a positive correlation with TAC. Adjusted SCFFFA significantly reduced disease risk. Total FFA had the greatest sensitivity and specificity for the prognosis of diabetes (AUC = 83.98, cut-off 919 μ M) and SCFFFA for the prognosis of prediabetes (AUC = 82.32, cut-off 39.56 μ M). Conclusion: Total FFA ($\geq 776\mu$ M), LCFFA ($\geq 613\mu$ M), SFFFA ($\geq 471\mu$ M), and USFFFA ($\geq 398\mu$ M) all increase the risk of disease by increasing OS, BMI, and HOMA-IR. On the other hand, SCFFAs ($\geq 38.7\mu$ M) and $\omega 3/6$ ($\geq 1/8.1$) reduce the risk of disease by reducing BMI, HOMA-IR, and OS. SCFFAs and total FFAs can be used for the prognosis of prediabetes and diabetes, respectively. Keywords: T2DM, prediabetes, free fatty acids, oxidative stress



چهاردهمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



β -arrestin suppression under high glucose conditions suggested dexamethasone and metformin influence other cellular signaling axes

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نوع پذیرش: پوستر | کد مقاله: G-04751

Abstract: Background: Metformin and dexamethasone are applied to reduce high blood sugar levels and anti-inflammatory effects, respectively. On high outbreak of atherosclerosis in diabetes, in this study the gene and protein expression levels of BARR2 in high glucose conditions were evaluated in VSMCs treated with metformin and dexamethasone. Methods and Materials: Human VSMCs were cultured in DMEM-F12 medium and were treated with different doses of metformin (1, 5 and 7 mM) and dexamethasone (10⁻⁵, 10⁻⁶ and 10⁻⁷ mM) in 24- and 48-hour periods. The cell viability was estimated using MTT assay. The BARR2 gene and protein expression levels were identified with RT-qPCR and western blotting techniques, respectively. The signaling axes were predicted from gene network made using Cytoscape software and annotated with Gene Ontology. Results: The BARR2 gene and protein expression levels reduced in vascular smooth muscle cells treated to dexamethasone and metformin after 24- and 48-hour periods. These effects were most considered after 48 hours. Furthermore, the filtered genes in annotated network showed many signaling axes related to BARR. Conclusion: Metformin and dexamethasone suppressed the BARR2 protein and gene expression levels in the VSMCs. Moreover, the gene networking data suggested other cell signaling axes related to BARR2 that may be affected by metformin and dexamethasone. Keywords:

Investigating the combined effect of Ursolic acid and Alpelisib on inhibiting cell proliferation and the expression of PI3K, AKT and mTOR proteins involved in the PI3K/AKT cell signaling pathway on mouse breast cancer cell line 4T1

عرفان شیخی،¹ محمودرضا آقامعالی¹ ©

دانشگاه گیلان

نوع پذیرش: پوستر | کد مقاله: G-84153

Abstract: Background: According to the WHO reports, cancer is the most common cause of human death in developed countries after cardiovascular diseases. Breast cancer has been reported as the second leading cause of cancer-related deaths in women worldwide. Using treatment methods such as; Chemotherapy, hormone therapy, and radiation therapy are often associated with side effects, so the successful treatment of breast cancer is still one of the challenges in this field. The PI3K/Akt/mTOR signaling pathway plays a critical role in controlling cell proliferation, apoptosis and tumorigenesis. Pieces of evidence showed that this signaling pathway is activated in most invasive breast cancers. Therefore, blocking this pathway provides a promising target for new therapeutic strategies. In this study, we further examined the effects of Ursolic acid and Alpelisib on the expression of PI3K, AKT, and mTOR protein levels in the 4T1 breast cancer cell line which are the main regulators in this pathway. Materials and Methods: 4T1 cell lines were cultured. Ursolic acid and Alpelisib were prepared in concentrations of 0.5, 1, 2, 4, and 8 μM and 25, 50, 100, 200, and 400 μM , respectively. The viability of 4T1 cells was evaluated by MTT assay after 24 hours of treatment with different concentrations of drugs, and the IC₅₀ was calculated by Compusyn software. Cells were treated with 0.5 \times IC₅₀ in combination groups and single-treated groups were used in 1 \times IC₅₀ concentration after cell passage. To evaluate whether Ursolic acid, Alpelisib, and a combination of these drugs are capable of modulating this signaling pathway to lead to inhibition of cell proliferation, we examined the effects of mentioned drugs on the expression of these signaling molecules on 4T1 cell lines by Western blot analysis. Results: The results of this study showed that the anti-proliferative effect of both drugs was concentration-dependent. so that in high doses, the highest decrease (74.17 % with UA and 64.04 % with Alp) in viability was observed in 4T1 cell lines. A combination of drugs significantly increased the inhibition of cell proliferation. Western blot analysis indicated that Treatment with drugs in single-treatment groups dramatically inhibited the expression of phosphorylated Akt and mTOR protein. We also detected a marked reduction in the PI3K proteins in a concentration-dependent manner. Also, a combination of drugs significantly decreased the expression level of PI3K, AKT, and mTOR proteins. Conclusion: To the best of our knowledge, this is the first study that shows the reduced expression level of PI3K, AKT and mTOR proteins in the 4T1 breast cancer cell line using Ursolic acid and Alpelisib. It seems that these drugs alone, and the desired combination may be useful as anticancer agents for breast cancer therapy. However, further investigations are needed in clinical trials to show the main mechanism of their role in breast cancer. Keywords:

Comparison of miR-7 and miR-29 expression in patients with Parkinson's disease and control

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نوع پذیرش: پوستر | کد مقاله: G-34259

Abstract: Background: Parkinson's disease is one of the most common neurological diseases, second only to Alzheimer's in terms of frequency. The most important cause of this disease is the loss of dopaminergic neurons in the substantia nigra of the brain and the formation of Lewy bodies. Parkinson's disease is a multifactorial disease in which various genetic and environmental factors play a role in its development, and the rate of this disease is more common in men than women. MicroRNAs (miRNAs) are small non-coding RNAs that are usually made of 20 to 25 nucleotides. They mediate post-transcriptional gene repression of target RNA transcripts. Therefore, in this study, we decided to compare the role of two microRNAs named miRNA29 and miRNA7 in these patients. Materials and Methods: In this study 75 patients with Parkinson's diagnosed by a specialist doctor were selected and 75 healthy people who were free of any neurological and metabolic diseases were selected. About 5 cc of blood was taken from each person and 16000 x g for 5 minutes in They were centrifuged at 4°C. Then, 100 microliters of the supernatant was transferred to a new tube using the serum/plasma kit to isolate total RNA, including miRNAs. First, 5 microliters of total RNA was reverse transcribed using the first strand cDNA synthesis kit. Subsequently, 2 µL of the product was used to detect the expression of miR29 and miR7 by quantitative PCR using the miRcute miRNA qPCR Detection kit. Data were evaluated using SPSS 19.0 (version 19.0; SPSS, Chicago, USA). And also statistical analysis was done using PRISM 5.0 (GraphPad Software Inc, USA). A significant difference was defined as P0.05. Results: Based on our study, comparing the expression level of miR-29 in the serum of controls and patients with PD, the mean expression level of miR-29 in patients with Parkinson's disease was lower than the control group, but compared to the expression level miR-7 in two cases, the level of expression of this gene in the group with Parkinson's disease was higher than in the control group (P 0.001), which was contradictory to some studies. Conclusion: Therefore, according to this experiment and the information obtained from this study, it can be suggested that the expression of miR-29 enzyme decreases in PD and the expression of miR-7 increased in PD in comparison to control group. In the central nervous system, miR-29 regulates neuronal and dendritic maturation. Dysregulation of miR-29 also has implications in aging and various neurological disorders. miR-7 expression contributes to normal development, physiology, and neurogenesis in the central nervous system and also maintains alpha-synuclein (α -Syn) at physiological levels. Second, PD patients show significant downregulation of miR-7 in brain regions associated with dopaminergic neurodegeneration. Downregulation of miR-7 in clinical samples is associated with α -Syn accumulation, loss of dopaminergic cells, and dopamine depletion in the striatum. Keywords: Parkinson's disease, miR-7, miR-29.

Effects of Cigarette Smoke and Opium on the CD36 Expression Levels in Human Macrophage THP-1 Cell Line

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نوع پذیرش: پوستر | کد مقاله: G-98635

Abstract: Background: Studies demonstrated that opium consumption and cigarette smoking increase the risk of inflammation and oxidative stress and are associated with lung diseases such as chronic obstructive pulmonary disease (COPD). Cigarette smoking increased the expression of CD36, as an activator of pro-inflammatory pathways. The aim of the present study was to evaluate the alone and in combination effects of opium and cigarette smoke extract (CSE) on the expression levels of CD36 at both mRNA and protein levels on human macrophage cell line THP-1. Materials and Methods: The THP-1 cell line was treated with CSE and opium, both alone and in combination forms during 24h incubation. The protein and mRNA levels of CD36 were evaluated by flow cytometry and quantitative reverse transcription-polymerase chain reaction (qRT-PCR) techniques, respectively. Results: CSE, both alone and in combination with opium, significantly up-regulated CD36 gene expression compared to the control (p0.001). however, only significant difference was found in monocytes treated with CSE in comparison with the control, opium and combination groups at the protein level, (p=0.016, p=0.031 and, p=0.049, respectively). No significant differences were observed in the CD36 gene expression and at the protein levels between opium-treated THP-1 cells and controls (p=0.470 and p= 0.965, respectively). Conclusion: CSE increased the expression of CD36 at the gene and protein levels in THP-1 cell lines. Therefore, CSE may play an important role in the pathogenesis and development of many inflammatory diseases including COPD, however, opium did not show significant effect on the expression of CD36. Keywords:

The effect of Sclareol on the expression of MDR-1 and glycoprotein P-genes in MKN-45 human gastric cancer cells

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نوع پذیرش: پوستر | کد مقاله: G-10692

Abstract: Objectiv: In recent years, the emergence of multidrug resistance in gastric cancer has been a major challenge in treatment of gastric cancer. To deal with the problem, studies and researches were conducted on Sclareol and have turned up the anti-cancer effect of the compound and have also determined the molecular mechanism of it to some extent. Therefore, the main purpose of this study was to investigate the effect of the substance extracted from *Salvia Officinalis* called Sclareol on MDR-1 gene expression and consequently on the rate of P-glycoprotein in human gastric cancer cell line MKN-45. Methods: Cell line MKN-45 was purchased from the Pasteur Institute of Iran and cultured in complete RPMI 1640 Medium with Fetal Bovine Serum, with 20, 40, 60, 80 and 100 μ M concentrations of Sclareol treatment for 5 hours. The rate of expression of MDR-1 gene was assessed by Real Time-PCR method and that of P-GP was assessed by Western blotting method. Results: The expression of MDR-1 gene was significantly reduced at doses of 20, 40 and 60 μ mol of Sclareol, while at doses of 80 and 100 μ mol there was not seen much effect (p 0.0001). Also, P-glycoprotein showed a very high decrease at doses of 40 and 60 μ mol of Sclareol, but no decrease was seen at doses of 80 and 100 μ mol (p 0.0001). Conclusion: From the results of this study, it seems that doses between 20 and 60 μ mol of Sclareol can be useful in reducing drug resistance, but doses above 60 mmol do not have such an effect. Keywords: Gastric cancer.Sclareol.MDR-1. Glycoprotein-P



Activation of HIF1a target genes led to hypoxia 5-FU resistance in Gastric cancer MKN-45 cells

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نوع پذیرش: پوستر | کد مقاله: G-27931

Abstract: Background: Gastric cancer (GC) is reported as the fifth most commonly diagnosed cancer and is the third most common cause of cancer-associated death in the world. Tumor cell hypoxia is one of the main factors causing 5FU resistance in gastric cancer cells. Herein, we intend to evaluate the efficacy of the drug 5FU on the MKN45 cell line by establishing in vitro hypoxic environment and compare them with results from normoxic conditions. Methods: MKN45 gastric cancer cell line were cultured in normoxic and hypoxic conditions. The cells were treated with various concentrations of 5-FU for 72 h. Then, cell viability was analyzed by the MTT method. Also, induction of apoptosis was analyzed by flowcytometry. Expression level of HIF-1 a, P53, BAX, Bcl2, MRP1 and Casp3 genes were quantified by real-time PCR. Statistical analysis of the results was done using SPSS software. Results: Our study showed that hypoxic condition leads to a higher resistance against 5-FU toxicity in MKN45 cells compared to normoxia. As a result of this drug resistance, we also found a significant low apoptotic cells in hypoxic conditions Data of gene expression in 5-FU treated MKN45 cells, indicated significant up-regulation of HIF1a in hypoxic conditions. we also showed an elevated level of pro-apoptotic genes (Bax and casp3) in normoxic and hypoxic group but this elevation was lower in hypoxia. in contrast, significant down-regulation of the anti-apoptotic gene (Bcl2) was detected just in the normoxic group. In the case of p53 and MRP1 genes, we found a higher level of gene expression in MKN45 cells treated under normoxic and hypoxic conditions compared to control, while this increase was more significant in hypoxic condition. There was no significant difference in level of expression of MRP1 gene in hypoxic condition compare to normoxia. Conclusion Altogether, our results demonstrated that the resistance to 5-FU in MKN45 gastric cancer cells might be due to the upregulation of the HIF-1 α gene and its regulated downstream target gene under hypoxic condition. Keyword: Gastric cancer, MKN45 , 5-FU, Hypoxia, HIF1a

Current Challenges of Cervical Cancer Surgery

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نوع پذیرش: پوستر | کد مقاله: G-53028

Abstract: Background: Cervical cancer is the fourth most common cancer in women worldwide, and it has the fourth highest mortality rate among cancers in women. The diagnosis of cancer can precede the application of certain therapeutic modalities as surgery, radiotherapy, chemotherapy, and hormone therapy, which opens a new challenging period in the life of women with cervical cancer. Surgery is a technique in combatting various early-stage cancers as it involves the physical removal of cancerous tissue. It can, however, also be used to remove metastatic tissues. Methods: In the current study, keywords including Cervical Cancer, Therapies, and Surgery were reviewed from the list of Mesh and other credible websites including PubMed, Science Direct and Google Scholar and the data was organized. The searches comprised all published paper from 2000 to 2022. All of full text was considered and the papers manifested as only abstract was excluded. The full papers selected that specific effect on cancers only. Totally 50 papers were selected and studied in this review. Results: Articles show currently, the types of surgery performed to treat cervical cancer include total hysterectomy, radical hysterectomy, loop electrosurgical excision procedure (LEEP), conization, trachelectomy, and cryosurgery. Also, the stage and extent of cervical cancer progression determines the treatment strategy needed and may include one or a combination of surgery, radiation and chemotherapy. The findings of the Laparoscopic approach to cervical cancer (LACC) trial revealed that radical hysterectomy performed using laparoscopy was associated with an increased rate of recurrence, loss of fertility and potential urinary dysfunction in the long-term. Scientifics believe that metastases in regional lymph nodes occurs in a fairly high percentage at all stages of the disease and that the primary cervical lesion spreads to surrounding anatomical structures without clear clinical symptoms and signs make the surgical method inefficiently effective. One literature review shows majority of the younger patients were treated with surgical resection; however, surgical resection in patients greater than 70 years is a rare occurrence. In one study grade one-two side effects in the surgery group included proctitis and cystitis (50%), and the rate of grade three-four side effects was 2%. In another study grade three side effects occurred in 5–11% and 8–12% of patients in the radiotherapy and surgery groups. In the surgery group, small intestine obstruction/perforation occurred in 4.2% of the cases, urethral stricture in 2.6%, vesicovaginal fistula in 1.6%, and rectovaginal fistula in 1.3%. In other research the cumulative incidence of severe late morbidity was higher in the surgery group at two years and at five years. One article demonstrated urinary and gastrointestinal complications were more prevalent after radiotherapy than after surgery. Also, the digestive and/or urinary systems were involved side effects in some studies. Conclusion: Current therapeutic options for cervical cancer are associated with debilitating side effects and tumor drug resistance. Despite considerable advancement with the use of combination therapies to improve the efficacy of single-agent treatments; new and improved therapies to treat cervical cancer are still urgently needed. Keywords:



چهاردهمین کنفرانس بین المللی آزمایشگاه و باالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



The effect of Ethanolic extract of *Trachyspermum ammi* on calprotectin levels in patients with Crohn's disease: a case series study

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نوع پذیرش: پوستر | کد مقاله: G-75486

Abstract: Background Inflammatory bowel disease (IBD) is an idiopathic and chronic inflammation of the intestine that includes ulcerative colitis and Crohn's disease. In Asia and the Middle East, the highest incidence of Crohn's disease is 5 per 100,000 per year. Crohn's disease is a chronic inflammatory disease that affects different parts of the gastrointestinal tract from the mouth to the anus, but in most cases it affects the end of the small intestine. Materials and Methods In this clinical trial study, which was initially conducted as a pilot study, four patients with Crohn's disease were selected for this study. Consent. Ethanolic extract of *Trachyspermum ammi* was given twice a day for 3 months and Clinical symptoms and their calprotectin levels were measured. Results The first patient was a 39-year-old woman with an initial calprotectin level of 840 mg/kg, after taking the drug the calprotectin level was 10.72 mg/kg after the second month. The second patient was a 22-year-old man whose initial calprotectin level was 760 mg/kg and after the intervention his calprotectin level was 260 mg/kg. The third patient was a 33-year-old man with an initial calprotectin level of 2225 mg/kg. After taking the drug, the calprotectin level became 1270 mg/kg after the second month. The fourth patient was a 35-year-old woman with an initial calprotectin level of 535 mg/kg. After taking the drug, calprotectin levels rose to 100 mg/kg after the intervention. Conclusion It seems that *Trachyspermum ammi* plant is effective in reducing calprotectin levels in patients with Crohn's disease, but its effect and mechanism need further studies in the future. Keywords:

Quercetin and Methotrexate in Combination have Anticancer Activity in Osteosarcoma Cells and Repress Oncogenic MicroRNA-223

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نوع پذیرش: پوستر | کد مقاله: G-07982

Abstract: Background: Osteosarcoma (OS) is one of the most common bone neoplasms in adolescents. Notable short- and long-term toxic effects of OS chemotherapy regimens have been reported. Hence, new chemotherapeutic agents with the ability to potentiate OS chemotherapy drugs and protect non-tumorous tissues are required. Materials and Methods: Saos-2 cells were treated with Methotrexate (MTX) and Quercetin (Que) (a polyphenolic flavonoid with anti-tumor effects) alone and in combination. MTT assay was performed to investigate the cytotoxicity of the drugs. Moreover, apoptosis-involved genes, including miR-223, p53, BCL-2, CBX7, and CYLD expression were analyzed via qRT-PCR. Annexin V-FITC/PI kit was employed to assess the apoptosis rate. Results: The MTT results showed that Que increases MTX cytotoxicity on OS cells. The measured IC50s are 142.3 μ M for QUE and 13.7 ng/ml for MTX. A decline in MTX IC50 value was observed from 13.7 ng/ml to 8.45 ng/ml in the presence of Que. Moreover, the mRNA expression outcomes indicated that the combination therapy significantly up-regulates the tumor suppressor genes, such as p53, CBX7, and CYLD, and declines anti-apoptotic genes BCL-2 and miR-223, which can lead to proliferation inhibition and apoptosis inducement. Furthermore, the apoptosis rate increased significantly from 6.03% in the control group to 38.35% in Saos-2 cells that were treated with the combination of MTX and Que. Conclusion: Que, with the potential to boost the anticancer activity of MTX on Saos-2 cancer cells through proliferation inhibition and apoptosis induction, is a good candidate for combination therapy. Keywords:



چهاردهمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Tissue engineering application on coronavirus pandemic: a systematic review

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نوع پذیرش: پوستر | کد مقاله: G-72653

Abstract: Background: The use of biomaterials in COVID-19 diagnosis and treatment has been investigated in various forms and origins (natural or synthetic). The creation of quick, ultra-sensitive field-effect transistor-based biosensing, antiviral platforms, vaccines, and nano-based materials accounted for the majority of studies on the use of biomaterials. The concept of tissue development, its behavior, and growth factors that are more readily supported in the medical setting are all covered by tissue engineering. This area can potentially aid the treatment of COVID-19-infected individuals and the overall battle against viral outbreaks. Materials and Methods: The Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) statement's guidelines for writing literature reviews were followed in this study. The two digital databases, Scopus and PubMed, were chosen. The best database for research in medicine and biomedical engineering is thought to be PubMed. In a variety of study fields, including medicine, health, science, technology, and engineering, Scopus is a reliable source. We conducted a systematic evaluation and obtained most of the data between June 2020 and April 30, 2022. In our study, topic headings (MeSH) keywords such as "coronavirus" and "Tissue engineering" were utilized. A precise selection strategy and exclusion criteria were used to screen the 1305 articles obtained. Only ten articles were thoroughly evaluated and included in this review, which only served to highlight how little research has been done in this crucial area. Results: The therapy approach is tissue engineering. This heterogeneous subject is particularly well adapted to applying engineering ideas to challenging therapeutic issues. These engineering methods concentrate on biomaterials, medication delivery systems, and the replacement of damaged tissues and organs. Some biodegradable biomaterials, including chitosan, mesoporous silica rods, and PLGA nanoparticles, have been utilized as vaccine platforms and can be used to create a SARS-CoV-2 vaccine. Notably, the suggested platform's size, shape, and other physicochemical characteristics should be carefully planned to accomplish the desired effects on the immune system. However, most of the newly presented preparations are still in the preclinical testing stage and have not yet entered the clinical setting. Conclusion: With their unique tools, tissue engineers can significantly advance our understanding of viral illness and the vital creation of diagnostic and therapeutic platforms. Future research on COVID-19 infection and drug testing are expected to benefit significantly from developing organ-on-a-chip technologies. However, developing innovative biomaterial-based techniques for preventing, treating, and monitoring COVID-19 require the collaboration of several disciplines. Keywords: COVID-19, Tissue engineering, Biomaterials

Serum level of melatonin in patients with osteoarthritis and its relation with 8-hydroxy-2-deoxyguanosine and vitamin D

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نوع پذیرش: پوستر | کد مقاله: G-35184

Abstract: Background: Osteoarthritis (OA) is one of the most prevalent degenerative joint diseases. According to the World Health Organization, approximately 9.6% of men and 18.0% of women aged over 60 have symptomatic OA. This study aimed to measure the serum levels of melatonin, 8-hydroxy-2-deoxy guanosine, and vitamin D in patients with OA. Based on the role of melatonin, we assumed that melatonin might be involved in the decrease of DNA damage and have a role in preventing OA. Materials and Methods: This study enrolled 47 patients with OA and 40 healthy controls. Serum levels of melatonin and 8-hydroxy-2-deoxy guanosine (8-OH-dG) were assessed. Also, serum levels of bone turnover biomarkers such as calcium, phosphorus, vitamin D, and alkaline phosphatase (ALP) were measured in OA patients and controls. Results: The serum level of melatonin was significantly lower in OA patients than the controls (6.18 ± 2.25 vs. 11.57 ± 3.87 pg/mL, P 0.05). In contrast, the serum level of 8-OH-dG was significantly increased in OA patients compared to controls (65.21 ± 16.12 vs. 22.51 ± 5.3 ng/dL, P 0.001). There was a negative correlation between serum melatonin and 8-OHdG levels in OA patients (P 0.05). There was a positive correlation between serum melatonin and vitamin D levels in OA patients (P 0.05). We found decreased calcium and vitamin D levels, and increased phosphorus and ALP levels in OA patients compared to controls (P 0.05). Conclusion: Our results showed a negative correlation between melatonin and 8-OH-dG, as a DNA damage marker, in the serum of patients with OA. Decreased levels of melatonin and elevated levels of 8-OH-dG might play a role in the pathogenesis of OA. Taken together, our findings indicated that melatonin might be involved in decreasing DNA damage and exerting a preventive function in OA. Moreover, it can be a potentially useful therapeutic agent for patients with OA. However, this study was limited by application of a single analysis method to measure each laboratory parameter, a relatively small sample size, and lack of outcome data from the patients. Consequently, this study requires a larger sample size to validate prognostic and diagnostic values of these biomarkers. Keywords:



چهارمین کنفرانس بین المللی آزمایشگاه و باالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Isolation and Characterization of Novel Bacteria Produced extracellular L-asparaginase enzyme

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نوع پذیرش: پوستر | کد مقاله: G-89317

Abstract: Background: L-asparaginase (E.C.3.5.1.1) is an important therapeutic enzyme that has been identified and purified for decades to evaluate its anti-cancer activity against various lymphoproliferative disorders such as acute lymphoblastic leukemia (ALL) and Hodgkin lymphoma. The ability of this enzyme to convert L-asparagine into aspartic acid and ammonia is the reason for its anti-cancer activity. Apart from medicinal and pharmacological uses, this enzyme is widely used in the food industry. Method: In this study, a bacterial strain was isolated from soil by repeated screening in Schlegel's synthetic medium and purified after several subcultures. The enzyme activity was assessed first by qualitative method with Schlegel's synthetic medium containing phenol red and then quantitatively by nesslerization method. The strain was identified by 16srRNA gene sequence and biochemical, morphological, and physiological tests. Result: The isolated bacteria was a member of the Kocuria genus. The enzyme activity of the cell-free supernatant was about 0.1 U/mL, without any glutaminase activity. Because no strain of this genus of bacteria that produces the L-asparaginase enzyme has been reported so far, the produced enzyme may have a new immunological property that can be used for patients with hypersensitivity. Conclusion: In this study, a new strain of bacteria from the genus Kocuria sp. was isolated, which can be a good source for the production of enzymes with low side effects. Keywords: L-asparaginase; glutaminase; leukemia; Kocuria



چهاردهمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Toxicity effects of Astragalus maximus extract on serum level of liver and kidney enzymes and hematological paramets in mice

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نوع پذیرش: پوستر | کد مقاله: G-21096

Abstract: Abstract Background: Considering the preventive and therapeutic uses of medicinal herbs, but, any herbal product should be evaluated in terms of toxicological studies before it is used as a medicinal form. Since, no documented study is existing on the toxicity characteristics of Astragalus maximus, here, we aimed to assess the sub-acute toxicity effect of A. maximus chloroform extract (AMCE) by assessing the kidney and liver enzymes, and hematological factors in male Balb/c mice. Materials: The effects of AMCE was investigated by studding the kidney and liver enzymes, and hematological factors followed by the oral treatment of mice with AMCE (0.1, 0.2, 0.4, and 0.8 g/kg) for 28 following days. Results: Lethal dose 50% (LD50) of the AMCE was 2.87 g/kg of body weight. We found that the kidney and liver enzymes has no significant modifications (p0.05). Likewise, blood parameters did now show significant modification (p0.05) in comparison to the control mice. Conclusion: We reported that AMCE at the doses of 0.1-0.8 g/kg had no significant sub-acute toxicity on kidney and liver function in Balb/c mice after 28 days' oral administration; but, supplementary surveys are mandatory to determine other toxicity phases, e.g. genotoxicity. Key words: liver, kidney, hematological, toxicity, herbal medicines



چهاردهمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Therapeutic effects of Fisetin in Letrozole-induced rat model of polycystic ovary syndrome

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نوع پذیرش: پوستر | کد مقاله: G-96430

Abstract: Background: Polycystic ovary syndrome (PCOS) is one of the most prevalent endocrine and metabolic disorders of the young women in reproductive age. It is accompanied by insulin resistance (IR), hyperandrogenism, and ovulation problems. Fisetin, a potent flavonoid, is known as an insulin sensitizer, anti-diabetic and anti-inflammatory agent. Therefore, in this study we aimed to investigate the alleviating values of fisetin on PCOS in a rat model. Materials and Methods: Female Wistar albino rats were randomly assigned into three sets. Control group (n=6) received carboxy methylcellulose (CMC 0.5 %), PCOS group (n=6) administered with 1 mg/kg letrozole in CMC 0.5 %, and Fisetin group (n=6) received 1 mg/kg letrozole + 10 mg/kg fisetin in CMC 0.5%. All administered doses were given by means of oral gavage. The serum fasting blood glucose, hormonal parameters (insulin, testosterone and estradiol), and histological examination were evaluated in all study groups. Serum levels of insulin was analyzed using ELISA kit and testosterone and estradiol were evaluated using chemiluminescence immunoassay kit. Hematoxylin and eosin staining were also used for histological examinations. Results: Our results showed that Fisetin treatment reversed letrozole induced PCOS related disturbances in hormonal parameters and histological alterations. Fisetin administration effectively reduced testosterone levels compared to the PCOS group. Nevertheless, a noticeable increase in estradiol was found in Fisetin treated group in comparison to the PCOS group. Also, Fisetin normalized Homeostasis model assessment index (HOMA-IR) levels in the rats with letrozole-induced PCOS. Furthermore, this flavonoid reduced the number of cystic follicles and increased corpora lutea compared to PCOS. Conclusion: It can be concluded that Fisetin administration resulted in noticeable alleviating effects by improving IR and hyperandrogenism in rat model of PCOS, suggesting that it may be a possible therapeutic candidate for combating PCOS. Keywords: PCOS, Fisetin, insulin resistance

Effects of melatonin in the regulation of non-coding RNAs in cancer: therapeutic potential and mechanisms

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نوع پذیرش: پوستر | کد مقاله: G-74812

Abstract: Background: Melatonin, an indolic chemical molecule that is secreted by the pineal gland, is associated to essential physiological functions including regulation of the circadian rhythm, redox balance, and the prevention of cancer. Over the last two decades, research knowledge of non-coding RNAs (ncRNAs) and their biological and pathological functions in numerous human diseases has grown. These structure are crucial in the regulation of a variety of biological processes, including cell proliferation, differentiation, apoptosis, and cell cycle, due to their ability to modify gene expression. A rising number of research findings have shown that melatonin affects the expression of several ncRNAs in a variety of diseases, including cancer. The regulation of ncRNAs expression is recognized as a vital potential in the treatment of cancer. Thus melatonin could be an effective therapy in cancer treatment by regulating of ncRNAs expression. Therefore, it is crucial to look into how melatonin affects the expression of ncRNAs in various types of cancer. Materials and Methods: A search was performed in published data in searching database (PubMed, Web of Science and Scopus) by following Keywords: “Melatonin, non-coding RNAs, cancer, and cellular mechanism.” Results: Melatonin's oncostatic properties have attracted focus in recent years. Melatonin, as a potent antioxidant, may help prevent the development of tumors by shielding cells from excess oxidative damage that is a major factor in the progression and growth of tumors. Further underlying mechanisms for melatonin's anticancer effects include: a) pro-oxidant activity; b) antiproliferative properties; c) angiogenesis suppression; and d) regulation of apoptosis and autophagy. Additionally, research has demonstrated that melatonin interacts with ncRNAs to have an anticancer effect. There is accumulating data suggested that melatonin partially modulates the expression and function of lncRNAs, miRNAs, and circRNAs, which could be important for slowing the development of cancer. Accordingly, melatonin affects certain non-coding RNAs (lncRNA, miRNA, and/or circRNA) in cancer, and thereby may lead to the promotion of tumor suppressor pathways or inhibition of cancer-inducing signals. These modifications in downstream signaling pathways (such as HIF1- α , AKT, Notch1, and PTEN) have major effect on the cancer cell's behavior, including increasing apoptosis, slowing proliferation, migration, invasion, cell growth, and lowering drug resistance. Conclusion: The interaction between melatonin and its effect on the expression of miRNAs, lncRNAs and circRNAs in cancer cells will improve our knowledge about melatonin signaling on the molecular processes of cancer cells and help to discover new therapeutic approaches. Further investigation into the molecular functions of melatonin in tumor cells and its connection to ncRNAs may highlight the significance of using this unique chemical in combination with other therapies to treat patients. Keywords: Melatonin, non-coding RNAs, targeted therapy, cancer



چهارمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Assessing the association of serum vitamin D levels in girls with precocious puberty

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Objective: Precocious puberty is a prevalent problem that can adversely affect the final growth and lead to social issues in children. The association between low serum vitamin D levels and precocious puberty has been recently suggested. This study investigated the association between precocious puberty and vitamin

Materials and Methods: Girls with a definitive diagnosis of precious puberty under the age of 11 were included. Subjects with genetic disorders, Down and Turner syndromes, Brain tumors and who were receiving vitamin D treatment, were excluded from the study. The control and case groups were clinically examined and their history was taken. Demographic, anthropometric, and laboratory data such as age, weight, height, 17 β estradiol, LH, FSH, free T4, free T3, and serum vitamin D levels were recorded. BMI, BMI z-score and weight-for-age z-score were calculated. Vitamin D levels were compared between case and control subjects, and their correlations with anthropometric and biochemical parameters were assessed.

Results: 134 girls were included (81 with precious puberty and 53 in the control group). The mean serum vitamin D level was 29.63 \pm 15.85 ng/ml and 41.00 \pm 21.62 ng/ml for the case and control groups, respectively (P=0.0002). The body mass index and weight-for-age Z score were significantly higher in the case group. Vitamin D serum level was significantly associated with weight to age Z score (P=0.016), weight to height Z score (P=0.018), T3 (P=0.049) and T4 (P=0.039) serum levels.

Conclusion: Serum vitamin D levels were significantly lower in girls with precocious puberty, suggesting its role in accelerating puberty. Therefore, supplementation with vitamin D in children may help prevent precocious puberty, which requires further studies.



An enhanced secretion RBD using modified α -factor signal sequence in *Pichia pastoris*

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نوع پذیرش: پوستر | کد مقاله: G-64235

Abstract: Vaccine design strategies against severe acute respiratory syndrome coronavirus 2 (SARS CoV-2) are focused on the Spike protein or its receptor binding domain (RBD) as the main antigen target of neutralizing antibodies. In this study, with the aim of the improvement of the RBD secretory production in *Pichia pastoris*, we used a modified alpha mating factor (α -Mat) signal sequence. The linearized pPICZ α consisting α -Mat ss::RBD or m α -Mat ss::RBD construct was integrated into X-33 P. *pastoris* genomic DNA by electroporation, and transformants were screened by PCR. The secretory expression of the RBD in both recombinant clones were validated by western blotting and Secretion and intracellular localization were compared between the transformants containing intact and modified α -Mat signal sequence by Bradford method. According to our findings, modified signal sequence enhanced secretion of RBD more than 5-fold compared to the levels obtained with the intact α -factor secretion signal. Overall, with regards to the data the recombinant yeast X-33 P. *pastoris* strain consisting the improved α -factor secretion signals is more suitable industrial candidate for the RBD production. Keywords:



چهاردهمین کنفرانس بین المللی آزمایشگاه و باالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



The effect of alcoholic extract of *Artemisia annua* on the expression of Bax and Bcl2 genes and Bax/Bcl2 ratio on HT29 cell line in vitro

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نوع پذیرش: پوستر | کد مقاله: G-09713

Abstract: Background: There is no complementary treatment for many cancers, and for this reason, treatment with high doses of chemotherapy drugs causes the toxicity of the patient's healthy cells, so the presence of a complementary combination along with these drugs to reduce the dose of chemotherapy drugs can be an effective step in the process of treatment. The Artemisia family is considered as an important medicinal plant around the world. In this research, the anticancer effect of *Artemisia annua* on HT-29 colon cancer cells was investigated. Materials and Methods: The methanolic extract of *Artemisia annua* was prepared with a rotary method. Cultured cancer cells were incubated with different concentrations of the extract for 48 hours and the level of cytotoxicity was checked by MTT test. The results were reported as IC50. After determining the IC50 of the cells, they were incubated for 48 hours under the effect of the extract, and after RNA extraction and cDNA synthesis, gene expression tests were performed by Real-time PCR method for Bax and Bcl2 genes. Results: From 20 to 2000 mg/ml doses, *Artemisia annua* significantly inhibited the proliferation of HT-29 cells assessed by MTT colorimetry, in both dose- and time-dependent manners (P less than 0.05). The compound also increased apoptosis after 48 h of exposure (P less than 0.05). Furthermore, examining gene expression indicated an increase in Bax gene expression, a decrease in Bcl2 gene expression, and an increase in the Bax/Bcl2 ratio. (P less than 0.05). Conclusion: *Artemisia annua* extract significantly reduces the growth of cancer cells by inducing apoptosis. Therefore, *Artemisia annua* can be used effectively and safely to prevent or treat cancers. Keywords:



چهاردهمین کنفرانس بین المللی آزمایشگاه و بائین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



The prevalence of Gestational Diabetes Mellitus (GDM) among women attending antenatal care at town public health facilities, FaryabCity, Kerman province.

مریم برخوردار مهنی، © P، ¹ پریسا دهقان، ¹ آذر دخت ایزدی فر، ¹ مجتبی عباسی جرجندی²

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نوع پذیرش: پوستر | کد مقاله: G-08193

Abstract: Background: Gestational Diabetes Mellitus (Gestational Diabetes Mellitus) refers to various degrees of carbohydrate intolerance that occurs or is diagnosed for the first time during pregnancy. Globally, Gestational Diabetes Mellitus (GDM) is rising, but it is a neglected health threat to mothers and their children in low resource countries. Gestational diabetes mellitus (GDM) is a major public health problem and threat to maternal and child health in The World. Materials and Methods: This study was aimed at determining the prevalence of GDM using the one-step 75-g Oral glucose tolerance test (OGTT) protocol, with plasma glucose measurement taken when patient is fasting and at 1 and 2 h and identify associated risk factors among pregnant. Institution based cross sectional study was conducted from April, 2022 to October, 2022 at antenatal care clinic of SPHMMC among sample of 572 eligible pregnant women. Descriptive statistics were used for analysis using SPSS. Results: The overall prevalence of GDM among study participants was 14/3%. GDM was prevalent among age 29 and 35 years, hypertension (2/4%), History of abortion (1/2%), Overweight (1/2%). Conclusion: Globally, the prevalence of Hyperglycemia first detected in pregnancy (Gestational Diabetes Mellitus) varies from 1 - 28 %. In this study, GDM is consistent with the global prevalence. Health services need to be aware of this and to understand the limitations of local data sources to ensure service planning. Public health education and dietary lifestyle modification be required for pregnant women who are at risk of GDM. Keywords: Gestational Diabetes Mellitus, prevalence, FaryabCity, Kerman

Investigating the effect of different concentrations of the alcoholic extract of *Artemisia annua* L. plant on morphological changes and p53 gene expression in HT-29 human colorectal cancer cell line in vitro

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نوع پذیرش: پوستر | کد مقاله: G-20894

Abstract: Background: Colorectal cancer (CRC) is the third most common cancer worldwide. Cancer often results from damage to several genes that control cell division and suppress tumors. Although recent advances in chemotherapy have improved the survival of patients with CRC, side effects and resistance to chemotherapy have led to the search for alternative treatments. The presence of supplements along with chemotherapy drugs to reduce their dose can be an effective step in the treatment process. Medicinal plants can be used for this purpose. There is considerable evidence that *Artemisia annua* L. (*A. annua*) extract has multiple anticancer effects on several types of cancer cells by inducing mitochondrial-dependent apoptosis. In this research, the anticancer effect of *A. annua* extract on CRC cell lines (HT-29) was investigated. Materials and Methods: *A. annua* plant was collected from areas around shahrood city, Iran in October 2021. After getting the herbarium number (voucher E-1347 FUMH) the methanolic extract was prepared under reduced pressure in a rotary evaporator at 40°C. HT-29 cells were cultured and incubated with different concentrations of *A. annua* extract (0.2-20 mg/mL) for 24 and 48 hours. The cytotoxicity was evaluated by MTT test. Furthermore, RNA extracted from cells treated with various concentration of *A. annua* extract (0.750-1 mg/ml) for 24h. After cDNA synthesis, the expression of the P53 gene was investigated by the Real-time PCR method. To investigate morphological changes, HT-29 cells were cultured and treated with 0.75 mg/ml concentration of *A. annua* extract and 4µM concentration of doxorubicin, which was considered as a positive control, for 24 and 48 hours. In addition, the percentage of apoptotic cells was analyzed by PI staining and flow cytometry. Results: The results of the MTT test demonstrated that the viability of HT29 cells was significantly decreased by increasing the concentration of *A. annua* methanolic extract, (IC₅₀ for 48h: 1358.1µg/ml). Analysis of gene expression by RT-qPCR showed a decrease in P53 gene expression compared to the control gene (p-value less than 0.05). Furthermore, the results of PI staining also confirmed the results of MTT, and morphological changes were observed in the cells treated with a concentration of 0.75 mg/mL of *A. annua* methanolic extract compared to the control groups. Conclusion: According to the results, it can be concluded that the methanolic extract of *A. annua* can induce apoptosis in HT29 cells and with further studies, it can be used in the treatment of colorectal cancer. Keywords: Colorectal cancer, *Artemisia annua* L. morphological changes, P53 gene

The effect of ZnO-Ag nanoparticles synthesized using Sophora pachycarpa extract on expression of caspase 3 and 6 genes of chronic myeloid leukemia cells (K562) in vitro

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نوع پذیرش: پوستر | کد مقاله: G-25690

Abstract: Background: Leukemia is a malignant disease that results from the unlimited proliferation of hematopoietic stem cells. However, limitations such as non-specificity, cytotoxicity, and multidrug resistance are fundamental challenge for optimal cancer treatment. Nanoparticles (1-100 nm) offer opportunities to destroy cancer cells due to their unique advantages such as biocompatibility, reduced toxicity, superior stability, The aim of this study was to evaluate the ability of ZnO/Ag nanoparticles synthesized using Sophora pachycarpa fruit extract to induce the expression of caspase 3 and 6 apoptotic genes in human chronic myeloid leukemia cells (K562 cells). Material and Methods: At first, hydroalcoholic extract of Sophora pachycarpa fruit was prepared. Then, synthesized ZnO-Ag nanoparticle was prepared using Sophora pachycarpa fruit extract. Then K562 cancer cells were treated with different doses (15, 250, 500, 1000 µg/ml) of ZnO-Ag nanoparticles synthesized using Sophora pachycarpa extract for 24 hours to investigate viability and gene expression. Viability of cells determined by MTT assay and IC50 calculated by CalcuSyn software. RNA extracted from treated cells by TRIZol, cDNA synthesis was done and using real-time PCR, the expression of caspase 3 and 6 genes in cells treated with ZnO-Ag nanoparticles synthesized using extract was determined and compared with beta-actin gene as an internal reference gene. The results were analyzed using Prism statistical software. Results: K562 Cell survival was considerably reduced with increasing concentration compared to control. RT-qPCR results showed that the expression level of caspase 6,3 genes increased (p-value less than 0.05) in cells treated with ZnO-Ag nanoparticles synthesized using the extract for 24 hours. Conclusion: The results showed that the biosynthesis of ZnO-Ag nanoparticles synthesized with Sophora pachycarpa extract is cheap and easy. Beside, anticancer properties of these nanoparticles against K562 cells were demonstrated. It can be induced apoptosis in leukemia cancer cells by changing the expression of genes involved in apoptosis although further studies are needed to clear precise mechanisms. Keywords: Sophora pachycarpa extract, ZnO-Ag nanoparticle, Cell line K562, Apoptosis

Evaluation and comparison of diagnostic tests for type 2 diabetes: a systematic review

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نوع پذیرش: پوستر | کد مقاله: G-19257

Abstract: Introduction: Diabetes is a very common disease that is considered as one of the global health problems. The most common type of diabetes is type 2 diabetes, which is often asymptomatic in the early stages of the disease. Early diagnosis of this disease can prevent its long-term complications, including blindness, kidney failure, cardiovascular disease, and amputation. There are many diagnostic tests to diagnose type 2 diabetes such as fasting plasma glucose (FPG), oral glucose tolerance test (OGTT) and glycosylated hemoglobin (HbA1c) test. This study was conducted with the aim of investigating the diagnostic tests of type 2 diabetes and comparing these methods with each other. Method This study was a systematic review that was conducted in 2022. Using the keywords (Type 2 diabetes), (Glycosylated Hemoglobin A1c), (Diagnosis Tests), (FPG), (OTTG) in the reliable databases of PUBMED, Scopus, Web of Sciences with a time limit of 2017 to 2022. . To ensure the completeness of the search results, the sources of the articles have been reviewed and after removing the duplicate titles from the endnote software and reviewing the titles and abstracts, the related articles were reviewed using JBi tools. After checking the quality of the articles, the findings were entered in the desired checklist. Results Research shows that the most commonly used tests for diagnosing type 2 diabetes are the FPG test and the OGTT test. In both of these tests, the blood glucose level is checked and the person must fast for at least 8 hours. Although the FPG test is widely used, the sensitivity of this test is not very high and about one third of people with diabetes remain undetected. Also, to use the FPG test, the blood sample must be examined within two hours at most. Otherwise, the blood glucose level will be shown as falsely low. To confirm the diagnosis of diabetes using this test, the test must be repeated at least twice. In the OTTG test, the fasting blood glucose level is first measured. Then they give a sweet drink to the patient and measure the blood glucose level after one, two and three hours. OTTG test, despite being widely used, is time-consuming and costly and has low reproducibility. Glycosylated hemoglobin (HbA1c) test is another test used to diagnose type 2 diabetes. This test can be done at any time without the need for the person to be fasting. The HbA1c test shows an average of two to three months of glucose. In the HbA1c test, the amount of glucose bound to hemoglobin (Hb), which is an oxygen-carrying protein in red blood cells, is measured. Discussion The results obtained from this study show that the combination of FPG test and HbA1c test is the best way to diagnose people with type 2 diabetes and to check the risk of developing type 2 diabetes in affected people. Keywords:

Investigating the relationship between the serum level of long non-coding RNA molecules (Lnc RNAs) and esophageal cancer

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۱) دانشگاه علوم پزشکی خراسان شمالی- دانشکده پزشکی - گروه پاتوبیولوژی و علوم آزمایشگاهی- استادیار بیوشیمی بالینی
۲) دانشگاه علوم پزشکی خراسان شمالی- دانشکده پزشکی - گروه فناوری های نوین- استادیار بیوتکنولوژی
۳) دانشگاه علوم پزشکی خراسان شمالی- دانشکده پزشکی - کارشناس آزمایشگاه

نوع پذیرش: پوستر | کد مقاله: G-48935

چکیده: مقدمه: امروزه تحقیق در مورد RNA های غیر کد شونده طویل یا Long noncoding RNAs به عنوان یک موضوع و ایده جدید در تحقیقات مرتبط با سرطان به حساب می آید. با وجود اینکه مطالعاتی در رابطه با تغییرات LncRNA های بافتی انجام شده، تا کنون مطالعات اندکی در زمینه ی Lnc RNA های سرمی در ارتباط با سرطان های مختلف از جمله سرطان مری انجام شده است. استفاده از نمونه سرم بیمار به دلیل غیر تهاجمی بودن و تشخیص زود هنگام چشم انداز وسیع و جدیدی را به روی محققان سرطان باز کرده است. به علت ظهور زود هنگام Lnc RNA ها و طول عمر نسبتا بالای آنها در سرم، می توانند از ارزش تشخیصی بسیار بالایی برخوردار باشند از این رو، نتایج حاصل از این تحقیق می تواند به شناسایی عوامل مرتبط با سرطان مری کمک کننده باشد. مواد و روش ها: 47 نفر از افراد مبتلا به سرطان مری که توسط بررسی های آندوسکوپیکن شناسایی و با مطالعات هیستوپاتولوژی تایید شده بودند وارد مطالعه شدند. در گروه شاهد نیز ۵۰ نفر از افراد مراجعه کننده به بیمارستان که آندوسکوپی سرطان مری آنها منفی بود، قرار داده شدند. نمونه ی خون افراد (۵ سی سی) بلافاصله پس از جمع آوری سانتریفیوژ و در دمای ۷۰- درجه سانتی گراد نگهداری شد. در ابتدا RNA سرمی افراد استخراج و از آنها cDNA سنتز و بر روی نمونه ها، تست Real Time PCR جهت اندازه گیری سطح سرمی مولکول های LncRNAs انجام گرفت و در آخر، نتایج Time PCR Real با فرمول $2^{-\Delta\Delta Ct}$ محاسبه گردید. یافته ها: در این بررسی مشخص گردید که غالب سرطان مری از نوع سنگفرشی (ESCC) بود (ESCC=72/3% (EAC=27/7%)). همچنین بررسی های این مطالعه نشان داد که ابتلا به سرطان مری در افرادی که دارای سابقه ی ابتلا به هرگونه سرطان در اقوام درجه یک و دو خود هستند بیشتر می باشد. نتایج Real Time PCR مشخص کرد که در گروه مورد میزان سطح سرمی LncRNA های MALAT1, TUG1, UCA1 بیشتر از گروه شاهد و تفاوت معنی دار آماری از لحاظ میزان بیان این ژن بین افراد گروه مورد و شاهد وجود داشت. (P=0.000) نتیجه گیری: در این مطالعه با توجه به تشخیص اسیدهای نوکلئیک در گردش خون و نیز با توجه به نمونه گیری آسان تر و تکرار پذیری بیشتر این روش به نسبت روش نمونه برداری از بافت، به نظر می رسد ارزیابی RNA های سرمی از جمله LncRNA های مرتبط با سرطان مری پس از تحقیقات بیشتر بتواند در کنار بررسی دیگر فاکتورهای سرطانی، در دستیابی به الگویی جهت تشخیص سریع تر سرطان مری کمک کننده باشد. با این وجود بررسی های بیشتر در این زمینه توصیه می شود.



چهاردهمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Green Synthesis and Antibacterial Activity of ZnO Nanoparticles Using plant *Sambucus nigra*

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نوع پذیرش: پوستر | کد مقاله: G-62741

Abstract: The aim of this study was to report the synthesis, characterization and evaluation of the antibacterial activity of zinc oxide (ZnO) nanoparticles (NPs) with *Sambucus nigra* extract. The physicochemical properties of these NPs such as crystal structure, size and morphology were investigated by X-ray diffraction (XRD), scanning electron microscopy (SEM) and transmission electron microscopy (TEM). The result was that the metallic ZnO NPs showed high antibacterial activity on *Escherichia coli*, while their antibacterial activity on *Staphylococcus aureus* was low. Keywords:

Epicardial Adipose Tissue; an Efficient Therapeutic Target to Improve Cardiac Function

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نوع پذیرش: پوستر | کد مقاله: G-84123

Abstract: Epicardial adipose tissue (EAT) or epicardial fat is located between the myocardium and the epicardium visceral layer. In the physiological conditions, EAT contributes greatly to cardiac function, primarily by metabolizing excess lipids and precluding development of atherogenesis. Nevertheless, EAT may exert detrimental effects on the cardiac function in pathological state due to inflammation or oxidative stress. Multiple findings have demonstrated a close relationship between EAT and the development of metabolic disorders as well as cardiovascular events. Recently, EAT has been recognized as a novel risk factor for cardiovascular diseases (CVDs), increasing interest in strategies that target cardiac adipose tissue. There is evidence that lifestyle changes, pharmacotherapy, and bariatric surgery can reduce EAT volume (EATV) via pleiotropic mechanisms, improving cardiac function. Based on findings, exercise or regular physical activity improve complications associated with the development of metabolic diseases with decreasing EAT thickness. Actually, physical exercise could diminish blood pressure, low-density lipoprotein (LDL) levels, inflammation markers, and EATV and subsequently ameliorate myocardial aerobic capacity. Nutritional interventions altering the composition of EAT fatty acids could also affect EAT inflammation and the risk of CVDs progression. A few studies have surveyed the surgical resection of EAT on CVDs and reported that the removal of cardiac fat may positively affect coronary artery disease as well as cardiac function. It has been demonstrated that epicardial fat can be considered as an effective therapeutic target for cardiometabolic drugs modulating adipose tissue, including glucagon-like peptide-1 (GLP-1) receptor agonists and sodium-glucose cotransporter 2 (SGLT2) inhibitors. As well, intensive statin therapy can reduce EATV and EAT thickness, proposing anti-inflammatory pleiotropic roles of statins in EAT attenuation. There are reports on other pharmacological therapeutic options affecting EAT, including glucose-lowering drugs (metformin and thiazolidinediones) proprotein convertase subtilisin/kexin type-9 (PCSK-9) inhibitors, dipeptidyl peptidase-4 (DPP-4) inhibitor and others. Lately, gene therapy could also be effective in targeting adipose tissue, despite the fact that it has primarily been applied to non-CVDs. The results of an experimental study revealed that an increase in fibroblast growth factor 21 (FGF21) expression in visceral adipose tissue was related to improved insulin sensitivity and decreased levels of inflammatory cytokines. Therefore, EAT may consider as a promising target for gene therapy to attenuate cardiovascular events. In conclusion, CVDs could be effectively managed by reducing EAT using different pharmacological interventions and non-pharmacologic procedures. However, some challenges still remain regarding therapeutic options that specifically target EAT. Hence, it is suggested that future studies be conducted in this field. Keywords:



چهاردهمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Role of the Nrf2-HER2 axis in cancer stem cells

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نوع پذیرش: پوستر | کد مقاله: G-06841

Abstract: Cancer is one of the main causes of death among humans, second only to cardiovascular diseases. In recent years, numerous studies have been conducted on the pathophysiology of cancer and it has been established that cancer is developed by a group of stem cells known as cancer stem cells (CSCs). Thus, cancer is considered a stem cell disease, although there is no consensus about the characteristics of these cells. CSCs change their metabolic pathways in order to access easy energy. Therefore, one of the key objectives of researchers in cancer treatment is to destroy CSCs. Nuclear factor erythroid 2-related factor 2 (Nrf2) plays an important role in chemotherapy by regulating antioxidants and detoxification enzymes. Human epidermal growth factor receptor 2 (HER2) is a member of the tyrosine kinase receptor family, which contributes to the protection of cancer cells against chemotherapy. Given the growing body of information in this field, in the present review, we attempted to shed light on the relationship between Nrf2-HER2 and CSCs. Keywords:

Evaluation of the simultaneous effects of progesterone and berberine on K562 cell line

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نوع پذیرش: پوستر | کد مقاله: G-49361

Abstract: Background: Chronic myeloid leukemia (CML) is an uncommon type of cancer of the white blood cells that starts in the bone marrow and invades the blood. Progesterone (P4) and berberine (BBR) inhibit the growth of tumor cells. Here, we assessed the simultaneous effects of progesterone and berberine on growth inhibition of K562 cells. Materials and Methods: K562 cells were cultured in medium containing serum and simultaneously exposed to IC50 different concentrations of P4 and BBR at 24 (P4:102.4 μ M; BBR:125 μ M), 48 (P4:78.4 μ M; BBR:114 μ M) and 72 h (P4:70 μ M; BBR: 45 μ M). Then, the cell viability was determined using MTT assay. Finally, apoptosis percentage of the cells was examined after exposing K562 cells to IC50 concentrations of p4 and BBR as a combination of two drugs and alone at 24, 48 and 72 h using AnnexinV staining and flow cytometry. Results: Our results showed that combining two drugs (P4 and BBR) compared to one drug alone more effectively induced apoptotic cell death and inhibited the cells. Conclusion: The combination of P4 and BBR may be considered as a promising therapeutic potential in CML patients in the future due to its high efficiency in killing cells. Keywords: Progesterone, Berberine, Apoptosis, Chronic myeloid leukemia

Evaluation of the photothermal effects of anti CD44 antibody-conjugated Fe₃O₄@Au core-shell nanoparticles in the presence of near infrared laser irradiation on gastric cancer stem cells

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نوع پذیرش: پوستر | کد مقاله: G-72053

Abstract: Background and Aim: Cancer stem cells (CSCs) due to characteristics, including self-renewal, differentiation, metastatic dissemination, and chemoresistance play an essential role in the initiation and progression of cancer. Gold nanoparticles are one of the most important photothermal agents that used in photothermal therapy. Here, we investigated photothermal effects of anti CD44 antibody-conjugated Fe₃O₄@Au core-shell nanoparticles in the presence of near infrared (NIR) laser irradiation on apoptosis and death of CSCs. Methods: After culturing CSCs in a serum-free medium containing EGF and B-27 supplement, examining CD44 expression in them using flow cytometry and exposing them to different concentrations (25-100 μ M) of the anti CD44 antibody-conjugated nanoparticles at 24, 48 and 72h, the cell viability was determined using MTT assay. In finally, apoptosis percentage was examined after exposing CSCs to conjugated nanoparticles (75 μ M) in the presence of laser irradiation at 24, 48 and 72h using AnnexinV staining and flow cytometry. Results: Our data showed that the conjugated nanoparticles inhibited the growth of CSCs in the dose- and time-dependent manners, as well as induced apoptotic cell death in these cells. Conclusion: The conjugated nanoparticles due to the apoptosis induction and death of CSCs may be considered a promising therapeutic potential in gastric adenocarcinoma patients in the future. Keywords: Nanoparticles, Photothermal, Cancer stem cells, Apoptosis, Gastric cancer

Interaction study of two natural compounds of Curcumin and Pectin on human albumin with an anticancer drug synthesis approach

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نوع پذیرش: پوستر | کد مقاله: G-43968

Abstract: Background: Human serum albumin (HSA) is a major protein in the blood plasma, with a molecular weight of 66 kDa. This protein transports most drugs and compounds into the bloodstream. Methods: In the present study, the interactions and side effects of natural anticancer compounds of curcumin and pectin on HSA the structure were investigated. Also, the side effects of the compounds, determination of the number of binding sites and the binding affinity of the binding were investigated using different spectroscopic techniques such as fluorescence and circular dichroism (CD) at 25° C. Results: The analysis of fluorescence spectra showed that the addition of these compounds resulted in a significant reduction of the HSA the fluorescence spectrum through the quenching mechanism. It can also alter the 3D structure of the protein. Analysis of circular dichroism spectra showed that the simultaneous binding of these compounds could alter the protein structure by transforming the regular structure of α -helix into a β -sheet. Conclusion: According to the results obtained, these results could help to synthesize new drugs with fewer side effects against cancer. Keywords: HSA, Curcumin, Pectin, Fluorescence, Interaction.

Development of an Indirect ELISA for Immunoassay against H5N1 Influenza Virus

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نوع پذیرش: پوستر | کد مقاله: G-23146

Abstract: Background: Avian influenza H5N1 virus which is a zoonotic pathogen causes severe and contagious illness in respiratory system. This virus is from type A and belongs to Orthomyxoviridae family. Avian influenza virus-mediated human infections are caused by H5, H9 and H7 subtypes which are very common. Materials and Methods: The aim of this study is to design an indirect ELISA for specific and rapid diagnosis of produced antibodies against avian influenza H5N1 virus. Therefore, the female Balb/c mice were infected by subcutaneous injection of H5N1 virus in three stages with 10 days intervals. Then the drawing blood and isolation of serum were performed. Different dilutions of the isolated serum were prepared and were incubated with different dilutions of coated antigens. Afterward, the titer of polyclonal antibody produced by immune system of mouse was determined by using indirect ELISA. Results: The results showed that the level of produced antibody in the serum of immune mice was considerable high and their assay by ELISA has been conducted efficiently. The comparison of immune mice with control ones showed a significant difference in the amount of produced antibodies. Conclusion: The results of this study present a promising future for designing more specific diagnostic kits for patients challenging with H5N1 virus. Keywords: H5N1, Polyclonal antibody, Orthomyxoviridae, Indirect ELISA.

Serum vitamin D levels in related to childhood obesity

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Background: Childhood obesity and vitamin D deficiency are two complications, both of which are prevalent and have an increasing incidence. Vitamin D plays an important role in bone growth; thus, its insufficiency or deficiency, especially in childhood, is of great importance. Evidence suggests that obesity is associated with a decrease in vitamin D levels. But so far there are not enough evidence to connect obesity in children with vitamin D deficiency. Therefore, the purpose of this study was to determine the relationship between vitamin D levels and obesity in children and adolescents, and compare them with normal healthy subjects.

Materials and Methods: This case/case study was performed on 174 children and adolescents aged 8 to 18 years old who were referred to the pediatric endocrinology clinic in Ali Asghar Children Hospital. The participants were categorized into two groups of obese and normal-weight children by measuring anthropometric indices and the calculation of BMI. Experimental data including vitamin D (measured by ELISA method), lipid profile, phosphorus and calcium levels were also recorded. The data were analyzed by SPSS software and t-test and Pearson tests were used for comparing the variables between the two groups and assessment of correlation between variables, respectively.

Results: According to this study, vitamin D level in obese subjects was significantly reduced compared to controls. When the subjects were categorized according to their vitamin D levels, it was found that lipid profile, except for HDL, was higher in vitamin D deficient group than those with normal levels of vitamin D. There was not any significant correlation between phosphorus and calcium levels with vitamin D levels, possible due to their normal levels.

Conclusion: The prevalence of obesity, similar to other studies, was associated with the risk of low vitamin D, and given the importance of complications of obesity and vitamin D deficiency and the two-way relationship between these two factors, controlling for vitamin D levels in all the children with obesity is suggested.

Keywords: Obesity, Vitamin D, children



چهاردهمین گنگره بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Sub-acute methadone administration suppresses serum butyrylcholinesterase activity without modulation of acetylcholinesterase in the hippocampus of rats

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نوع پذیرش: پوستر | کد مقاله: G-69427

Abstract: Background: Cholinesterase enzymes are responsible for the hydrolysis of choline-based esters in order to terminate the impulse transmission of acetylcholine neurotransmitter. A sub-acute exposure of methadone in a rat model was designed to study its effect on the activity of cholinesterase enzymes. Changes in the activity of serum butyrylcholinesterase and acetylcholinesterase in the hippocampus of Wistar rats were investigated. Materials and Methods: Determination of butyrylcholinesterase activity in serum was performed by a colorimetric method using a biochemical auto-analyzer. Activity of acetylcholinesterase in the hippocampus was performed following the release of the enzyme from tissue by a similar colorimetric method. The rats were assigned to receive doses of 1.5, 3, and 6 mg/kg methadone orally by gavage. Following completion of the treatment, the heart blood was drawn for serum separation, WBC count, and the differential leucocytes. Furthermore, hippocampus was surgically removed for acetylcholinesterase activity in methadone-treated rats. Results: The results showed a significant decrease in butyrylcholinesterase activity in the methadone treated rats ($p=0.006$). However, methadone did not alter the acetylcholinesterase activity in the hippocampus. The ratio of butyrylcholinesterase to acetylcholinesterase was 1.4 to 1. WBC count and the differential leukocytes indices following the sub-acute exposure to methadone did not change significantly. Conclusion: The pattern of cholinergic modulation in the brain and serum were not the same following methadone in vivo exposure. Methadone sub-acute administration in rats suppressed serum butyrylcholinesterase activity without modulation of acetylcholinesterase in the hippocampus. Keywords: Methadone, serum, hippocampus, cholinesterase, rats



چهاردهمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Assessment of oxidative stress and mitochondrial dysfunction associated with brain lesions in patients with multiple sclerosis

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نوع پذیرش: پوستر | کد مقاله: G-89740

Abstract: Multiple Sclerosis (MS) is a disease of the central nervous system, which ultimately may lead to various disabilities in patients. There is No definitive cure and diagnosis for the disease. MRI is method of imaging neuronal degradation, which would be useful in disease diagnosis as it becomes progressive. Many complex molecular defects lead to neurodegeneration in people with MS. Serval studies emphasizes on mitochondrial dysfunction and reactive oxygen species (ROS) that attack the myelin sheath and destroy neurons in the central nervous system, resulting in wounds in the brain called plaque or scarring. Adenine nucleotide translocase 1 (ANT1) is the most abundant protein in the mitochondrial inner membrane and is important for maintaining the mitochondrial membrane potential and apoptosis. This study aimed to evaluation of oxidative stress and the role of dysfunctional mitochondria in MS and their possible relationship with brain lesions in MS patients. Keywords:

Association between Vitamin D and Migraine Headaches: A systematic review

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نوع پذیرش: پوستر | کد مقاله: G-90745

Abstract: Background: Migraine is defined as a highly prevalent headache for which various non-pharmacologic agents have so far been proposed, given that the existing treatments have had common adverse effects. Riboflavin (B2) magnesium and coenzyme Q10 combination with vitamin D appears to reduce the amount of pain experienced during a migraine. In this review, we discuss the current evidence regarding the association between vitamin D and migraine headaches. Materials and Methods: PubMed, Science Direct, SID, and Google Scholar databases were searched for eligible articles up to January 2023, using the keywords of “migraine” and “vitamin D”. Studies were chosen according to the following inclusion criteria: I) patients had to have been diagnosed with migraine, II) interventions consisted of vitamin D versus placebo, usual care or supplementation with any other compound. Among the 48 articles found in this regard, 27 related articles were used at the end. All articles were selected from English and Persian articles. Results: Finally, 27 articles were included in this study. Serum levels of 25(OH)D were found to be lower in subjects diagnosed with migraine compared with healthy individuals. In a number of studies, no significant correlation was found between 25(OH)D serum concentrations; however, different migraine parameters, including frequency, severity, attack duration, migraine disability assessment questionnaire (MIDAS), etc., were shown to be negatively correlated with vitamin D serum levels in others. After treatment of vitamin D deficiency, many migraine characteristics improved significantly. In some interventional studies, which included adult migraineurs of both genders with deficient, insufficient, or normal serum levels of vitamin D, it was demonstrated that D3-vitamin supplementation in a dosage of 50 µg/day (equal to 2000 IU) to 100 µg/day (equal to 4000 IU) for an intervention period of 12-24 weeks could significantly decrease migraine frequency and even migraine severity in some cases. Although most interventions were focused on adults. Some existing evidence suggested that vitamin D, due to its fewer adverse effects compared with conventional medications, could also be regarded as a prophylactic agent in children suffering from migraine. Moreover, some positive effects, caused by pharmacological medications, e.g. amitriptyline, could be magnified, while coupled with this vitamin supplementation. Finally, newly published meta-analyses could reveal additional benefits of supplementation with vitamin D on migraine characteristics. Conclusion: It appears that vitamin D supplementation is a well-tolerated option that can improve migraine headaches. However, further research needs to be done on the topic. Keywords: Migraine; Vitamin D; 25(OH)D



چهارمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Clinical scores, inflammation and demyelination ameliorated in mice model of multiple sclerosis fed with high cholesterol diet

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نوع پذیرش: پوستر | کد مقاله: G-17238

Abstract: Background: In multiple sclerosis (MS) which is an autoimmune demyelinating disease, disturbing lipid metabolism especially cholesterol has been reported. The aim of this study is to examine the effects of high cholesterol supplementation in improvement of clinical scores, reducing inflammation and finally control of demyelination in EAE, as the main animal model of MS disease. Materials and Methods: C57BL/6 strain female mice were used and randomly divided to three groups in which two treated-groups (n=6 animals in per group) were fed with an appropriate diet containing more than 4% cholesterol. Thereafter, one of treated group was induced animal model of MS or experimental autoimmune encephalopathy (EAE) using MOG 35-55 peptide and pertussis and related adjuvant. The clinical scores were recorded in cholesterol-fed treated EAE model in comparison with non-treated EAE and cholesterol-fed mice. At the peak of clinical scores in non-treated EAE model, blood samples were taken from the mice to evaluate the cytokines and other inflammation markers and after sacrificing all the mice, brains and spinal cords tissues were obtained to examine demyelination by histopathological assays. Results: The data showed that the cholesterol supplementation could ameliorate the clinical scores of cholesterol-fed treated EAE model as well as inflammation factors in comparison with non-treated EAE mice and cholesterol-fed mice. Meanwhile, histological examination showed that cholesterol has the relatively preventive effects on myelin destruction and can reduce inflammatory cell infiltration and astrocyte accumulation. Conclusion: It seems that appropriate amount of cholesterol supplementation not only has no adverse effects on clinical scores in EAE model of MS disease, but also can reduce the inflammation which is an important reason of the disease. It also seems that metabolism of cholesterol is the hallmark point for more investigation about its roles in pathogenesis of this disease. Keywords: Cholesterol, myelin, Multiple sclerosis, Clinical scores, EAE

Determination of the genotype and frequency of glutathione transferase-P (GSTP) alleles in tumor biopsies from Iranian patients with oral squamous cell carcinoma

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نوع پذیرش: پوستر | کد مقاله: G-39251

Abstract: Background: Glutathione S-transferases (GSTs) play an important role in protecting cells from oxidative stress and the metabolism of chemical carcinogens. The oral mucosa expresses the predominant form of glutathione S-transferases pi (GSTP1). GSTs could exist in different genetic polymorphic forms in different ethnical groups. Genetic polymorphism can affect the enzyme activity related to the metabolism of xenobiotic agents. Therefore, this study aims to compare genotypes of GSTP1 in Iranian individuals diagnosed with oral squamous cell carcinoma (OSCC). Materials and Methods: The major GSTP1 genotypes and allele frequency in tissue biopsies from Iranians OSCC (n=43) and gingiva biopsies (n=5) from healthy individuals were determined using the PCR-RFLP technique. Sanger sequencing was used to confirm the results. Results: The Ile/Ile genotype was more prevalent in patients than in healthy individuals. OSCC risk was relatively lower in individuals with AG genotype (OR=0.387, %95CI=0.253-0.593, P=0.001) and G allele (0.276, %95CI=0.129-0.589, P=0.001) in GSTP1 rs1695. Whereas, the AA genotype was significantly higher in OSCC cases. In OSCC cases, the AA genotype was significantly higher which was associated with increased GST activity in plasma. Conclusion: The Ile/Ile genotype of GSTP1 has a positive correlation. Such association was not detected in the patients with the Ile/Val genotype. This finding showed that people with the AA genotype might be more vulnerable to OSCC incidence. Further studies with larger sample sizes and different ethnicities are required to validate these findings. Keywords: Oral Squamous Cell Carcinoma, Single Nucleotide Polymorphism, Glutathione transferase P, PCR-RFLP

Cardiac infarction diagnosis using neural networks

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نوع پذیرش: پوستر | کد مقاله: G-37149

Abstract: Background: One of the most important causes of death in the world is heart disease. A myocardial infarction occurs when one of the coronary arteries is completely blocked. 12-lead ECG, along with patient history and biochemical markers, are commonly used in the emergency department to diagnose AMI. A 12-lead ECG has the advantage that it is always available, but it is difficult to interpret. Therefore, computer-aided ECG interpretation is important to detect AMI and can improve the early diagnosis of AMI. Therefore, a study on the diagnosis of cardiac infarction using neural network was evaluated. Materials and Methods: In this project, we have used the possible artificial network as a tool to diagnose AMI patients using 12-lead ECG. We evaluated the data of 294 patients using MATLAB software. Results: In this article, Q wave amplitude, ST level deviation and T wave amplitude are used as features extracted from twelve ECG leads. We extract the ST segment using the end point of the QRS and the start point of the T wave, or we can directly consider the 80ms long point after the J point. Read 5 cycles and calculate the amplitude and integral of R and Q and the amplitude of T and the total integral. It should be noted that the values are the average of 5 cycles. That is, we obtain the values separately and divide by 5. Then the characteristic of 70% of healthy people and 70% We give % of the patient to the neural network and leave 30% for testing. We introduce the obtained features, i.e., Q, R, and T domains, as well as the training and testing set for the classifier. Finally, the network has the ability to classify the remaining 30% in healthy people and 30% in patients using the features to The random face can determine whether a person is healthy or sick, and secondly, what kind of disease (MI) he has. Final results for ECG signal Classification to detection of Myocardial Infarction (Probabilistic Neural Network (PNN)84.4 % Multilayer Perceptron (MLP)78.13 % k-Nearest Neighbors (KNN)84.4 % Kmeans61.68 %) Conclusion: By using feature extraction from lead two and input to the artificial neural network without a doctor, we can determine whether the person in question is sick or healthy and if there is a disease (MI), which type of disease he has. The shortcomings of this work are as follows. Only lead 2 is used if some types (MI) show themselves in other leads and the features are only selected from five selection cycles at different points and this is one of the problems of this project. Keywords: Infarction, neural network, Electrocardiography

case report of Catastrophic frequent false reports of blood calcitonin levels in a patient with a history of medullary thyroid carcinoma

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نوع پذیرش: پوستر | کد مقاله: G-30869

Abstract: Background: Calcitonin is a peptide hormone that is produced by the C cells or perifollicular cells of the thyroid gland. Calcitonin levels decrease with age and during pregnancy and breastfeeding. Its amount in serum is higher than in plasma. It is an effective marker for the diagnosis of medullary thyroid carcinoma (MTC). Calcitonin testing is also effective for the follow-up and treatment response of medullary thyroid carcinoma. (Normal base values (plasma): Men: ≤ 19 pg/ml, Women: ≤ 14 pg/ml). Case presentation: A 58-year-old woman with a history of swelling in the neck underwent surgery to remove a thyroid mass following initial para-clinical procedures. The pathological examination revealed medullary thyroid carcinoma. After that, according to the guidelines, she performed a calcitonin test for control every three months for three years. The first calcitonin level after surgery was 80 pg/ml, but after three months it dropped to 4 pg/ml and serial testing with three month intervals was near 4-7 pg/ml. Approximately three years later, the results were again 6 pg/ml. However, on that same day a suprasternal adenopathy was detected during an ultrasound examination, and a metastatic medullary carcinoma has been diagnosed through a pathological examination. The patient was immediately referred to another laboratory, where the calcitonin level was found to be 160 pg/ml. Upon returning to the primary laboratory, the patient's calcitonin level was determined to be 8 pg/ml, and the patient filed a complaint with the court regarding the primary laboratory. For three years, the laboratory has given false reports, and as both ultrasound and other laboratory tests proved otherwise, the fault of the primary laboratory was confirmed. However, the exact cause of the error has not been determined and was reported to have an unknown cause. The most likely cause of the error was the use of an ELISA kit to test the calcitonin level. Initially, the test was performed using the closed method, which gave the result of 80 pg/ml. In other tests, the open (ELISA) method was used. Thus, the authenticity of the Eliza kit was questioned. Conclusion: Since closed methods are more accurate than open methods, it is recommended to follow-up patients with medullary thyroid carcinoma using the closed method, in particular with electrochemiluminescence (ECL). Keywords: Medullary thyroid carcinoma, open test, closed test, calcitonin, laboratory fault

Preparation and characterization of encapsulated anionic liposomes with melittin gene for targeting the BT-474 breast cancer cells

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نوع پذیرش: پوستر | کد مقاله: G-30471

Abstract: Background: Breast cancer is the main cause of cancer-related death among women worldwide. Current treatment methods are insufficient, so novel treatment strategies are needed. The main component of bee venom, melittin, has anti-cancer properties. Transferring the melittin encoding gene to breast cancer cells is an appropriate tool for precise diagnosis and treatment of the disease. Materials and Methods: Phospholipon 90H, Cholesterol, and DSPE-PEG2000 lipids were used to synthesize the PEGylated liposomes using thin film hydration technique. Plasmids containing the melittin gene were encapsulated in liposomes by the passive loading method. Transmission electron microscopy (TEM) and dynamic light scattering technique (DLS) were applied to illustrate the morphology, size, and zeta potential of the synthesized liposomes. The MTT assay was used to measure the cytotoxicity of BT-474 breast cancer and NIH/3T3 mouse normal fibroblast cell lines. To check the GFP expression, the fluorescent microscope was used. Results: The TEM images confirmed the spherical appearance and monolayer structure of the synthesized liposomes. Based on DLS results, the size of encapsulated nanoparticles was about 140 nm and their charge was negative. The encapsulation efficiency was estimated as 57±38 % (mean ± SD). The estimated IC50 of nanoliposomes transfecting BT-474 cells was 12.04 and 9.86 µg/ml for 48 and 72 hours, respectively. However, these nanoparticles had less effect on the viability of normal NIH/3T3 cells. The fluorescent microscopy results also exhibited the expression of GFP in transfected cells which confirms the expression of the target gene. Conclusion: Anionic PEGylated liposomes were able to efficiently transfer the melittin gene to BT-474 cancer cells and reduce the viability of the cells, while normal cells were almost unaffected by this cytotoxicity. Thus, these targeted nanoparticles could be suggested as an effective alternative tool for the diagnosis and treatment of breast cancer. Keywords: Liposomes, Melittin, Plasmids, Breast Cancer.

Prevalence of Microalbuminuria and Its Association with Severe Urinary Reflux and Renal Scarring with Reflux Nephropathy in Children Aged Less Than 12 Years in Ilam, Iran

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نوع پذیرش: پوستر | کد مقاله: G-57019

Abstract: Background: Vesicoureteral reflux is a common urinary tract abnormality, which could damage the renal parenchyma. The present study aimed to investigate the prevalence of microalbuminuria and its association with the severity of urinary reflux and renal scarring with reflux nephropathy in children aged less than 12 years referred to Imam Khomeini Hospital in Ilam, Iran. Methods: This longitudinal study was conducted during one year on the hospitalized patients who had tested positive for urine and urine culture. After the treatment of urinary tract infection and obtaining a negative urine culture, isotope cystography or radiographic cystography was performed to diagnose urinary reflux. Data analysis was performed in SPSS version 20 using descriptive statistics, chi-square, and correlation-coefficients. Results: The prevalence of microalbuminuria in Ilam province was 35.7%. No significant difference was observed between the rates of microalbuminuria and reflux (P 0.05). However, the inverse correlation in this regard was not considered significant (P 0.05). A direct correlation was observed between the rate of microalbuminuria and the incidence and severity of scars, which was considered significant (P 0.05). Conclusion: According to the results, the mean rate of microalbuminuria in reflux decreased with the increased degree of reflux. Due to the changes in microalbuminuria compared to the severity of urinary reflux, this method cannot be used to determine the severity of reflux, which it could be considered an influential factor and a method used for the early diagnosis and follow-up of patients and preventing final kidney damage and renal failure. Keywords: Microalbuminuria, Urinary Reflux, Scar, Children, Ilam

The potential of cancer stem cells in Breast tumors initiation, progression, metastasis, and drug resistance

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نوع پذیرش: پوستر | کد مقاله: G-95473

Abstract: Introduction: Breast Cancer (BC) has been recognized as the second malignancy that could lead to death among women worldwide. Investigations have concentrated on the BC subordinating regarding the presence of immunohistochemistry biomarkers, including the ER, PR, and HER2. Nonetheless, It has been perceived that tumors are constituted of miscellaneous associations of the cells organized hierarchically and operated by Cancer Stem Cells (CSCs), known as BCSCs in Breast tumors. In spite of numerous therapeutic methods for BC, including hormone therapy, radiotherapy, chemotherapy, surgery, or the combination of these methods, BC patients' treatment might eventually lead to failure, increase in reoccurrence and progression rate, metastasis, drug resistance, and survival reduction due to the existence of BCSCs that have the potential of self-renewal trait, transformation and are capable for Breast tumor commencement and conservation. Methods: This study was conducted by searching verified databases, such as Pubmed, Scopus, Science Direct, and Springer, with breast cancer stem cells, signaling pathways, markers, drug resistance, and therapeutics keywords. Results: Based on the studies carried out on BSCSs, there was a panel of CD markers, some enzymes, and specific proteins, including CD44, CD24, CD29, CD133, PROCR, ESA, MUC1, DLL1, DNER, PKH, CK18, GATA3, Osteonectin, and Vimentin for the definition of the BSCS subpopulation that could be assessed and indicate tumor initiation, metastasis, resistance, and epithelial-mesenchymal or mesenchymal-epithelial transitions, individually. BCSCs are unstable and can shift to a stem/non-stem-like state by being involved in several signaling transductions. For instance, Notch pathway has an essential role in the balance between apoptosis, proliferation, and differentiation, Wnt signaling transduction plays an important role in stemness and differentiation balance, and Hedgehog (Hh) cascade has an effect on carcinogenesis and typical mammary development. Regarding the phase and the type of BC cells, every pathway can be affected by a unique drug targeting a protein. For example, Tamoxifen, Docetaxel, Vismodegib, Exemestane, Letrozole, and a combination of Paclitaxel and Carboplatin target γ -secretase in Notch signaling, Paclitaxel modulates Frizzled7 in Wnt pathway and RO4929097, and composition of Paclitaxel, Epirubicin, and Cyclophosphamide influence the Smoothened in Hh cascade. Other factors can also affect the stem/non-stem-like condition. Tumor microenvironments, such as TAMs, CAFs, MSCs, and ECM, can provide vital elements, including growth factors and cytokines for BCSC self-renewal, maintenance, angiogenesis, and metastasis. In addition, diverse non-coding RNAs (ncRNA), both long ncRNAs (lncRNA) and microRNAs (miRNAs) are associated with BCSCs features inhibition or promotion. Several miRNAs are responsible for drug resistance in BC, including miR-10, miR-7, miR-15a, and let-7. The clusters of miR-183, miR-221, miR-200, miR-222, miR-142, miR-214, and let-7 regulate gene expression in the maintenance of BCSCs. Conclusion: To conclude, BCSCs play a crucial



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role in BC's development, progression, migration, invasion, and drug resistance. Targeting the essential intermediates for BCSCs preservation could inhibit the stem-like traits and reverse the drug resistance. However, further investigations should carry out to reveal signaling pathways, modulators, therapeutics, and the other properties of BCSCs. Keywords: Breast cancer stem cells, Notch, Wnt, Hedgehog, non-coding RNA

آدرس دبیرخانه:

تهران، خیابان کارگر شمالی، رویروی مرکز قلب تهران،
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miR-27a as a novel agent against atherosclerosis

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نوع پذیرش: پوستر | کد مقاله: G-70284

Abstract: Background: Cardiovascular Atherosclerosis is the most common cause of death around the world, and is a chronic inflammatory disease that manifests with myocardial infarction (MI). Endothelial dysfunction is one of the risk factors that initiates atherosclerosis alongside hypercholesterolemia. During the process, endothelial cells' function disrupt so that they upregulate their adhesion molecules (e.g., P-selectin) which results in facilitating monocytes adhesion to endothelial cells. microRNAs (miR) are small (21-25N) RNA molecules which bind to 3' UTR of mRNAs and mediate their destruction. Several studies have reported the atheroprotective effects of various miRs. Therefore, we aimed to investigate the possible protective effects of miR-27a on atherosclerosis initiation in HUVECs. Materials and Methods: HUVEC cells were cultured in DMEM-F12. To simulate endothelial dysfunction and inflammation, LPS (1µg/mL) was added to culture medium. After 48h, HUVEC cells overexpressed P-selectin. miR-27a was designated by bioinformatics databases and was transfected to the cells by PEI vehicle with an N/P ratio of 20. Then, miR-PEI delivery was assessed by flowcytometry. P-selectin mRNA expression levels were measured by RT-qPCR. Finally, monocytes adhesion to HUVECs was measured with the commercial kit. Results: Our data indicated that miR-27a significantly downregulated the P-selectin expression which led to a remarkable decrease in monocytes adhesion to endothelial cells. Flowcytometry results showed that delivery rate of miR-27a was 98%. Conclusion: The results of the present study supported the previous reports regarding protective effects of miRs on the etiopathology of atherosclerosis. However, more investigations are needed to broaden the information about the signaling pathways through which miRs involve in the atherosclerosis. Keywords: Atherosclerosis, miR-27a, microRNAs, P-selectin

The effects of magnesium supplementation on blood glucose and gene expressions related to insulin and lipid metabolism in gestational diabetes

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نوع پذیرش: پوستر | کد مقاله: G-52073

Abstract: Background Aims Gestational diabetes mellitus (GDM) is defined by abnormal lipid and carbohydrate metabolism as well as hyperinsulinemia that appear or detected during pregnancy. GDM is a typical endocrine condition that affects pregnant women. Magnesium is a mineral that performs a crucial part in several metabolic processes, including carbohydrates and lipids metabolism. It also works as a particular activator for many various enzymes. Accumulated evidence shows that magnesium has useful effects such as antiglycemic and antilipidemic function. Based on epidemiological studies, there is an inverse relationship between the consumption of magnesium and the risk of diabetes. It has been reported in an interventional study that magnesium supplementation by participants of normal weight ameliorated glycemic control. Therefore, the aim of this study was to investigate the effects of magnesium therapy supplementation on blood glucose and genes related to insulin and lipid metabolism in women with GDM who did not use oral hypoglycemic drugs. Methods: This randomized, double-blind, placebo-controlled clinical trial was performed on 40 patients with GDM. The patients were randomly assigned into an intervention and a placebo group, who respectively received 250 mg/day of magnesium supplements in the form of magnesium oxide or placebo (for 6 weeks). Fasting blood was collected at the baseline and end of intervention to measure FPG and also peripheral blood mononuclear cells (PBMCs) for assess the gene expression related to insulin and lipid metabolism was isolated in using RT-PCR method. Clinical trial registration number: <http://www.irct.ir>: IRCT201704235623N111. Results Subjects who received magnesium had significantly lower FPG (P0.001) compared with placebo group. Results of RT-PCR showed that magnesium supplementation, decreased gene expression of oxidized low-density lipoprotein receptor (LDLR) (P = 0.001) and increased gene expression of peroxisome proliferator-activated receptor gamma (PPAR- γ) (P= 0.003) and glucose transporter 1 (GLUT-1) (P = 0.004) and in PBMCs of women with GDM. Conclusion Overall, our study indicated that magnesium supplementation for 6 weeks among GDM women had beneficial effects on FPG levels, and of PPAR- γ , GLUT-1, and LDLR expression Keywords: Magnesium, gestational diabetes, Supplementation, Lipid, gene expression



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Evaluation of exosomal biogenesis and autophagic response in lung tissue of streptozotocin-induced diabetic rats

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نوع پذیرش: پوستر | کد مقاله: G-24763

Abstract: Background: Diabetes is a chronic disease that occurs either when the pancreas does not produce enough insulin or when the body cannot effectively use the insulin it produces. The development of cellular injuries and impaired energy metabolism are involved in the pathogenesis of diabetes mellitus, leading to severe diabetic complications in different tissues such as the lung tissue. Autophagy is a double-edged sword mechanism required for maintaining cell survival and hemostasis. Any abnormalities in autophagic response can lead to the progression of many diseases. Here, we aimed to assess the potency of diabetic conditions on the autophagic response and exosome secretion in a rat model of type 1 diabetic Mellitus. Materials and Methods: Animals were received 45 mg/kg STZ dissolved in 0.1 M sodium citrate. After 4 weeks, we monitored autophagic response and exosome biogenesis in the lung tissue using Immunohistochemical (IHC) staining and Real-time PCR analysis, respectively. Results: IHC staining displayed an enhanced autophagic response indicated with the induction of Beclin1, LC3 and P62 compared to the control rats. These changes coincided with significant induction of CD63, Alix and Rab-27 in STZ-induced diabetic rats relative to control rats (p0.05). Conclusion: In conclusion, a diabetic condition can increase the autophagic response and exosomal biogenesis in lung tissue. Keywords: Diabetes, Autophagy, Exosome, lung, Rat

Evaluation of Changes in the renal indices in COVID-19 Patients

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نوع پذیرش: پوستر | کد مقاله: G-52394

Abstract: Background: Coronavirus disease 2019 (COVID-19), caused by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), mainly manifests as an acute respiratory illness. It leads to multi-organ dysfunctions in liver, blood vessels, heart, kidney, and etc. A large number of studies have reported the adverse effect of COVID-19 infection on renal function indices. Therefore, we aimed to evaluate the laboratory renal factors in the patients with positive and negative COVID-19 PCR results. Methods: A total of 979 (811 PCR positive and 168 PCR negative) participants were enrolled in our study from July to March 2021 who were admitted to Taleghani hospital, Urmia, Iran. Blood urea and creatinine levels were measured with an auto-analyzer biochemistry system. Later, SPSS 25 (t-test) was used to analyze the values of the aforementioned factors based on the PCR results of the participants. Results: The results of serum levels of urea and creatinine in PCR positive (47.55 ± 42.12 , 1.32 ± 2.63) showed significant decrease compared to patients with PCR negative (58.23 ± 50.99 , 1.96 ± 3.66) ($p < 0.05$). Conclusion: Analysis of creatinine and urea levels in patients with PCR-positive and negative showed that impaired kidney function occurs in COVID-19 patients, but due to low numbers of PCR-negative participants compared to PCR-positive ones, more investigations are suggested to be done. Keywords: COVID-19, Urea, Creatinine



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Investigating the effect of vitamin D on insulin resistance in patients with type 1 diabetes: A review article

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نوع پذیرش: پوستر | کد مقاله: G-30691

Abstract: Background: Type 1 diabetes (T1DM) is a disease characterized by absolute deficiency of endogenous insulin secretion. Insulin resistance (IR) may occur among patients with T1DM. Vitamin D deficiency has been reported as a risk factor in the development of IR. The aim of this review is to investigate the effect and relationship between vitamin D and IR in patients with T1DM. Materials and Methods: By searching and reviewing the articles of the last few years in the Google Scholar and PubMed databases with the keywords of type 1 diabetes, insulin resistance and vitamin D. Results: No significant and specific relationship was found in the reviewed studies. In some studies, vitamin D deficiency has a positive effect on insulin resistance, and in the long term, clinical symptoms are expected to increase the risk of metabolic diseases, but in studies on children, this was not expected and no relationship was found between them. Conclusion: Vitamin D serum concentration has a negative relationship with insulin resistance in patients with T1 diabetes, and in children it has no relationship with insulin and can even increase the risk of metabolic diseases in the future, but its deficiency can cause insulin resistance to some extent. Keywords: Type 1 diabetes, Vitamin D, Insulin Resistance



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دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



The effect of nutritional status on benzene toxicity: A systematic review

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نوع پذیرش: پوستر | کد مقاله: G-09736

Abstract: Background: Benzene is widely used in the chemical industry. Excessive benzene exposure leads to acute leukemia, diabetes, kidney disease, respiratory allergies, skin rashes, and death. An appropriate nutritional status is crucial to human health and has an essential role in supporting the immune system. We discuss the effect of nutritional status on benzene toxicity. Materials and Methods: This review article was performed within articles published at PubMed, Science Direct, Google Scholar, SID, and Cochrane until January 2023. The keywords were benzene, nutrition, trace minerals, trace elements, and reactive oxygen species (ROS). By searching these databases 41 articles were found. 28 articles were selected under the inclusion criteria. Results: Finally, 28 articles were included in this study. Occupational exposure to benzene caused oxidative stress and immune suppression. Inadequate nutritional status of nutrients including iron, selenium, methionine, and ascorbic acid enhanced susceptibility to adverse effects caused by benzene. Nicotinamide adenine dinucleotide (NAD), nicotinamide adenine dinucleotide phosphate (NADP), niacin-containing enzymes, and vitamin E, A, and C supplementation reduced oxidative stress and improved antioxidant enzymes that protected cellular structures from harmful effects of free radicals. We could find them in sweet potato, carrots, spinach, broccoli, tomatoes, and eggs while pre-formed vitamin A sources were shrimp, eggs, cheese, yogurt, chicken, beef, and lamb. Vitamin D had a vital role in controlling systemic inflammation and oxidative stress that was present in salmon, mushrooms, cow's milk, soy milk, orange juice, and fortified foods. Pro-vitamin K3 induced oxidative stress by the production of hydroxyl radicals. Vitamin B2 recycled glutathione which was the most crucial antioxidant that protected against free radicals in the body. Zinc could reduce oxidative stress by participating in the synthesis of antioxidant enzymes. The best source of zinc was in red meat, poultry, beans, nuts, crab, lobster, and dairy products. Selenium helped lower oxidative stress in the body, which reduced inflammation and enhanced immunity presented in seafood and organ meats. Selenium supplementation affected the occurrence of benzene-induced leukemia. Magnesium had antioxidant capacities and prevented oxygen radical formation by inhibiting xanthine oxidase and NADPH oxidase. Conclusion: It seems that sufficient nutritional status can reduce oxidative stress from benzene long-term exposures and toxicological responses of workers. However, further research needs to be done on the topic. Keywords: Benzene, nutrition, trace elements, reactive oxygen species

Development of a Reverse Hybridization Method for Simultaneous Identification of 1691G A (Leiden), 20210G A (PTH) and 677C T (MTHFR) Mutations.

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نوع پذیرش: پوستر | کد مقاله: G-13958

Abstract: Background: Cardiovascular diseases (CVD) is a general term for conditions that affect the heart and blood vessels and cause various types of diseases. Atherosclerosis and venous thromboembolism (VTE) are two major manifestations of CVD which are caused by complex environmental and genetic interactions. Thrombosis can cause by some negative factors like use of female hormones, inactivity, surgery, cancer, drug and alcohol usage and changes in the responsible genes for the coagulation system. Mutations in the following genes are the most common causes of VTE which result in Recurrent Spontaneous Abortion (RSA): factor V Leiden, PTH, and MTHFR. Common mutations associated with CVD can be detected by various molecular methods. However, due to the high amounts of reagents and time consumption, and lack of simultaneous identification of several effective mutations, the reverse hybridization line probe assay was developed. In this method, several mutations can be detected simultaneously, the sequences with the same length are separated by prob, and it is not necessary to choose different amplicon lengths to identify genes. Materials and Methods: First of all, primers were designed to place on the both sides of the mutation, therefore they can be used in a multiplex reaction, as well, they do not interact with each other. DNA samples were extracted by standard methods. After that, DNA were amplified by PCR and were sequenced. All reactions (mutations) were performed as a singleplex, then the test was performed as a multiplex PCR. Finally, the binding and reaction of the Multiplex PCR product on all probes were optimized. After that, Line probe assay method were done. Results: a multiplex PCR method was developed to identify and amplify simultaneously the gene regions of 1691GA (Leiden), 20210GA (PTH) and 677CT (MTHFR) mutations. Keywords: Reverse Hybridization, FV liden, PTH, MTHFR, Mutation

The study of the frequency and correlation between HLA-DQB1*02 allele and two genetic variants associated with tissue transglutaminase protein reduced function in celiac patients

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نوع پذیرش: پوستر | کد مقاله: G-85130

Abstract: Background: Celiac is the result of the interaction of genetic, immunological and environmental factors that can occur at any age. This disease is a malabsorption disorder of the small intestine. As a result of eating gluten, which is a part of the structure of many grains, it leads to damage of the intestinal mucosa with an inappropriate immune response. Since the 1990s, with the help of celiac antibodies including anti-endomysial antibody, anti-tissue transglutaminase antibody and anti-gliadin antibody, it was determined that celiac disease is a common disease and it is classified into four types: typical, atypical, silent and latent. Materials and Methods: In this case-control study, 103 saliva samples were collected, 53 were patient samples and 50 were control samples. DNA samples were extracted by phenol chloroform method. Samples carrying the HLA-DQB1*02 allele were determined by PCR method. Then, the carriers of HLA-DQB1*02 allele were examined by tetra primer-amplification refractory mutation system based polymerase chain reaction (T-ARMS-PCR) method to determine the frequency and genotype of single nucleotide polymorphisms rs45629036 and rs41274716. Results: In this study, the frequency of A allele in single nucleotide polymorphism rs45629036 (21%) and its frequency in single nucleotide polymorphism rs41274716 (3.9%) were reported. Out of 73 samples carrying HLA-DQB1*02 allele, the frequency of HLA-DQB1*02 allele in Sick men were significantly more carriers of this allele than sick women ($p = 0.051$), considering that the number of sick women was more than sick men. In the examination of clinical manifestations, it was observed that the patients without the HLA-DQB1*02 allele had significantly higher incidence of bone pain ($p=0.056$), neurological disorders ($p=0.035$) and long-term fatigue ($p=0.025$). They showed a higher frequency than patients with this allele. Conclusion: The presence of genotypes of single nucleotide polymorphisms rs45629036 and rs41274716, which lead to a decrease in tissue transglutaminase 2 enzyme activity

Genetics science helps patient with Marfan syndrome: diagnosis and cure

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Background:

Marfan syndrome is a genetic disorder that changes proteins that help build connective tissue. This disorder disrupts the growth of the connective tissue that supports bones, muscles, organs, and tissues. In most cases, there is a mutation in the FBN1 gene.

Materials and Methods:

This syndrome is autosomal dominant and occurs in 1 in 20,000 people. Genetic testing of the FBN1 gene detects 70-93% of mutations and is available in clinical laboratories. Marfan syndrome may not be diagnosed until the teenage years because it does not always appear in childhood.

Results:

Symptoms

myopia, lens dislocation, dolichostenomelia, pectus excavatum (chest) or pectus carinatum (pigeon chest), scoliosis, cardiovascular abnormalities (aortic dilatation, mitral valve prolapse, tricuspid valve prolapse, severe tricuspid valve prolapse). Pileps andlapepst. It gets progressively worsens as the patient ages.

Diagnosis

This genetic disorder can be diagnosed with a genetic test with 99% accuracy. Unfortunately, this is an expensive process, given that the FBN1 gene can mutate in more than 3,000 different ways. Therefore, in most cases, diagnosis is based on physical examination and evaluation of the patient's medical and family history.

Clinical diagnosis can be used to screen family members even before birth as implantation. The choice Currently, the technique of of mutation screening method largely depends on its success rate and cost. trench sequencing is very powerful and extensive, but it cannot detect deletions or large repeats in the DNA sequence unless combined with multiplexing. The latest technique used is whole genome/exome sequencing.

If one of the parents is affected by the genetic mutation of this syndrome, the following are used:

Prenatal diagnosis:

1. Sampling of chorionic villi or amniocentesis (performed between 10 and 12 weeks of pregnancy and has a risk of miscarriage between 1 and 2 percent)
2. Placental villi sampling (performed between 14 and 20 weeks of pregnancy and has a risk of miscarriage between 0.5 and 1 percent)

Genetic diagnosis before implantation:

- Natural harvest
- Gamete donation (egg or sperm).
- Adoption


Conclusion:

Cure

There is no cure for Marfan syndrome. Therefore, treatment focuses on managing symptoms and reducing the risk of complications. Patients with Marfan syndrome are treated by a multidisciplinary medical team including geneticists, cardiologists, ophthalmologists, orthopedists, and cardiac surgeons. People with Marfan syndrome are treated by a multidisciplinary medical team including geneticists, cardiologists, ophthalmologists, orthopedists, and cardiac surgeons. With the emergence of new technologies such as Crispr, we hope that this disease will be treated with the help of this technology in the future

Keywords: Marfan syndrome, FBN1, mutation

The long non-coding RNAs (lncRNAs) gene expression: MEG3 and H19 in obese women adipose tissues and its association with insulin resistance and obesity indices

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نوع پذیرش: پوستر | کد مقاله: G-05826

Abstract: Background: There are ample evidences regarding the role of MEG3 and H19, two lncRNAs in the pathomechanism of obesity and related disorders. Here, we evaluated the expression of MEG3 and H19 in visceral adipose tissues (VAT) and subcutaneous adipose tissues (SAT) of obese women (n = 18), in comparison to the normal-weight women (n = 17). Furthermore, we sought to identify the association of MEG3 and H19 expression in SAT and VAT with obesity parameters, insulin resistance, and the mRNA expression of possible target genes involved in adipogenesis and lipogenesis including peroxisome proliferator-activated receptor gamma (PPAR γ), fatty acid synthase (FAS), and acetyl-CoA carboxylase (ACC). Materials and Methods: Real-time PCR was performed to evaluate the mRNA expression of the above-mentioned genes in VAT and SAT from all participants. Results: The data revealed lower mRNA levels of H19 in SAT of obese women, comparing to the normal-weight women, while MEG3 expression was significantly higher in the SAT of the obese group rather than controls. Correlation analysis indicated that the transcript level of H19 had an inverse correlation with obesity indices and HOMA-IR values. However, MEG3 expression displayed a positive correlation with all the indicated parameters in all participants. Interestingly, a positive correlation was found between transcript level of MEG3 in SAT with FAS and PPAR γ . However, there was an inverse correlation between SAT expression of H19 and FAS. Conclusion: It appears that lncRNAs, MEG3 and H19, are involved in obesity-related conditions. However, more clinical investigations are needed to clarify the relationships between lncRNAs with obesity and related abnormalities. Keywords: Adipogenesis, Lipogenesis, Long non-coding RNAs, Obesity

Association study of rs7482144 variant in *HBG2* gene with HbF level in beta-thalassemia minors with the IVS-II-1 (G>A) mutation

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Abstract

Background and aims:

The severity of the disease in people with beta-thalassemia major is very variable. Previous studies have shown that the level of fetal hemoglobin (HbF) plays a major role in reducing the symptoms of the disease. According to the conflicting results of studies regarding the association of different variants with HbF level, in this study the association of rs7482144 variant in *HBG2* gene with HbF levels in individuals with beta thalassemia minor carrying IVS-II-1(G>A) mutations was investigated.

Methods:

Based on the results of hematological and beta thalassemia genetic tests, beta thalassemia minor carriers of IVS-II-1 mutation (G>A) were identified. Based on HbF level, the samples were divided into two groups with HbF lower than 1.5% and people with HbF level above 2%. DNA extraction from blood was done by salting out method. ARMS-PCR was used to genotyping. Chi-square test was used to evaluate the Hardy-Weinberg equilibrium and examine the association between the SNP and HbF level.

Results:

The frequency of individuals with T allele for the rs7482144 variant in the group with high and low HbF levels was 0.85 and 0.60, respectively. Hardy-Weinberg equilibrium was established for both groups. In this study, no significant difference was observed between the investigated variant and the HbF level.

Discussion:

Considering the importance of fetal hemoglobin level in the severity of thalassemia disease, in this study, a variant that previously had shown a relationship with HbF level was investigated in carriers of IVS-II-1 mutation. Repeating this study with a larger sample size can help to obtain more accurate information.

Key words:

Beta thalassemia minor, fetal hemoglobin, *HBG2* gene



چهاردهمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



A Meta analysis of the association between the SLC6A4 gene polymorphisms and bipolar disorder

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نوع پذیرش: پوستر | کد مقاله: G-49812

Abstract: Background: Bipolar disorder is a complex psychiatric disorder which genetic factors are known to contribute to its etiology. A number of studies have reported associations between the three polymorphisms of serotonin transporter gene (SLC6A4/5-HTT) and bipolar disorder. This study reports the effect of these three polymorphisms using meta analysis method. Materials and Methods: Electronic searches were performed using PubMed. In the extensive electronic literature search, keywords “5-HTT gene” and “bipolar disorder” were searched for prospective studies. The pooled effect sizes (ORs) along with 95% confidence intervals (CIs), in “cases” and “controls” groups for these three polymorphisms (5-HTTLPR, 5-HTTVNTR and 5-HTT 44bp insertion/deletion) were calculated. Further subgroup analyses were conducted if the data were available. Results: Twenty eight studies with 15005 participants (6333 cases and 8672 controls) were included in the analyses. The main analysis revealed that the “5-HTTVNTR” pooled OR is 1.070 ; 95%CI is (0.905 - 1.234) and its p-value is less than 0.0001. The “5-HTT 44bp insertion/deletion” pooled OR is 1.560 ; 95%CI= (0.113 - 3.007) and its p-value is 0.0349. For “5-HTTLPR” , pooled OR is 1.084 ; 95%CI is (1.016 – 1.152) and its p-value is less than 0.0001. Conclusions: From the p-value of “5-HTT 44bp insertion/deletion” polymorphism, which is 0.0349, we found that compared with the other 2 polymorphisms, it’s not capable to cause bipolar disorder so much, as we know a p-value should be less than 0.05 (0.05) to be statistically significant, which is also true about this one. But we found the other two polymorphisms with the p-value 0.0001 are statistically significant. They indicate strong evidences against the null hypothesis. (The null hypothesis is a typical statistical theory which suggests that no statistical relationship and significance exists in a set of given single observed variable, between two sets of observed data and measured phenomena.) Keywords: SLC6A4, 5-HTT, bipolar disorder, polymorphism, 5-HTTLPR, 5HTTVNTR

Comparative analysis of Xist gene exon 1 repeat A sequence in human with similar sequences in Bos species and Mus musculus

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نوع پذیرش: پوستر | کد مقاله: G-05728

Abstract: Background: Xist (X-inactive specific transcript) as a large polyadenylated RNA molecule that is expressed from the inactive X chromosome, has no extended open reading frame for protein translation and suggested to have a regulatory role in gene expression. There is a conserved repeat A region in the 5' end of the Xist encoding gene consists of nine repeat of 5' GCCCATCGGGGCCTCGGATACCTGC-3' sequence in human and mouse with a high important role in the RNA molecule function. Method: The A-repeat sequences of Xist molecule registered in GeneBank from human, Bos Taurus, Bos indicus and Mus musculus were analyzed using the BioEdit software and were compared to the samples taken from human blood after RNA extraction and cDNA synthesis procedure followed by the A-repeat region sequencing. Results: The most differences in nucleotide sequences is seen in the nucleotide numbers 12,13 and 14 flanked in a highly conserved sequence of the total 24 residues in the exon 1, A repeat region that makes an eight different repeat sequences which comes in an conservative arrangements in every analyzed species. Conclusion: It is suggested that the consequence arrangement of eight different repeat sequences has an important role in Xist RNA molecule function. Key words: Xist, RNA, Repeat A

Bioinformatics-derived expression data from Trypanosoma cruzi-infected human primary fibroblast cells

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نوع پذیرش: پوستر | کد مقاله: G-31256

Abstract: Bioinformatics-derived expression data from Trypanosoma cruzi-infected human primary fibroblast cells Ata moghimi¹, Ehsan Ahmadpour^{2*} 1. Department of Medical Laboratory Science, Tabriz University of Medical Sciences, Tabriz, Iran. 2. Infectious and Tropical Diseases Research Center, Tabriz University of Medical Sciences, Tabriz, Iran *Corresponding authors: Ehsan Ahmadpour, Ph.D Email: ehsanahmadpour@gmail.com, ahmadpoure@tbzmed.ac.ir Address: Department of Parasitology and Mycology, Tabriz university of Medical Sciences, Tabriz, PO Box: 14155-6446, Iran Tel: +98 413 5428595, Fax: +98 413 337 3745 Background: Trypanosoma cruzi (T. cruzi) is an obligate intracellular protozoan parasite that causes human chagas disease, a leading cause of heart failure, cardiovascular complications and romana. Using these cells, we investigated gene expression and its effect on the cell cycle in human foreskin fibroblast cells infected by T. cruzi. Material and Methods: We obtained microarray data from GEO and selected expression data from human primary fibroblasts, endothelial cells, and smooth muscle cells infected with Trypanosoma cruzi (GSE13791), which included T. cruzi-infected and non-infected cells. We chose fibroblasts that were either infected or not with T. cruzi, and after using the Transcriptome Analysis Console (TAC) to analyze our data and identify upregulated genes, we used wikipathway to look into how these genes affected the cell cycle. Results: The results of the analysis showed 5287 genes with altered expression. 3304 of which are upregulated, and 1983 of which are downregulated (P-value: 0.01). Six of the upregulated genes, including CCND2, CCND4, E2F2, MDM2, ATR, and STAG1, have cell cycle effects. Conclusion: Genes whose expression increases are effective in the production of various proteins. For example, STAG1 plays a role in the production of storm antigen 1, ATR plays a role in ATR serine/threonine kinase, MDM2 plays a role in the MDM2 proto-oncogene, and other genes play a role in the production of different types of other proteins, each of which can increase its expression and have different effects on the cell cycle and can cause several complication. Key words: Trypanosoma cruzi, upregulated genes, GEO, cell cycle



چهاردهمین کنفرانس بین المللی آزمایشگاه و باالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Maturation in ANTXR2 in a patient with hyaline fibromatosis syndrome: A case report

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Background: Hyaline fibromatosis syndrome (HFS) is a rare autosomal recessive syndrome caused by the accumulation of amorphous hyaline material in the papillary dermis and other tissues. It can present with subcutaneous nodules, joint contractures, gingival hypertrophy, osteopenia, and protein-losing enteropathy. Mutations in the gene encoding anthrax toxin receptor two protein (ANTXR2) cause this progressive disease.

Case presentation: A 2-month-old girl was referred to our clinic due to hypothyroidism, but her mother noticed some nodules over the fingertips and external ears. Moreover, a firm tissue was presented over the mouth. Skin ulcer, joint stiffness, progressive flexion contractures, abnormality of the face, and gingival hypertrophy were observed. The genetic analysis was done and showed a pathogenic homozygous variant (c.1073dupC; p. A359CfsTcr13) in ANTXR2 gene. The diagnosis of HFS was confirmed at the age of one year.

Conclusion: As of now, there is no treatment option available for HFS, a disabling disease. So, genetic analysis and prenatal diagnosis for the next pregnancy are of particular importance for couples.

Keywords: ANTXR2, Hyaline Fibromatosis Syndrome, Systemic Hyalinosis



چهاردهمین کنفرانس بین المللی آزمایشگاه و بالین

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Epidemiological study of Carbapenem-Resistant Enterobacteriaceae in patients admitted to Sari Cardiovascular Hospital

مریم اندیشگر © (P), معصومه باقری آستانی^۱, فرنوش فدایی^۱, مهناز نصراللهی^۱, روشنک حقیری سنته^۱, مانده کاظمی^۱

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نوع پذیرش: پوستر | کد مقاله: G-36591

Abstract: Background: Enterobacteriaceae is a large family of Gram-negative bacteria, which can cause a variety of severe infections such as bloodstream, soft tissue infections, intra-abdominal, respiratory tract, and urinary tract infections. Enterobacteriaceae are constantly finding new ways to avoid the effect of antibiotics used to treat the infections they cause. Their high resistance to different groups of antibiotic is concerning as it is becoming prevalent as a health problem. Enterobacteriaceae are becoming increasingly resistant to many previously effective antibiotics and it makes them difficult to treat. The emergence and spread of carbapenem-resistant enterobacteriaceae (CRE) has become a serious threats to public health. In this research, enterobacteriaceae's resistance to carbapenem is studied in cardiovascular patients. The World Health Organization published a list of antibiotic-resistant bacteria in which carbapenem-resistant enterobacteriaceae (CRE) was in the critical priority group for an urgent need to develop new antibiotics. Methods: A total of 91 enterobacteriaceae-positive cultures was studied from July 2020 to March 2022. Antimicrobial susceptibility testing was performed on all samples and the carbapenem antibiotic disc used was Imipenem (IPM). Samples collected were blood, urine, endotracheal tube, sputum and wound from the patients in various wards. Results: 91 patients tested positive for enterobacteriaceae and 62 of them showed high level of resistance to carbapenem in Sari cardiovascular hospital. Conclusion: This study shows the level of resistant of carbapenem to enterobacteriaceae in hospital and emphasizes on the urgent need to develop new antibiotics to prevent spread of these pathogens. Keywords: enterobacteriaceae, carbapenem resistance, imipenem

A review of the application of CRISPR-Cas9 in the treatment of epithelial ovarian cancer

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نوع پذیرش: پوستر | کد مقاله: G-23461

Abstract: Epithelial ovarian cancer (EOC) is the fifth leading cause of cancer-related deaths among women in the United States and the most lethal gynecological cancer. Because of its rapid growth and lack of effective early-detection strategies, 70% of EOC patients are diagnosed at an advanced stage, accompanied by peritoneal carcinomatosis (PC). Most EOC patients also eventually become refractory to platinum, the major drug for treating EOC. Importantly, there are few molecularly targeted agents available for treating EOC, likely because EOC has high intertumor and intratumor heterogeneity at the molecular and epigenetic levels. Therefore, the mortality rate of EOC has not significantly changed for several decades. To improve the poor prognosis of EOC, the discovery of new drug targets is sorely needed. As one of the most potent gene-editing tools to date, clustered regularly interspaced short palindromic repeats (CRISPR)-CRISPR-associated protein 9 (Cas9) technology has demonstrated applicability, simplicity, and efficient gene-editing capability compared to previously developed gene manipulation tools. **Methods:** This review has been achieved by using an organized search of the scientific data published on the effects of CRISPR-Cas 9 in EOC treatment in various databases, including PubMed, Scopus, and Science Direct. **Results:** based on the investigations done, several candidate drug targets for EOC were identified using a combination of shRNA and CRISPR/Cas9 library screening. Among these drug targets, it's shown that inhibition of one, KPNB1, by ivermectin has promising antitumor effects and synergizes with paclitaxel in the treatment of EOC. **Conclusion:** the newest gene-editing technology CRISPR-Cas9 is a breakthrough in the treatment of diseases deemed untreatable or hard to treat only up until now. And a new era can begin using this technology and its potential. **Keywords:** epithelial ovarian cancer (EOC), clustered regularly interspaced short palindromic repeats (CRISPR)-CRISPR-associated protein 9 (Cas9), cancer

Investigating the effect of Lecithin Cholesterol Acyltransferase genetic variants on prognosis and suffering from low HDL level

سپیده صرفی @¹، دکتر فریدون عزیزی ©²

دانشجو کارشناسی ارشد ایمنی شناسی دانشگاه علوم پزشکی بیرجند
استاد ممتاز غدد درون ریز و متابولیسم (بالغین) گروه غدد درون ریز بالغین، دانشکده پزشکی مرکز تحقیقات غدد درون ریز پژوهشگاه علوم غدد درون ریز و متابولیسم بیمارستان آیت الله طالقانی دانشگاه علوم پزشکی شهید بهشتی

نوع پذیرش: پوستر | کد مقاله: G-54819

Abstract: Background: Among the most common lipid abnormalities, a low level of high-density lipoprotein-cholesterol (HDL-C) is one of the first risk factors identified for coronary heart disease. Lecithin cholesterol acyltransferase (LCAT) has a pivotal role in the formation and maturation of HDL-C and in reverse cholesterol transport. Methods: To identify genetic loci associated with low HDL-C in a population-based cohort in Tehran, the promoter, coding regions and exon/intron boundaries of LCAT were amplified and sequenced in consecutive individuals (n=150) who had extremely low or high HDL-C levels but no other major lipid abnormalities. Result: A total of 14 single-nucleotide polymorphisms (SNPs) were identified, of which 10 were found to be novel; the L393L, S232T and 16:67977696 CA polymorphisms have been previously reported in the SNP Database (as rs5923, rs4986970 and rs11860115, respectively) and the non-synonymous R47M mutation has been reported in the Catalogue of Somatic Mutations in Cancer (COSM972635). Three of the SNPs identified in the present study (position 6,531 in exon 5, position 6,696 in exon 5 and position 5,151 in exon 1) led to an amino acid substitution. The most common variants were L393L (4886C/T) in exon 6 and Q177E, a novel mutation, in exon 5, and the prevalence of the heterozygous genotype of these two SNPs was significantly higher in the low HDL C groups. Univariate conditional logistic regression odds ratios (ORs) were nominally significant for Q177E (OR, 5.64; P=0.02; 95% confidence interval, 1.2 26.2) Conclusion: this finding was attenuated following adjustment for confounders. Further studies using a larger sample size may enhance the determination of the role of these SNPs Key words: lecithin cholesterol acyltransferase, high-density lipoproteins, single nucleotide polymorphism, mutation

Evaluation of common ALDOB gene mutations in Iranian patients suspected of having inherited fructose intolerance

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نوع پذیرش: پوستر | کد مقاله: G-45216

Abstract: Background: Hereditary fructose intolerance (HFI) is an autosomal recessive metabolic disorder characterized by loss of function of both alleles of the Aldolase B (ALDOB) gene. There are more than 50 known mutations in the ALDOB gene that can cause symptoms of HFI. Symptoms of HFI can be severe if undiagnosed quickly and patients continue to consume sugars such as fructose, sorbitol, and sucrose. Additionally, different populations of HFI patients have different types and frequencies of ALDOB gene mutations. In order to facilitate rapid diagnosis of HFI patients, and limited knowledge of Iranian population for the ALDOB gene mutations, this study has attempted to investigate the type and frequency of ALDOB gene mutations using Sanger Sequencing. Materials and Methods: 15 Iranian patients suspected of having HFI based on clinical symptoms were included in this study. 5 cc of peripheral blood was collected from suspected HFI patients and transferred to sterile tubes containing EDTA anticoagulant for genetic analysis. White blood cells were used to extract genomic DNA. Spectrophotometry and electrophoresis on a 1% agarose gel were used to evaluate the quality and quantity of DNA extracted. Primers were designed for each exon and PCR was used to determine the mutation's presence and genotype. A 2% agarose gel was used to electrophorese the PCR products. In order to identify common mutations in hot spots and mutations in other regions of the ALDOB gene, Sanger sequencing was conducted Results: We have found 4 patients with mutation rs1800546 in exon 5 and 5 patients with mutation rs118204427 / rs78340951 in exon 9. One patient had both mutations rs1800546 and rs76917243 / rs386626618 in exon 5. No mutation was found in the DNA of 6 patients. Conclusion: In order to identify individuals with HFI and asymptomatic carriers before weaning, population-based screening methods using DNA analysis are necessary. In addition, further investigation about other mutations in ALDOB gene and using more advanced techniques such as Next-generation sequencing (NGS) are needed to screen patients who do not have common mutations. Keywords:



چهاردهمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Personalized medicine is essential to the management of chronic myeloid leukemia

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نوع پذیرش: پوستر | کد مقاله: G-49182

Abstract: Background: The first neoplastic disease for which a characteristic genetic alteration has been identified is chronic myeloid leukemia (CML). As a consequence of the t9; 22(q34; q11) translocation, it bears a genetic marker, the BCR::ABL1 rearrangement. Patients with chronic myeloid leukemia are prescribed TKIs as a targeted therapy to treat the disease. Clinical practice has demonstrated that several patients receiving TKI therapy have poor primary response rates, develop resistance to the drug, or relapse after an initial clinical response despite Imatinib's excellent efficacy and improved clinical response rates. Results: The Pharmacogenetics of cancer drugs has become more and more important due to the variation in responses between individuals to the same cancer drugs. An extensive study of pharmacogenetics and sequencing has permitted the identification of new recurrent mutations in CML that have a significant prognostic impact. Additionally, whole-genome sequencing is likely to become a standard diagnostic test in the near future, allowing for the molecular diagnosis of disease Conclusion: Researchers are investigating the effect of different factors, such as BCR-ABL point mutations, efflux, and influx transporters, on the response to targeted drugs in CML. As a result, it is necessary to develop molecular targets that will provide new therapeutic perspectives and enable individualized treatment of patients suffering from this progressive disease. Keywords:

Iranian chronic myeloid leukemia patients' response to imatinib mesylate and clinical outcome as affected by ABCG2 C421A and ABCG2 G34A genetic polymorphisms

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نوع پذیرش: پوستر | کد مقاله: G-36510

Abstract: Background: Chronic myeloid leukemia (CML) is a multifactorial clonal myeloid neoplasm that mainly caused by the Philadelphia chromosome. Despite imatinib mesylate (IM) being the gold standard for first-line treatment of CML, a number of patients displaying IM resistance have been reported. A number of factors influence IM resistance, including pharmacogenetic variability. The present study evaluated whether two common ABCG2 single nucleotide polymorphisms (SNPs) (G34A and C421A) contribute to the development of IM resistance and/or good responses among Iranian CML patients. Materials and Methods: Patients with Ph-positive CML (37 females and 35 males) were treated with 400 mg IM daily. Before participating in this study, patients had been diagnosed with chronic phase CML at Omid Hospital (Isfahan, Iran). After obtaining written consent, blood samples were collected in tubes containing EDTA. Genomic DNA was isolated from peripheral blood lymphocytes using the PrimePrep Genomic DNA isolation kit. In order to genotype G34A, HRM techniques were used after identification of polymorphism genotypes. PCR-RFLP using BseMI enzyme was used in the absence of primers of 80 to 100 bp to genotype the C421A polymorphism. To confirm the results, sanger sequencing was used. SPSS version 26 was used to analyze the data. Results: The distribution of ABCG2 C421A and ABCG2 G34A polymorphism genotypes between the two groups did not differ significantly. Furthermore, these alleles were not associated with resistance, and their frequency was not significantly different between the two groups. Hematological indices were not significantly different between genotype groups, nor did drug therapy with IM affect them. The genotype and allele frequencies of C421A (P= 0.146, P= 0.170 respectively) and G34A (P= 0.235, P= 0.398 respectively) did not provide any statistically significant association with IM response. The hematological index did not differ significantly before and after the administration of the drug. A significant effect of genotypes on hematologic outcomes (WBC, Plt, and Hb) was not observed. Conclusion: ABCG2/C421A and ABCG2/G34A polymorphisms are not significantly associated with optimal response rates to IM or cytogenetic/hematologic response, and cannot be used as a predictor of optimal response or primary failure. Our study is the first to investigate the relationship between hematologic index and drug consumption among responders and resistant groups. there was a small statistical population for assessing the relationship between combined SNPs and the response to treatment. In order to evaluate the relationship between ABCB1, SLC22A1, CYP3A4, and CYP3A5 polymorphisms and IM response/resistance, additional studies in larger and diverse populations are recommended. Keywords: BCR-ABL; CML; Drug resistance; Pharmacogenetics; Philadelphia chromosome



چهاردهمین گنگره بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Screening test and genetic analysis in children with diagnosis of phenylketonuria

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نوع پذیرش: پوستر | کد مقاله: G-16329

Abstract: Background: Phenylketonuria (PKU) is an autosomal recessive disorder affecting the essential amino acid phenylalanine (Phe). A deficiency of phenylalanine hydroxylase (PAH) leads to the accumulation of phenylalanine in body fluids and, if not treated, negatively impacts cognitive function. Individuals with classic PKU almost always have intellectual disability unless levels are controlled through dietary or pharmacologic treatment. This study aimed to investigate when genetic analysis should be performed on phenylketonuric children. Materials and Methods: This cross-sectional descriptive study was conducted on children under 18 years with a diagnosis of phenylketonuria who were referred to a pediatric clinic in Yazd. Screening and HPLC tests were done for all of them over the years. If children had Phe above 6 mg/dl, dietary treatment should be initiated. Results: Out of 30 children with hyperphenylalaninemia, 27 had Phe levels greater than 6 mg/dl, so dietary treatment was initiated. The Phe level of others ranged from 2 to 6 mg/dl. Genetic analysis was done for them to diagnose and prove this disease definitively. All three children had the gene for PKU. Moreover, these children perform the regular Phe monitoring test and are still under observation. Conclusions: Patients with a positive screening test require a diet if phenylalanine is confirmed to be greater than 6 mg/dL. In the cases of phe 2-6 mg/dl, although there is no need for a diet, they must be constantly monitored, so genetic testing is used to confirm the diagnosis. However, it is recommended that all patients with a positive test (6 mg/dl or 2-6 mg/dl) undergo genetic testing. Keywords: Hyperphenylalaninemia, Phenylketonuria, Genetic Testing

Antileishmanial and cellular mechanisms of formononetin against *Leishmania tropica*

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نوع پذیرش: پوستر | کد مقاله: G-07619

Abstract: Background: At present, the synthetic drugs such as pentavalent antimony compounds are considered as the most effective drugs for treating cutaneous leishmaniasis (CL); however, the use of these drugs are associated with various adverse side effects. The present study aimed to investigate the leishmanicidal and cytotoxicity effects of formononetin (FMN), a natural isoflavone, against *Leishmania tropica*. Materials and Methods: We used the MTT (3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyl tetrazolium bromide) assay to determine the leishmanicidal effects of FMN against promastigotes and its cytotoxicity effects on J774-A1 macrophage cells, where, the macrophage model was applied to assess the effect of FMN against amastigotes of *L. tropica* as well as assessing cytotoxicity. The Griess reaction assay was used to determine the nitric oxide (NO) produced by treated macrophage cells with FMN. Results: Based on our findings, the FMN significantly (P<0.001) reduced the viability and number of promastigotes and amastigotes forms of *L. tropica* compared with the negative control. The 50% inhibitory concentrations value for FMN and glucantim was 9.3 and 14.3 µg/mL for promastigote and amastigote, respectively. We found that the macrophages exposed with FMN especially at concentrations of 1/3 IC₅₀ and 1/2 IC₅₀ significantly activated the NO release compared to the control group. Our findings displayed that pre-incubation of *Leishmania* parasites with FMN markedly dropped the rate of cell infection by 60.3% compared with non-treated parasites. Conclusion: The findings of the current investigation showed the promising antileishmanial effects of formononetin, a natural isoflavone, against promastigote and amastigote stages of *L. tropica* through inhibition of infectivity rate of macrophage cells and triggering the NO production. However, more studies are required to evaluate the efficacy and safety of FMN in animal model before use in the clinical phase. Key words: Leishmaniasis, promastigote, amastigote, nitric oxide, infectivity



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Cockayne syndrome in an Iranian pedigree with a homozygous missense variant in the ERCC6 gene

Ali Nikfar, Mojdeh Mansouri, Hossein Chiti, Gita Fatemi Abhari, Negin Parsamanesh

Cockayne syndrome (CS), a rare autosomal recessive multisystem disorder, is characterized by mental retardation, progressive growth failure, neurodegeneration, microcephaly, retinal degeneration, sensorineural deafness, cutaneous photosensitivity and premature aging. This genetic disorder is a member of the nucleotide excision repair (NER) disorder family. Excision repair cross-complementing, group 6 (ERCC6) and excision repair cross-complementing, group 8 (ERCC8) gene mutations underlie most CS cases. Furthermore, a small number of CS cases are caused by mutations in other NER genes. Furthermore, a small number of Cockayne syndrome cases are caused by certain mutations in the XP genes. This article describes the symptoms of Cockayne syndrome in an 8-year-old Iranian child. Using whole exome sequencing, we discovered a homozygous missense mutation in the ERCC6 gene, c.2551 T > A; p Trp851Arg.

Key words: Cockayne syndrome, ERCC6, DNA-repair deficiency disorders, Whole exome sequencing

A novel homozygous variant in an Iranian pedigree with cerebellar ataxia, mental retardation, and dysequilibrium syndrome type 4

©¹ محسن ناصری

هیئت علمی¹

نوع پذیرش: پوستر | کد مقاله: G-49710

Abstract: Background: Cerebellar ataxia, mental retardation, and dysequilibrium (CAMRQ) syndrome is a rare and early-onset neurodevelopmental disorder. Four subtypes of this syndrome have been identified, which are clinically and genetically different. To date, altogether 32 patients have been described with ATP8A2 mutations and phenotypic features assigned to CAMRQ type 4. Herein, three additional patients in an Iranian consanguineous family with non-progressive cerebellar ataxia, severe hypotonia, intellectual disability, dysarthria, and cerebellar atrophy have been identified. Materials and Methods: Following the thorough clinical examination, consecutive detections including chromosome karyotyping, chromosomal microarray analysis, and whole exome sequencing (WES) were performed on the proband. The sequence variants derived from WES interpreted by a standard bioinformatics pipeline. Pathogenicity assessment of candidate variant was done by in silico analysis. The familial cosegregation of the WES finding was carried out by PCR-based Sanger sequencing. Results: A novel homozygous missense variant (c.1339G A, p.Gly447Arg) in the ATP8A2 gene was identified and completely segregated with the phenotype in the family. In silico analysis and structural modeling revealed that the p.G477R substitution is deleterious and induced undesired effects on the protein stability and residue distribution in the ligand-binding pocket. The novel sequence variant occurred within an extremely conserved subregion of the ATP-binding domain. Conclusion: Our findings expand the spectrum of ATP8A2 mutations and confirm the reported genotype-phenotype correlation. These results could improve genetic counseling and prenatal diagnosis in families with clinical presentations related to CAMRQ4 syndrome. Keywords: ATP8A2, Cerebellar ataxia, dysequilibrium syndrome 4, mental retardation, whole exome sequencing

Bisulfite sequencing, one of the methods for detecting epigenetic changes (specifically: methylation)

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نوع پذیرش: پوستر | کد مقاله: G-95406

Abstract: Background: Bisulfite sequencing is the treatment of DNA with bisulfite before conventional sequencing to determine the methylation pattern. This method is the gold standard for DNA methylation detection. DNA methylation is an epigenetic modification in the genome and plays a vital role in embryonic development, cell proliferation, transcriptional regulation, and imprinting. Methylation mainly involves the addition of a methyl group to the 5-carbon position in the cytosine of CpG islands and represses transcriptional activity. Materials and Methods: In this review study, information related to bisulfite sequencing was searched and analyzed using the keywords Bisulfite Genomic Sequencing, Methylation, and Epigenetic Changes, through PubMed, Science Direct, Google Scholar, and Springer Link databases. Results: In this study, the history and various aspects of the bisulfite sequencing method, including its applications in biological research and new treatments for diseases, especially cancer treatment, have been discussed. Treatment of DNA with bisulfite converts cytosine residues to uracil but leaves 5-methylcytosine residues unaffected. DNA methylation, which often occurs at the C5 cytosine loop in CpG islands, is often found in gene regulatory sites such as promoters. Bisulfite sequencing uses conventional sequencing on bisulfite-treated DNA to determine the methylation status of CpG islands. Conclusion: Bisulfite sequencing can reliably determine DNA methylation changes in the desired DNA region, and in this way can help a lot in the investigation and diagnosis of various diseases, especially cancer. Keywords:



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Monkeypox virus Real Time PCR kit

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نوع پذیرش: پوستر | کد مقاله: G-89413

Abstract: Background: Monkeypox virus is an enveloped double-stranded DNA (200 kb) virus that belongs to the Orthopoxvirus genus of the Poxviridae family. The virus is usually transmitted from animals to humans through being bitten by an infected animal, direct contact with blood, monkeypox lesions, body fluids, and eating an infected animal that has not been properly cooked. This virus can be transmitted by direct contact with the body fluids of an infected person as well as clothing. An infected mother can also transmit this virus to the fetus through the placenta. The symptoms of this disease are similar to smallpox but milder, such as high fever, lymphadenopathy, headache, and systemic rashes, which have a mortality rate of about 1 to 10%. Recently, this disease has occurred in Europe and North America, and it is believed that threatens a wider population. Materials and Methods: Detecting the presence of the gene expressing complement binding protein F3L, which is one of the protection genes. This virus has been designed using primers and probes performing Real-Time PCR tests under optimal conditions. Contents of the kit Real-Time PCR - Master Mix, primers and probes for the MPXVgp052 gene and TE buffer (10mM, pH 8.1 ± 0.2) Results: The existence of a melting curve at the Tm optimum temperature limit indicates the replication of the sequence related to the virus MPXV is the JOE signal with a specific hybridization probe indicating the identification of the MPXV virus. Conclusion: This kit is not produced in Iran, and by producing this kit, it saves time and diagnosis, as well as prevents the spread of the disease in the country. Keywords: Monkeypox Virus, KIT, Real-Time PCR



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PEAR1 polymorphisms as a prognostic factor in hemostasis and cardiovascular diseases

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نوع پذیرش: پوستر | کد مقاله: G-80951

Abstract: Platelet Endothelial Aggregation Receptor (PEAR1), as a platelet receptor, plays a vital role in hemostasis. This receptor, by its extracellular part, causes platelet adhesion and consequently initiates platelet aggregation. Dysfunction of PEAR1 can disrupt platelet aggregation in patients with cardiovascular diseases (CVDs). The content used in this paper has been taken from English language articles (2005–2020) retrieved from Pubmed database and Google scholar search engine using “Cardiovascular Disease”, “PEAR1”, “Polymorphism”, and “Platelet Aggregation” keywords. Some PEAR1 polymorphisms can disrupt homeostasis and interfere with the function mechanism of cardiac drugs. Since polymorphisms in this gene affect platelet function and the platelet aggregation process, PEAR1 could be further studied in the future as an essential factor in controlling the treatment process of patients with cardiovascular diseases. PEAR1 polymorphisms through disruption of the platelet aggregation process can be a risk factor in patients with CVDs. Therefore, controlling patients through genetic testing and the evaluation of PEAR1 polymorphisms can help improve the treatment process of patients. According to the studies on the PEAR1 gene and the effect of different polymorphisms on some crucial issues in CVDs patients (changes in platelet activity), it is clear that if there is a significant relationship between polymorphisms and CVDs, they can be used as prognostic and diagnostic markers. This study aims to evaluate the prognosis and drug treatment of the PEAR1 gene in CVDs patients. Keywords:

Evaluation of Radiotherapy on CCL5/miR-214 -3p /MALAT1 Genes Expression in the immune pathway in Breast Cancer Patient Blood Samples

فضل اله شکری, @¹ حسین مزدرانی, ©¹ میردادود عمرانی²

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نوع پذیرش: پوستر | کد مقاله: G-59234

Abstract: Background: Current cancer therapies include chemotherapy, radiation therapy, immunotherapy, and surgery. Despite these treatment methods, a major point in cancer treatment is early detection. RNAs (mRNA, miRNAs, and LncRNA) can be used as markers to improve cancer diagnosis and treatment. This research examined how radiotherapy affected CCL5, miR-214, and MALAT-1 gene expression in the immune pathway in peripheral blood samples from radiation therapy-treated breast cancer patients. Methods: Before and after radiotherapy, peripheral blood was collected from 15 patients in four steps. Blood samples were collected in an outpatient facility from 20 healthy female volunteers with no history of malignant or inflammatory conditions. RNA was extracted from the blood samples and cDNA was synthesized. CCL5, miR-214, and MALAT-1 gene expression were determined by real-time polymerase chain reaction (RT-PCR). CCL5 protein levels in the serum were determined in 80 samples (60 BC and 20 healthy controls) using Quantikine Enzyme-Linked Immunosorbent Assay (ELISA) kits (R&D Systems). The data was then statistically evaluated. Results: There was a significant difference between CCL5 levels in tumoral and adjacent normal blood samples (p 0.05). The results also show that the level of gene expression and serum concentration of CCL5 protein in different phases of radiotherapy is significantly different. On the other hand, the expression level of the miR-214 gene was significantly decreased in patients compared to the control group, but this decrease was not significant for the MALAT-1 gene (p 0.05). Also, after each stage of radiotherapy, the expression level of these two genes showed a decrease, but in the fourth week after radiotherapy, this decrease was significant (p 0.05). Conclusion: radiotherapy is associated with a decrease in the expression of miR-214 and MALAT-1, as a result, an increase in the expression of CCL5. An increase in the concentration of CCL5 protein is accompanied by an increase in the level of monocytes, which ultimately causes the infiltration of macrophages and can ultimately cause cancer recurrence. It is suggested that these genes can probably be used as diagnostic and therapeutic radiotherapy markers in breast cancer. Keywords: Breast cancer, Biomarker, Radiotherapy, ELISA, Mir-214, CCL5, MALAT-1

Rel-A/PACER/miR 7 axis may play a role in radiotherapy treatment in breast cancer patients

فضل اله شکری^۱، حسین مزدارانی^۱، © میر داود عمرانی^۲

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نوع پذیرش: پوستر | کد مقاله: G-42587

Abstract: Background: Cancer development and treatment include a variety of immunological mechanisms. Activation of the proinflammatory transcription factor, nuclear factor-kappaB (NF- κ B), in particular, is a frequently noted event in breast cancer. Current cancer treatments include surgery, radiation therapy, chemotherapy, and immunotherapy. Early detection remains a significant issue in the treatment of cancer despite these interventions. RNAs (miRNAs, lnc-RNA) can be used as markers in cancer diagnosis and treatment. This study investigated the effect of radiotherapy on PACER and miR-7 expression and Rel-A of their target genes in the NF-B signaling pathway in peripheral blood samples from radiotherapy-treated breast cancer (BC) patients. Methods: Blood samples were collected from participants at four different time points: 72 hours before the start of RT, one week after RT completion, and two and four weeks following RT completion. In addition, blood samples were collected from healthy women who did not have any immune or cancer-related diseases. Blood RNA was extracted and cDNA was synthesized. The expression of Rel-A, PACER, and miR-7 was determined using real-time polymerase chain reaction (RT-PCR). Results: There was a statistically significant difference in Rel-A levels between tumoral and adjacent normal blood samples (p 0.05). After four weeks of radiotherapy, quantitative RT-PCR revealed significant down-regulation of miR-7 and up-regulation of Rel-A and PACER in BC patients. Also, there is a significant association between Rel-A expression and blood monocyte levels during radiotherapy (0.001). Conclusions: PACER and miR-7 expression, and that of its target gene, Rel-A, changed after radiotherapy. These genes can likely be used as diagnostic and therapeutic radiotherapy markers in BC. Keywords: Biomarker, Breast cancer, Radiotherapy, Rel-A, PACER and miR-7



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Association of human papillomavirus with breast cancer: a new perspective on an old debate

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نوع پذیرش: پوستر | کد مقاله: G-67058

Abstract: Background: Breast cancer is a common cancer in the female population. Despite remarkable progress in the treatment of this cancer, its exact etiology is still unknown. Since the first evidence of an association between breast cancer and human papillomavirus (HPV) was provided in 1992, numerous studies have explored this subject but have reached contradictory results. Materials and Methods: The search in the extensive literature of peer-reviewed articles published from the inception to December 2021 was conducted to identify the relevant studies, using the electronic databases of MEDLINE/PubMed, Embase, Scopus, the Cochrane Library, and the Web of Science. Results: In this review, the authors examine the existing evidence and hypotheses regarding the pathways whereby HPV infection can reach breast cells and the mediators linking HPV oncoproteins to breast cancer pathogenesis. Furthermore, the authors discuss contradictory findings regarding the association of HPV with breast cancer. Showing the link between HPV infection and increased genomic instability, reduced apoptosis, immune system dysfunction and progression of metastasis. Conclusion: the reviewed findings highlight the importance of active presence or history of HPV infection as a prognostic factor for breast tumor development. Keywords:

A Case Report: Identifying a New VPS13A Mutation in an Iranian Family with Chorea-Acanthocytosis

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نوع پذیرش: پوستر | کد مقاله: G-13294

Abstract: Background Chorea-acanthocytosis (ChAc) is a rare neurodegenerative disease that clinically resembles other pathologies such as Huntington's disease-like 2, McLeod's syndrome, pantothenate kinase-associated neurodegeneration, all grouped into the Neuroacanthocytosis syndrome. ChAc is characterized by onset at adult age, often between 30 and 40 years and by the combination of movement disorders due to degeneration of basal ganglia and acanthocytosis in the peripheral blood non often reported as a beginning symptom but may appear late during the disease course. Clinically, ChAc is heterogeneous and presents mainly with chorea, parkinsonism, dystonia, tics and involuntary movements. Self-mutilation such as tongue and lip biting are common and can be considered pathognomonic of the disease. Other symptoms as epilepsy, neuropsychiatric and neuromuscular symptoms may be added, and sometimes it can be in an atypical form presenting as epilepsy or obsessive-compulsive behavior. It is caused by mutations in VPS13A gene with autosomal recessive pattern of inheritance. Case presentation Here we report two affected brothers belonging to a non-consanguineous marriage who present with movement disorder pathology. Older brother was a 32-year-old man presented with progressive disorders including lingual dystonia, dysphasia, dysarthria, abnormal gait and speech disorder. Age onset of disease was at 27 years old. He has a 31 years old brother with the same clinical phenotypes. His brother developed symptoms at age 22. His parents are not consanguineous and his father is deaf-mute. In the enlarged families of both parents, there is a known individual (mother's first cousin) with mental retardation and (father's second cousin) with clinical phenotypes like this affected man and his brother. His grandfather (father-side) was suffering from dysphagia. Based on clinical/para-clinical investigations the referring physician suggested Mc Leod syndrome or Acanthocytosis as possible diagnoses for them. Thus, whole-exome sequencing was performed for precise diagnosis and identified a homozygous novel frameshift deletion c.6348delA (p.K2117Nfs*16) in exon 47 of VPS13A in older affected brother. This frameshift deletion mutation was validated by Sanger sequencing in all the family members showing a co-segregation of the mutation with the disease (unfortunately the younger brother showed the same mutation. So, the two patients were homozygous and the parents were heterozygous for mutation). Conclusion Here, we report a novel frameshift deletion p.K2117Nfs*16 in VPS13A identified by whole-exome sequencing, which caused ChAc in an Iranian family. This is the first description of ChAc in Iran with genetic confirmation, that expands the mutation diversity of VPS13A and provide clinical, neuroimaging and deep brain stimulation findings. Keywords: Chorea-acanthocytosis, neurodegenerative, VPS13A gene

A Missense Presenilin 1 Mutation Associated with early-onset Alzheimer's Disease without any Amyloid Plaques: An Important challenge in Neuropsychiatric Diagnosis

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نوع پذیرش: پوستر | کد مقاله: G-73569

Abstract: Introduction: early-onset familial Alzheimer's disease (EOFAD) is a rare form of Alzheimer's disease which causes symptoms before the age of 65 and accounts for 5 to 10 percent of all Alzheimer's cases. PSEN1 is a protein coding gene encodes presenilin-1 protein which is one of the four subunits of gamma secretase complex and play an important role in generation of amyloid beta (A β) from amyloid precursor protein (APP). According to the Alzheimer Disease Mutation Database (<http://molgen-www.uia.ac.be/ADMutations>), several mutations in exon sequences of PSEN1 have been detected in families with FAD. Here, we describe a 40-year-old female with progressive disorders (age of onset: ~34 years old) including dementia, mobility impairment, without remarkable findings in her brain computed tomography (CT) scan (absence of extracellular β -amyloid deposit) who's the father and two siblings respectively at Ages 41, 52 and 38 died with the same phenotypes. Based on clinical/para-clinical investigations, the referring physician suggested CADASIL disease or mitochondrial leukoencephalopathy as possible diagnoses for her. Methods: Genomic DNA was isolated from Peripheral blood of the affected individual and her non-affected mother and two siblings. Whole Exome Sequencing (WES) carried just for the proband individual. Afterwards, Sanger sequencing was used to confirm candidate variants to determine whether they co-segregated with FAD in family members. Results: Among all mutations that proband carries, a heterozygote novel (in Iranian population) missense mutation (V272A) in PSEN1 exon1 (Position: Chr14:73664784 TC, dbSNP ID: rs63750680) was the most probable mutation responsible for proband clinical phenotypes. Sanger sequencing determined the above-mentioned mutation in proband whereas, segregation analysis showed benign homozygosity in her mother as a healthy control and her sister and brother as unaffected siblings. This result strongly reinforces the possibility that V272A mutation is the main cause of Alzheimer's disease in this case. Conclusion: Consequently, the following case-report study declares that V272A missense mutation could alter presenilin-1 protein sequence somehow that results in dementia phenotype and its associated characteristics with autosomal dominant inheritance. Keywords:

The Role of microRNAs and circularRNAs in diagnostic, Prognostic and therapy response as Personalized Oncology Biomarkers in prostate cancer

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نوع پذیرش: پوستر | کد مقاله: G-82316

Abstract: Background: Small noncoding RNAs known as microRNAs (miRNAs) control protein expression at the post transcriptional level as well as Circular RNAs (circRNAs) are a unique family of noncoding RNAs that could regulate multiple biological processes, which play a crucial role in carcinogenesis, progression and chemotherapy resistance of cancers. These RNAs influence a wide range of biologic processes and are often deregulated in cancer. circRNAs and microRNAs play a key role in the development of cancer and are therefore a potential marker for diagnosis, prognosis, and therapeutic choices in prostate cancer (PCa) patients. To review the currently available data on circRNAs and microRNAs as biomarkers in PCa and as possible tools for early detection and prognosis Materials and Methods: Review was performed searching the PubMed and Science direct, Embase, Scopus database for articles in English using the following terms: circularRNA, circRNA, microRNAs, miRNAs, cancer, prostate cancer, circRNA and miRNAs profiling, diagnosis, prognosis, therapy response, and predictive marker. We summarize the existing literature concerning the profiling of circRNA and microRNAs in PCa detection, prognosis, and response to therapy. Results: The circRNAs and miRNAs are important regulators of biologic processes in PCa progression. A common expression profile characterizing each tumor subtype and stage has been identified for Pca diagnosis, prognosis and therapy response, Large-scale studies that should provide additional important information are still missing. Further studies, based on common clinical parameters and guidelines, are necessary to validate the translational potential of circRNAs and miRNAs in PCa clinical management Conclusion: The literature shows that circularRNAs and miRNAs hold potential as novel biomarkers that would aid prostate cancer management, but additional studies with larger patient cohorts and common guidelines are necessary before clinical implementation. Keywords: prostate cancer, circular RNA, biomarker, micro RNA



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DNA Microarray in Cancer Diagnosis

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نوع پذیرش: پوستر | کد مقاله: G-82567

Abstract: Background: Cancers are associated with multistep and accumulative genetic and epigenetic changes. Therefore, it is of importance to elucidate the molecular events and genetic markers of carcinogenesis. Gene expression profiling based on DNA microarray is a versatile and powerful platform for genome-wide scale identification of genetic alterations in cancer and other disorders. Materials and Methods: Here, we have summarized the recent major findings concerning the key applications of DNA microarrays technology in the field of cancer research and discussed their potential in clinical context. These include, mutation detection, chromosomal gains and losses, as well as tumor classification. Results: Distinct oncogenic pathways lead to identification of different molecular subclasses of solid tumors which could be characterized by DNA microarray data. These data may lead to development of multigene prognostic or predictive models that could be superior to existing clinical methods. Several genomic abnormalities identified by these assays are being used as predictive markers for cancer treatment with targeted therapeutics such as ovarian cancers, oral cancers, melanomas, colorectal carcinomas and prostate carcinomas. Conclusion: DNA microarray analysis can be a reliable method for the classification of tumors. This approach can potentially complete the underlying genetic mechanisms of many types of disease. Keywords: DNA microarray, Cancer, Diagnosis



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Over-Expression of Immune-Related lncRNAs in Inflammatory Demyelinating Polyradiculoneuropathies

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نوع پذیرش: پوستر | کد مقاله: G-18503

Abstract: Background: Long non-coding RNAs (lncRNAs) have crucial roles in the pathogenesis of immune-related disorders. However, their role in the pathobiology of inflammatory demyelinating polyradiculoneuropathies remains unclear. Materials and Methods: In the current study, we measured the peripheral expression of four lncRNAs, namely TUG1, FAS-AS1, NEAT1, and GAS5, in patients with acute/chronic inflammatory demyelinating polyradiculoneuropathies (AIDP/CIDP) compared with healthy subjects by real-time PCR method. RNA was isolated using the RNA isolation kit produced by the Gene All Company. Then, the Thermo Fisher kit was used for cDNA synthesis. Expression levels of four lncRNAs were measured in all enrolled persons using the appropriate PCR master mix. Results: Notably, all lncRNAs were overexpressed in patients compared with controls (P value less than 0.0001 for all lncRNAs). When assessing their expressions in AIDP and CIDP groups separately, TUG1 and NEAT1 were up-regulated in both patient groups compared with controls, yet FAS-AS1 and GAS5 were only up-regulated in CIDP cases Conclusion: There were remarkable pairwise correlations between expression levels of these lncRNAs in all study groups. Based on the above-mentioned data, we suggest the participation of these four lncRNAs in the pathogenesis of inflammatory demyelinating polyradiculoneuropathies. Moreover, FAS-AS1 and GAS5 lncRNAs have type-specific roles in this regard. Future functional studies are needed to elaborate on the molecular mechanisms of the contribution of these transcripts in AIDP/CIDP. Keywords: lncRNA. TUG1. FAS-AS1. NEAT1. GAS5



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A biallelic loss-of-function variant in TMEM147 causes profound intellectual disability with neuromuscular phenotypes

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نوع پذیرش: پوستر | کد مقاله: G-09451

Abstract: Background: Intellectual disability, occurring in syndromic or non-syndromic forms is the most common neurodevelopmental disorder inflicting huge burden on the health care systems worldwide. Significant part of cases is caused by single gene defects making it the most heterogenous genetic disorder. Materials and Methods: A consanguineous family with two affected members with ID along with movement disorders such as spastic quadriparesis or spasticity was included in the study. Whole exome sequencing and validating sanger sequencing were utilized to confirm the identified causal variant. Results: Here, we report a novel loss-of-function variant in TMEM147 causing intellectual disability and neuromuscular phenotypes. Variants in TMEM147, a transmembrane protein have been recently linked to intellectual disability with specific facial features. TMEM147 is believed to localize in endoplasmic reticulum membrane and nuclear envelope and regulate the proteins involved in protein transport and translation. Conclusion: Our findings were in line with the previously described patients with TMEM147 variants manifesting intellectual disability as a major clinical sign. This study brings more evidence on the pathogenicity of TMEM147 in causing intellectual disability plus other specific clinical characteristics and expands the phenotypic and variant spectrum linked to this gene. Keywords: Intellectual disability, Movement disorders, TMEM147, Whole exome sequencing

Investigation of next-generation sequencing in cancer diagnosis in clinical laboratories: a systematic review

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G-16528 نوع پذیرش: پوستر | کد مقاله:

Abstract: Background: Genomic sequencing has provided important insights into the etiology of simple and complex diseases. Technological advances have led to the introduction of next-generation sequencing (NGS) platforms in cancer research. Next-generation sequencing technologies have been and continue to be deployed in clinical laboratories, enabling rapid developments in genomic medicine. These technologies enable the sequencing of a large number of nucleotides in a short period of time at an affordable cost. NGS enables extensive parallel sequencing, which provides the maximum genomic evaluation of the tumor. The aim of this study is to investigate Next-generation Sequencing is used in the diagnosis of cancer in clinical laboratories. Methods: This study is a systematic review study that was conducted in 1401. By using the keywords of Next-generation sequencing, clinical laboratory, and cancer in reliable databases including PubMed, Scopus, Cochrane, Web of Science, Embase, and Google scholar search engine without a time limit. To ensure the completeness of the search results, the sources of the articles were checked and after removing the duplicate titles from the endnote software and checking the titles and abstracts, the related articles were checked using JBi tools, after checking the quality of the articles, the findings in the checklist the target was entered. Results: 92 articles were reviewed and finally 21 articles related to the purpose of the research were selected. According to the reviews, the results of some studies have shown that the development of next-generation sequencing (NGS) techniques, commercially available since 2006, enabled cost- and time-effective tumor DNA sequencing, leading to the "genomic era" of diagnosis and cancer treatment. NGS has many advantages such as the ability to completely sequence all types of mutations for a large number of genes (hundreds to thousands) and sensitivity, and speed in a single test at a relatively low cost compared to other sequencing methods. Recently, NGS technology has been used due to many advantages Compared to traditional methods, it has revolutionized the molecular diagnosis of cancer and for new diagnosis and rare cancer mutations, detection of translocations, inversions, insertions and deletions, detection of copy number variants, identification of familial cancer mutation carriers, providing molecular logic for Targeted, therapeutic and appropriate prognosis is used. Whole-genome sequencing can be used to provide the most comprehensive description of the cancer genome, whose complexity we are only just beginning to understand. Conclusion: The findings showed that clinical research centers should develop multigene sequencing as a tool to screen eligible patients for clinical trials and accelerate drug development, and prospectively develop data that can inform more about how to optimize the use of this technology. Due to the high speed and lower cost of this technology, it can be used for faster and more cost-effective diagnosis of all types of cancers. Keywords:



چهاردهمین گنگره بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Targeted Genome Editing via CRISPR and Theoretical System on Diagnostic and Therapeutic Applications of CRISPR-Cas9

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Abstract: CRISPR-Cas is a technique whose function and structure are derived from bacteria and have been the most important tool in recent years. Efficiency of CRISPR/Cas in genome editing is dependent on the ability to bind and cause double-stranded fractures in DNA by Cas9 endonuclease using a short sequenced gRNA. The identification of the Cas9 protein is an important discovery in the biology. The CRISPR/Cas9 system consists of two primary components: gRNA and Cas9 protein. Cas9/gRNA complex can be used to cause a double-stranded fracture in a specific area of the target gene. Using CRISPR/Cas9 system, it is possible to create animal models including all genetic and epigenetic changes, and this has been made available to researchers by studying the molecular mechanism of disease development and progression and also could help identification of oncogenes and tumor suppressor genes. Integration of CRISPR/Cas9 system and human induced pluripotent stem cells has provided a new strategy for modeling human diseases in vitro. Stem cells with impaired ABCC8 gene expression are more inhibitive of insulin secretion than their normal peer cells. In addition, it has been found that excess insulin secretion can be controlled by drugs and the structure of k-ATP channel is considered as a new target for the design of these drugs. The CRISPR-Cas 9 system has been employed by numerous researchers to diagnose developing infectious diseases. CRISPR-Cas 9 technology is advancing the understanding of the relationship between hosts and bacteria that has not been possible before and has been added to develop new diagnostic methods for infectious diseases. Perhaps the biggest improvement in CRISPR-based diagnosis for infectious diseases is non-specific nucleic acid incision, which is observed in CRISPR-CAS III, V and VI systems to provide accurate and targeted diagnosis. DNA methylation, methylation and histone acetylation, which regulate gene expression, are epigenetic factors. In some cancers, the enzymes responsible for these changes are difficult and cause the inactivation of cancer-suppressing genes or the activation of cancerous genes. Using the CRISPR-CAS9 system, the desired genes can be turned off and on. It can even be used by dead Cas9 (dCas9), who has lost his endonuclease activity to influence the activity of epigenetic-related enzymes and perform reversible activity of methylcytes and acetylation. CRISPR will create gene mutations in epigenetic-related magnesium with the process of cutting DNA and recombination of homologous or restorative system. CRISPR-Cas 9 is able to identify and modify mutations caused by single gene disorders, it prevents the occurrence of abnormal phenotypes resulting from these mutations. In addition, CRISPR-Cas 9 has made it possible for researchers to make adaptive changes in the genome of pathogens such as HIV, thus helping to improve people with high health by inducing immune system mutations or treatment mutations in host tissue. The potential abilities of this technology in gene therapy of different types of cancers cannot be ignored. CRISPR technology can also be used as a new method in future

planning for diagnosis of infectious diseases treatment. Keywords: Infectious Diseases, Systems CRISPR-Cas, Genome Editing

Autophagy; a viable option for targeted radio-chemotherapy in breast cancer

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نوع پذیرش: پوستر | کد مقاله: G-79536

Abstract: Background: Breast cancer (BC) is one of the most common types of malignancy in women so more than 2 million new cases are diagnosed each year throughout the globe. Due to the limitation and obstacles of using conventional therapies like radiotherapy, different targeted therapies have been introduced to circumvent the hurdles. There are different compensatory mechanisms that cancer cells utilize to resist stressful conditions including radiotherapy. Therefore, renewing and finding up-to-the-minute therapy is of the essence. One of the most important radiotherapy-resistant mechanisms that are considered to be targeted by inhibitors in BC is autophagy. Autophagy is a cytoprotective process in which cancerous cells recycle damaged organelles and superfluous cellular contents in a lysosomal-dependent pathway. In this study, we tried to shed light on the effect of autophagy inhibition on the efficacy of radiotherapy on breast cancer cell development. We also assessed the expression levels of two well-known autophagy-related circRNAs MUC16 and MTO1 in two BC cell lines. Materials and Methods: The expression levels circRNAs MUC16 and MTO1 were evaluated by qRT-PCR before and after treatment with radiation and 3-Methyladenine (3-MA) (a potent autophagy inhibitor) in breast cancer cell lines MCF-7 and MDA-MB-231. Cells were cultured in DMEM medium, supplemented with 10% Fetal Bovine serum (FBS), antibiotics (Penicillin/Streptomycin), and kept under optimal conditions (37°C and an atmosphere with 5% CO₂). Cells were treated with 3-Methyladenine (3-MA) and irradiated with a 6 MV linear accelerator with a dose of 4 Gy (for 24 hours). Then, RNA extraction was done for both cell lines, cDNA was synthesized and the expression level of circular RNAs, MUC16 and MTO1 as well as LC3B and Becn1 genes, was measured by real-time PCR. GAPDH served as an internal control housekeeping gene in this study. Data were analyzed using 2- $\Delta\Delta$ CT method. Furthermore, the proliferation rate by trypan blue exclusion assay and by utilizing MTT assay was determined. Results: Our results showed that inhibition of autophagy in combination with radiation resulted in a significant decrease in the expression of oncogenic circRNA MUC16, while it caused the increase of tumor suppressor circRNA MOT1 in both BC cell lines. However, the expression change in circRNAs in MCF7 cells was more significant than MDA-MB-231. Moreover, it induced apoptosis and reduced the proliferation rate in the cells. Conclusion: Due to the vital role of autophagy in participating in the radio-sensitivity of BC, considering this potent process for targeted therapy may be a viable approach for the treatment of breast cancer. Moreover, circRNAs MUC16 and MTO1 may be considered as prognostic markers based on the correlation that exists between, them and autophagy in breast cancer. Keywords:



چهاردهمین گنگره بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



CRISPR-Cas-mediated targeted genome editing and Theoretical System on Diagnostic and Therapeutic Applications of CRISPR-Cas9

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نوع پذیرش: پوستر | کد مقاله: G-16527

Abstract: Background: CRISPR-Cas is a technique whose function and structure are derived from bacteria and have been the most important tool in recent years. efficiency of CRISPR/Cas in genome editing is dependent on the ability to bind and cause double-stranded fractures in DNA by Cas9 endonuclease using a short sequenced gRNA. The identification of the Cas9 protein is an important discovery in the biology. Methods: The CRISPR/Cas9 system consists of two primary components: gRNA and Cas9 protein. Cas9/gRNA complex can be used to cause a double-stranded fracture in a specific area of the target gene. Using CRISPR/Cas9 system, it is possible to create animal models including all genetic and epigenetic changes, and this has been made available to researchers by studying the molecular mechanism of disease development and progression and also could help identification of oncogenes and tumor suppressor genes. Integration of CRISPR/Cas9 system and human induced pluripotent stem cells has provided a new strategy for modeling human diseases in vitro. Stem cells with impaired ABCC8 gene expression are more inhibitive of insulin secretion than their normal peer cells. In addition, it has been found that excess insulin secretion can be controlled by drugs and the structure of k-ATP channel is considered as a new target for the design of these drugs. The CRISPR-Cas 9 system has been employed by numerous researchers to diagnose developing infectious diseases. CRISPR-Cas 9 technology is advancing the understanding of the relationship between hosts and bacteria that has not been possible before and has been added to develop new diagnostic methods for infectious diseases. Perhaps the biggest improvement in CRISPR-based diagnosis for infectious diseases is non-specific nucleic acid incision, which is observed in CRISPR-CAS III, V and VI systems to provide accurate and targeted diagnosis. DNA methylation, methylation and histone acetylsion, which regulate gene expression, are epigenetic factors. In some cancers, the enzymes responsible for these changes are difficult and cause the inactivation of cancer-suppressing genes or the activation of cancerous genes. Using the CRISPR-CAS9 system, the desired genes can be turned off and on. It can even be used by dead Cas9 (dCas9), who has lost his endonuclease activity to influence the activity of epigenetic-related enzymes and perform reversible activity of methylcytes and acetylsion. CRISPR will create gene mutations in epigenetic-related magnesium with the process of cutting DNA and recombination of homologous or restorative system. Results: CRISPR-Cas 9 is able to identify and modify mutations caused by single gene disorders, it prevents the occurrence of abnormal phenotypes resulting from these mutations. In addition, CRISPR-Cas 9 has made it possible for researchers to make adaptive changes in the genome of pathogens such as HIV, thus helping to improve people with high health by inducing immune system mutations or treatment mutations in host tissue. The potential abilities of this technology in gene therapy of different types of cancers cannot be ignored. CRISPR technology can also be used as

a new method in future planning for diagnosis of infectious diseases treatment. Keywords: Infectious Diseases, Systems CRISPR-Cas, Genome Editing

Decreased cell proliferation and induced apoptosis in human B-chronic lymphocytic leukemia following miR-221 inhibition through modulation of p27 expression

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Abstract: Background: This study aimed to investigate the effects of the miR-221 inhibition on the human B-chronic lymphocytic leukemia (B-CLL) cell viability and the p27 gene expression, to introduce a new treatment approach for this type of cancer. In this context, the cyclin-dependent kinase (Cdk) inhibitor 1B (p27Kip1) is considered as an enzyme inhibitor that encodes a protein belonging to the Cip/Kip family of the Cdk inhibitor proteins. Materials and Methods: The affected miR-221 inhibition in the B-CLL cell viability was initially assessed. The inhibition of miR-221 in the B-CLL cell line (183-E95) was thus performed using locked nucleic acid (LNA) as an antagomir. After the LNA-anti-miR-221 transfection, the miR-221 quantification, cell viability, and apoptosis assays were evaluated at different intervals by the reverse transcription-quantitative polymerase chain reaction (RT-qPCR), the 3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyl-2H-tetrazolium bromide (MTT) assay, and flow cytometry (FC), respectively. The qRT-PCR was also completed for the p27 gene. The data were subsequently analyzed by independent-samples t-test and one-way analysis of variance (ANOVA). Results: A gradual reduction was observed in the B-CLL cell viability, and consequently the transfected LNA-anti-miR cell viability reached below 55% of the untreated cells after 72 h of transfection. A statistically significant difference was found in the cell viability between the LNA-anti-miR-treated and control groups (p -value ≤ 0.043). The downregulation of miR-221 in the B-CLL (183-E95) cells was further conducted by LNA-anti-miR-221. Conclusion: The miR-221 inhibition significantly decreases cell viability through augmenting the p27 gene expression and inducing apoptosis. Moreover, the findings demonstrated that the inhibition of miR-221 might be a new treatment approach for B-CLL, although more confirmation is needed by investigating appropriate animal models. Keywords:



چهاردهمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Involvement of progranulin (PGRN) in the pathogenesis and prognosis of breast cancer

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نوع پذیرش: پوستر | کد مقاله: G-14270

Abstract: Background: Breast cancer constitute a common type of oncological disease with a highlighted mortality rate. In recent years, researchers have introduced progranulin (PGRN) as a novel potential biomarker and associated its function with higher risk factor for development of breast cancer. Materials and Methods: The present review article collects evidence on the association of PGRN with clinicopathological features and drug resistance in the patients with breast cancer. Results: The results of this study suggested the use of routine determination of PGRN in the clinic as a reliable biomarker for screening people at high risk or as early indication of breast cancer. Conclusion: Targeting PGRN and its associated signaling pathways and receptors, such as sortilin (SORT1), could also cover a novel therapeutic strategy in the breast cancer. Keywords:



چهاردهمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Study of CYP1B1 Gene Mutations in Families with Primary Congenital Glaucoma in Southern Iran

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نوع پذیرش: پوستر | کد مقاله: G-74825

Abstract: Abstract Background and Aim: Primary Congenital Glaucoma (PCG) is a type of childhood glaucoma and one of the major causes of irreversible blindness in children due to developmental defects of the aqueous humor outflow pathway structures. PCG often presents with an autosomal recessive pattern, due to obstruction in the drainage of the aqueous humor due to congenital anomalies of trabecular meshwork growth and anterior chamber angle structures during fetal development. This disease leads to damage to the optic nerve and loss of vision by increasing congenital intraocular pressure (IOP) due to decreased aqueous humor outflow due to dysfunction of the trabecular meshwork. PCG occurs mainly in the first 3 years of life. The CYP1B1 gene is the most commonly reported gene and is currently the major known genetic cause of PCG. CYP1B1 expression plays an important role in regulating the growth and functions of the trabecular meshwork. This study was performed to evaluate the genetic mutations of CYP1B1 gene in 11 patients with primary congenital glaucoma in southern Iran by sequencing the exons of this gene by Sanger sequencing. Method: In this study, 11 families of PCG patients in southern Iran were studied. Conscious consent was obtained from all patients. Patients' familial pedigrees were also drawn. Exons encoding the CYP1B1 gene, including exons 2 and 3, as the main gene responsible for the disease, were amplified by PCR and then sequenced by Sanger sequencing. For one family, Segregation Analysis was performed on Proband and his parents. All variants found were interpreted based on genetic guidelines. Results: In this study, 5 different mutations such as c.182G A (p.Gly61Glu) and c.1103G A (p.Arg368His) were reported in seven families. Some of the mutations were the most common mutations in about half of our cases. Conclusion: The percentage of patients we studied had at least one pathogenic mutation in the CYP1B1 gene. The frequency of mutations observed in CYP1B1 gene in the studied patients compared to other breeds in the world and other parts of Iran seems to be slightly different, which indicates the role of other known genes in PCG or the possibility of other unknown mutant genes in these Patients. Keywords: Primary congenital glaucoma, CYP1B1 gene, mutation analysis



چهاردهمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Prevalence of Human papillomavirus Genotypes in patients referred to the genetics department of ART Center of Tabriz ACECR

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نوع پذیرش: پوستر | کد مقاله: G-19786

Abstract: Background: Human Papillomaviruses (HPV) are a family of small non-enveloped icosahedral viruses with double-stranded circular DNA. HPV lesion increases cancer risk in some organs like the cervix, vulva, vagina, penis, anus, mouth, tonsils, or throat, and is leading cause of approximately 1/3 cervical cancer and anal neoplasms. Its influences in recurrent miscarriages (RM) is under investigation. Materials and Methods: HPV DNA was Extracted from cervico-uterine smears or biopsies from Women and Men who had referred to the ART center of Tabriz ACECR (n = 225, cases). Viral genotyping was performed using reverse blot technique that allows qualitative detection in DNA samples. We investigate 37 human Papillomavirus subtypes Including – Medium-high risk and Low risk. Results: Among the samples, only 68 samples out of 225 were negative. the highest frequency genotypes 6 and 42 were more prevalence low risk subtypes, respectively. While, subtypes 51 and 16 showed had the highest frequency in High-Risk categories. Conclusion: HPV infection should be considered as a risk factor among RM patients and some cancers. Keywords:



چهارمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Molecular Study of Mutations in Axin2 Gene in Colorectal Cancer

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نوع پذیرش: پوستر | کد مقاله: G-18254

Abstract: Background: A Colorectal cancer (CRC) is one of the most common cancers, after skin, breast, and stomach cancers. Changes in the WNT pathway are commonly reported in this cancer. Axin1 reduces the oncogenic activity of beta-catenin and plays as a tumor suppressor in the WNT pathway. Axin2 acts as a negative regulator in the WNT / TCF pathway and helps to form the formation of the beta-catenin destruction complex. The aim of this project is to investigate the mutations on exon7 in axin2 in association with CRC demographic and pathologic data. Materials and Methods: A samples in this current project study contains 147 fresh frozen samples from CRC patients and 3 cell lines, including HT29, SW480, and CACO-2. And 25 healthy samples were used. Single nucleotide polymorphism (SNP) selection was performed using the NCBI, Ensembl, and Polyphen databases. The chosen SNPs are placed in exon7/ axin2 with rs370618491 at position C2140T. By utilizing the PCR-RFLP method, mutated samples that were mutated were identified and sent for sequencing. Results: The results showed that mutations in the SNP in axin2 were observed in 1 out of 147 patient samples (0.68%). In the three of sequences examined in axin2 (exon7), mutations in SNP with rs79024445 at A2052C were observed. Statistical analysis of clinical and pathological data of patients showed a significant relationship between the tumor size (T) factor and grade of cancer (P-value = 0.016) as well as the degree of tumor diffusion to the lymph nodes (N) factor with a grade of cancer (P-value = 0.001). Conclusion: The multi-factorial nature of cancer, high genetic diversity in the Iranian population, and limited statistical population can be effective in these outcomes. The observed mutations in each sample can also indicate the importance of personalized Medicine in study of diseases. Keywords: Axin2, SNPs, Colorectal Cancer, RFLP

Platelet-derived growth factor receptor beta (PDGFR- β) mRNA in blood circulation of patients with esophageal cancer

علیرضا عباسپور¹، هادی محمد دوست²، © رضا سالاری نیا³، علی بابایی⁴

1) دانشگاه علوم پزشکی خراسان شمالی- دانشکده پزشکی - گروه پاتوبیولوژی و علوم آزمایشگاهی- استادیار بیوشیمی بالینی

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4) دانشگاه علوم پزشکی خراسان شمالی- دانشکده پزشکی - کارشناس آزمایشگاه

نوع پذیرش: پوستر | کد مقاله: G-53109

مقدمه: سرطان یکی از شایع ترین علل مرگ و میر در جهان می باشد، که بروز و شیوع آن در حال افزایش است. تشخیص هر چه زودتر این سرطان در درمان آن نقش بسزایی دارد. این در حالیست که بیش از ۵۰ درصد افراد دارای سرطان مری، هنگامی تشخیص داده می شوند که سرطان به نقاط دیگر بدن متاستاز داده است. با توجه به تهاجمی بودن روش تهیه ی بیوپسی و تحمیل هزینه ی زیاد به بیمار و از طرفی احساس نیاز جهت گسترش و افزایش شناخت بیومارکرها در پیش بینی طول عمر و پاسخ به درمان بیماران مبتلا به سرطان مری ما را بر آن داشت که mRNA رسپتور فاکتور رشد مشتق از پلاکت نوع بتا (PDGFR- β) در گردش خون بیماران مبتلا به سرطان مری را بعنوان مولکولی که ممکن است ارزش تشخیصی داشته باشد، بررسی نماییم مواد و روشها: ۳۳ نفر از افراد مبتلا به سرطان مری که توسط بررسی های آندوسکوپیک شناسایی و با مطالعات هیستوپاتولوژیک تایید شده بودند وارد مطالعه شدند. نمونه ی خون همه ی شرکت کنندگان (۵ سی سی) بلافاصله پس از جمع آوری با سرعت ۲۰۰۰ r/min برای ۱۵ دقیقه در دمای ۴ درجه سانتی گراد سانتریفیوژ شد. RNA سرمی افراد توسط کیت شرکت کبازن (QIAamp Circulating Nucleic Acid) استخراج و سپس غلظت RNA توسط دستگاه نانودراپ اندازه گیری شد. سپس تمامی نمونه ها از نظر غلظت RNA یکسان سازی و از آنها cDNA سنتز شد. بر روی نمونه ها، تست Real Time PCR جهت اندازه گیری سطح mRNA سرمی رسپتور فاکتور رشد مشتق شده از پلاکت نوع بتا (PDGFR- β) انجام گرفت و در آخر، نتایج Time PCR Real با فرمول $2^{-\Delta\Delta CT}$ محاسبه گردید. نتایج: غالب سرطان مری از نوع سنگفرشی (SCC) بود. (EAC=27% _ ESCC=73%) همچنین بررسی های این مطالعه نشان داد که ابتلا به سرطان مری با داشتن سابقه ی ابتلا به هرگونه سرطان در اقوام درجه یک و دو، در ارتباط است. بررسی بیان ژن PDGFR β در سرطان مری در دو گروه سالم و بیمار با تکنیک Real Time PCR مورد ارزیابی قرار گرفت. نتایج مشخص کرد که تفاوت معنی دار آماری از لحاظ میزان بیان ژن PDGFR β در بین افراد بیمار و سالم وجود دارد. (p0.05) نتیجه گیری: با توجه به ارزش تشخیصی اسیدهای نوکلئیک در گردش خون و از طرفی نمونه گیری آسان این روش، بررسی های بیشتر در این زمینه جهت یافتن الگوی تشخیصی و افتراقی مناسب سرطان مری می تواند راهگشا باشد در ضمن بررسی های انجام شده در این مطالعه، از میزان بیان رسپتور فاکتور رشد مشتق از پلاکت می توان در تشخیص بیماران مبتلا به سرطان مری نوع سنگفرشی (ESCC)، میزان پیشرفت تومور و نیز افتراق آنها از سرطان مری نوع غده ای (EAC) بهره جست.

Small non coding micro RNAs; as a powerful tools in diagnosis of the recurrent miscarriages

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نوع پذیرش: پوستر | کد مقاله: G-81530

Abstract: Abstract Introduction: miRNA molecules are small non-coding RNAs whose expression in maternal blood during pregnancy plays an important epigenetic role in fetal growth and development. They cause frequent miscarriages by targeting the immune system, apoptosis, and angiogenic gene function. This study aimed to determine the significant difference in the expression of miRNAs miR-223, miR-155 among patients with recurrent miscarriage (RM) as a cases compared to normal control group (control) to determine whether these miRNAs can be used as diagnostic biomarkers? Or not. Methodology: Blood samples were collected from 120 causes and control groups who referred to Fertility Center of ACECR in Tabriz. Total RNA was extracted followed by synthesized cDNA of miRNAs and the gene expression assay by Real-Time PCR method. Spss21 and GraphPad Prism software were used for data analysis. Results: this study showed a significant difference in the expression of miR-155 ($p=0.005$) and miR-223 ($p=0.002$) in cases compare to controls. The examination of the Roc test showed that according to the value obtained for the area under the curve (Auc), miRNAs with values of 0.617 for miR-155 and 0.658 for miR-223 can be used as diagnostic biomarkers with medium to high power in early diagnosis of RM. Discussion and conclusion: Based of the finding of study, miRNAs can be effective in the early diagnosis of recurrent miscarriage in mothers; therefore, it is suggested to use them to identification of RM. Keywords: recurrent miscarriage, biomarker, miR-155, miR-223.

Killing and eating of pups by pregnant mother after delivery before lactation in Wistar rat and NMRI

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نوع پذیرش: پوستر | کد مقاله: G-81025

Abstract: Background: Killing and eating of pups by the pregnant mother during childbirth before breastfeeding and feeding the babies can be seen in Wistar rats and NMRI in laboratory conditions. which is influenced by environmental conditions and nutrition. This damage and losses can reduce the number of puppies, as well as reduce the efficiency of the test results, as well as waste time. Due to familiarity with the way of mating and pregnancy of Wistar rats and NMRI in laboratory conditions, further losses can be prevented. Materials and Methods: In this experiment, we used adult male and female Wistar rats of the same age, first and second generation, weighing 180-220 grams, born from the same mother, and male and female NMRI rats, first and second generation, weighing 25 grams, born from the same mother. After adapting to the environment and laboratory conditions, adult male and female Wistar and NMRI rats were placed in separate special cages in groups of 2 for mating during the night with free access to water and food under standard laboratory conditions with controlled light. They were placed and kept in the animal house and humidity of 40-50%, controlled environmental temperature (20-25 degrees Celsius). Results: The obtained results show that male and female mice that were born from the same family and from the same mother, after mating and pregnancy, the female mouse killed or ate her born cubs during childbirth. Conclusion: According to the results and observations obtained from the losses, killing and eating the pups can be caused by genetic defects, including family matings, inappropriate environmental conditions for nutrition, as well as the use of hormone stimulating substances and drugs in pregnant rats at the time of delivery. Keywords: wistar rat, NMRI, pups, Killing , eating , pregnant

Whole exome sequencing revealed a causative mutation in the PGAP3 gene related to the Hyperphosphatasia with impaired intellectual development syndrome-4

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نوع پذیرش: پوستر | کد مقاله: G-60274

Abstract: Background: Hyperphosphatasia with impaired intellectual development syndrome-4 (HPMRS4) is an autosomal recessive neurologic disorder caused by a glycosylphosphatidylinositol (GPI) biosynthesis defect. The PGAP3 gene encodes a GPI-specific phospholipase A2 that is expressed in the Golgi. The enzyme is involved in fatty acid GPI remodeling, critical for a proper association between GPI-anchored proteins and lipid rafts. This study identified a deleterious variant in the PGAP3 gene in two affected brothers. Methods: Two affected siblings with severe intellectual disabilities and other clinical symptoms, their parents, and other sibs in the family were included in this study. The patients were studied by whole exome sequencing. Sanger sequencing, co-segregation analysis, and in silico analysis were carried out to verify the candidate variant. The identified variant was interpreted based on the ACMG guideline. Results: We identified a missense variant in the PGAP3 gene, NM_033419.5:c.850CG (NP_219487.3:p.His284Asp), in two siblings with severe intellectual disabilities, Cleft palate, Developmental delay, Aggressive behavior, Lack of speech, and Dysmorphic facies in an Iranian consanguineous family that was related to the clinical features of two patients known as Hyperphosphatasia with mental retardation syndrome 4 (HPMRS4). The variant was found to be pathogenic. Conclusion: The current study findings expand the existing knowledge of the variant of the PGAP3 gene implicated in Hyperphosphatasia with mental retardation syndrome 4 (HPMRS4) and it presents a detailed clinical feature associated with the related condition. The data has implications for genetic diagnosis and counseling in families with the same disorders. Keywords:

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نوع پذیرش: پوستر | کد مقاله: G-81025

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Whole exome sequencing revealed a causative mutation in the PGAP3 gene related to the Hyperphosphatasia with impaired intellectual development syndrome-4

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نوع پذیرش: پوستر | کد مقاله: G-60274

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Investigating the effect of hesperetin on Cyclin D1 gene expression in MDA-MB-231 breast cancer cell line

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نوع پذیرش: پوستر | کد مقاله: G-97640

Abstract: Background: Breast cancer is one of the most important and common malignant cancers in women. This cancer is caused by the uncontrollable proliferation of cells in the lobular part (mammary glands) and the duct leading to the nipple. Hesperidin (Hsd) is a glycosylated flavanone found in citrus fruits. After entering the digestive tract, Hsd is enzymatically hydrolyzed, loses its sugar part and becomes hesperetin (Hst). The anticancer effects of Hst have been of interest in recent years, and many studies have been conducted in relation to the molecular pathways related to this compound. Studies have shown that Hst can decrease G1 protein but this decrease was not significant. On the other hand, since cyclin is one of the regulatory proteins in the G1 phase, therefore, in this study, we examined the expression of the Cyclin D1 gene in the MDA-MB-231 cell line. Material and method: MDA-MB-231 cell line was obtained from Institute Pasteur and cultured in RPMI-1640 with 5% FBS. After evaluating IC50 through MTT viability assay, cells were seeded on 6-well plates and treated with concentrations of 0, 25, 50, 100 and 200 mM hesperetin for 24 hours. Then RNA was extracted by Parstos kit and cDNA was synthesized. After that, gene expression analysis using SYBR Green method and Real Time-PCR thermocycler (ABI-USA). $2^{-\Delta\Delta ct}$ was entered into version 16 SPSS software for analysis. Results: Cytotoxicity results by MTT test showed that MDA-MB-231 cells have about 51.1% viability in 200 mM hesperetin concentration. Real-time PCR results showed a decreasing mRNA level at all concentrations of hesperetin, and the results were significant at concentrations of 100 and 200 mM (P -Value ≤ 0.05 was confirmed). Conclusion: Previous studies have shown that Hst induces apoptosis in MDA-MB-231 cancer cells through its effect on caspases such as caspase 3 and 9. Previous studies have shown that hesperetin prevents the growth of colon cancer. Also, in a study conducted by L Ye and his colleagues in 2012, it was shown that hesperetin prevents the growth of MDA-MB-231 cells and does this by stopping the cell cycle in the G1 phase. STAT3 is involved in the expression of genes such as apoptosis genes as well as cell cycle genes. The possible pathways by which hesperetin can reduce Cyclin D1 gene expression can be mentioned STAT3 as well as SP1 and cAMP-PKA pathways. But more studies are needed to prove this. Keywords: hesperetin, MDA-MB-231, breast cancer, Cyclin D1

New insight into the application of STR in paternity

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نوع پذیرش: پوستر | کد مقاله: G-21356

Abstract: Background: Short tandem repeats (STRs), also known as microsatellites are a polymorphic locus present in all eukaryotic genomes. They typically consisted of tandem matrices of 2 to 6 base pair short repeating patterns. They are one of the most often employed genetic markers in forensic science, anthropology, archaeology, and population genetics. STR loci are identified for the presence of mutations in order to enhance the quality of conclusions in disputed paternity instances. Materials and Methods: Articles indexed in Google scholar and Pubmed databases; applied MeSH available keywords for this topic were: “STRs” AND “Paternity tests” AND “Human identification” AND “Microhaplotype” during 2020 to 2022 were included. Finally, 11 articles were selected based on the criteria of the research. Results: In a study the combined power of discrimination (CPD) and the combined power of exclusion (CPE) of the new-generation autosomal STR amplification system in the Hotan Uyghur is 9,9999-E01 and 9,9999-E01, respectively. Population genetic studies indicate that the Hotan Uyghur show a close genetic relationship with geographically different Uyghurs and Kazakhs, while significant genetic differentiation exists between the Hotan Uyghur and some ethnicities from other non-Turkic-speaking populations. The results of population comparisons among the 52 worldwide populations demonstrate that geographically approached intercontinental populations have close genetic relationships. In two studies the ABO-rhesus/hemoglobin electrophoresis examination of the fourteen trios under study showed ten plausible inclusion instances, three exclusion cases, and one unclear paternity. Out of the ten possible inclusions with ABO-rhesus/hemoglobin electrophoresis assay, DNA STR analysis indicated five paternity inclusions as opposed to nine paternity exclusions. In several studies in the population under study, two marker sets with 19 STR markers each outperform 20 enlarged CODIS loci. Additionally, 20 paternity cases with CPI values of 7.62×10^{11} and 7.16×10^{11} demonstrated the usefulness of these marker sets. Penta E, Penta D, and SE33, three non-CODIS STR markers, shown amplification in 50 difficult samples with 0.80 heterozygosity. Conclusion: Because of their small size, polymorphic makeup, simplicity of amplification, development of the multiplex system, and speed of analysis, STR markers have become an indispensable component of the majority of DNA analysis labs. The results showed that STR analysis was not only very effective for paternal testing but also had potential value for kinship analysis and forensic records. Keywords: STRs; Microhaplotype; Paternity tests

A Novel Homozygous Pathogenic Variant in CYP11B1 in a Female Iranian Patient with 11 β Hydroxylase Deficiency

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نوع پذیرش: پوستر | کد مقاله: G-52487

Abstract: Background: Congenital Adrenal Hyperplasia (CAH) addresses a number of autosomal recessive disorders characterized by the enzyme defects in steroid hormones biosynthesis. The second common cause is related to 11 β -hydroxylase deficiency (11 β OHD) (OMIM: 202010), due to the CYP11B1 gene mutations, which account for 5–8% of all cases. 11 β -hydroxylase (CYP11B1, EC 1.14.15.4) is a P450 type I mitochondrial enzyme that catalyzes the hydroxylation of 11-deoxycortisol and deoxycorticosterone (DOC) to cortisol and corticosterone, respectively. 11 β OHD is characterized by a reduction in cortisol synthesis leading to an elevated plasma level of adrenocorticotrophic hormone (ACTH) and accumulation of DOC, a less potent mineralocorticoid, activates mineralocorticoid receptors, referring to salt retention and hypertension. CYP11B2 and CYP11B1 genes contain highly homologous sequences with about 93% homology in the coding region and about 90% in introns that make a major challenge for routine used molecular genetic diagnostic methods. Indeed, homologous regions introduce complexity to discriminate calls from these sequences, hence different diagnostic approaches need to be refined to identify variants in CYP11B2 and CYP11B1 genes in homologous regions. Here, we reveal a novel mutation in the CYP11B1 gene related to the 11 β OHD. Methods and Results: The present study was launched by exploiting the combined strategy of phenotype-directed genotyping and hotspot exon prioritization to clarify the molecular basis of 11 β OHD. We identified a novel likely pathogenic variant (CYP11B1:c.1351CT) in an Iranian 19-year-old girl with 11 β OHD by using CYP11B1 gene-specific primers. Proper Bioinformatic tools and three-dimensional (3D) protein structure models predicted the destructive molecular consequences of this mutation on the human CYP11B1 protein. In silico analysis and Molecular Docking were done. Protein docking showed destructive effects of the variant on the CYP11B1 protein-ligand interactions. Results: Sequence analysis of CYP11B1 exons led to the identification of a novel missense variant (c.1351CT), which causes leucine to phenylalanine substitution (p. L451F). The variant, C to T transition, located in exon 8, was inherited in a homozygous manner in the proband. The variant was found to be co-segregating with the phenotype: Both parents were heterozygous for the mutation, and her sister was normal homozygous. The variant was absent from NCBI dbSNP human build 147, 1000 genomes project, Genome Aggregation Database, NHLBI GO exome sequencing project (ESP), the Human Gene Mutation Database, and the ClinVar database. Accessed information showed novelty and probably evidence for the damaging effect of the



چهاردهمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



variant in the protein based on in silico predictive tools. Multiple sequence alignment of the CYP11B1 protein from different species showed conservation of the L451 residue in human, rat, mouse, pig, bovine, and sheep. The native and p.L451F mutant 3D spatial models indicated a larger size of F451 compared to L451 in the heme-binding peptide. The ligand binding energy of heme estimated -5.53 kcal/Mol in the normal and -2.51 kcal/Mol in the mutant protein. The comparison of the results suggested that the L451F variant in the CYP11B1 protein affects its structure and reduced the tendency of the ligand to the protein. Conclusion: This study broadened the CYP11B1 mutation spectrum and introduces the novel p.L451F likely pathogenic. Keywords:



چهاردهمین گنگره بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



A new mutation in NTRK1 gene is associated with congenital insensitivity to pain without anhidrosis

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نوع پذیرش: پوستر | کد مقاله: G-86370

Abstract: Background: Congenital insensitivity to pain with anhidrosis (CIPA) is a very rare autosomal recessive disease characterized by pain insensitivity, frequent intermittent fevers, anhidrosis, self-mutilating actions and mental retardation. Germline mutations in NTRK1 gene have been associated with CIPA. Materials and Methods: In the current study, we describe the first reported case from Iran. The patient was a 10-month old girl born to a healthy consanguineous Iranian parent with family history of CIPA. Unexpectedly, the cases had normal sweating. Results: Whole exome sequencing revealed a new likely pathogenic mutation in the exon 13 of NTRK1 gene (NM_002529.3) in the proband in homozygote state (c.1524_1531dupGGACATCG, p.Val511Glyfs*39). The frameshift mutation leads to early termination of the coding sequence, which is anticipated to affect the protein function. Sanger sequencing confirmed the results in the proband and other affected members of the family. In addition, Sanger sequencing showed that parents carry the same mutation in heterozygote state. Conclusion: The current study shows a different phenotypic variant of CIPA in Iranian population and adds to the repository NTRK1 mutations. Keywords:

Characterization of a Novel Androgen Receptor Gene Variant Identified in an Iranian Family with Complete Androgen Insensitivity Syndrome (CAIS): a Molecular dynamics simulations study

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نوع پذیرش: پوستر | کد مقاله: G-78513

Abstract: Background: Androgen insensitivity syndrome (AIS) is the most prevalent type of 46, XY disorder in sex development disease (DSD). It is due to the androgen receptor (AR) gene mutations and is inherited as an X-linked recessive genetic disease. AIS includes clinical subgroups of complete AIS (CAIS) and partial AIS (PAIS), along with a vast area of clinical heterogeneity of completely normal female external genitalia to male infertility. Method: The Whole Exome Sequencing (WES) detect the cause of DSD in a consanguineous Iranian family with 2 female patients with normal external genitalia and 46, XY karyotype. Sanger sequencing was applied to validate the candidate variant in family. Furthermore, the structural alteration induced by the variant on AR protein predicted using bioinformatics analysis such as molecular dynamic (MD) and molecular docking simulations. Results: WES results identified a novel hemizygous p.L763V variant in the AR gene in the proband that was compatible with the X-linked recessive pattern of inheritance. Moreover, co-segregation confirmed variant in family and bioinformatics studies approved the loss of AR function. Based on the American College of Medical Genetics and Genomics (ACMG) guidelines, it was categorized as pathogenic. Conclusion: This study broadens the AR mutation spectrum and introduces the novel p.L763V missense pathogenic variant leading to AR failure to bind to its ligand, and the resulting CAIS clinical subgroup. This study presents a prosperous application of WES and bioinformatics analysis to recognize the underlying cause of DSD in Iran, necessary for its clinical/psychological management. Keywords:



چهاردهمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



The Role of Non-Coding RNAs in Cervical and Head and Neck Cancer: A Review

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Abstract: Background: Cervical and head and neck cancer are leading causes of cancer-related deaths worldwide. The development and progression of these types of cancer are complex and multifactorial, involving a variety of genetic and epigenetic changes. Non-coding RNAs (ncRNAs), including microRNAs, long non-coding RNAs, and circular RNAs, have been shown to play important roles in the regulation of gene expression and have been implicated in the development and progression of various types of cancer, including cervical and head and neck cancer. The aim of this study is to review recent literature on the role of ncRNAs in cervical and head and neck cancer, specifically focusing on the potential mechanisms and applications of ncRNAs in these types of cancer. Methods: A comprehensive search of the literature was conducted using multiple databases and the articles included in this review were published between 2016 and 2022. Discussion: Studies have shown that ncRNAs can act as oncogenes or tumor suppressors and can regulate various cellular processes, such as cell proliferation, apoptosis, angiogenesis, and the epithelial-to-mesenchymal transition, which are important in the development and progression of cervical and head and neck cancer. NcRNAs have also been demonstrated to be potential biomarkers for cervical and head and neck cancer, and they may be therapeutic targets for the treatment of these cancers. For instance, miR-154 could be used as a potential biomarker for head and neck squamous cell carcinoma (HNSCC) by influencing the development and progression of HNSCC through the regulation of the epithelial-to-mesenchymal transition process. Moreover, it has been shown that in HPV-induced head and neck squamous cell cancer, computational approaches could be employed to identify novel functions of PIWI-interacting RNAs. Finally, non-coding RNAs play role in the autophagy process in cervical carcinogenesis. Conclusion: The studies reviewed in this paper suggest that ncRNAs play important roles in the development and progression of cervical and head and neck cancer and have potential as biomarkers and therapeutic targets for these types of cancer. Further research is needed to fully understand the mechanisms by which ncRNAs regulate the development and progression of cervical and head and neck cancer and to develop effective therapeutic strategies targeting ncRNAs. Keywords: ncRNAs, Cervical Cancer, Head and Neck Cancer

Evaluation of CD56+CD16+ / CD56dim/bright Natural Killer Cell subsets in Severe/Critical COVID-19 patients

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نوع پذیرش: پوستر | کد مقاله: G-35816

Abstract: Background: The severity of COVID-19 disease in patients is determined by both the viral infection and the host immune response. Innate immunity-as the first line of defense of our immune system-plays a crucial role in defending against SARS-CoV-2 infection and also its immunopathogenesis. Due to the importance of immune system responses in the recovery or progression of the disease and the relationship of laboratory parameters with the severity of the disease, the present study was designed. The population of the cells with CD56 and CD16 markers and their subsets in patient's blood samples and their relationship with the severity of patients' clinical symptoms and several laboratory factors were evaluated. Materials and Methods: After taking blood samples from the admitted COVID-19 patients in University hospital, peripheral blood mononuclear cells were isolated from 20 healthy individuals and 44 COVID-19+ patients. The PBMCs were separated by Ficoll-Hypaque density gradient and centrifugation. The immunophenotype of NK cell subsets were detected by flow cytometry. Results: The percentage of CD56+ CD16+ NK cell population was significantly decreased in COVID-19 patients ($p=0.0001$). The population of CD56dim CD16- NK cell subsets were increased ($p=0.0001$) in sever COVID-19 patients. CD56bright NK cell subsets was significantly decreased in the patient's blood. The percentage of total NK cells, CD56+ CD16+ NK cells negatively correlate with LDH levels. Conclusions: The declined of NK cells in COVID-19 patients were associated with disease severity and progression. Total NK cells, CD56+ CD16+ NK cells, could be used as meaningful indicators for assisting diagnosis of severe/critical COVID-19. Keywords:

Assessment of Hrd1 and Sel1L genes associated with endoplasmic reticulum stress response in major depressive disorder follow-up sertraline treatment

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Background: The role of endoplasmic reticulum stress (ERS) in the pathogenesis of major depressive disorder (MDD) is not well understood. The Hrd1/Sel1L (*HMG-CoA reductase degradation 1/Suppressor/Enhancer of Lin-12-like*) complex is involved as a part of cellular response to the ERS. This complex has a special function in the pathogenesis of various diseases, ranging from mental disorders to inflammatory diseases. Hence, the role of inflammation in the pathogenesis of depression raised the assumption that the Hrd1/Sel1L complex may play a role in the pathogenesis of major depression. Therefore, this study was conducted to investigate the expression of these two genes in MDD patients before and after treatment with sertraline.

Materials and Methods: The mRNA expression level of Hrd1 and Sel1L was measured in two groups containing 17 patients with major depression and 17 healthy controls by Real-time qPCR. We assessed the expression level of these genes before and after 8 weeks of consecutive treatment with sertraline.

Results: Compared to the healthy control, the expression level of Hrd1 and Sel1L genes was not significantly different from the MDD patients ($p=0.869$, $p=0.35$). It should be noted that after 8 weeks of treatment with sertraline, the expression level of both these genes increased, which was not statistically significant ($p=0.796$, $p=0.097$). However, the expression level of Sel1L increased significantly after treatment compared to the patients before treatment ($p=0.03$). Furthermore, there was a correlation between the Sel1L expression and the improvement of the depression index in patients with MDD.

Conclusion: Several studies have shown an involvement of the Hrd1/Sel1L complex in mental and inflammatory disorders. According to previous findings, there is persistent ER stress in MDD patients. Consistently, we found an increase in the expression of Hrd1 and Sel1L, although it was not significant. However, our data indicate that further studies require in this case.

Keywords: Hrd1, Sel1L, MDD, ER stress

Comparison of the Expression Level of TLR2, TLR4, NLRP3 and NOS2 Genes in Peripheral Blood Monocytes of Colorectal Cancer Patients and Healthy Controls

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نوع پذیرش: پوستر | کد مقاله: G-51632

Abstract: Abstract Introduction: Colorectal cancer (CRC) is the third most common cancer diagnosed and the second leading cause of cancer related death for both men and women in the United States of America (US) and also, is the third and fourth common cancer in Iranian men and women, respectively. It is curable in its early stages; we hypothesized” the inflammatory gene expression level of the peripheral monocytes of CRC patients is different from control healthy persons”. Therefore, this research was done with the aim of finding of the role of inflammation in the formation of CRC to help diagnosis and treatment of CRC in its early stages on the basis of its immunopathological view. Materials and Methods: In this case-control study, the expression level of TLR2, TLR4, NLRP3 and NOS2 genes was compared following RNA extraction and cDNA synthesis from isolated monocytes of stage II CRC patients (confirmed by TNM method and before any chemotherapy and radiotherapy n=12) versus non-CRC healthy/controls (referred for CRC screening n=12) by qPCR method. The β - actin gene was used as the reference gene in this research. Results: In CRC patients’ monocytes, the expression levels of TLR2 and TLR4 genes were significantly less than those of healthy controls (P0.05). The NLRP3 gene expression level in CRC group was slightly higher but, not significant. In contrast, the expression level of NOS2 gene in CRC group was significantly higher than that of in healthy controls (P0.05). Conclusion: On the basis of the variations of the gene expression levels of TLR2, TLR4 and NOS2 in monocytes of stage II CRC patients and the role of inflammation in its formation, it is possible using this variations as CRC prognosis and in time treatment along with other methods; though, it needs more investigations. Keywords:

Comparison of the Expression Level of TLR2, TLR4, NLRP3 and NOS2 Genes in Peripheral Blood Monocytes of Colorectal Cancer Patients and Healthy Controls

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نوع پذیرش: پوستر | کد مقاله: G-34502

Abstract: Introduction: Colorectal cancer (CRC) is the third most common cancer diagnosed and the second leading cause of cancer related death for both men and women in the United States of America (US) and also, is the third and fourth common cancer in Iranian men and women, respectively. It is curable in its early stages; we hypothesized” the inflammatory gene expression level of the peripheral monocytes of CRC patients is different from control healthy persons”. Therefore, this research was done with the aim of finding of the role of inflammation in the formation of CRC to help diagnosis and treatment of CRC in its early stages on the basis of its immunopathological view. Materials and Methods: In this case-control study, the expression level of TLR2, TLR4, NLRP3 and NOS2 genes was compared following RNA extraction and cDNA synthesis from isolated monocytes of stage II CRC patients (confirmed by TNM method and before any chemotherapy and radiotherapy n=12) versus non-CRC healthy/controls (referred for CRC screening n=12) by qPCR method. The β - actin gene was used as the reference gene in this research. Results: In CRC patients’ monocytes, the expression levels of TLR2 and TLR4 genes were significantly less than those of healthy controls (P0.05). The NLRP3 gene expression level in CRC group was slightly higher but, not significant. In contrast, the expression level of NOS2 gene in CRC group was significantly higher than that of in healthy controls (P0.05). Conclusion: On the basis of the variations of the gene expression levels of TLR2, TLR4 and NOS2 in monocytes of stage II CRC patients and the role of inflammation in its formation, it is possible using this variations as CRC prognosis and in time treatment along with other methods; though, it needs more investigations. Keywords:



چهاردهمین کنفرانس بین المللی آزمایشگاه و باالین

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Investigating the effectiveness of stress coping skills training on the immune system and natural killer cells (NKC) and the level of pain in breast cancer patients

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Abstract: Cancer causes many problems in physical, psychological and social dimensions, including pain tolerance and reduced quality of life. Objective: This study was conducted with the aim of the effectiveness of stress coping skills training on immune system (NKC) and pain level and quality of life of breast cancer patients living in Dezful city. Method: This research is a semi-experimental study with a pre-test-post-test design with a control group with follow-up. For this purpose, through informal invitations, 34 patients who met the conditions of the study were enrolled. These patients were randomly divided into two groups of 17 people, experimental and control. The experimental group was trained in 8 weeks of 1.5 hour stress coping skills program (Lazarus and Folkman, 1984) and the control group received their normal treatment program until the end. Both groups completed a short pain intensity questionnaire before and after the program and were examined in terms of the activity of natural killer cells in two stages. Findings: Descriptive results showed a better condition of the experimental group in the level of natural killer cells (NKCs), the amount of pain and its dimensions, compared to the control group. The results of multivariate analysis of covariance, by controlling the pre-test effect, showed that stress coping skills training improved the function of natural killer cells (NKCs) in breast cancer patients. Also, this program reduces pain intensity and reduces pain interference. Keywords:



Lymphocytosis in all age groups following COVID-19 infection in Tehran, Iran

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نوع پذیرش: پوستر | کد مقاله: G-80457

Abstract: Background: Investigating the possibility of lymphocytosis in patients with Covid-19 Material and methods: In this study, which was conducted in a Khanevadeh Hospital, in Tehran, Iran, in the first step, individuals were given an information sheet, and then their referrals were collected. The study included 161 individuals, 71 (44%) were female and 90 (56%) of whom were male. These people were divided into two age groups under five years (43%) and older than five years (57%). For people with respiratory symptoms, nasal swab samples were taken, and a Real-time PCR test was performed for all these samples. In the end, 14 (8.7%) positive samples of severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2) were obtained from 161 pieces. Results: Among 14 positive cases of severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2), nine were for people under five years old, and five patients were for people over five years old. We examined these 14 people for symptoms, and cough was the only symptom seen in all 14, and also shivering was one of the symptoms seen in just one patient. For patients whose Real-time PCR test for SARS-CoV-2 result was positive, CBC was performed to determine the hematological characteristics of these people. Overall, 12 cases of lymphocytosis and 2 cases of lymphopenia out of 14 patients with severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2) have been observed Conclusion: we concluded that in this statistical group, lymphocytosis is more common than lymphopenia. And we have observed that most of the patients infected with SARS-CoV-2 have lymphocytosis. Key words: COVID-19, SARS-CoV-2, lymphocytosis, Clinical symptoms In



چهاردهمین گنگره بین المللی آزمایشگاه و بالین

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Inhibition of tumor growth by blockage of adenosine receptor

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نوع پذیرش: پوستر | کد مقاله: G-87425

Abstract: Title: Inhibition of tumor growth by blockage of adenosine receptor Vida Hashemi^{1*}, Farhad Jadidi Niaragh^{2, 3} 1. Department of basic science, faculty of medicine, Maragheh University of medical Science, Maragheh, Iran 2. Department of Immunology, Faculty of Medicine, Tabriz University of Medical Sciences, Tabriz, Iran 3. Immunology Research Center, Tabriz University of Medical Sciences, Tabriz, Iran Background: The expression of immune-checkpoint inhibitors molecules on infiltrating T cells is one of the chief reasons for the unsuccessfulness of various cancer immunotherapies. So, we decided to suppress one of the most important inhibitory checkpoint molecule expressed on tumor-infiltrating T cells (A2aR). Ligation of adenosine with A2aR significantly inhibit T cell responses against cancer cells. Materials and Methods: we well designed NPs with high functional properties for delivery of A2aR siRNAs to cancer cells and then evaluated the potential of NPs loaded siRNA alone or in combination with DC-based vaccines in cancer treatment (4T1 and CT26 Mice tumors). Results: It has been shown that that NPs loaded with A2aR siRNA molecules significantly inhibited the expression of A2aR target genes in tumor-infiltrating T cells. Also noticeably induced anti-tumor immune responses, reduced tumor growth, suppressed Treg differentiation, and increased survival time in mice. Conclusion: our findings demonstrate that a combination therapy based on magnetic nanocarrier NPs loaded with anti-PD-1/A2aR siRNAs and DC-based vaccines can be regarded as a promising therapy for cancer patients in the near future. Keywords: Nanoparticle, siRNA, A2aR and Cancer.

The relationship between the cellular immunity and the clinical course, imaging findings and mortality rate of n-Covid 19 affected patients.

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نوع پذیرش: پوستر | کد مقاله: G-69574

Abstract: Background: In numerous pathological conditions, Cell mediated immunity plays a significant role in immune responses and has a very potential to regulate humoral response as well native immunity. So, careful study of T cells has an important effect on accurate information in SARS-CoV-2 disease pathogenesis. Method: In this research, the function and frequency of several T cells involved in immune responses evaluate in SARS-CoV-2 disease with various disease severity compared to normal groups. This study was done on asymptomatic recovered patients (n =20), ICU hospitalized or severe patients (n =30), non-ICU hospitalized or mild patients (n =30), and normal groups (n = 20). To exactly examine T cells function and their cytokine secretion after purification. Also after purification of Treg, their immunosuppressive activity on T cells was evaluated. Results: SARS-CoV-2 disease with severe disease not only had a remarkable increase in Th1cells and Th17 cells but also a significant reduction in Th2 cells and Treg. More importantly, as the IFN- γ and IL-17 secretion was sharply increased in ICU hospitalized, the secretion of IL-4 and IL-10 was reduced. Moreover, the inhibitory action of Treg was decreased in ICU hospitalized in comparison to other groups. In severe COVID-19 disease, current findings indicate when the inflammatory responses of cell immunity is meaningfully increased, a considerable decrease in anti-inflammatory and regulatory responses happened. Conclusion: In end, the inhibitory and regulatory action of Treg cells was decreased in severe patients in comparison to other control groups. In severe COVID-19 disease current show when the inflammatory arm of cell immunity is significantly increased, a significant decrease in anti-inflammatory arm and regulatory arm happened. Key word: COVID-19, T cells, Cell mediated immunity, Inflammation.



چهاردهمین کنفرانس بین المللی آزمایشگاه و بالین

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Correlation of IL-17 serum level with disease severity and onset of symptoms in patients with rheumatoid arthritis

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نوع پذیرش: پوستر | کد مقاله: G-10764

Abstract: Abstract Background: Rheumatoid arthritis (RA) is one of the most common autoimmune diseases often leading to joint damage and physical disability. This study aimed to investigate the relationship of serum levels of IL-17 and anti-CCP factor with disease severity in RA patients. Materials and Methods: Fifty-four patients with RA confirmed by clinical and laboratory criteria were recruited. A 5 ml venous blood sample was taken from every patient, its serum was separated. Based on clinical data and the severity of symptoms, patients were classified into three groups of those with mild, moderate, and severe symptoms. Serum levels of IL-17 and anti-CCP in all samples were measured using ELISA. Results: Analysis of IL-17 serum levels in different groups showed that its amount was higher in the group with mild clinical symptoms than in other groups. Comparison of IL-17 serum levels between mild and moderate disease severity groups showed a statistically significant relationship. There was also a positive linear relationship between anti-CCP and serum IL-17 levels in different groups of the disease and serum IL-17 levels were inversely related to the duration of exposure to the disease. Conclusion: Higher IL-17 serum levels in patients with mild symptom severity confirm that this highly specific marker is involved in the pathogenesis of RA and may be effective in initiating patients' clinical symptoms. Keywords: IL-17, Anti-CCP, Rheumatoid Arthritis

Autophagy potential of nanoparticles in breast cancer: A systematic review

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نوع پذیرش: پوستر | کد مقاله: G-37528

Abstract: Background: Breast cancer is commonly known cancer and the leading cause of cancer death among females. An effective and specific strategy for killing cancer cells is to target the cellular subdivisions associated with the signaling networks. One of these routes is autophagy signaling. Nanocarriers, with enhancing pharmacokinetic and pharmacodynamics qualities, help to make less undesirable side effects of the drug and able to overcome traditional drug delivery roadblocks that currently prevent many types of treatments from becoming viable therapies. Materials and Methods: A systematic review was related to) "Breast Neoplasms" OR "Breast Cancer" OR "Breast Carcinoma" OR "Breast Tumors" OR "Mammary Cancer") AND ("Autophagy" OR autophag*) AND ("Nanoparticle" OR "Nanocrystalline Materials" OR "Nonocarrier" OR "Nanocrystals"). The full texts of all relevant articles, when the studies met the inclusion criteria were carefully examined in detail to confirm their compliance with the defined eligibility criteria, and then the studies assessing autophagy potential of nanoparticles (NPs) in breast cancer were classified. Results: Of the 19 articles included in the analysis, carried out on MCF-7, MDA-MB-231, MDA-MB-231-TXSA, MDA-MB-468, SUM1315, and 4T1. 19 in vitro studies and 1 in vivo studies and applied 5 different autophagy tests: Acridine orange, western blot, Cyto-ID Autophagy Detection kit, confocal microscope, and qPCR. NPs in the basic-format including Ag, Au, Y2O3, Se, ZnO, CuO, Al, Fe, vanadium pentoxide, and liposome were prepared in included articles. Three behavior of NPs related to autophagy seen: Induction, inhibition, and no-action. Conclusion: The present study systematically reviewed laboratory studies that evaluated the three behavior of NPs related to autophagy: induction, inhibition, and no-action. Screened and presented data suggesting that most of the involved NPs (metallic NPs) in this systematic review had ROS mediated pathway with the induction of autophagy. Otherwise impressive percentage of studies (31%) did not examine the NP-related autophagy pathway. Keywords:

Progesterone-induced blocking factor (PIBF) enhances the expression of Foxp3 in peripheral CD4+ T cells

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نوع پذیرش: پوستر | کد مقاله: G-61248

Abstract: Abstract: Background: The fetus is a semi-allogeneic graft makes pregnancy a unique characteristic in the immune system. Women with a normal immune system have the tolerance to the fetus during pregnancy. Immunomodulatory effects of progesterone-induced blocking factor (PIBF) help in persevering the fetus from rejection. In addition to some identified mechanisms of CD25+ performance, this work introduces a new possible aspect of the immunomodulatory function of PIBF. Methods: Peripheral blood mononuclear cells (PBMCs) were stimulated by anti-CD3, anti-CD28, and IL-2 in the presence of varying concentrations of PIBF. Cells were maintained in a culture medium at 37 °C for 5 days. Finally, the percentage of CD4+ CD25+ Foxp3+ T cells was evaluated by Flow cytometry. Results: The experiments showed a marked increase of Foxp3 expression in the PIBF treated CD4+ CD25+ T cells. Conclusion: PIBF induced Foxp3 expression in peripheral CD4+ T cells may provide an alternative for Treg development during normal pregnancy, which may be useful in immunotherapy treatments. Keywords: fork head box P3; Progesterone-induced blocking factor; Regulatory T-cells.



چهاردهمین کنفرانس بین المللی آزمایشگاه و بائین

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CD33 as a Leukocyte-Associated Marker Expressed on Human Spermatozoa

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نوع پذیرش: پوستر | کد مقاله: G-21763

Abstract: Abstract Background: Sialic acid-binding immunoglobulin-type lectins (Siglecs) are commonly present on immune cells and often mediate cell-to-cell interactions and signaling. Studies have shown the presence of Siglecs 1, 2, 5, 6, 10 and 14 on human spermatozoa. To the best of our knowledge, the expression of CD33 on spermatozoa has not yet been studied. Methods: Semen samples were collected from 25 healthy men with normal semen status. CD33 expression on purified spermatozoa was evaluated by flow cytometry methods. Results: The results demonstrate the expression of CD33 on the surface of purified spermatozoa. The mean (\pm SD) of MFI (mean fluorescence intensity) was 12.85 (\pm 1.33) and the mean percentage of spermatozoa that express CD33 was 73.75 (\pm 3.75). Results were obtained showing that spermatozoa express CD33 (or Siglec-3) on their surface. Conclusion: The physiological role of these molecules on spermatozoa remains to be determined. It is recommended that further research should be undertaken regarding the role of Siglecs (such as CD33) on spermatozoa apoptosis. Keywords: Spermatozoa, CD33, Siglecs

Progesterone induces the expression of membrane progesterone receptors (mPRs) on peripheral CD4+ T lymphocyte cells in normal fertile females

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دانشجو
استاد راهنما
همکار

نوع پذیرش: پوستر | کد مقاله: G-79640

Abstract: Introduction: Progesterone (P4) is an immunomodulatory hormone with beneficial effects on the immunologic tolerance of the semi-allogeneic fetus. The effects of P4 on target cells are associated with progesterone receptors (PRs). One of the important immune cell types which is affected by P4 in pregnancy is T cell. The expression of membrane progesterone receptors in women with recurrent spontaneous abortion have decreased on T cell and may be associated with abortion. The purpose of this study was to evaluate the effect of P4 on the expression of membrane progesterone receptor β (mPR β) on CD4+ T cells. Materials and methods: Isolated peripheral blood mononuclear cells (PBMCs) from 20 healthy women were stimulated by anti-CD3 and anti-CD28 monoclonal antibodies (mAb). The cells were (or were not) exposed to P4 at the concentration of 4 μ g/ml in the cell culture (37 °C, 5% CO₂, 90% humidity) for 3 days. Then, the mean fluorescence intensity (MFI) of mPR β was evaluated using polyclonal and monoclonal antibodies on CD4+ T cells. Results: P4 was able to significantly increase mPR β expression on the surface of peripheral CD4+ T cells ($p \leq 0.05$). Conclusion: The present study demonstrated the increasing effect of P4 on the expression of mPR β on CD4+ T cells. P4 can strengthen its own immunomodulatory effect on T cells. So during normal pregnancy increase in P4 concentration is in parallel with an increase in the immunomodulatory effect of P4 on T cells -at least, somewhat- due to an increase in mPR β expression. Keywords:

Comparing of 25-hydroxyvitamin D serum level in patients with psoriasis and healthy individuals

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نوع پذیرش: پوستر | کد مقاله: G-54097

Abstract: Background: Psoriasis is a common skin disease that presents with papulosquamous lesions (scaly papules and plaques) and can have psychological and physical consequences. Due to the anti-inflammatory role of vitamin D, studies have been conducted on the relationship between serum levels of this vitamin and psoriasis. In recent years, conflicting results have been obtained, all of which emphasize the importance of investigating this issue. The aim of this study was to compare the serum level of 25-hydroxyvitamin D in patients with psoriasis and healthy individuals. Materials and methods: This study was a case-control study on patients with psoriasis referred to the dermatology clinic of Vasei Hospital and people referred to Sabzevar Blood Transfusion Center between December 2019 and September 2020 year. Patients with chronic psoriasis (more than 6 months) aged 18 to 65 years were included in the study regardless of the type of psoriasis. In this study, the sample size of 180 people was estimated to be 90 in each case and control group. The data collection method was questionnaire and blood sample. In both groups, the amount of 25-hydroxyvitamin D was evaluated by ELISA laboratory method within 24 hours after sampling. The outcome of this study was 25-hydroxyvitamin D. Chi-square test or Fisher's exact test was used to compare qualitative variables between the study groups. SPSS software version 25 was used for data analysis and the value of P-value 0.05 was considered statistically significant. Results: In this study, data of 177 people were available, of which 88 people were in the case group (49.7%) and 89 people (50.3%) were in the control group. Of these, 78 (44.10%) were male and 99 (55.90%) were female. The mean age in the case group was 36.95 ± 13.30 and in the control group was 21.34 ± 12.60 that there was no statistical difference between the two groups. Conclusion: The findings of this study showed that there is no relationship between the serum level of 25-hydroxyvitamin D and psoriasis. Keywords:

Seroprevalence of anti-SARS-CoV-2 antibodies among Staff of Sabzevar Vasei Hospital

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نوع پذیرش: پوستر | کد مقاله: G-27984

Abstract: Background: In December 2019, an unknown outbreak of pneumonia caused by a new virus named coronavirus disease 2019 (COVID-19) was identified in Wuhan, China. This virus has spread to more than 220 countries and more than 600 million people have been infected with this disease. This study was conducted in order to investigate IgM and IgG antibodies against SARS-CoV-2 among the healthcare workers of Vasei Sabzevar Hospital. Materials and Methods: This cross-sectional and descriptive-analytical study was conducted on 165 health care workers. Between March 1 and March 29, 2019, blood samples were collected from the health care personnel of Vasi Sabzevar Hospital. Enzyme-linked immunosorbent assay (ELISA) was used to detect and measure IgM/IgG antibodies against SARS-CoV-2 using kits manufactured by Pishtaz Teb Company, Tehran, Iran. The data was analyzed by SPSS version 16 software and a significance level of 0.05 was considered. Results: Out of a total of 165 participants, the result of the IgM antibody test against SARS-CoV-2 was positive in 9 people (5.5%) and the anti-SARS-CoV-2 IgG antibody test was positive in 106 people (64.2%). Based on the results, service staff and medical staff had significantly more positive antibody tests than administrative staff ($p=0.03$). The study subjects were in 3 groups, 95 people in the medical staff group, 44 people in the service staff, 26 people in the administrative staff, and according to the place of work, there were 22 people in the 4 parts of the administrative building, 26 people in the ICU, 35 people in the emergency room, 82 people in the ward, They were working and among them 16 people had underlying diseases. Conclusion: The results of the present study showed that the seroprevalence of covid-19 among the healthcare workers of Vasi Sabzevar Hospital was high. It seems that this finding is due to the early exposure to Covid-19 and the lack of awareness and preparation to deal with this epidemic in Iran compared to other countries. Keywords:



چهاردهمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Modeling and Optimization of Hepatitis C Treatment Method Using Differential Evolution Algorithm

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نوع پذیرش: پوستر | کد مقاله: G-83425

Abstract: Background: Hepatitis C disease has not been vaccinated so far, and researchers has attracted the many attention. Materials and Methods: In this study, an effective treatment strategy for hepatitis C disease is presented based on the method of differential evolution algorithm, which aims to achieve the desired dose of the drug. To achieve the right dose of the drug, we need all the variables of the system state, which due to the unavailability of all the variables, the Luenberger nonlinear observer was used to estimate the unmeasured variables. Using Lyapunov stability theory, which proves the stability of the closed-circuit system in the presence of observer dynamics, the performance of the control method has been investigated and modeled Results: The results indicate the appropriateness of the proposed treatment method. The proposed method is optimized using the differential evolution algorithm in MATLAB. Conclusion: The objective function is defined with the aim of minimizing the number of infected cells in the patient's body and taking into account the number of healthy cells in the person. Keywords: Hepatitis C, Differential Evolution Algorithm, Luenberger Nonlinear Observer, Lyapunov Stability Theory Highlights • Provide appropriate treatment for hepatitis C disease with method differential evolution algorithm • Estimation of unmeasured variables using the, Luenberger Nonlinear Observer • Closed-circuit system stability in the presence of observer dynamics using Lyapunov Stability theory. Keywords:



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Development of an mRNA vaccine candidate for breast cancer; An attempt from Islamic Republic of Iran

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نوع پذیرش: پوستر | کد مقاله: G-16954

Abstract: Doing the active immunization in cancer therapy has various advantages, which the most important aspect can be specific immune responses to the tumors without toxicity for normal cells. Here, we are trying to develop a tumor vaccine based of mRNA technology. In fact, after the successful experience of SARS-CoV-2 vaccines that developed by Pfizer and Moderna companies, this platform got more attention for various vaccines development. It is clear that the concurrent expression of several cancer antigens through an mRNA structure is possible. In addition, this type of vaccine is not limited to MHC and also the low cost, fast and easily production of vaccines in this platform, encouraged us to concentrate on the development of an mRNA vaccine against breast cancer encoding angiogenic antigens. Herein VEGFR2 and c-MET as angiogenic elements were selected and immunoinformatic analysis was performed for cytotoxic T lymphocyte activation. We also selected a few T helper epitopes as a helper agent for CTL response, given the role of Th in helping CTL. Analyzes were performed with UniProt, IEDB, NCBI and RCSB databases, BioEdit, MEGA and Chimera tools. Finally, we have selected some epitopes of these antigens and the project is ongoing to develop an mRNA vaccine.

Keywords:

Assessing the immunologic properties of a novel immunoinformatic based designed multiepitope DNA vaccine against human SARS coronavirus-2

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نوع پذیرش: پوستر | کد مقاله: G-53709

Abstract: Background: The Covid-19 as a respiratory syndrome disease is responsible for significant mortality and morbidity in human population in the current worldwide pandemic. The development of multiepitope DNA vaccines by using the reverse vaccinology (RV) approach could be an innovative strategy for vaccine development. Materials and Methods: A multiepitope DNA vaccine (fuspMA) previously was designed according to the usage of nucleocapsid epitopes, membrane glycoprotein, and ORF8 proteins of SARS-CoV-2. In the next step, the 3D structure of fuspMA protein is predicted using the I-TASSER server. Interactions of fuspMA of SARS-CoV-2 with human MHC I, MHC II, TLR3, and TLR4 were investigated by protein-protein docking procedure. Molecular docking study was performed using the ClusPro server in antibody-mode to predict and measurement the affinity of fuspMA of SARS-CoV-2 structure after 50 ns MD simulation as a ligand to TLR3, TLR4, MHCI and MHCII as receptors. Results: According to the obtained results, the model with the clash score of 30.5 and RMSD of 0.505 Å° was the most favorable one. During simulation time, the average of RMSD for the Cα of fuspMA was just 0.93951 nm in comparison with the minimized generated structure of fuspMA of SARS-CoV-2. Docking scores in antibody mode included the center lowest energy of -305.8, -313.9, -452.6, and -381.2 for human MHC I, MHC II, TLR 3, and TLR 4 as respectively. Conclusion: Our docking study confirmed the proper interaction of validate structure of fusMA of SARS-CoV-2 with HLA class I histocompatibility antigen/beta-2-microglobulin that could result in a strong and effective cell-mediated immunity. Keywords: DNA vaccine, immunoinformatic, COVID-19, SARS-CoV-2, Major histocompatibility complexes.

Role of zinc, selenium, vitamin D and vitamin C in boosting respiratory system: A metaanalysis approach

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نوع پذیرش: پوستر | کد مقاله: G-02518

Abstract: Back ground: Respiratory tract infections consist of many diseases such as colds, pharyngitis, tonsillitis, influenza and respiratory diseases. Therefore, this meta-analysis study was performed to assay the effect of zinc, selenium, vitamin D, vitamin C on respiratory tract infections. Methods: In this systematic review of data on the effects of zinc, selenium, vitamin D and vitamin C on respiratory tract infections in the last 20 years in the world (2010- 2001) with a review of 30 studies (5351 cases) including English and Persian articles, Reputable domestic and foreign sites were performed. Data were analyzed using meta-analysis: The odds ratio of respiratory tract infections in vitamin D users was estimated to be 0.797 (confidence interval 95%, 0.808-0.786). The Rate of odds of respiratory infections in consumers of vitamin C, 0.0496 (confidence interval 95%, 0.55-1.441) was estimated. The odds ratio of respiratory infections in zinc users was estimated to be 0.437 (confidence interval 95, 0.51-0.366). The odds ratio of respiratory tract infections in selenium users was estimated to be 0.624 (confidence interval 95, 0.696, 0.545). Results: Respiratory infections are seen in consumers of vitamin D, vitamin C, zinc, selenium. Proper use of vitamin D, vitamin C, zinc, and selenium is essential in addition to monitoring the epidemiology of regional respiratory infections. CONCLUSION: Ass results of the previous study and the present study, it seems, results of the studies as well as statistical indicators, a heterogeneity and fluctuation in the odds ratio of respiratory infections in consumers of vitamin D, vitamin C, Zinc and selenium are observed. Keywords: Vitamin D, vitamin C, zinc, selenium, respiratory infections.



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Designing a novel multiepitope DNA vaccine against human SARS coronavirus-2 based on immunoinformatics approaches

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نوع پذیرش: پوستر | کد مقاله: G-87591

Abstract: Background: Human SARS coronavirus 2 (SARS-CoV-2) causes the current worldwide COVID-19 pandemic. Vaccination may be the main approach to prevent the contagion of an infection and subsequent challenges. Attenuated-infectious agents to the novel DNA vaccines are between various procedures have been developed for vaccine design and production. Here, we have designed a novel multiepitope DNA vaccine against SARS-CoV-2 using reverse vaccinology and DNA vaccine methods. Using these strategies led to reduce the time and costs of vaccine development and also increase the immune protective characteristics of the vaccine. Materials and Methods: Epitopes of nucleocapsid, membrane glycoprotein, and ORF8 proteins of SARS-CoV-2 chose as targets for designing a multiepitope vaccine. Furthermore, the Kozak and tissue plasminogen activator sequences were added into the epitope sequences for proper protein expression and secretion as respectively. In addition, interleukin-2 and beta-defensin 1 preproprotein sequences were incorporated to vaccine as an adjuvant. Modeling and refinement of fused protein composed of SARS-CoV-2 multiepitope antigens (fuspMA) have performed based on homology modeling of orthologous peptides. Results: Three linear B-cell epitopes and 10 T-cell related epitopes were selected and mentioned as a vaccine candidate. Our obtained results confirmed the selected ones have shown appropriate antigenic features and lack of allergenic and toxic properties. Conclusion: It seems the designed multiepitope DNA vaccine have great chance to be introduced as an efficacious vaccine against COVID-19 after more in vivo evaluations. Keywords:



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The role of tumor-isolated exosomes on suppression of immune reactions and cancer progression: A systematic review

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نوع پذیرش: پوستر | کد مقاله: G-51967

Abstract: Background: Exosomes are Extracellular Cells (EVs) released by various cell types and involved in cell to cell communication. In cancer diseases, through the horizontal transfer of various molecules such as proteins and miRNAs, exosomes emerge as local and systemic cells to cell mediators of oncogenic information and play an important role in the progression of cancer. Materials and Methods: Databases of Scopus, Science Direct, PubMed, EMBASE, ISI web of science and Cochrane for English resources were written from 66 articles and searched up to December 2018. Results: The biological distribution of cancer cell-derived exosomes in tumor tissue is an important factor to detect those roles in tumor increase; on the other hand, a limited number of studies have interrupted the biodistribution of exosomes in tumor tissues. while exosomes function as cancer biomarkers and support in cancer treatment, we have a long way to improve the anti-tumor treatment of exosomes and develop exosome-based cancer diagnostic and therapeutic strategies. Conclusion: This review describes the current science and significance in cancer pathogenesis and exosomes relative to cancer treatment resistance. Key words: exosome- cancer pathogenesis- tumor- metastasis- immune system

Role of PDL-1 and PD-1 in Immune Reactions and expression Blood Cancer cells: A Systematic Review

غزال پوربیرق, ¹ فائزه مهدی زاده, ¹ مهرداد پاشازاده ©²

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نوع پذیرش: پوستر | کد مقاله: G-94230

Abstract: Background: One of the most important immune pathways is the programmed cell death 1 (PD1) protein. PD1 is expressed on the surface of T-cells and controls immune reactions. CD274, B7-H1, or PD-L1 (Programmed death-ligand1) are expressed by cells of the myeloid lineage, including macrophages and dendritic cells and effector CD8+ T cells and Tumor cells and tumor-associated suppressor cells. Methods: Databases of Scopus, Sciencedirect, PubMed, EMBASE, ISI web of science, and Cochrane for English resources were written from 70 articles and searched up to October 2022. Results: expression of PDL-1 molecule in cancer has been linked to worse prognosis and resistance to anti-cancer therapies in several malignancies. In this review, we update on the expression of CD274 molecule in malignant tumor cells and hematological. In this review, we update on the expression of CD274 molecule in malignant tumor cells and hematological and describe these molecules which inhibit the immune response to cancer cells. Conclusion: we describe the current science and significance in immunotherapy strategies that can be further developed to target this molecule. Key words: Immunotherapy, Programmed death-1: programmed death-ligand 1 blockade, B7-H1 (programmed death-ligand 1), T cells, tumor

The role of the immune system in schizophrenia: Focus on the function of microglia

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نوع پذیرش: پوستر | کد مقاله: G-98123

Abstract: Background: Schizophrenia (SCZ) is a severe psychological disorder. The exact cause of schizophrenia has not been determined yet, but malfunctions in the immune system has been seen. Microglia cells are one of the most important members of the innate immune system in the central nervous system (CNS) that includes 10 to 20% of the CNS cells. These cells are involved in maintaining homeostasis in the CNS, removing apoptotic cells through phagocytic activity, helping oligodendrocyte cells for myelination; they also play a part in the development of the nervous system, and synaptic pruning. So, microglia can play both protective and pathological roles. The aim of the current study is to describe the function of microglia cells in the progression of schizophrenia. Materials and Methods: In this review, data were searched via keywords including immune system, schizophrenia, microglia and pathophysiology in PubMed, ISI web of knowledge, Scopus, Google Scholar, ProQuest, Oxford and Ovid databases from 2000 to 2022. Results: In response to changes in the environment and danger signals (including injury, infection, stress, disease, and lack of light) microglial cells can be activated by altering their morphology and function because this condition led to compromise the CNS homeostasis. In SCZ patients. There are malfunctions in the immune system such as enhanced microglia density and activity. Reactive microglia can have phagocytic activity or act as antigen presenting cells to lymphocytes. Microglia activated by increased expression of TLR, phagocytic receptors (CR3, CR4), scavenger receptors (CD36, CD91), release of cytokines and complement proteins, and production of active oxygen and nitrogen mediators (ROS, RNS) and phagocytic NADPH oxidase, causes neuronal destruction, increased synaptic pruning and white matter abnormalities and eventually leads to SCZ. Conclusion: In SCZ, activation of microglia cells, cytokines released during inflammation (IL-1 β and TNF α) can lead to increased brain endothelial permeability and blood-brain barrier dysfunction. Dysfunction of the blood-brain barrier causes cytokines, antibodies and immune cells to be transferred from the blood to the brain and can increase brain inflammation. Therefore, the dysfunction of the blood-brain barrier and the disruption of microglia cells can play an important role in pathophysiology SCZ. Keywords: Immune system, Schizophrenia, Microglia, Pathophysiology



چهاردهمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



The effect of COVID-19 on B lymphocyte and BAFF cytokine: A cross-sectional study

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نوع پذیرش: پوستر | کد مقاله: G-53760

Abstract: Background: As Coronavirus disease 19 (COVID-19) impacts the human immune system, we aimed to investigate whether changes in BAFF ligand and the supply of BAFFR receptor on the surface of peripheral blood monocular cells (PBMC) affect the incidence and severity of COVID-19. Materials and Methods: This cross-sectional study was included 120 participations (60 patients with COVID-19 and 60 healthy controls). Their information was collected over 14 days (the first, seventh, and fourteen days). Separating of PBMCs from peripheral blood of patients done by using ficoll and concentration gradient and flow cytometric analysis done by the protocol of Biolegend.Co company. Blood samples were taken to measuring BAFF plasma concentration by ELISA assay. The Real-Time testing was conducted over extracted DNA from PBMCs. Results: In the present study, the average of the participations was 43.15 ± 13.24 years. Regarding the severity of COVID-19, 8.4% were severe, 33.3% were moderate, and 58.3% were mild. The findings of flow cytometric analysis demonstrated that the number of BCD19 cells, and also the average number of B cells with BAFFR receptors, in the test group on the seventh day is higher than on the first and fourteen days, as well as greater than the average number of BCD19 cells and BAFF receptors in the control group. The ELISA assay showed on the seventh day the BAFF ligand had increased dramatically from the beginning of the disease, and were considerably higher than the control group. In the Real-Time testing, there was a significant relationship between the BAFF and BAFFR gene expression and also highly increased in the case group than the control group. Conclusion: Our findings revealed COVID-19 is linked to elevated the level of BAFF ligand and BAFFR receptor. It is possible the activation of B lymphocytes and regulation of the immune system are both influenced by COVID-19 via the BAFF axis. Keywords: BAFF Receptor, BAFF Ligand, COVID-19

Investigating the immunomodulatory effects of mesenchymal stem cells to treatment of infectious diseases

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نوع پذیرش: پوستر | کد مقاله: G-54081

Abstract: Mesenchymal stem cells (MSCs) are non-hematopoietic stem cells with features such as self-renew and multilineage differentiation. Modulation of immune responses is one of the characteristics of these cells. Due to the effectiveness of these cells to migrate towards the site of infections, production soluble factors, cell-cell communication mechanisms and releasing extracellular vesicles (EVs) containing immunomodulatory molecules and cytokines are hypothesized to modulate the immune system. The characteristics of innate and acquired immune system regulation are the therapeutic applications of these cells, which include anti-inflammatory, anti-apoptotic, chemotactic and tissue repair stimulator in response to injury. The mechanism of action of MSCs is by using the production of growth factor, enzymes, chemokines and the effect of these factors on the response to the site of damage and the stimulation of progenitor cells for tissue regeneration; such as: inhibiting infiltration of neutrophils, induce a “tolerogenic” phenotype in monocytes, effect on maturation of dendritic cells, stimulation of anti-inflammatory phenotype in macrophages, secretion of programmed death-ligand 1 (PD-L1) and PD-L2 in T cells, effect on proliferation, differentiation and chemotactic behavior of B cells for immune-mediated disorders, inhibiting proliferation and cytotoxicity of natural killer (NK) cells and regulatory T cells which cause the migration of these cells to the site of infection. MSCs also inhibit NK proliferation through factors such as indoleamine 2,3-dioxygenase (IDO) and prostaglandin E2(PGE2). In recent studies, in addition to examining the effects of these cells on non-infectious complications, the use of mesenchymal stem cells as one of the immunotherapy methods for infectious diseases has been considered. Recent studies have shown new ideas of treatment approaches against infectious agents such as bacteria, viruses, fungal agents and parasites. population of these cells has the ability to produce the cytokine IL-17, which unlike conventional mesenchymal stem cells, not only does not suppress the immune system but also acts as a stimulant inhibiting the growth of fungi such as *Candida albicans*. But the source of isolation, administration method, dosage and duration of treatment can affect the regenerative function caused by MSCs. key words: MSCs, immunomodulatory effects, infectious diseases

Effects of azithromycin (AZT) and extracellular vesicles derived from mesenchymal stem cells (MSC-EVs) injection on biochemical parameters in a mouse model of sepsis

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نوع پذیرش: پوستر | کد مقاله: G-39258

Abstract: Effects of azithromycin (AZT) and extracellular vesicles derived from mesenchymal stem cells (MSC-EVs) injection on biochemical parameters in a mouse model of sepsis Fatemeh Ahangari¹, Zahra Mirsanei¹, Sara Soufi², Sara Soudi³, Seyed Mahmoud Hashemi¹* 1. Department of Immunology, School of Medicine, Shahid Beheshti University of Medical Sciences (SBMU) 2. Department of Animal Biology, Faculty of Natural Sciences, Tabriz University 3. Department of Immunology, School of Medicine, Tarbiat Modarres University (TMU) *Corresponding Author: smmhashemi@sbmu.ac.ir, Department of Immunology, School of Medicine, Koodakyar Dead End, Daneshjou Blvd, Velenjak, Tehran, Iran. Phone number: +989353717433 Background: Recent studies showed that both azithromycin (AZT) and extracellular vesicles derived from mesenchymal stem cells (MSC-EVs) can protect vital organs from being damaged in sepsis mouse models. This study evaluated the effects of combinational therapy of AZT and MSC-EVs on biochemical parameters, including alanine transaminase (ALT), aspartate aminotransferase (AST), blood urea nitrogen (BUN), and creatinine. An increase in the serum level of these biochemical factors can represent tissue damage to different organs. Materials and Methods: C57BL/6 female mice were randomly divided into the sham group, the cecal ligation and puncture (CLP) group, the AZT group, the MSC-EVs group, and the AZT+MSC-EVs group. The CLP group underwent abdominal surgery and received sterile saline via intravenous injection (i.v.), the AZT group received 100 mg/kg AZT via intraperitoneal injection (i.p.), the MSC-EVs group received 200 mg/kg of MSC-EVs via i.v. injection, and the AZT+MSC-EVs group received i.p. injection of 100 mg/kg of AZT and a tail vein injection of 200 mg/kg of MSC-EVs. After 24 hours mice were euthanized by exsanguination under anesthesia. The serum was separated from blood clot and biochemical parameters, including ALT, AST, BUN, and creatinine were measured. Results: AST and creatinine levels of serum reduced significantly (P<0.05) in the AZT+MSC-EVs group in comparison with the CLP group. However, ALT and BUN levels in the serum of mice receiving combinational therapy of AZT+MSC-EVs did not decrease significantly. None of the treatment groups could reduce ALT levels significantly. In the AZT+MSC-EVs group the level of BUN was not significantly reduced compared to the CLP group. However, each single treatment group, including the AZT group and the MSC-EVs group could decrease the BUN levels in comparison with the CLP group. Conclusion: The co-administration of AZT and MSC-EVs with the dose of 100 mg/kg and 200 mg/kg, respectively, could reduce some biochemical levels in the serum, including AST and creatinine. However, due to the lack of reduction in ALT and BUN levels in the AZT+MSC-EVs group, tissue histopathological examinations are required to further investigate the intensity of damage to the vital organs and make a final decision about the protective effects of this combinational in the CLP model of sepsis. Keywords: Extracellular Vesicles, Exosomes, Mesenchymal stem cells, Sepsis

Effects of rituximab treatment on interleukin-21 serum levels in patients being treated for Multiple sclerosis compared to newly diagnosed patients and healthy controls

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نوع پذیرش: پوستر | کد مقاله: G-90253

Abstract: Background: Multiple sclerosis (MS), as a demyelinating and neurodegenerative disease, is identified by auto-inflammatory immune responses in which both adaptive and innate immune systems are involved in disease pathogenesis. Among major pro-inflammatory CD4 T-cells associated with MS, T follicular helper cells (Tfh), such as Th17 CD4 T-cells, are considered a key subset, that mostly secrete interleukin 21 (IL-21) into the circulation. To control the responses caused by the aforementioned T cells, as well as B cells, a wide variety of medications have already been introduced. In this context, Rituximab (RTX) is a monoclonal antibody that targets B cells through the process of MS therapy; however, the effects of RTX on Tfh cells are not so clear in MS patients. Thus, in the current study, we evaluated the serum concentrations of IL-21, as the major cytokine originated from Tfh cells, in RTX-treated MS patients versus newly diagnosed patients and healthy controls. Materials and Methods: Two groups of MS patients from MS clinic of Kashani Hospital, Isfahan, Iran, were recruited to this study: One group (n=30) was clinically defined as relapsing-remitting MS (RRMS) according to the McDonald criteria who treated with RTX for at least 6 months and the other group (n=30) was newly diagnosed patients, who did not receive any immunosuppressive drugs. Moreover, 30 age-and-sex-matched healthy controls were enrolled in this study. Blood specimens were collected from newly diagnosed MS patients that they had not received any medication, and MS patients treated with RTX, as well as healthy subjects. Serum samples were obtained by centrifugation, and then transferred into new tubes. Eventually, serum concentrations of IL-21, produced by Tfh cells, were measured by an ELISA kit (BD Bioscience, USA), according to the manufacturer's instructions. Statistical differences between control and experimental groups were analyzed by one-way analysis of variance (ANOVA) and multivariate analysis of variance (MANOVA) with post-Tukey's multiple comparisons tests, using the GraphPad Prism Software version 6.0 (San Diego, CA). Results: Our findings revealed a decrease in the serum concentrations of IL-21 in RTX-treated MS patients compared to newly detected cases and healthy controls. Based upon the statistical analyses, the above-stated decline was statistically significant (p-value less than 0.001). Notwithstanding, no significant difference was found in IL-21 levels between newly diagnosed cases and healthy controls. Conclusion: The decrease in IL-21 concentration literally reflects the decrease in the number of Tfh cells. Hence, it can be concluded that RTX has the ability of reducing Tfh cells, and subsequently Tfh cells-related responses in MS patients. Additionally, the interaction between B cells



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and Tfh cells could result in the mitigation of cTfh cells population and function following the RTX treatment. Further Flow cytometric analyses confirmed the corresponding decrease. Keywords: Multiple sclerosis, Rituximab, T follicular helper cells, Interleukin-21.

آدرس دبیرخانه:

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Investigating the effect of Pycnogenol supplementation (French maritime pine bark extract) on tumor growth rate and immunological factors in a murine model of colon cancer

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نوع پذیرش: پوستر | کد مقاله: G-05493

Abstract: Background: During the past decades, anti-oxidants attracted much attention due to their anti-tumor properties. Several studies have reported the antioxidant activity of the Pycnogenol extracted from French maritime pine in the past decades, focusing on the polyphenols. However, additional surveys are needed to clarify the underlying mechanisms behind the anti-tumor activity of Pycnogenol. Methods: Two groups of C26 tumor-inoculated BALB/c mice received Pycnogenol (100 mg/kg/day) and tap water was determined. On day 30 from receiving treatment 4 mice from each group were sacrificed to evaluate T cell subsets by flow cytometry and cytokine gene expression by qRT-PCR. Results: Flow cytometry analysis showed that subsets of the CD8+ T cell population were significantly increased in the Pycnogenol-receiving group (P 0.05). The population of regulatory T cells and CD4+ T helper 1 and 2 cells were not altered. The expression of IFN- γ , perforin, and granzymes genes was statistically enhanced in the intervention group. However, the levels of IL-2, IL-4, IL-13, and TGF- β were not changed. Regarding the effects of Pycnogenol on tumor growth, there was no statistically significant difference between the two groups. Conclusion: The results showed that in addition to its anti-oxidant properties, the use of Pycnogenol can also strengthen T lymphocyte activation. Keywords: Pycnogenol, Cancer, Immune-responses, Anti-oxidants

Prevalence of specific antibodies against SARS-COV-2 in the Serum of Newborns from Pregnant Mothers with a History of COVID_19 Infection

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نوع پذیرش: پوستر | کد مقاله: G-26513

Abstract: Background: It should be noted that COVID_19 changes immune responses in relation to mother and fetus and can affect the well-being of mothers and babies. The specific IgG antibody test for COVID_19 is a method to study the immunity of babies born from mothers infected with SARS_cov-2. It needs a deeper analysis. The purpose of this study is to investigate the safety of newborns born to mothers with a history of COVID-19 by measuring the serum level of specific antibodies to COVID_19 in hospitals in Khorram Abad city. Materials and Methods: The current research is an analytical cross-sectional study. 45 pregnant women who tested positive for the PCR test of Covid-19 during pregnancy and were hospitalized for childbirth were selected as available samples after explaining the research design and obtaining consent. From the mentioned qualified mothers, 2 cc of blood from pregnant women hospitalized for delivery and babies born from them in the first 24 hours of birth were taken, their serum was separated with the help of a centrifuge and collected with the help of an ELISA kit to measure specific IgM and IgG antibodies. Corona, the concentration of antibodies was measured in two groups of mothers and their newborn babies. Descriptive and analytical statistics were used to analyze the data. Results: The number of mothers whose serum was examined for antibody levels was 45, whose average age is 28.84 ± 6.12 , and the youngest mother was 14 years old and the oldest mother was 43 years old, and the largest population of mothers were in the age group of 30-34 years. . In this study, 16 mothers in the first trimester, 10 mothers in the second trimester, and 9 mothers in the third trimester were infected with Covid, in 31 cases it was mild and in 14 cases it was severe. Of these mothers, 20 were girls and 25 were boys, and 7 out of 45 babies were diagnosed with Covid. Conclusion: According to the analysis of the results, a significant correlation was found between the amount in the blood of mothers and the concentration of covid antibody in the blood of babies born from them, but there is a correlation between the concentration of corona antibody in the baby and the time the mother contracted the covid virus during pregnancy and Also, the gender of the baby and the final hospitalization of the baby were not seen. Keywords: COVID-19, newborn, Antibody



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Autoantibodies against central nervous system antigens in patients with schizophrenia

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نوع پذیرش: پوستر | کد مقاله: G-31026

Abstract: Background: Schizophrenia is a disease of the nervous system and immune system disorders can affect its pathogenesis. Activation of microglia, disruption of the blood-brain barrier (BBB) due to inflammation, activation of autoreactive B cells, and consequently the production of autoantibodies against system antigens are among the immune processes involved in neurological diseases. This study aimed to measure the frequency of autoantibody positivity against several nervous system antigens in patients with schizophrenia. Material and Methods: This study was conducted on 40 patients with schizophrenia and 40 healthy individuals in the control group. The frequency of autoantibodies against Hu, Ri, Yo, Tr, Amphiphysin, and SOX1 antigens was measured by the indirect immunofluorescence method. Results: The frequency of autoantibodies against Ri antigens in patients with schizophrenia was significantly higher than in the control group. Autoantibodies were positive in 6 patients for Ri antigen. Autoantibodies were also positive in 1 patient for Hu. Negative results were reported for other antigens. Conclusion: Our findings suggest that autoantibodies against RI antigens may be a reflection of immune system dysregulation in patients with schizophrenia. Keywords: Schizophrenia; Microglia; Autoantibodies

Protective effects of Cinnamic acid against hyperglycemia induced oxidative stress and inflammation in HepG2 cells

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نوع پذیرش: پوستر | کد مقاله: G-49681

Abstract: Background: Cinnamic acid, a naturally occurring aromatic fatty acid, is considered a plant hormone, regulating cell growth and differentiation. This compound is reported to have multiple biological activities including antioxidant, anti-inflammatory, hepatoprotective, antityrosinase, antidiabetic activities, anti-malarial and anti-cancer properties. The present study was designed to investigate the effects of cinnamic acid as a therapeutic potential on reducing oxidative stress, expression of inflammatory factors, and inhibition of DPP-4 in HepG2 cell line in the presence of high glucose concentration. Methods: In the first stage, the viability of HepG2 cells at different concentrations of glucose and CA was assessed by MTT assay. Oxidative stress markers (GSH, and MDA) were measured spectrophotometrically. After RNA extraction, the effect of different concentrations of CA on the expression of DPP4 and inflammatory factors (NF- κ B) in HepG2 cells was assessed using real-time PCR. Results: In HepG2 cells, CA increased catalase and glutathione peroxidase activity and GSH production in a dose-dependent manner in the presence of high glucose concentrations, with the greatest effect seen at a concentration of 75 mg/ml. CA also reduced the amount of MDA in high-glucose HepG2 cells. Furthermore, CA decreased the expression of DPP4, NF- κ B genes in HepG2 cells in the presence of high glucose levels. Conclusion: The results of our study indicated that CA reduced hyperglycemia-induced complications in HepG2 cells by decreasing inflammatory gene expression NF- κ B and inhibiting the expression of DPP4, and limiting oxidative stress. Keywords:



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Correlation between the levels of Immunologic Tests in SLE Patients

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نوع پذیرش: پوستر | کد مقاله: G-04359

Abstract: Correlation between the levels of Immunologic Tests in SLE Patients Mahsa Khatibi¹, Amir Gholamzad¹, Ghazaleh Daryoushi¹, Hoda Haghani¹, Mehrdad Gholamzad²* 1. Department of Laboratory Medicine, Faculty of Paramedical Sciences, Tehran Medical Sciences, Islamic Azad University, Tehran, Iran 2. Department of Microbiology and Immunology, Faculty of Medicine, Tehran Medical Sciences, Islamic Azad University, Tehran, Iran, Mgholamzad@iautmu.ac.ir *Corresponding Author: Department of Microbiology and Immunology, Faculty of Medicine, Tehran Medical Sciences, Islamic Azad University, Tehran, Iran, Mgholamzad@iautmu.ac.ir Background: Nowadays, laboratory diagnostic tests are used as a main key factor for the final diagnosis in systemic autoimmune diseases. It is very important to measurement should be done with automatic immunoassay analyzers, and therefore its quality control is also very important. Also, the relationship between these tests is important for the final diagnosis of the disease. Antinuclear antibody), anti-native DNA levels, serum hemolytic complement, and complement components C3 and C4 were determined in this study. Materials and Methods: Antinuclear antibody, anti-native DNA levels, serum hemolytic complement, and complement components C3 and C4 were measured in 550 serum samples taken from 311 patients with active and 239 with inactive systemic lupus erythematosus. Results: Increased anti-DNA levels were shown in 82% of the samples from patients with SLE and in 57.8% of those from inactive SLE. Decreased levels of CH50, and C3, C4 was seen in 37, 50, and 80% of the samples taken from active and in 22, 29, and 67% of those from inactive, diseases, respectively. ANA test was positive in 94.7% of the patients with SLE and 87.9% of those with inactive disease. Significant differences were found between the two patient groups for all tests. Conclusion: Relationship between anti-DNA antibodies and Complement levels, as well as between serum hemolytic was also demonstrated. Six subgroups for expressing the positivity of five parameters, 32 patterns of positive tests were found and their possible applications were suggested. In combining these tests and using appropriate patterns, their determination may be helpful not only for the diagnosis but also for the assessment of disease activity. Keywords: SLE, Immunoassay, Autoimmune Diseases

Effect evaluation of different serums on the growth pattern in a murine macrophage cell line by the MTT method

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نوع پذیرش: پوستر | کد مقاله: G-67802

Abstract: Background: Animal cell culture is used to achieve a long-term continuous culture of normal cells exhibiting differentiated properties of their tissue of origin. Beyond a basal nutrient mixture of salts, sugars, amino acids, and vitamins, cells in vitro require the proliferation of a supplement of poorly defined biological fluids or extracts. These include embryo extract, spinal or amniotic fluid, lymph, milk or colostrum, and plasma or serum from various sources. Because of availability and ease of storage, the most commonly used supplement is serum. Since these supplements will support the survival and growth of cells in vitro, we evaluated the possible effect of the serum of different species from apparently healthy animals, including chicken, horse, goat, sheep, dog, human, and rabbit serum, compared to Fetal Bovine Serum (FBS) in J774.A1 cell line viability. Materials and Methods: J774.A1 murine “macrophage-like” cells, obtained from the Pasteur Institute of Iran, were cultured in RPMI 1640 medium containing phenol red, L-Glutamine, Penicillin/Streptomycin, and 10% FBS. Cells were removed from the culture flask via gentle scraping and then re-suspended in a complete medium before centrifugation at 300 g for 4 min. Cell viability was determined using Trypan blue (0.4% solution) exclusion. Cells were adjusted to a suspension of 2.5×10^5 cells ml⁻¹ in a complete medium and used for all subsequent experiments. Cell viability was determined via the ability of the J774.A1 cells to reduce the tetrazolium salt 3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide (MTT). The animal sera were received from researchers working on these animals' clinical samples (including whole blood) and examined in five concentrations on the murine cell line. Results: Compared to FBS control, the results indicated that culture media enriched with the filtered chicken, horse, and rabbit sera could support the growth of the J774.A1 cell line and can be used for their cultivation. And culture media enriched with the filtered dog, goat, sheep, and human sera cannot support the growth of the J774.A1 cell line. Conclusion: According to our findings, utilizing animal sera like horses, rabbits, and chickens could be a cost-efficient, standard and available option in some cases during the experiment process. We need more tests to examine if adding some supplements, growth factors, or hormones increases enrichment. Keywords: Fetal Bovine Serum, Culture media, Cell lines, Cell Viability

In silico exploration of Neohesperidin inhibitory mechanism on TGF- β pathway and improving its bioavailability

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نوع پذیرش: پوستر | کد مقاله: G-13429

Abstract: Background: Neohesperidin, a natural compound obtained from orange, which is widely used as an industrial sweetener, has proven anti-cancer and anti-inflammatory properties but a low bioavailability and unknown functional mechanism. Some papers have shown that Neohesperidin can prevent the phosphorylation and oligomerization of SMAD proteins in the TGF β pathway, however, the detailed molecular mechanism of the process is largely unexplored. In this research, we investigated the mechanism of the effect of Neohesperidin on the intracellular domain kinase of TGF β membrane receptor type 2 and the inhibitory effect of this molecule on SMAD protein phosphorylation, Also, using peptide-drug conjugate technology, we designed a peptide structure to Increase the bioavailability of this compound for the intracellular target. Materials and Methods: The SMAD protein structure and, TGF β type 2 intra-cellular kinase domain structure were obtained from the PDB database. The 3D conformer of Neohesperidin was also achieved from the PubChem database. The interactions between the SMAD protein and TGF β type 2 kinase domain were investigated through the ClusPro docking web server, and the interaction between Neohesperidin and this kinase domain was explored through Molegro molecular docking software. After confirming the binding of Neohesperidin to the active site of the second TGF β kinase and intending to increase the bioavailability of this compound, we designed a peptide-drug conjugate structure using HyperChem software. Results: As expected, the results of docking simulation analysis between SMAD and TGF β type 2 kinase domain, show that the SMAD carboxyl terminal is completely placed in the kinase domain active site. The analysis of the interaction of SIS3 and Neohesperidin with the kinase domain also shows that both of these molecules occupy the kinase active site with relatively comparable binding site and energy. The result from OPM server also suggest that designed Neohesperidin-peptide conjugate have a membrane binding capability. Conclusion: The results of this study demonstrate that the Neohesperidin molecule, as a natural compound, can bind to the TGF β type 2 receptor with the same energy and site as its chemical counterpart, SIS3, to block the kinase functional region and prevent the phosphorylation of the SMAD carboxyl-terminal. On the other hand, the peptide-drug conjugate stability and membrane binding capability show this structure's probable potential to improve the compound bioavailability. These results provide the basis for the design of new pharmaceutical compounds based on Neohesperidin. It also suggests an approach for the optimal transfer of this compound to cells. Keywords: cancer, natural compound, peptide

The progress and future prospect of Therapeutic vaccines for colorectal cancer

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نوع پذیرش: پوستر | کد مقاله: G-85139

Abstract: Background: Cancer vaccines are usually derived from the patient's tumor cells or the antigens found on their surface, which may help the immune system to identify and kill these malignant cells. Current focus of many researches is designing vaccines with the hope of triggering the immune system to attack cancer cells in a more effective, reliable and safe manner. Methods: Although colorectal cancer (CRC) is recognized as the third leading cause of death by cancer, but significant advances in therapy strategies have been made in recent years, including cancer vaccine. In this review, we present various vaccine platforms that have been used in the border battle against CRC, some of which have been approved for clinical use and some are in late-stage clinical trials.. Results: Until now there is approximately 1940 clinical trials of cancer vaccines on patients with different cancer types, and many more trials are in the planning stages, which makes it the most important period of therapeutic cancer vaccines studies in the history of the immunotherapy. In cancer vaccines clinical trials, there are several considerations that must be taken into account including engineering of antigen-presenting cells, potential toxicity of antigenic areas, pharmacokinetics and pharmacodynamics of vaccines, and monitoring of the patients' immune response. Conclusion: The need to overcome immunosuppression mechanisms/immune tolerance is a critical step for the success of introducing therapeutic vaccines into the widely used drugs on market. In this way, better understanding of neoantigens, tumor immune surveillance escape mechanisms and host-tumor interactions are required to develop more effective and safe cancer vaccines. Keywords: Colorectal cancer, Immunotherapy, Cancer vaccine, mRNA vaccine, Cellular vaccines

Procalcitonin as a diagnostic biomarker of sepsis in neonates

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نوع پذیرش: پوستر | کد مقاله: G-80279

Abstract: Background: Neonatal sepsis is a dynamic process where the precious evaluation of clinical signs along with appropriately biomarkers guides the diagnosis of sepsis. Blood culture as a standard method for diagnosis of neonatal sepsis is a time consuming method, so other biochemical markers such as Procalcitonin (PCT) as part of the complex pro-inflammatory response of the innate immune system should be considered to improve early diagnosis. This study aimed to determine the diagnostic value of PCT in sepsis. Materials and Methods: In this cross-sectional study, 56 hospitalized neonates in the NICU and neonatal ward divided into two groups including proven and suspected sepsis. CRP, PCT levels, blood culture and Cell Blood Count were analyzed. The differences between the factors were statistically analyzed, and the receiver operating characteristic curve (ROC curve) was plotted to obtain the optimal cut-off values of PCT to diagnose sepsis sensitivity and specificity. Results: We collected 56 neonates with proven (40.74% females & 59.26% males) and suspected sepsis (44.83% females & 55.17% males) with a mean age of 11.74 ± 7.35 and 13.96 ± 6.29 days, respectively. PCT values were significantly different in the two groups ($P 0.001$). Based on our ROC curve of PCT; sensitivity, specificity, predictive values of PCT were determined 70.4%, 72.4% and % 70, respectively. Conclusion: Procalcitonin have a good reference value for diagnosis of sepsis in neonates. To improve its accuracy in practice, further studies are required to confirm these findings. Keywords: Procalcitonin, Sepsis, Neonate



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Diagnostic Accuracy of Salivary Biomarkers including Lactate Dehydrogenase and Hemoglobin A1c for Screening Chronic Periodontitis

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نوع پذیرش: پوستر | کد مقاله: G-93178

Abstract: Background: Periodontitis is one of the most common chronic bacterial infections in humans involving the tooth-supporting tissue. The present study aimed to evaluate and compare salivary biomarkers, including lactate dehydrogenase (LDH) and hemoglobin A1c (HbA1c), between patients with severe chronic periodontitis and healthy individuals. Materials and Methods: This study was performed on 29 patients with severe chronic periodontitis and 30 healthy individuals at Zahedan University of Medical Sciences, Zahedan, Iran, in 2021. Salivary samples were taken, and clinical parameters, including the clinical attachment loss (CAL) and probing pocket depth (PPD), were measured. Besides, the levels of LDH and HbA1c were measured using ELISA kits. The sensitivity, specificity, and positive and negative predictive values of HbA1c and LDH were examined for chronic periodontitis diagnosis. Results: Based on the present results, the levels of LDH and HbA1c did not show adequate sensitivity or specificity for screening chronic periodontitis. Conclusion: According to the present findings, salivary biomarkers, including LDH and HbA1c, cannot be used with certainty for screening chronic periodontitis.

The effect of ethanolic extract of wild pistachio leaf (*Pistacia Khinjuk*) on the expression of genes involved in the metastatic power of human breast cancer cells

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نوع پذیرش: پوستر | کد مقاله: G-30712

Abstract: Background and Aim: Breast cancer is one of the most common types of cancer among women. According to the World Health Organization, the prevalence and death rate of this type of cancer will increase in the future. Although chemotherapy methods are initially beneficial in most patients, acquired drug resistance is a major problem in this type of cancer treatment. Therefore, there is a need for more effective and safe treatment methods for this type of cancer. Considering the need to identify new treatment methods for breast tumors and considering the presence of polyphenol compounds and flavonoid glycosides in the leaves and aerial parts of dark pistachio plants and the anticancer effects of *Pistacia Khinjuk* species on cervical cancer and breast cancer cell lines, a study The present was chosen with the aim of determining the effect of the ethanolic extract of *Pistacia Khinjuk* leaves on the expression of genes involved in the migration power of human breast cancer cells. Methods: In this laboratory study, ethanolic extract of wild pistachio plant was extracted and cytotoxicity was evaluated by MTT method. After calculating the IC₅₀, the effect of the extract on the expression of genes related to migration in breast cancer cells was evaluated by Real-time PCR method. The data was analyzed through SPSS statistical software and by one-way ANOVA and Student's t-test. Results: MTT test results showed that the IC₅₀ of the extract decreased respectively for 24, 48, 72 and 96 hours. Real-time PCR data showed that after 24 hours of treatment with the IC₅₀ concentration of the extract, the level of MMP-2 and -9 genes in breast cancer cells decreases significantly (p less than 0.05). The expression of TIMP-1 and -2 genes showed a significant increase (p less than 0.05). The expression of uPA and uPAR genes showed a significant decrease (p less than 0.05). Conclusion: Wild pistachio leaf extract has anti-metastasis effects in breast cancer cells. Keywords: ethanol extract, *Pistacia Khinjuk*, gene expression, breast cancer

Frequency of Anti-Thyroid Peroxidase Antibodies in Autoimmune Hypothyroidism Suspected Patients in Sari, during 2021-2022

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نوع پذیرش: پوستر | کد مقاله: G-25678

Abstract: Background: Hashimoto's thyroiditis is the most frequent autoimmune thyroid disease which is diagnosed by clinical characteristics and Anti-Thyroid Peroxidase (Ani-TPO) titer. The aim of the study was to evaluate the serum concentration of anti-TPO in autoimmune hypothyroidism suspected patients. Materials and Methods: In a cross-sectional study, blood samples were collected from 3425 suspected patients and serum concentration of Ani-TPO were determined by Electrochemiluminescence assay. Participants were categorized based on their age group, gender and the serum anti-TPO titer. Results: The total of 3425 hypothyroidism suspected patients (2697 females and 728 males) with age-baseline of 48 years were included in this study. According to the data analysis, relative frequency of anti-TPO positive samples in considered population was 29.8% (n=1022). There was a positive correlation between anti-TPO positive hypothyroidism and gender (81.51% of females). Moreover, the average age of positive-anti-TPO-patients was lower in females (39.5) rather than males (45.53). Conclusion: The frequency of anti-TPO positive individuals was significantly higher in our female population. Based on our results, we suggest periodic screening of anti-thyroid antibodies that is important in ascertaining thyroid function especially for middle-aged females. We also recommend a close follow-up of thyroid function for these females especially before and during pregnancy.



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Assessment of Tumor Markers in Patients Suspected of Cancer in Sari, during 2021-2022

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نوع پذیرش: پوستر | کد مقاله: G-18362

Abstract: Background: Several tumor markers are widely used in clinical experiments to monitor and screen various tumors. The aim of this study was to evaluate the serum concentration of common tumor markers including Alpha-Fetoprotein (AFP), Cancer antigen (CA) 125 and 15-3 in patients suspected of cancer. Materials and Methods: In a cross-sectional study, blood samples were collected from 2523 suspected patients and serum concentration of AFP, CA15-3 and CA125 were determined by Electrochemiluminescence assay. Participants were categorized based on their age group, genders, and pregnancy or nonpregnancy. Then, results were compared with the normal ranges. Results: The total of 2523 patients suspected of cancer (794 Males, 1739 Females) with age-baseline 48 years were included in this study. According to the data analysis, in comparison with normal range, high serum concentration of AFP, CA15-3 and CA125 were 8.8%, 16.87% and 14.60% respectively. Additionally, outcomes revealed that most positive titer of tumor markers correlated to the age of 41 (AFP), 52 (CA15-3), and 46 (CA125) in average. Conclusion: The results confirmed that the routine clinical evaluation of serum tumor markers is useful in early screening the patients suspected of cancer. Keywords:

Correlation of Expression of MMP-2, ACE2, and TMPRSS2 Genes with Lymphopenia for Mild and Severity of Covid-19

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نوع پذیرش: پوستر | کد مقاله: G-12497

Abstract: Introduction: Some risk causes may be associated with the infectivity and severity of Covid-19. The central host-pathogen factors that might be to affect infection are human receptor angiotensin-converting enzyme 2 (ACE2), trans-membrane protease serine 2 (TMPRSS2), and SARS-CoV-2 surface spike (S)-protein. The main purpose of this study was to determine the differences in the expression of MMP-2, MMP-9, ACE2, and TMPRSS2 genes and their correlation with lymphopenia in the mild and severe types of the COVID-19 patients. Methods Eighty-eight patients, aged 36 to 60 years old with the mild (n=44) and severe (n=44) types of COVID-19 were enrolled. Total RNA was isolated from the peripheral blood mononuclear cells (PBMCs). The changes of MMP-2, MMP-9, ACE2 and TMPRSS2 genes expression in PBMCs from mild and severe COVID-19 patients were examined by the real time-quantitative polymerase chain reaction (RT-qPCR) assay and, compared between the groups. Data were collected from May 2021 to March 2022. Results The mean age of the patients in both groups was 48 (interquartile range, 36–60), and there were no appreciable differences in age or gender distribution between the two groups (P0.05). The present study showed a significant increase in the expression of ACE2, TMPRSS2, MMP-2, and MMP-9 genes in the severe type of COVID-19 patients compared to the mild type of COVID-19 patients. Conclusion Overall, it suggests the expression levels of these genes on PBMC cells surface in the immune system are susceptible to infection by SARS-CoV-2 and therefore could potentially predict the patients' outcome. Keywords: Covid-19, ACE2, TMPRSS2, MMP-2, MMP-9.

Characterization of mouse monoclonal antibodies against human gamma interferon

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نوع پذیرش: پوستر | کد مقاله: G-72168

Abstract: Introduction: A monoclonal antibody (mAb) is a useful tool for unambiguous identification, quantification, and large-scale purification of an antigen or an epitope. This type of antibody is superior to conventional polyclonal antibodies in that they are specific for the antigenic determinant as opposed to conventional polyclonal antibodies that are not as precise. Methods: In this study, mouse spleen B lymphocytes immunized with recombinant IFN- γ were combined with mouse SP2/0 cells, and hybridized cells were selected in HAT medium, which were then panned and yielded monoclonal clones. We conducted indirect enzyme-linked immunosorbent assay (ELISA) tests, sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE) tests, and western blot tests to confirm the existence of antibody-secreting hybridoma cells. Results: mAb against IFN- γ were produced by fusing SP2/0 mouse non-secretory myeloma cells with spleen cells from immunized mice. Indirect ELISA Optical Density (OD) of the desired antibody was 2.055 on average, and in comparison to Septicol (commercial antibody), the desired antibody was able to bind to the antigen in the western blot. Conclusion: A mouse mAb was produced through the immunization of Balb/C mice and the fusion of SP2/0 cells with spleen cells from these mice in this study. It has been shown that it is capable of binding to recombinant human IFN- γ and can be used to detect IFN- γ secretion in all types of intracellular infections, including latent tuberculosis. Keywords: Interferon Gamma, Monoclonal Antibody, Hybridoma, SP2/0



چهاردهمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



B7-H7 Suppression Increases the Expression of CTLA-4 and VISTA Genes in Gastric Cancer Cell Line

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نوع پذیرش: پوستر | کد مقاله: G-40126

Abstract: Background: Gastric cancer (GC) is a multifactorial genetic malignancy that tumor metastasis is one of the principal characteristics of this disease. The B7 family immune checkpoints have important functions in maintaining the immune system's equilibrium that participates in the regulation of invasion, metastasis, and development of tumors. Silencing of gene expression via small interference RNA (siRNA) delivery technology is one of the significant approaches in gene therapy. The main goal of the current study was to determine the effect of B7-H7 suppression by siRNA on the expression of CTLA-4 and VISTA in the MKN-45 GC cell line. Methods: For this purpose, MKN-45 cells were transfected with B7-H7-siRNA. Then, transcript levels of CTLA-4 and VISTA genes following the suppression of the B7-H7 gene were investigated using quantitative real-time PCR. Results: This research demonstrated that the transcript levels of CTLA-4 and VISTA were increased after transfection of B7-H7-siRNA compared to the control cells. These experiments revealed that the knockdown of B7-H7 altered the expression of two immune checkpoints in the GC cell line. Conclusion: In conclusion, these results strengthen the supposition that upregulation and downregulation of VISTA and CTLA-4 expression in MKN-45 GC cell line may be affected by expression of the B7-H7 gene. The results of this investigation showed that suppression of B7-H7 gene expression led to upregulation of CTLA-4 and VISTA expression in MKN-45 GC cells. The present study will serve as a base for future studies, and it is suggested that the association of elevated CTLA-4 and VISTA genes expression following the suppression of the B7-H7 gene in other GC cell lines is investigated in future studies. Keywords:



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Breast cancer-derived exosomes: their role in cancer progression, metastasis, drug resistance, immune evasion and therapy

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نوع پذیرش: پوستر | کد مقاله: G-05489

Abstract: Almost all living cells secrete a set of extracellular vesicles (EVs). The naming of EVs depends on various factors, including their origin cells, function, and size. Extracellular vesicles (EVs) were first observed 50 years ago in plasma. Since then, all biological fluids tested have been shown to contain vesicles, and also in vitro grown cell lines have been shown to release vesicles to different extent. Extracellular vesicles (EVs) are classified into three groups typically based on their size and biogenesis: exosomes (30–200 nm), micro vesicles (MVs) (100–1000 nm) and apoptotic bodies (1000 nm). EVs are natural carrier systems that can transfer nucleic acids, proteins, and lipids between donor and recipient cells in an autocrine, paracrine, and endocrine manner. tumor cells possess more exosomes-releasing properties when compared to normal cells. Tumor-derived exosomes (TEX) have been widely studied in various types of cancer, such as renal cancer, hematological cancer, breast cancer and melanoma. TEXs, according to growing evidence, play a critical role in BC. In This review discusses the potential clinical application of exosomes in BC by summarizing how exosomes participate in BC proliferation, metastasis, drug resistance, therapeutic effect and other biologic progress. Moreover, we propose exosome as a candidate biomarker in predicting and monitoring the therapeutic drug response of BC and as a potential target or carrier to reverse the drug resistance of BC. Keywords:

Inflammation and cytokines as predictors of acute stress symptoms after injury

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نوع پذیرش: پوستر | کد مقاله: G-64739

Abstract: Background: Tissue and skeletal system damage may cause a hyper-inflammatory reaction in the immune system, which is characterized by increased levels of pro-inflammatory cytokines (PICs) and it can eventually cause the development of systemic inflammatory response syndrome (SIRS). The degree of this inflammatory reaction depends on the severity of the injury, which is known as the first hit. A secondary inflammatory reaction in patients with multiple traumas during and after surgical procedures (for example, immediately after fracture fixation) is known as secondary hit. The development of these hyper-inflammatory reactions is characterized by the activation of the immune system, which leads to the increase in the secretion of PICs such as IL-8 and IL-6. Results: PICs elevation is evident soon after injury (6 hours after initial injury) and persists for 24 to 48 hours in many cases. The secondary hit of the inflammatory reaction in severe injuries may exacerbate acute SIRS. Also, it may also lead to the development of acute respiratory distress syndrome and multiple organ failure with high mortality and morbidity. The high secretion of PICs usually stimulates the regulatory cytokines such as TGF- β and IL-10 upregulation of anti-inflammatory cytokines (AICs) such as IL-4, which causes a decrease in the intensity of the inflammatory reaction. An imbalance between the initial systemic inflammatory response and the subsequent compensatory anti-inflammatory response may be responsible for organ failure and elevated susceptibility to infections. Secretion of anti-inflammatory cytokines including IL-4 to reduce inflammatory activity. The increase in the levels of PICs following injuries indicates their role in the body's response to trauma. TNF- α and IL-1 stimulate chemokines, the recruitment of leukocytes in infected tissues, and epithelial adhesion molecules. IL-6 is produced by macrophages and T lymphocytes, which stimulate, the production of antibodies, the maturation and proliferation of T cells, and the proliferation of B lymphocytes. IL-8 is released by activated monocytes and plays a key role as a chemokine for macrophages and neutrophils and in the accumulation of leukocytes in inflammatory areas. IL-12 is secreted by Th1 cells and is necessary for stimulate the proliferation of B cells and differentiation, proliferation, and growth of Th1 cells. The AIC IL-4 in the later stages of the immune response increases the suppression of PICs. TGF- β and IL-10 are regulatory cytokines that are secreted by macrophages and T cells and play a central role in regulating wound healing, angiogenesis, and cell differentiation and proliferation. Conclusion: Low levels of regulatory cytokines such as IL-10 and TGF- β and AICs such as IL-4 and high serum levels of PICs such as IL-8 and IL-6 are predictors of high levels of acute stress signs immediately after injury. In addition, lower serum levels of TGF- β and higher serum levels of IL-8 are predictors of post-traumatic stress signs. PICs such as IL-6 may cause or aggravate the patient's psychological signs. These results show that high levels of inflammation caused by an injury event may be a risk factor in the occurrence of psychological signs after the injury. Keywords:

Inflammatory cytokines (IL-6 and TNF- α) as main reference indicators to endometriosis and subsequent infertility

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نوع پذیرش: پوستر | کد مقاله: G-52906

Abstract: Background: It is well accepted that endometriosis is a hormone-dependent chronic inflammatory disease that is usually associated with elevated local estrogen levels and abnormal cytokine levels. Endometriosis is characterized by stroma and ectopic endometrial cells outside the uterine cavity. Also, endometriosis is one of the important causes of infertility in women. Estrogen is closely related to the occurrence and progression of endometriosis, which is dependent on Th2 immune cells and dysregulation of Th2 cytokine expression. The function of inflammatory cells, including the infiltration and activation of peritoneal macrophages, as well as the secretion of cytokines by these macrophages, can cause the inflammatory response caused by endometriosis. Results: Macrophages stimulate the secretion of various inflammatory cytokines, which play an essential role in the occurrence, maintenance and development of endometriosis. As a part of the innate immune system, the activation of macrophages causes the release of growth factors and various cytokines that play a role in the development and growth of endometriosis. Functional deviation of local immune cells such as macrophages, T lymphocytes, monocytes B, natural killer (NK) cells, and lymphocytes in the peritoneal fluid may play a key role in the pathophysiological process of endometriosis. Inflammation is considered as the main key in evaluating the components of signaling pathways such as mitogen-activated protein kinase (MAPK) in endometriosis. Also, IL-13, IL-6, TNF- α and IL-10 are more expressed in the peritoneal fluid of women with endometriosis. The interaction between the body's immune system and the endometrial tissue has a major impact on the development and progression of this disease. IL-6 is a type of cytokine with several effects that is produced by the offending cells such as monocytes and lymphocytes. IL-6 is a Th2 cytokine that causes migration, location and growth of endometrial cells in patients with endometriosis. TNF- α is involved in many pathological and physiological reproductive processes and has both harmful and beneficial effects. TNF- α is produced by activated lymphocytes, neutrophils, NK cells and macrophages and is recognized in mesothelioma stromal cell cultures. TNF- α induces the proliferation of endometriosis stromal cells through the induction of interleukin 8 gene and its protein expression, and it can be concluded that it is one of the main factors in the pathogenesis of endometriosis. The development of endometriosis is associated with increased levels of pro-inflammatory cytokines including monocyte IL-6, TNF- α and chemoattractant protein type 1 and macrophages. Conclusion: IL-6 is a type of macrophage activator that can encourage the proliferation of endometrial cells. Then the activated macrophages induce the secretion of IL-13, TNF- α and IL-13. TNF- α can mediate immune and inflammatory responses and cause local pelvic adhesions, fibrosis and immunological disorders that lead to the formation of ectopic lesions. Also, high concentrations of TNF- α in peritoneal fluids can directly



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reduce sperm motility, which affects the processes of implantation and fertilization, and as a result, decreases fertility in patients with endometriosis. Therefore, these inflammatory factors such as IL-10, IL-6, TNF- α and IL-13 can be used as main reference indicators to diagnose endometriosis and subsequent infertility

The key roles of Inflammation in sub- fertility/ infertility

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نوع پذیرش: پوستر | کد مقاله: G-39547

Abstract: Background: Infertility in men is basically due to a disorder in the process of spermatogenesis, which causes the absence or inability of spermatozoa. Various spermatogenic factors and signs are considered as the cause of infertility, which include: low sperm count, reduced sperm motility, low sperm quality, and damage to sperm DNA. Inflammation affects the dual roles of the testis, including spermatogenesis and steroidogenesis. During the presence of inflammation, a significant decrease in the amount of LH and testosterone in the blood circulation has been observed. Cytokines are proteins that can act as modulate cellular reactions such as inflammation and signaling molecules. Cytokines induce an inflammatory response by binding to their receptors. Results: Innate immunity is mediated by the presence of leukocytes in the testicles, which are located in the interstitial space. Macrophages are the main group of leukocytes, while significant amounts of mast cells and lymphocytes can also be found in this area. macrophages/ Monocytes can promote the inflammatory process by secreting chemo-attract molecules, inflammatory cytokines such as IL-1, TNF- α and producing ROS. Cytokines are physiologically produced in testicular tissue by many diverse cell populations and can be found in seminal plasma. There is a positive correlation between the levels of different cytokines and the presence of leukocytes in the semen. Increased levels of IL-8 and TNF- α in semen infected with pathogens have been detected and indicate a large number of leukocytes. However, high levels of IL-6 observed during leukocyte infiltration into semen even in the absence of pathogens suggest that IL-6 can also be used as an indicator of non-pathogenic inflammation in semen. Men with different sperm defects have different profiles of cytokines in their semen. For example, men who are asthenospermic (decreased sperm motility) have increased levels of IL-8 and IL-10 in their semen while infertile men who suffer from oligospermia (decreased sperm count) have increased levels of IL-6 and IL-10 in their semen. In sub-fertile men with obstructive azoospermia (due to blockage in the reproductive system), higher levels of IL-10, TNF- α and IL-6 have been observed. In the testes, TNF- α regulates the steroidogenesis of leydig cells and the apoptosis of germ cells. TNF- α inhibits steroidogenic enzyme gene expression in leydig cells by activating NF- κ B. Inhibition of steroidogenic enzymes causes a decrease in testosterone production. Increased levels of TNF- α have also been observed in the semen of sub-fertile and infertile men. Also, in the conditions of infiltration of leukocytes into the semen, the presence of high levels of TNF- α in the semen has been observed, which indicates that inflammation directly mediates azoospermia through TNF- α levels. Conclusion: Inflammation in the male reproductive system is mainly mediated by cytokines such as interleukins and TNF- α . Inflammation affects leydig cells (due to the reduction of testosterone hormone secretion) and Sertoli cells (due to the destruction of the blood-oval barrier function), which ultimately causes the prevention and destruction of the spermatogenesis process. Contamination of semen with inflammatory agents causes disruption in the physiology and morphology of sperm, which eventually leads to sub-fertility/ infertility.



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دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



The Rise of the Novel Therapeutic Antibodies Derivates for Cancer Treatment and Precise Tumor Immunotherapy

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نوع پذیرش: پوستر | کد مقاله: G-64739

Abstract: Background: Targeted cancer therapy has been transformed by therapeutic antibodies over the past 3 decades. Monoclonal antibodies offer an improvement in the body's natural immune system to inhibit the activity of cancer cells and neutralize them. Antibody-drug conjugates (ADCs) promise the most specific transportation of antineoplastic agents to the desired location. In this paper, we review the efficacy and the future of these antibodies and how biotechnology can help us get closer to finding a final solution for cancers. Results: ADCs are made of four major parts which are, the target antigen, an antibody construct payload (generally a cytotoxic agent), and a linker moiety that pairs the antibody to the payload. After the binding of the ADC to the target antigen of the tumor, the ADC is internalized and the payload will detach. The detachment can be caused by the degradation of the whole ADC structure. The therapeutical features of the ADC are determined by its components. ADCs are designed in a way to drop their toxic payload on any cell that expresses the targeted antigen. Linkers can be divided into two types of cleavable and non-cleavable. The cleavable type's stability may vary in the circulation and may degrade in plasma. On the other hand, non-cleavable linkers are more stable in plasma. Early ADCs were made to deliver traditional chemotherapy drugs but their efficacy was not superior to the standard cytotoxic drugs of the time. Therefore, experiments with highly toxic chemotherapy drugs began. The drug-to-antibody ratio is the mean number of payloads attached to a monoclonal antibody and varies between different types of ADCs. Conclusion: ADCs are now one of the most complicated biochemical agents used in treating cancer which uses antibodies and cytotoxic drugs to make special mechanisms and pharmacokinetic properties. Progress in biotechnology leads to the development of linkers and making novel payloads which results in more effective ADCs that are highly selective and take us one step closer to the cancer cure. Keywords:

Implementing PSMA Targeted Therapies in Treatment Algorithm of Prostate Cancer

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نوع پذیرش: پوستر | کد مقاله: G-87436

Abstract: Background: Prostate cancer has the highest occurrence rate in men worldwide and also is the second cause of mortality in western countries. As of now, the options for treating prostate cancer include radical prostatectomy to external radiotherapy. Unfortunately, most tumors will turn into castration-resistant prostate cancer (CRPC) or metastatic castration-resistant prostate cancer (mCRPC) which is the main cause of mortality. Current therapies still face many disadvantages including high systemic toxicity, drug resistance, and low selectivity in tissues. Moreover, these therapies usually can't prolong the lifetime of patients more than 6 months. In this paper, we study the potential advantages of PSMA-targeted tumor therapy over traditional methods. Results: PSMA is a type II glycoprotein on the membrane of the Prostate cancer cell line LNCaP. PSMA expression is very low in non-prostatic tissues whereas in cancerous tissues, the expression level can increase 100-1000 folds compared to normal tissues and this level is even higher in metastatic, poorly differentiated, and castration-resistant prostate cancer tissues. Therefore, PSMA levels have acceptable specificity for the diagnosis and treatment of the disease. Currently, there are three major methods to target PSMA ligands, including, monoclonal antibodies, aptamers, and small molecule inhibitors. Monoclonal antibodies are made to only target certain preprogrammed epitopes. Aptamers are small sequences of artificial DNA or RNA which bind to a certain target such as proteins, phospholipids, nucleic acids, and other molecules. Small molecule inhibitors are compounds that can affect the proteins and decrease their biological activities such as inhibitors, transfer factor inhibitors, and ion channel blockers. PSMA-targeted treatment can be achieved using methods such as Radioligand therapy in which a certain dose of radionuclide-labeled ligand into the body. Another method is based on Antibody-drug conjugates which is a leap forward in tumor therapy. Compared with traditional antineoplastic drugs, systemic toxicity is avoided in this method. After the binding of antibodies to PSMA, ADCs break into the tumor cells, followed by releasing of the cytotoxic drug which kills the targeted cells. Cellular immunotherapy is getting more attention as it is showing potential in cancer therapy. In adoptive cellular therapy, human autoimmune cells are collected and then amplified in the laboratory to improve their function in the killing of the patient's cancer cells. Conclusion: With fast-paced advancements in biotechnology, a new path has been paved for treating cancers in a more selective and precise way. It is clear that soon a paradigm shift will happen in the medical world and we should start focusing and investing on new methods so we can be a part of this new bright world. Keywords:

Immunomodulatory and tissue regenerative effects of phytosomal curcumin are associated with regulation of related-biomarkers in human dental pulp derived-mesenchymal stem cells

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نوع پذیرش: پوستر | کد مقاله: G-03126

Abstract: Background: Human dental pulp stem cells (hDPSCs), as one type of mesenchymal stem cells (MSCs), have the capability of selfrenewal, multipotency, as well as immunosuppressive properties. They are ideal candidates for regenerating damaged dental tissue and treating many diseases. Recently, genetic variation is one of the methods to improve the immunomodulatory activity of MSCs. Phytosomal curcumin (PC) is a nanoparticle form of curcumin that eliminates the disadvantages of curcumin. Curcumin is notable for its pleiotropic medicinal benefits, like its anti-inflammatory activity. This study was conducted to investigate the effect and underlying mechanisms of PC on the immunomodulatory and regenerative function of hDPSCs and whether treating these cells with PC can improve therapeutic efficacy. Materials and Methods: hDPSCs were isolated from dental pulp and then treated with PC. Cell viability rate was observed in hDPSCs after treatment of PC by MTT assay. Real-time quantitative (RT-PCR) was applied to estimate the expression of immunomodulatory and regenerative genes after treatment of PC. Results: The RT-PCR results showed that PC significantly reduced the expression of RelA, STAT3, VCAM1 and HLA-G5 genes up to many times over while optimally enhanced the expression of DSPP and VEGF-A genes, although this enhance was statistically significant only for VEGF-A (all P 0.001). Conclusion: Our findings demonstrate that PC can enhance the immunomodulatory and regenerative effects of hDPSCs and improve their therapeutic efficacy. These findings can give an understanding of the mechanism for improving restorative and immunomodulatory activity in hDPSCs by PC. Keywords:

Cancer immunotherapy

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نوع پذیرش: پوستر | کد مقاله: G-89563

Abstract: Background: Today, cancer is considered one of the serious and dangerous diseases in the world, and its treatment can be effective or ineffective depending on the type of cancer. Among the many methods used to treat cancer, cancer immunotherapy is one of the treatment methods for this disease. Cancer immunotherapy means the treatment of the disease by the cells of the body's immune system. However, this method, like other cancer treatment methods, also has limitations, such as the patient's lack of response to treatment, the lack of suitable immunotherapy options for some cancers, the inaccessible and suppressive nature of the immune system. But this method can be mentioned. It can be one of the strong and powerful treatment methods for advanced cancers and metastases. The initial start of cancer immunotherapy dates back to 1893 when William Coley used live bacteria as an immune stimulant to treat cancer. However, due to limited clinical effectiveness, cancer immunotherapy did not make much progress at that time. But in the last few decades, many advances have been made to prevent the escape of the immune system. Clinical studies show that people who respond to cancer immunotherapy have fewer metastatic recurrences. However, fewer people respond positively to cancer immunotherapy. Cancer immunotherapy includes several treatment methods, including vaccines, monoclonal antibodies, oncolytic virus, and host cell transfer. The growth and development of the tumor occurs in different stages in the body, in which the body's immune system tries to prevent the progress of the tumor to other parts of the body. Tumor growth and development has different stages, including initiation, promotion, and progression. In the initial stage, which begins with DNA mutation and oncology, the formed cancer cells try to survive and escape from the immune system. This stage consists of 3 phases (elimination, equilibrium, escape). Cancer cells that survived in the initial phase form a tumor and enter the progression phase and can cause tumor proliferation in the body and metastasis. The initial phase of cancer cell development includes three phases: elimination, equilibrium and escape. In the elimination phase, the innate immune system starts to eliminate cancer cells. The main cells of the innate immune system in this phase include NK cells and macrophages. . NK cells use the histocompatibility complex (MHC) to lyse cancer cells, and macrophages' hempenin using IL12 stimulates the production of TH and CTL and also causes phagocytic cancer cells. In the equilibrium phase: the longest phase is the initiation phase and it may last for years and the tumor grows and proliferates during this long period because the cancer cells that survived the elimination phase start to proliferate and it is possible that the resistant parts to collect immune cells. In the escape phase: In this phase, according to the mutations that the cancer cells had in the equilibrium phase, they escape from the immune system. During the balance phase, cancer cells overcome the immune system through immune editing and a strong immune response is not created in the body. This phenomenon

Different types of immune escape mechanisms in leukemic cells in chronic lymphocytic leukemia

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نوع پذیرش: پوستر | کد مقاله: G-53071

Abstract: Background: CLL (Chronic lymphocytic leukemia) is a heterogenous-incurable diseases and the most common adult leukemia in the western country that determines with clonal proliferation and continuous accumulation of cancerous CD19+/CD5+ B cells in peripheral blood, bone marrow and lymphoid organs. CLL allocates to approximately 25% of all leukemia, 1.3% of all cancers and something about 70% of lymphoid leukemia. This disease is more common in male than female (about 1.5-2 versus 1) and its incidence in USA is about 4.1 in each 100000 inhabitants. CLL is an age-adjusted disease which affect older people who are 65 years and older. The aim of this study is to prepare more comprehensive understanding of the evasion mechanisms of CLL cells from the host immune system and help to the improvement of the current therapeutic approaches. Materials and Methods: A comprehensive literature search was performed from 1993-2022, in several known databases including pubmed and google scholar. Search terms was CLL, immune scape, immune checkpoint and signaling pathway. Results: Overall, cancers including CLL, are associated with changes in the immune system properties. Various cells in the tumor microenvironment have different cytokine/chemokine receptors and secrete different cytokines/chemokines such as IL-4, IL-10, IL-13, CCL2, CCL3, CXCL12, CXCL13, that lead to recruiting tumor cells to the tumor microenvironment and their reaction with the bystander cells and eventually leads to immune suppression, tumor cells evasion, increased resistance of leukemic cells to apoptosis and their survival. Besides the increasing in frequency of CD4+ T and CD8+ T cells in the early stages of CLL disease, there are defects in the formation of immunological synapses with antigen presenting cells, in degranulation/cytotoxicity, cytokine production, shift of Th cells towards Th2 and Treg cells, the expression of inhibitory markers such as PD-1, Tim-3, CTLA-4, Gal-9, TIGIT and also the occurrence of exhaustion phenotype, especially in CD8+ cells. BCR signaling plays a significant role in the pathogenesis of CLL. Binding of BCR to antigen leads to the activation of LYN and SKY kinases and then phosphorylates BTK, which can activate downstream signaling pathways such as MAPK, AKT, ERK1,2, PLC γ 2, PI3K, JAK/STAT and NF- κ B, resulting proliferation of tumor cells and their survival. On the other hand, high expression of the CD200/CD200R, Notch1/Notch2 receptors and their ligands, B and T lymphocyte attenuator/ Herpes Virus Entry Mediator (BTLA/HVEM) axis and also lack of IRF4 which lead to the downregulation of MHC-II molecules on the CLL cells surface, reduce function of the immune cells and eventually lead to tumor expansion. Conclusion: The survival of CLL cells in the tumor microenvironment depends on their interactions with bystander cells, including stromal cells, such stromal cells, endothelial cells, T lymphocytes, NK cells, NLCs, monocytes/macrophages which occurs through a complex network of adhesion molecules, cell surface ligands, chemokines/cytokines and their receptors, leads to the downregulation of the immune system, the evasion of tumor cells, resistance to apoptosis and finally tumor expansion. Further studies are required for a better understanding of the tumor escape mechanisms and to find new therapeutic approaches. Keywords:



چهاردهمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Formulation of Inactivated SARS-CoV-2 Virus in MF-59 adjuvant; Analysis of Cellular and Humoral Immune Responses

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نوع پذیرش: پوستر | کد مقاله: G-59071

Abstract: Vaccination is the most and rationale way in the prevention of infectious disease. Various vaccines are developed in order to prevent infectious disease. But, it is proven that adjuvant and vaccine formulation is a critical parameter in the immunogenicity and vaccine efficacy. In this study, inactivated SARS-CoV-2 virus was formulated in MF-59 adjuvant and the potency of this vaccine in the induction of cellular and humoral immune responses was assessed in experimental mice. Experimental BALB/c mice were immunized subcutaneously, three times with MF-59- and Alum-based vaccines. In addition, a PBS as a control group was considered. Three weeks after the vaccine immunization, lymphocyte proliferation of spleen cells was performed by BrdU method, IL-4 and IFN- γ cytokines were assessed on the spleen cell culture supernatant by quantitative ELISA kits. Furthermore, specific total IgG and IgG1/IgG2a were assessed with an optimized indirect ELISA. The results of the present study show that immunization with MF-59-inactivated SARS-CoV-2 vaccine lead to a robust cellular and humoral immune responses which showed a significant differences versus Alum-based vaccine and PBS control group. It seems that MF-59 could be used as a suitable adjuvant in SARS-CoV-2 vaccine development.

Keywords:

Investigating the effect of royal jelly on the infertility in patients with multiple sclerosis disease

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نوع پذیرش: پوستر | کد مقاله: G-05472

Abstract: Background: Multiple sclerosis (MS) is a chronic disease that may lead to a variety of symptoms and disabilities, including infertility in both sexes. Royal jelly (RJ) is a yellowish white, creamy liquid for the nutrition of young larvae in the colony and the queen bee. Multiple pathomechanisms (immunodeficiency, hypoxia, oxidative stress, neuroinflammation and mitochondrial dysfunction) can play a significant role in the MS pathogenesis. RJ has important effects improvement menopausal symptoms, decreasing fatigue and has a positive effect on steroidogenic and spermatogenic and is known as a complementary treatment. In this study we review affect of royal jelly on the infertility in patients with MS. Methods: In this review were used PubMed, Google Scholar and Scopus databases. The keywords that were used included Royal Jelly, Infertility, Multiple Sclerosis and MS. Articles from 2010 to 2022 were reviewed. After searching for keywords, we analyzed the articles that matched our inclusion and exclusion criteria among the displayed results. Results: About 26 articles were selected including animal and human studies in this field and we mostly focused on human studies. Human studies showed that the protective effect of the testis is related to increasing the number of sperm and their quality, increasing the concentration and mobility of sperm. RJ can increase seminal fructose, ejaculation volume, sperm output and sperm motility. Some human studies have also evaluated its effect on hormonal disorders in postmenopausal and infertile women. Royal jelly compounds can improve testosterone and testicular function, thereby increasing the resistance of the testicle against thermal stressors. A cohort study male infertility is associated with MS; showed that men diagnosed with male factor infertility had a higher risk of prevalent (odds ratio= 1.61, 95% confidence interval (95% CI) 1.04-2.51) and incident MS (hazard ratio= 1.28, 95% CI 0.76-2.17) when compared to the reference group. Abnormalities of the levels of sex hormones and gonadotrophins, decline follicle count and ovarian artery Doppler as a result reduced ovarian reserve women with MS, lower AMH levels in young women with relapsing–remitting MS compared with controls, reproductive endocrine abnormalities in MS, including hyperprolactinaemia and hyperandrogenism, and hence reduced fertility. Also one study found that males with MS had reduced semen quality and hypogonadotrophic hypogonadism. Conclusion: Interestingly in MS patients of other study; characteristics, motor function, a proinflammatory cytokine and demyelination were ameliorated by RJ. thereby making RJ a promising possible preventive and therapeutic treatment of sub/infertility in MS patients. Keywords: Royal Jelly; Infertility; Multiple sclerosis; MS.

Investigating the effects of adipose-tissue derived MSCs on proliferation and apoptosis of the healthy individual's PBMCs in co-culture with HeLa cell line

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نوع پذیرش: پوستر | کد مقاله: G-05397

Abstract: Background: Cervical cancer, the most common cancer of the reproductive system in women, is the fourth cause of cancer-related deaths. Today, the use of mesenchymal stem cells (MSC) has been investigated in the treatment of various diseases, but its use in cervical cancer has not been well-studied. This study investigated the effect of adipose tissue-derived MSCs on apoptosis and proliferation of peripheral blood mononuclear cells (PBMCs) in co-culture with the HeLa cell line. Materials and Methods: MSCs were isolated from adipose tissue by enzymatic method using collagenase I, and then MSCs, PBMCs, and HeLa cells were co-cultured in DMEM low glucose medium containing 10% heat-inactivated fetal bovine serum (FBS), and 1% penicillin/streptomycin for 24, 48 and 72 hours. The ratio of MSCs to HeLa cells was 1:1 and the ratio of PBMCs to MSC/HeLa was 5:1 in co-cultures. Cell apoptosis and proliferation were evaluated using an Annexin V/PI kit and CFSE assay kit, respectively. Results: The presence of MSCs in the co-culture of MSC, HeLa, and PBMC cells, enhanced the proliferation of PBMCs after 24 hours. Also, in the 24-hour co-cultures of HeLa-MSC and PBMC-MSC, it was observed that the presence of MSCs decreased the apoptosis of PBMCs and increased the apoptosis of HeLa. However, these results were observed in 48- and 72-hour treatments. Conclusion: Results of this study suggest that MSCs may secrete some metabolites that can increase the proliferation of PBMCs in the tumor microenvironment and improve immune defense, and they can also increase the apoptosis of cervical cancer cells. Key words: MSC (mesenchymal stem cell), PBMC (Peripheral blood mononuclear cell), HeLa (human cervical cancer cell line)

Seroprevalence of VZV IgG antibody in kidney transplant recipients: A systematic and meta-analysis review

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نوع پذیرش: پوستر | کد مقاله: G-95614

Abstract: Background Varicella-zoster virus (VZV) is a human neurotropic virus that becomes latent in nerve ganglia. VZV infection rarely occurs after kidney transplantation but causes severe clinical features and is associated with higher mortality rates. This study was performed to survey the reports on the seroprevalence of VZV IgG antibodies in kidney transplant recipients. Material and methods Relevant studies were obtained by an online review of international databases (Web of Science, PubMed, Scopus, Science Direct, and Google scholar), and suitable studies were selected. The NOS checklist was used for the quality assessment of the selected studies. Heterogeneity assay among the primary studies was conducted by Cochran's Q test and I2 index (significance level 50%). Statistical analysis was performed using the Comprehensive Stata software (Version 14 package). Results Seroprevalence of VZV IgG in transplant recipients has been reported in ten studies. After combining the results of preliminary studies using a random effect model, the overall estimate of IgG positivity to VZV in transplant recipients was obtained equal to 98%. Conclusion In this study, our results demonstrated that VZV is a prevalent infectious agent in kidney transplant recipients. A prophylactic vaccine may provide an effective strategy for preventing VZV in renal transplant recipients and also provide prophylaxis against the occurrence of post-herpetic neuralgia in immunocompetent patients. Keywords:

Seroprevalence and geographical distribution of parvovirus B19 antibodies in pregnant women: A-meta analysis

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نوع پذیرش: پوستر | کد مقاله: G-70593

Abstract: Parvovirus B19 has been identified to infect pregnant women and cause anemia, spontaneous abortion, and fetal death. Given the significance of parvovirus B19 complications, this study aims to determine the seroprevalence and geographical distribution of parvovirus B19 antibodies in pregnant women to improve health control policies in the community. Online international databases and national Persian databases were used to define appropriate studies published between 2000 and January 2021. The quality of all papers was determined by a NOS checklist. The statistical analyses were performed using the Stata version 11 package (StataCorp, College Station, TX, USA) software. Heterogeneity among the primary studies was calculated using Cochran's Q-test and I² index. The Egger test and the funnel plot chart with a significance level of less than 0.1 were used to evaluate the publishing bias. The seroprevalence of parvovirus B19 IgG antibodies among pregnant and non-pregnant women in Iran was assessed in 12 primary studies. Our finding showed that the seroprevalence of parvovirus B19 IgG antibodies among pregnant women varies from 21% to 76%. Combining the results of 5 primary studies based on the random effect model, the seroprevalence of parvovirus B19 IgG antibody among pregnant women in Iran was estimated to be 54% (95% CI: 33-76). The seroprevalence of parvovirus B19 IgM antibodies has been reported in 9 studies. By combining the results of these studies using a random effect model, the seroprevalence of parvovirus B19 IgM antibody among pregnant women was estimated to be 3% (95% CI: 1-6). Generally, it is suggested that appropriate screening programs should be performed for the treatment and prevention of diseases. According to this point, the prevalence of parvovirus B19 is low among pregnant women, but it can cause serious manifestations such as hydrops fetalis and severe anemia, therefore, antibody determination using ELISA can be recommended for all pregnant women.

Keywords:

The Prognostic value of CD44 stem cell biomarker expression in patients with non-small cell lung cancer: a systematic review and meta-analysis

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نوع پذیرش: پوستر | کد مقاله: G-86275

Abstract: CD44 is an interesting prognostic marker and potential therapeutic target in non-small cell lung cancer (NSCLC). Although CD44 expression is associated with poor prognosis of NSCLC in most literatures, some controversies still exist. Since there are a limited number of independent studies in this field, we conducted a systematic review and meta-analysis to elucidate the correlation between CD44 expression and prognosis and clinicopathological features in NSCLC patients. Using Google Scholar, Scopus PubMed, Web of Science, EMBASE, and Cochrane databases, studies published in English until December 2022 were identified. Then, data from eligible studies related to CD44 expression, evaluation of clinicopathological features in NSCLC patients in primary lesions and survival data reported based on CD44 expression were extracted. To collect the effect estimates of the input studies, event rates and 95% confidence intervals were identified and described by a forest plot. Heterogeneity across included studies was determined using Cochran's and Higgins I2 tests. In all evaluations, P 0.05 was considered statistically significant. To investigate sources of heterogeneity between included studies, subgroup analysis was performed. The overall event rate of subgroups was determined based on histology (SCC, ADC, and LCC), tumor differentiation (good, moderate, and poor), tumor stage (I, II, III, and IV), survival rate. All statistical analyzes were performed by meta-analysis (CMA) software. We carried out a very last evaluation of 2692 sufferers from 23 evaluable studies for prognostic value and clinicopathological features. Our findings showed that the pooled HR of overexpression CD44 for overall survival in NSCLC turned into 53%. Overexpression of CD44 is associated with tumor differentiation (poor differentiation, OR = 1.89, 95% CI: 1.32-2.65), tumor histological type [squamous cell carcinomas (SCC), OR = 2.8, 95% CI: 1.70-4.82], clinical TMN stage (TMN stage III, OR = 2.45, 95% CI: 1.64-3.47) in patients with NSCLC. However, there has been no massive association among CD44 and tumor size [OR = 1.42, 95% CI: 0.93-2.58]. Our meta-analysis confirmed that CD44 is an efficient prognostic thing for NSCLC. Overexpression of CD44 become extensively associated with tumor differentiation, tumor histological type, medical TMN degree. However, there was no great affiliation among CD44 and tumor size. Large potential research is now needed to verify the clinical utility of CD44 as an unbiased prognostic marker. Keywords:



چهارمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Correlation of HLA-G and HLA-E Tissue Distribution and Degree of Tumor Malignancy in Breast Cancer

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نوع پذیرش: پوستر | کد مقاله: G-51804

Abstract: Background: Human leukocyte antigen (HLA) molecules play a substantial role in T lymphocyte-mediated adaptive immune response. Down regulation of HLA expression may help tumor to escape from immune surveillance. The aim of this study was to evaluate correlation of HLA-G and HLA-E tissue distribution and degree of tumor malignancy in human breast cancer. Material and Methods: Tissue samples of 145 patients with breast cancer were chosen. Distribution of HLA-G and HLA-E molecules was determined by immunohistochemistry method. Results: From a total of 145 patients, 79.3% of tumors did not express HLA-G, 17.9% of them expressed (+), 2.8 % expressed (++) and no patients expressed (+++). Moreover 51% of tumors did not express HLA-E, 36.6 % of them expressed (+), 8.3% expressed (++) and 4.1% expressed (+++). Generally, 20.7% and 49% of patients showed expression of HLA-G and HLA-E tissue distribution, respectively. A significant correlation was seen between grade of disease and expression of HLA-G ($p=0.001$) and HLA-E ($p=0.02$). Significant correlation was seen between simultaneously expression of HLA-G and HLA-E and grade ($p=0.034$, $r=0.176$). There was a significant correlation between HLA-G and HLA-E expression with degree of malignancy. Conclusion: Expression of these biomarkers may be contributed in prognosis and progression of breast cancer disease. Keywords: HLA-G, HLA-E, Breast cancer, Tumor malignancy

Seroprevalence of VZV IgG antibody in kidney transplant recipients: A systematic and meta-analysis review

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نوع پذیرش: پوستر | کد مقاله: G-95614

Abstract: Background Varicella-zoster virus (VZV) is a human neurotropic virus that becomes latent in nerve ganglia. VZV infection rarely occurs after kidney transplantation but causes severe clinical features and is associated with higher mortality rates. This study was performed to survey the reports on the seroprevalence of VZV IgG antibodies in kidney transplant recipients. Material and methods Relevant studies were obtained by an online review of international databases (Web of Science, PubMed, Scopus, Science Direct, and Google scholar), and suitable studies were selected. The NOS checklist was used for the quality assessment of the selected studies. Heterogeneity assay among the primary studies was conducted by Cochran's Q test and I2 index (significance level 50%). Statistical analysis was performed using the Comprehensive Stata software (Version 14 package). Results Seroprevalence of VZV IgG in transplant recipients has been reported in ten studies. After combining the results of preliminary studies using a random effect model, the overall estimate of IgG positivity to VZV in transplant recipients was obtained equal to 98%. Conclusion In this study, our results demonstrated that VZV is a prevalent infectious agent in kidney transplant recipients. A prophylactic vaccine may provide an effective strategy for preventing VZV in renal transplant recipients and also provide prophylaxis against the occurrence of post-herpetic neuralgia in immunocompetent patients. Keywords:

Association of peripheral blood CD11b⁺/CD33⁺/HLA-DR⁻ myeloid cells with increasing CRP in children with infectious diseases

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Background: Recurrent or persistent infections correlate with increased serum C-reactive protein (CRP) in childhood. Also inflammatory mediator release inhibitory cells named myeloid-derived suppressor cell (MDSC) into circulating and tumor tissues. Herein, we evaluated the percentage and count of peripheral blood CD11b⁺/CD33⁺/HLA-DR⁻ MDSCs or myeloid cells at infants, children, and adolescents with infection disease and increased CRP.

Materials and Methods: We enrolled 40 patients with infection disease and 20 healthy as control. CD11b⁺/CD33⁺/HLA-DR⁻ MDSCs or myeloid cells was evaluated in peripheral blood samples by flow cytometry. The association between the percentage and absolute count of MDSCs with clinical parameters were evaluated.

Results: We significantly found a higher level of MDSCs in patients with increased CRP compared to healthy controls (P=0.003). However, the results of analysis showed no correlation between MDSC percentage and count with grouped age and sex in patient groups.

Conclusion: Our findings showed a positive correlation between the high level of serum CRP and peripheral blood CD11b⁺/CD33⁺/HLA-DR⁻ MDSCs in infants and children, as the CRP increases, the percentage of blood MDSCs increases. This study could be a roadmap for future studies to use increased CRP as a potential prognostic biomarker to target MDSCs in children with recurrent or persistent infections.

Keywords: CRP, MDSC, Infectious disease

Immunomodulatory effects of potential probiotic *Lactobacillus gasseri* ATCC 33323 on the expression level of inflammation-related genes in HT-29 cell line

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نوع پذیرش: پوستر | کد مقاله: G-38129

Abstract: Background: Colon cancer develops from a polyp inside the colon or rectum Probiotics are live microorganisms that improve overall health when used in adequate amounts. Recent clinical studies demonstrated that probiotics are highly effective in preventing and treating gastrointestinal cancers. Potential probiotic *Lactobacillus gasseri* ATCC 33323 bacteria are able to modulate inflammatory response in colorectal cancer cells. Methods: *L. gasseri* strain ATCC 33323 was cultured on MRS agar. Colorectal cancer HT-29 cells were cultured in complete DMEM medium in a CO₂ incubator. The impact of live *L. gasseri* probiotic bacteria was examined on mRNA expression level of TLR4, MyD88, and NF- κ B genes in HT-29 cells following 24 h by RT-qPCR assay. Results: *L. gasseri* strain ATCC 33323 significantly down-regulated the gene expression level of TLR4, MyD88, and NF- κ B genes in HT-29 cells after 24 h of treatment. Conclusion: The potentially probiotic strain of *L. gasseri* used in this study could possibly ameliorate the expression of inflammation-related genes in HT-29 cells during in vitro conditions. This beneficial microbe could be developed as an efficient supplementation to the current prevention and treatment drugs administrated against inflammatory response caused in patients with colorectal cancer. Keywords: *Lactobacillus gasseri*; Probiotics; Colorectal cancer; Inflammation; HT-29 cells



چهاردهمین گنگره بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Investigation of the latest immunotherapy methods for colon carcinoma malignancy

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نوع پذیرش: پوستر | کد مقاله: G-03271

Abstract: Background: Colon carcinoma is one of the most common malignancies that can cause death in the world. Despite the lack of definitive treatment, immunotherapy techniques smooth the process of diagnosis and treatment of this disease. Materials and Methods: A literature review using web databases PubMed, Scopus, Google Scholar, and Embase from 2015 to 2023 Results: The results showed that adoptive cellular therapy, Car-T cell, Car-NK cell, DNA vaccines, peptide vaccines, and DC-based therapy are different immunotherapy methods used to fight colon carcinoma, which can effectively anti-tumor activities. Conclusion: Since a definitive treatment for colon carcinoma disease, which is one of the most common malignancies and one of the leading causes of death in the world, has not yet been found, by examining the methods and clinical results of colon carcinoma immunotherapy, it shows that the way to develop new methods such as Car-T cells, Car-NK cells and other techniques in immunotherapy have paved the way for the treatment of this disease and other cancers without harming other organs of the body. Keywords: Immunotherapy, colon carcinoma, cancer

The Inflammatory Role of Interleukin-33 in breast cancer and idiopathic granulomatous mastitis

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نوع پذیرش: پوستر | کد مقاله: G-92716

Abstract: Background: Breast cancer (BC) is the main cause of cancer death in women. Idiopathic granulomatous mastitis (IGM), a rare and chronic disease mimics breast carcinoma clinically, which is related to the high rate of mortality. Immediate and accurate diagnosis decreases its mortality and morbidity rates. Interleukin-33 (IL-33) has an induction role in the network of pro-inflammatory cytokines and is expressed in numerous human tissues. The aim of this study was to investigate the levels of IL-33 in BC, and IGM patients. Material and Methods: In this descriptive- analytical study, 28 patients with BC, and 25 patients with IGM were sampled after obtaining written consent. Histopathological pattern of BC and IGM were confirmed by specialized pathologists. In addition, 25 healthy volunteers with normal screening reports consist of the control group. The serum concentration of IL-33 was measured using enzyme-linked immunosorbent assay (ELISA) according to the kit manufacturer's instructions. Results: The mean age of the participants with BC, IGM, and control groups were 49.1, 37.1, and 36.8 years, respectively. IL-33 assay indicated a significant difference between BC ($p = 0.011$), and IGM ($p = 0.031$) groups compared to the control group, but the comparison levels of IL-33 between the IGM and BC groups didn't show a significant difference. Also, there was no significant difference in all groups by considering age, marriage, BMI, and menopause with the IL-33. Conclusion: IL-33 is a significant factor in IGM and BC patients compared to the control group, but it couldn't be used to diagnose and differentiate BC from IGM. Keywords: Breast cancer, Idiopathic granulomatous mastitis, Interleukin-33



چهاردهمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Increase levels of interleukin-6 in Hashimoto's thyroiditis

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نوع پذیرش: پوستر | کد مقاله: G-04729

Abstract: Background: Hashimoto's thyroiditis is an autoimmune disorder that happened when thyroid cells devastate through cell and antibody-mediated reactions. Recently indicated a group of cytokines have crucial role in pathogenesis this disease. The purpose of this study was to investigate the levels of interleukin 6 in the serum of Hashimoto's disease and control group. Materials and Methods: In this study, 30 patients with Hashimoto thyroiditis and 30 control groups were included in the study. The level of interleukin 6 was evaluated by ELISA kit. Results: The level of interleukin 6 was higher in patients with Hashimoto's thyroiditis than in the control group (p 0.05). Conclusion: Increased levels of IL-6 in patients with Hashimoto's thyroiditis may play a role in the pathogenesis of the disease. Keywords: Interlukin-6, Hashimoto's thyroiditis, Cytokine



چهاردهمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



The Effects of Asthma on the Endothelial Dysfunction Factors in Children with Pneumonia

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نوع پذیرش: پوستر | کد مقاله: G-82613

Abstract: Background: Pulmonary vascular endothelial activation has been implicated in adverse clinical outcomes of community-acquired pneumonia (CAP). Although chronic lung problems such as asthma may affect the consequences of pneumonia, the exact mechanism of this effect remains unclear. The present study aimed to assess the effects of asthma on the endothelial activation biomarkers in children pneumonia. Materials and Methods: A cross-sectional study designed with a total of 75 children including both severe CAP and asthma (as group I), severe CAP alone (as group II), and healthy children (as group III) was conducted. Fasting blood samples were taken to the assay of serum soluble vascular cell adhesion molecule-1 (sVCAM-1) and plasminogen activator inhibitor-1 (PAI-1). Results: VCAM-1 and PAI-1 levels as the endothelial dysfunction biomarkers were significantly higher in group I (1.5 ± 0.62 mmol/l, 10.52 ± 3.2 AU/ml, respectively) compared with groups II (1.06 ± 0.53 mmol/l and 8.23 ± 3.4 AU/ml; P value = 0.009, P value = 0.000, respectively) and III (0.6 ± 0.35 mmol/l and 2.39 ± 0.83 AU/ml; P value = 0.000, P value = 0.000, respectively). Also, VCAM-1 and PAI-1 levels were significantly higher in group II compared with groups III (P value = 0.000, P value = 0.000). Conclusion: can exacerbate the vascular dysfunction of pneumonia in children. Keywords: Community-Acquired Pneumonia, Asthma, the vascular dysfunction.



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Misleading issues and challenges in the diagnosis of eosinophilic gastrointestinal disorders

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نوع پذیرش: پوستر | کد مقاله: G-34178

Abstract: Background: Eosinophilic gastrointestinal disorders (EGIDs) are a group of diseases that are associated with an increased presence of eosinophils in the gastrointestinal tract. Although the available evidence shows that the prevalence of this group of diseases is increasing, there is no specific and standardized criteria for diagnosing them, and the defects of the current criteria cause delays in diagnosis and misdiagnosis for patients with EGIDs. Materials and Methods: By evaluating the available literature, we examined the pitfalls of the existing diagnostic criteria for EGIDs and described factors that attention to them can improve the diagnosis of these diseases. Results: In this review, the defects and pitfalls in the EGIDs diagnosis guideline were discussed. Also, the factors related to the disease beyond what is considered in the current diagnostic criteria such as cytokines, genetics, etc. were introduced, which by putting them together can achieve a comprehensive and effective diagnostic criteria for EGIDs. Conclusion: Since the existing diagnostic criteria for detecting EGIDs is not sufficiently developed and may miss a number of patients, defining a new guideline by considering various factors can lead to more accurate and faster diagnosis of patients with these diseases. Keywords:

Immunopharmacological Perspective on Zinc in SARS-CoV-2 Infection

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نوع پذیرش: پوستر | کد مقاله: G-69084

Abstract: The novel SARS-CoV-2 which was first reported in China is the cause of infection known as COVID-19. In comparison with other coronaviruses such as SARS-CoV and MERS, the mortality rate of SARS-CoV-2 is lower but the transmissibility is higher. Immune dysregulation is the most common feature of the immunopathogenesis of COVID-19 that leads to hyperinflammation. Micronutrients such as zinc are essential for normal immune function. According to the assessment of WHO, approximately one-third of the world's society suffer from zinc deficiency. Low plasma levels of zinc are associated with abnormal immune system functions such as impaired chemotaxis of polymorphonuclear cells (PMNs) and phagocytosis, dysregulated intracellular killing, overexpression of the inflammatory cytokines, lymphopenia, decreased antibody production, and sensitivity to microbes especially viral respiratory infections. Zinc exerts numerous direct and indirect effects against a wide variety of viral species particularly RNA viruses. The use of zinc and a combination of zinc-pyridione at low concentrations impede SARS-CoV replication in vitro. Accordingly, zinc can inhibit the elongation step of RNA transcription. Furthermore, zinc might improve antiviral immunity by up-regulation of IFN α through JAK/STAT1 signaling pathway in leukocytes. On the other hand, zinc supplementation might ameliorate tissue damage caused by mechanical ventilation in critical COVID-19 patients. Finally, zinc might be used in combination with antiviral medications for the management of COVID-19 patients. In the current review article, we review and discuss the immunobiological roles and antiviral properties as well as the therapeutic application of zinc in SARS-CoV-2 and related coronaviruses infections.

Keywords:



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Investigation of IL-10 serum level in patients with severe COVID-19 undergoing treatment

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نوع پذیرش: پوستر | کد مقاله: G-24695

Abstract: Background: In coronavirus disease 19 (COVID-19), serum levels of L-10 increase along with cytokines such as IL-6, IL-8, and TNF- α . Furthermore, increased serum IL-10 levels are associated with the severity of COVID-19. The aim of this study was to investigate the serum levels of IL-10 in patients with severe form of COVID-19 undergoing treatment. Methods: 30 patients with severe form of COVID-19 hospitalized in intensive care unit (ICU) undergoing treatment in Imam Reza Hospital of Kermanshah and 30 patients with mild COVID-19 (outpatients) were included in the study. Blood was collected from patients and serum IL-10 levels were measured using a human IL-10 ELISA kit (Zell Bio GmbH, Germany). Results: The results of this study showed that the serum level of IL-10 in patients with severe form of COVID-19 (62.13 ± 20.39) was significantly lower than in patients with mild form of the disease (83.23 ± 11.76) (P value less than 0.0001). Conclusion: In general, these results showed that therapeutic processes in patients with severe form of COVID-19 reduce the serum level of IL-10 in these patients even lower than its level in patients with mild form. Keywords: COVID-19, IL-10, Treatment, ELISA



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Comparison of exosome isolation methods: A brief review

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نوع پذیرش: پوستر | کد مقاله: G-73685

Abstract: Background: Exosomes (30-150 nm) are membrane-bound extracellular vesicles produced in the endosomal compartments of most eukaryotic cells. In multicellular organisms, exosomes and other extracellular vesicles have been discovered in biological fluids including blood, urine, cerebrospinal fluid, and various tissues. Methods: In this context, many biotech companies are developing different methods to isolate exosomes. These procedures include centrifugation, chromatography, filtration, polymer-based precipitation, and immunological isolation. In this study, different databases were used to receive articles. Recent advances have led to easier and faster isolation of exosomes. Contamination of isolated exosomes with small apoptotic vesicles, apoptotic bodies of lipoproteins, and exomers can lead to wrong conclusions about the exosomes biological activities. Results: Therefore, the separation method affects the purity and yield of exosomes. The use of ultrafiltration and chromatography yielded 58-fold more exosomes than ultracentrifugation. Exosomes secreted from body fluids usually play an important role in the pathogenesis of diseases. Different methods have been developed to separate exosomes from biological fluids. Conclusion: In general, centrifugation techniques are very common, however, other methods such as immunological and filtration procedures also show positive results; therefore, these options can be effectively used in laboratory research as well. Key words: Exosome, Ultracentrifuge, Filtration, Body fluids.

The impact of multi strains of probiotics on Th17-related cytokines in patients with asthma: a randomized, double-blind, placebo-controlled trial

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نوع پذیرش: پوستر | کد مقاله: G-49382

Abstract: Background: Asthma is known as one of the most common chronic inflammatory diseases characterized by recurrent obstruction and inflammation of the airways. Probiotics are defined as a group of beneficial living microorganisms that are beneficial in many disorders, including allergies. The aim of this study was to investigate the probiotic supplement effects on improvement of clinical asthma symptom and changes in the pattern of Th17-related inflammatory cytokines in asthmatic patients. Methods: This was a randomized controlled clinical trial with parallel, double-blind groups. Forty patients with asthma were enrolled and received 1 capsule/day of a probiotic supplement for 8 weeks. Respiratory function tests; and the level of IL-6, IL-17, IL-21 and TGF- β were evaluated at the baseline and end of intervention. Results: The results showed that the level of IL-6 and IL-17 in patients after receiving probiotics was reduced and expression of TGF- β was increased as compared to the baseline. Also, the expression of IL-17 and IL-21 in the probiotic group was significantly lower than the placebo group at the end of the intervention. In addition, an improvement in pulmonary function tests and clinical symptoms was observed after receiving probiotics. Conclusion: Eight-weeks treatment with a probiotic supplementation suggests that it may effect on Th17 cells-associated IL-6, IL-17 and TGF- β ; and Forced Expiratory Volume in 1 second and Forced Vital Capacity. Taken together, these results suggest that probiotics may have the ability to affect neutrophilic asthma and they can possibly be used besides common treatments for patients with neutrophilic asthma. Keywords:

Investigating traces of antibodies caused by natural infection with covid-19 in breast milk. Systematic review

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نوع پذیرش: پوستر | کد مقاله: G-27049

Abstract: Background: Since the beginning of the Corona pandemic, babies have taken a large share of concerns to be safe from the global virus, Covid-19. Even today, common vaccines against this disease have not been approved for injection for babies. A 2020 meta-analysis found that the SARS-CoV-2 genome was generally not found in the milk of lactating women with Covid-19. The World Health Organization also emphasizes the continued breastfeeding and its harmlessness during the mother's infection with the corona virus. However, in the very large studies that were conducted in the past with different goals on breast milk, in addition to helping the growth and development of the baby, they proved its important role in shaping the child's immune system, but due to the emerging and widespread nature of this infection. There is the importance of investigating different aspects of this disease. Our aim in this study is to investigate antibodies against covid-19 in breast milk due to natural infection. Materials and Methods: In this systematic review study, which was conducted by two people at the same time, 14 studies were included in the review process. The search strategy using the words "antibody", "breast milk" and "Covid-19" as well as similar words were extracted from the MeSH database and free search and were performed in the PubMed and Google Scholar databases until November 18, 2022. The inclusion criterion is to be in line with the main purpose of the study, the studied study must be original and published in English. The exclusion criterion was lack of access to the complete file of the study. Results: In the total of the studies included in this review, the milk samples of 816 lactating women with an average age of 32.1 ± 4.7 years, all of whom had a definite history of covid-19 infection, were collected. Only 13 samples (1.59%) were not capable of neutralizing SARS-COV-2 infection in laboratory conditions. In all the reviewed studies, the presence of IgG and IgA antibodies was confirmed, but only 6 studies indicated the presence of IgM antibodies along with other antibodies. Among these three antibody classes, the highest titers were related to IgA, IgG and IgM respectively. Of all the participants, 62.5% had IgA class antibodies and 56.25% had IgG antibodies specific to this RBD (receptor-binding domain) virus. No significant difference has been reported between the titers of antibodies in symptomatic and asymptomatic women during their illness to this virus. Conclusion: According to the findings of this study, breast milk is a suitable source and a safe method for creating passive immunity against this virus in infants. And the importance of encouraging mothers to breastfeed their babies to help achieve collective immunity against this virus as soon as possible. Keywords: Antibody, Breast milk, Covid_19



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Role of neurotransmitters in immune-mediated inflammatory disorders: a crosstalk between the nervous and immune systems

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نوع پذیرش: پوستر | کد مقاله: G-04687

Abstract: Immune-mediated inflammatory diseases (IMIDs) are a group of common heterogeneous disorders, characterized by an alteration of cellular homeostasis. Primarily, it has been shown that the release and diffusion of neurotransmitters from nervous tissue could result in signaling through lymphocyte cell-surface receptors and the modulation of immune function. This finding led to the idea that the neurotransmitters could serve as immunomodulators. It is now manifested that neurotransmitters can also be released from leukocytes and act as autocrine or paracrine modulators. Increasing data indicate that there is a crosstalk between inflammation and alterations in neurotransmission. The primary goal of this review is to demonstrate how these two pathways may converge at the level of the neuron and glia to involve in IMID. We review the role of neurotransmitters in IMID. The different effects that these compounds exert on a variety of immune cells are also reviewed. Current and future developments in understanding the cross-talk between the immune and nervous systems will undoubtedly identify new ways for treating immune-mediated diseases utilizing agonists or antagonists of neurotransmitter receptors. Keywords:



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Immunogenicity of the COVID-19 vaccines in adult patients with autoimmune inflammatory rheumatic diseases: A systematic review and meta-analysis

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نوع پذیرش: پوستر | کد مقاله: G-98012

Abstract: Background COVID-19 vaccines approved by the FDA have been studied mainly in healthy individuals and there is limited information on their immunogenicity and safety in individuals with autoimmune diseases. Therefore, in this meta-analysis study, we comprehensively investigated the immunogenicity of these vaccines in patients with autoimmune inflammatory rheumatoid diseases (AIIRD). Method: A literature comprehensive search was performed on various databases, including PubMed, Google Scholar, Web of Science, Scopus, and Embase to select cohort and clinical-trial (RCT) studies up to January 2022. Also, to quality assessment and heterogeneity tests of the selected studies, the PRISMA checklist protocol and the I2 statistic were used, respectively. Fixed and random-effects models were estimated based on the heterogeneity tests, and pooled data were determined as the standardized mean difference (SMD) with a 95% confidence interval (CI). Result As a result, we found that vaccines can cause favorable immunogenicity in vaccinated AIRD patients with an acceptable safety profile; however, older age and the concomitant consumption of glucocorticoids, rituximab, mycophenolate mofetil (MMF), and methotrexate (MTX) drugs could significantly reduce the vaccine immunogenicity. Conclusion: Consequently, our findings revealed a significant humoral response (seropositive) and no apparent side effects in AIRD patients following the administration of COVID-19 vaccines. Keywords: COVID-19, Vaccine, AIIRD, Safety, efficacy



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دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Investigating the role of monoclonal antibodies in recognizing the infectious intracellular parasite leishmania

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نوع پذیرش: پوستر | کد مقاله: G-67084

Abstract: Introduction: Leishmaniasis is one of the most important infectious diseases that is widespread all over the world. Three forms of this disease have been identified in humans. Leishmaniasis is the most dangerous form of this disease, which is endemic in different countries of the world, including the Mediterranean areas and Iran, and according to the studies conducted, its causative agent is known to be *Leishmania infantum* in most parts of the world. Despite all the efforts made, leishmaniasis is still one of the health problems of the world and the region. According to the above, the aim of this study is to investigate the role of monoclonal antibodies in recognizing the infectious intracellular parasite *Leishmania*. Methods: *Leishmania infantum* parasite was cultured as promastigote. Then antigen was prepared from the resulting parasites in order to stimulate the tested mice. Integration of the spleen cells of the immunized mice with SP20 cells was done and monoclones were obtained from the resulting hybridomas. Results: Monoclonal antibodies obtained against the promastigote form of *Leishmania infantum* were investigated. Those who had higher antibody titers were selected and their effect on the mentioned parasite antigens was tested. Discussion: These antibodies may also react against *Leishmania infantum* amastigote and help in the diagnosis of leishmaniasis and it seems that they can be used for diagnostic kits. Keywords: monoclonal antibodies, intracellular parasite, infectious agent, *Leishmania*

The modulatory effects of two bioflavonoids, quercetin and thymoquinone on the expression levels of DNA damage and repair genes in human breast, lung and prostate cancer cell lines

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نوع پذیرش: پوستر | کد مقاله: G-19632

Abstract: Background: The recent decade has witnessed the increasing potential of various flavonoids such as quercetin and thymoquinone in inhibiting cancer cells proliferation and growth and their therapeutic effects in various cancers. Therefore, in the current study, we aim to evaluate the expression levels of key factors of DNA damage response in human breast, lung and prostate cancer cell lines in response to treatment with quercetin and thymoquinone. Materials and Methods: MTT assay was applied to assess the effects of quercetin and thymoquinone on the viability of MCF-7, A549, and PC3 cancer cells. Quantitative reverse transcription-polymerase chain reaction (qRT-PCR) was used to evaluate the expression levels of p53, RAD51, Ku70, XRCC1, and H2AX in treated cells. In addition, the expression rate of 8-hydroxy-deoxyguanosine (8-OH-dG) was assessed by ELISA kit. Results: The quercetin and thymoquinone induce cytotoxicity in breast, lung, and prostate cancer cells effectively; MCF-7 cells were the most sensitive cells to quercetin with an IC50 value of 50 μ M and PC3 cells were more sensitive to thymoquinone with an IC50 value of 20 μ M. The expression levels of DNA damage markers, H2AX, and 8-OH-dG were significantly increased in all cancer cells treated with quercetin and thymoquinone ($p < 0.05$). Moreover, both flavonoids significantly decreased the expression levels of DNA repair mediators, RAD51, Ku70, XRCC1, in cell lines. P53 was also increased in MCF-7 and A549 cells. Conclusion: We found that flavonoid, quercetin and thymoquinone significantly increased DNA damage and suppressed the expression levels of DNA repair genes in cancer cells. We showed that the anticancer effects of quercetin and thymoquinone could be mediated by the effects of the DNA damage response. According to our results and multiple studies, p53 is located in the hot point of anti-cancer effects of quercetin and thymoquinone, p53 increase apoptosis and cell cycle arrest after exposure with quercetin and thymoquinone and in the other hand can suppress DNA repair machinery system. All in all, bioflavonoids have anti-cancer effects through multiple pathways like DNA damage response. Keywords:

The effects of methotrexate on the immune responses to the COVID-19 vaccines in the patients with Immune-mediated inflammatory disease: A systematic review of clinical evidence

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نوع پذیرش: پوستر | کد مقاله: G-08124

Abstract: Background: COVID-19 vaccines exhibit high levels of immunogenicity in the overall population. Data on the effects of immunomodulators on the consequences of COVID-19 in patients with Immune-mediated inflammatory diseases (IMIDs) remains scarce. This systematic review aimed to evaluate the immune responses to the COVID-19 vaccines in IMID patients receiving methotrexate (MTX) compared with healthy individuals. Materials and Methods: A comprehensive search for literature was carried out using electronic databases such as PubMed, Web of Science, Scopus, Google Scholar, and Embase up to August 2022 to identify eligible RCT evaluating the effect of MTX on immune responses in patients with COVID-19. The PRISMA checklist protocol was applied for quality assessment of the selected trials. Results: Our findings demonstrated that MTX lowered the responses of T cells and antibodies in IMID patients compared to healthy controls. We also discovered that young age (60 years) was the main parameter influencing antibody response after vaccination, while MTX dose had little effect. Age linked inversely with immune response on MTX patients, and all patients with antibody titers below the threshold were over the age of 60. Following vaccination, the period effect was more significant than before vaccination, with 10 days being the critical discontinuation. Because many IMID patients did not have adequate humoral and cellular responses, our findings highlighted the importance of second/booster vaccine doses and temporary MTX discontinuation. Conclusion: As a result, it implies that individuals with IMIDs should be subjected to more research, particularly humoral and cellular immunity efficiency trials after COVID-19 vaccination, until a credible information is achieved. Keywords:

The effect of Coronavirus on the rate of brain disease: a systematic review

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نوع پذیرش: پوستر | کد مقاله: G-51680

Abstract: Background: COVID-19 first occurred in Wuhan, China, in late 2019. The COVID-19 pandemic had killed 232,478 people and infected 3,291,008 people as of May 1, 2020. Cough, sputum production, exhaustion, shortness of breath, and most symptoms of the respiratory tract are the most typical clinical signs. But a growing number of instances have also included neurologic symptoms, such as olfactory and gustatory issues. No aspect of life has been unaffected by the COVID-19 epidemic. In addition, to having a direct impact on the person's health, it has also had important societal, psychological, and economic repercussions. Materials and Methods: Between December 2019 and April 30, 2021, we carried out a systematic review and gathered the majority of the data using PubMed and Google Scholar. Medical subject headings (MeSH) keywords were used in our investigation, including "coronavirus", and "neurological effects of coronavirus". Peer reviews were conducted on most of the publications utilized in this study. This research decided to include participants of every age and gender. For our search strategy and flowchart, we followed the Preferred Reporting Items for Systematic Reviews and Meta-Analyses (PRISMA) criteria. Results: 12 papers were removed after 87 articles in total were assessed and their quality evaluated. According to research, headaches, nausea, disorientation, reduced awareness, and seizures are all neurological symptoms. Due to the disease's novelty, relatively few researchers have examined the psychological implications of the COVID-19 pandemic. The survey's result demonstrated a broad spectrum of worries and behavior about the impact of the fear and present epidemic of coronavirus throughout the community. Overall, the neurological features of the viral onslaught must, therefore, be taken into mind in establishing the treatment methods and recovery paragons intended for sufferers of COVID-19. Headache (11–13%), vertigo (8–17%), and altered state of awareness (8–9%) are some of the most prevalent neurological symptoms. Up to 5% of patients are now documented to additionally include several peripheral nervous system abnormalities, such as neuralgia, hypogeusia, and hyposmia or anosmia. Ataxia (1%), epilepsy (1%), and acute cerebrovascular illness (3%), which are less frequent, have also been noted. Conclusion: The neurotropic potential of the COVID-19 virus might be clarified by a consistent report on the patients exhibiting neurological symptoms of the virus together with other study discoveries including involuntary loss of control over breathing, seizures, headaches, and decreased awareness. Clinical suspicion for both acute and chronic neurologic problems in COVID-19 patients must be high, according to clinicians. Keywords: COVID-19 - Pandemics- Nervous System Diseases

A narrative review on Mesenchymal stem cells (MSCs), their properties and recent clinical findings

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نوع پذیرش: پوستر | کد مقاله: G-58092

Abstract: Background: Mesenchymal stem cells (MSC) are subtypes of immature multipotent cells with self-renewing potency that can differentiate into mesenchymal cell lines including osteoblasts, chondrocytes, myocytes, cardiomyocytes, and adipocytes. MSCs can be isolated from different tissues but it is better to separate them from the umbilical cord. MSCs present low levels of MHC-I, CD80, CD86, and CD40. They don't express MHC-II. Studies show that CD106 (VCAM-1), CD146, and ITGA11 are MSC special markers. In this review study, we attempted to express some properties and medical discoveries of these amazing cells. Materials and Methods: We searched different electronic databases, such as Google scholar, PubMed, Medline, and other relevant sources published in English globally, by using the search terms "MSCs and different disease treatments", "Stem cells and new medical applications", also "perspective and challenges in MSCs field". Results: Studies display that in the presence of MSCs, M1 macrophages alter to M2 macrophages which led to a decrease in inflammation. Also, MSCs can disturb the activation, proliferation, and differentiation of T cells. As well as in inflammation conditions, they inhibit the differentiation process of Th1 and Th17 and marvelously advance Th2 and Treg formation. MSCs' Impression on B cells is not completely clear. MSCs can produce some growth factors (for tissue regeneration), immunomodulators, anti-apoptotic and anti-inflammatory cytokines. Conclusion: Studies indicate that mesenchymal stem cells with their regenerative and immunomodulatory specialties can help us miraculously to improve cardiovascular injuries, autoimmune diseases, cancers, and neurodegenerative diseases and they can even reduce transplant complications. Keywords: Mesenchymal stem cell, Immunomodulation, Inflammation, Transplant, Treatment.

Evaluation of HLA-DRB1 in patients with Type 1 diabetes

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نوع پذیرش: پوستر | کد مقاله: G-49673

Abstract: Background: Many studies and research have shown that type 1 diabetes is related to the polymorphism of HLA region genes in chromosome 6 (P21 6), chromosome 6 is specific for DRB1 and some HLA class II genes. Type 1 diabetes, formerly called insulin-dependent diabetes, affects all ages but is more common in children and young adults. Materials and Methods: Serum samples from 35 patients with Type 1 diabetes (T1DM) were evaluated for the level of HLA-DRB1 biomarker and compared with 35 negative controls who did not have diabetes. The measurement of the HLA-DRB1 level was detected quantitatively using the HLA-DRB1 ELISA Kit according to the manufacturer's instructions, and an ELISA reader measured the HLA-DRB1 level. Results: The average age of patients (26.78 ± 13.11) and healthy people (29.98 ± 3.9) had no significant difference. HLA-DRB1 was significantly higher in patients than in controls. The increasing trend in HLA-DRB1 levels was directly related to the blood glucose level of people with diabetes. So, in patients with Type 1 diabetes (T1DM), HLA-DRB1 was reported in the range of (1850 ± 5.12) pg/ml and in the control group in the range of (987 ± 8.74) pg/ml. And there was a statistically significant ($p < 0.05$) difference. Conclusion: Our study shows that HLA-DRB1 is associated with the severity of clinical symptoms of type 1 diabetes. However, more studies are needed in this area.. Keywords: HLA-DRB1, Type 1 diabetes (T1DM)



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دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Association between Interleukin-32 gene polymorphism and susceptibility to preeclampsia

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نوع پذیرش: پوستر | کد مقاله: G-20985

Abstract: Background: Preeclampsia (PE) is a multi-system, hypertensive disorder of pregnancy that complicates 5–10% of pregnancies. PE is a placental disease and the immune system plays an important role in a normal placentation. This study aims to determine association between IL-32 gene polymorphism, and serum levels of IL-32 and susceptibility to preeclampsia. Methods: Totally, 199 women diagnosed with PE, and 228 healthy women were recruited. The frequency of IL-32 rs9927163 and rs4786370 polymorphisms was determined by PCR-RFLP. Also ELISA was used to determine the levels of serum IL-32 in the two groups. Results: Regarding rs4786370 C/T SNPs, the frequencies of CT, TT genotypes and T allele showed to be higher in the PE patients. Also the serum level of IL-32 significantly increased in the PE patients (161.86 ± 58.85 vs. 118.28 ± 45.27 pg/ml, $p=0.0001$). Conclusion: Variety in allele and genotype IL32 rs4786370 as well as a rise in serum level of IL-32 can be regarded as a risk factor for PE. Key Words: Gene polymorphism, IL-32, Preeclampsia, Pregnancy

In vitro differentiation of dendritic cells from peripheral blood mononuclear cells (PBMCs)-derived monocytes

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نوع پذیرش: پوستر | کد مقاله: G-24058

Abstract: Background: Human immune system is structured from innate and adaptive immunity. The innate immune system is considered the primary line of defense against different pathogens and it is made up of various cells consisting of innate lymphocyte cells (ILCs), macrophages, neutrophils, natural killer cells (NKs), and dendritic cells (DCs). DCs are the most potent antigen presenter cell (APC) that possess the capability to present antigens to T lymphocytes and augment the adaptive immune response. DCs comprise some subsets including plasmacytoid DCs (pDCs), conventional DCs (cDCs), Langerhans cells, and monocyte-derived DCs (moDCs). moDCs are known as potent cells in the process of cell therapy and their development and homeostasis depend on some cytokines like interleukin-4 (IL-4) and granulocyte-macrophage colony-stimulating factor (GM-CSF). Material and method: First of all, peripheral blood mononuclear cells (PBMCs) were isolated from the whole blood of healthy donors by fractionation over Ficoll gradients. Magnetic activated cell sorting (MACS) technique was recruited for separating the CD14+ monocytes from PBMCs. After being separated, 1×10^6 monocytes/ml were seeded in a 6-well plate and were then cultivated in complete medium (CM) (Roswell Park memorial institute (RPMI) containing 10% FBS) that had been supplemented with $50 \mu\text{M}$ 2-Mercaptoethanol (2ME), 40 ng/mL of rhGM-CSF, and 25 ng/mL of rhIL-4. On day 3, fresh CM containing rhGM-CSF and rhIL-4 was added to the remaining half of the media to feed the cultures. On day 5, cells were collected and assayed based on their morphological and phenotypic features. Results: Above 90% of monocytes were isolated from PBMCs by MACS technique. Finally, monocytes differentiated to immature DCs after 5 days in the presence of GM-CSF and IL-4. Based on phenotypic features evaluated by flow cytometry, 70 percent of collected cells on the day 5 were CD11c+ immature DCs. Conclusion: Monocyte differentiation to DCs has been considered a potential approach for immunotherapy in some diseases including various cancers. Keywords:

Xanthohumol: An underestimated, while potent and promising chemotherapeutic agent in cancer treatment

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نوع پذیرش: پوستر | کد مقاله: G-91437

Abstract: Today, there is a growing interest nowadays in the use of herbal substances as cancer therapeutic agents. Over recent years, Xanthohumol (XTL) has been brought out as a prenylated chalcone that is found in hops (*Humulus lupulus*) and beer. XTL is being investigated for its potential properties, and it has been found to have various biological effects, including anti-microbial, anti-viral, and immunomodulatory. Other than these biological effects, it has also been found that XTL exerts anti-tumor effects. In the beginning, XTL, by modulating cell signaling pathways, including ERK, AKT, NF- κ B, AMPK, Wnt/ β -catenin, and Notch signaling in cancer cells, inhibits tumor cell functions. Moreover, XTL, by inducing apoptotic pathways, either intrinsic or extrinsic, promotes cancer cell death and arrests the cell cycle. Furthermore, XTL inhibits metastasis, angiogenesis, cancer stemness, drug resistance, cell respiration, etc., which results in tumor aggressiveness inhibition. XTL has low solubility in water, and it has been hypothesized that some modifications, including biotinylation, can improve its pharmacogenetic characteristics. Additionally, XTL derivatives such as dihydroXTL and tetrahydroXTL can be helpful for more anti-tumor activities. Using XTL with other anti-tumor agents is another approach to overcome tumor cell resistance. XTL or its derivatives, it is believed, might provide novel chemotherapeutic methods in future cancer therapy. Keywords: Xanthohumol, Chalcone, Cancer, Phytotherapy, Chemotherapy



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Gut microbiome and multiple sclerosis: New insights and perspective

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نوع پذیرش: پوستر | کد مقاله: G-69250

Abstract: Background: The human gastrointestinal microbiota, also known as the gut microbiota living in the human gastrointestinal tract, has been shown to have a significant impact on several human disorders including rheumatoid arthritis, diabetes, obesity, and multiple sclerosis (MS). Materials and Methods: A narrative review article. Results: MS is an inflammatory disease characterized by the destruction of the spinal cord and nerve cells in the brain due to an attack of immune cells, causing a wide range of harmful symptoms related to inflammation in the central nervous system (CNS). Despite extensive studies on MS that have shown that many external and genetic factors are involved in its pathogenesis, the exact role of external factors in the pathophysiology of MS is still unclear. Recent studies on MS and experimental autoimmune encephalomyelitis (EAE), an animal model of encephalitis, have shown that intestinal microbiota may play a key role in the pathogenesis of MS. Therefore, modification of the intestinal microbiome could be a promising strategy for the future treatment of MS. Conclusion: In this study, the characteristics of intestinal microbiota, the relationship between intestine and brain despite the blood-brain barrier, various factors involved in intestinal microbiota modification, changes in intestinal microbial composition in MS, intestinal microbiome modification strategies, and possible use of intestinal microbiome and factors affecting it have been discussed. Keywords:

Distribution of HLA-DRB1 and HLA-DQB1 alleles in Lak population of Iran

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نوع پذیرش: پوستر | کد مقاله: G-13948

Abstract: Background: Human leukocyte antigen (HLA) genes are the most polymorphic loci in the human genome and encode the highly polymorphic molecules critically involved in immune responses. Anthropological studies based on highly polymorphic HLA genes provide useful information for bone marrow donor registry, forensic medicine, disease association studies, as well as designing peptide vaccines against tumors, and infectious or autoimmune diseases. The aim of this study was to determine the HLA-DRB1 and HLA-DQB1 allele frequencies in 100 unrelated Lak individuals from Lorestan province of Iran. Methods: In this study, blood samples were collected with informed consent from 100 unrelated Lak individuals 20–30 years old, male and female each 50, inhabitant of Lorestan province of Iran. All participants were third generation natives of the selected area and none had personal or family history of cancer or autoimmune diseases. Their genomic DNA was extracted from peripheral blood leukocytes using EXTRA GENE I kit (BAG Health Care GmbH, Lich, Germany). Commercial HLA-Type kits were used for determination of the HLA-DRB1 and HLA-DQB1 allele frequencies. Differences between populations in the distribution of HLA-DRB1 and HLA-DQB1 alleles were estimated by χ^2 test with Yate's correction and Fisher's exact test. Results: The frequency of HLA-DRB1 and HLA-DQB1 alleles in the Iranian Lak population was investigated. We identified 24 alleles for HLA-DRB1 and 10 alleles for HLA-DQB1 in our population sample of 100 Lak individuals. The most frequent HLA-DRB1 alleles were 1103 = 4 (23%), 1502 (9.5%), 0701 (9%), 0301 (8.5%), 1101 (7.5%) and 1501 (6%) while HLA-DQB1 0301 (40%), 0201 (15%), 0502 (10.5%), 0303 (10%), 0602 = 3 (9.5%), and 0501 (7.5%) were the most frequent alleles in Lak population. HLA-DRB1 0409, 0804, 1102, 1112, 1405, and HLA-DQB1 0503, 0604 were the least observed frequencies in Lak population. Neighbor-joining tree based on Nei's genetic distances and correspondence analysis. based on HLA-DRB1 and HLA-DQB1 allele frequencies show the genetic relationship of Laks with other Iranian subpopulations. As illustrated, the Laks are close to Lurs of Khorramabadi and Kurd but far from Lurs of Kohkiluyeh/ Boyerahmad and Bakhtiari. Conclusion: our results based on HLA-DRB1 and HLA-DQB1 allele frequencies showed that the Lak population possesses the previously reported general features of the Lur and Kurd populations, with some additional interesting differences. In other words, the Lak population is close to Lurs of Khorramabadi and Kurd but far from Lurs of Kohkiluyeh/Boyerahmad and Bakhtiari. Keywords: HLA class II, Lak population, Iran, PCR-SSP

Serological Changes during the Pulmonary Mucormycosis; A Systematic Review on Molecular Approach of Laboratory Diagnosis

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نوع پذیرش: پوستر | کد مقاله: G-74618

Abstract: Mucormycosis is a disease caused by the Mucormycete fungus, found in mammals' mucosa and can spread easily in hospital conditions. Early diagnosis is very vital for a safe treatment, so if diagnosis and treatment are not done on time, it can cause necrosis. pathological sampling from lung tissue is too hard, and time-consuming, it can be one of the problems during the diagnosis of this fungal infection. On the other hand, Filamentous fungi cannot be diagnosed with radiological techniques, so serological diagnosis is useful way. This article was amassment by reviewing published articles with related keywords in valid databases from 1995 to 2022. Many tests are prepared to check the level of Antibodies (Ab) in the blood, which does not have the hardness of other diagnostic methods (e.g., histopathology). Although examining the serum extracted from patients' blood is not very accurate, it is very useful in early diagnosis. Different serologic methods based on Immunofluorescence Assay (IFA), Hemagglutinin-Inhibition Assay (HI), precipitation, and complementation, and Enzyme-Linked Immunosorbent Assay (ELISA) have been defined to check the amount of Immunoglobulins(Ig) or Abs and Antigens (Ag) in the blood. There are many diagnostic tests in this regard, for example, neutralization tests, Direct Agglutination Tests (DATs), immunoblotting tests, and immunodiffusion tests. Mucorales (formerly Zygomycota), are usually observed in the mucosal layer of various organs, including the respiratory system. After creating a colony in the mucosal layer, this fungus penetrates the lower layers of the tissues and enters the circulatory system. When this fungus leaks into the blood it can flow throughout the body. But before its entry, the host's immune system tries to fight the fungal infection by releasing cytokines and Abs. In serologic methods, by examining different levels of immune cells and immune parameters, we can confirm or rejects the possibility of mucormycosis in patients.

Expression pattern of Drug-Resistance Genes ERG11 and TAC1 in *Candida albicans* Clinical Isolates

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نوع پذیرش: پوستر | کد مقاله: G-41356

Abstract: Background: *Candida albicans* (*C. albicans*) is an opportunistic fungus and the most common cause of vulvovaginal candidiasis (VVC). In recent years, the use of antifungal drugs has led to the incidence of drug-resistant *C. albicans* strains. The purpose of this study is twofold: to determining the pattern of drug sensitivity and the relationship between risk factors and the incidence of drug resistance among *C. albicans* isolates and investigated the expression pattern of drug-resistance genes ERG11 and TAC1 in these isolates. Materials and Methods: This descriptive cross-sectional study was conducted on 50 *C. albicans* isolates from women with VVC. Antifungal susceptibility of the isolates was tested by M27-A3/S4 broth microdilution method following the Clinical and Laboratory Standards Institute (CLSI) guidelines. The change in ERG11 and TAC1 genes expression was determined by qPCR. The expression levels of genes (ERG11 and TAC1) were evaluated using the $2^{-\Delta\Delta CT}$ method, where Ct was the average threshold cycle number from three independent experiments. The threshold value 1 fold was considered over-expression. Data were presented as the fold change in gene expression normalized to the Act1 gene as internal control. Results: High susceptibility rates were recorded for itraconazole and voriconazole (68%), followed by ketoconazole (46%). Fluconazole had the lowest susceptibility on *C. albicans* with 36% sensitivity. The mean ΔCt values of ERG11 and TAC1 genes were significant difference between fluconazole-resistance and susceptible groups ($p < 0.001$). Interestingly, we found that 77% of fluconazole-susceptible isolates were remarkably upregulated ERG11 gene (2.9-99.0 fold). In addition, the expression of TAC1 was upregulated in 44% of fluconazole-susceptible isolates (3.86-89.8 fold). Conclusion: Our finding revealed that the over-expression of ERG11 and TAC1 genes may cause azole resistance; Incidence of drug resistance in *C. albicans* is not simply controlled by genes but is a multi-factorial phenomenon, where several factors and mechanisms are involved in the process. Keywords:



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Evaluation of cdr1b gene expression in voriconazole-resistant aspergillus flavus and a. fumigatus isolated from patients with pulmonary aspergillosis

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نوع پذیرش: پوستر | کد مقاله: G-31587

Abstract: Background: Aspergillus sections fumigatus and A. flavus are the common causes of invasive aspergillosis and pulmonary aspergillosis (PA). We evaluated of the relationship between voriconazole resistance and gene expression of efflux pump/Cdr1B in PA. Materials and Methods: This study was performed on 87 patients with PA. Isolated A. flavus and A. fumigatus were identified using the BTU-sequencing. Voriconazole sensitivity test was performed according to the CLSI M38-A2 guideline. The Cdr1B gene expression was conducted in voriconazole-resistant isolates compared with A. flavus PTCC 5004 and A. fumigatus PTCC 5009 using real-time PCR. Results: Out of 87 samples collected, 58 and 29 isolates were identified as A. flavus and A. fumigatus, which 4% and 3% were resistant to voriconazole, respectively. The qRT-PCR results showed that, overexpression of Cdr1B gene in voriconazole-resistant isolates was 7.8-fold. Overall, A. fumigatus isolates demonstrated overexpression of Cdr1B compared to A. flavus. Conclusion: Our results demonstrated that the Cdr1B gene expression associated with increased resistance to azole in PA. Keywords:



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Signature Polymorphisms in ITS rDNA Region for the Differentiation Species of the *T. interdigitale* and *T. mentagrophytes*

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نوع پذیرش: پوستر | کد مقاله: G-97018

Abstract: Background: Fungi of the *T. mentagrophytes* and *T. interdigitale* are important pathogenic dermatophytes that known to be the most common cause of various human skin infections in Iran. Communicating epidemiological statistics of these dermatophytes is greatly impeded because taxonomic schemes are constantly changing. The aim of this study was to identify, type and differentiate *T. mentagrophytes* and *T. interdigitale* species and evaluate the applicability of the current taxonomy on this isolates. Materials and Methods: A total of 27 isolates of dermatophytes belonging to *T. interdigitale* and *T. mentagrophytes* were analyzed by the use of the sequence of the ITS region. Results: Among the 27 isolates, 21 belonged to the *T. interdigitale* after molecular identification. Analysis of the sequences distinguished three allele types of among our *T. interdigitale* species and three allele types of among our *T. mentagrophytes*. Conclusion: PCR sequencing was useful for distinguishing *T. mentagrophytes* and *T. interdigitale* species. Also, the applicability of the current taxonomic concept was successful in differentiate *T. mentagrophytes* and *T. interdigitale* species. The isolates previously identified as *T. mentagrophytes* should be relabeled as *T. interdigitale* according to current taxonomy. Keywords:

Bacterial and Fungal Coinfections among patients with COVID-19 in Zanjan, Northwest of Iran; a single-center observational with meta-analysis of the Literature

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نوع پذیرش: پوستر | کد مقاله: G-21578

Abstract: Background: There is a poor understanding about the prevalence and clinical differentiation of secondary bacterial and fungal infections from Coronavirus diseases 2019 (COVID-19) superinfection in hospitalized patients. This study aimed to determine the prevalence of bacterial and fungal secondary infections in COVID-19 patients admitted to a COVID-specialized center in Northwest Iran, Zanjan, between February 2020 and February 2021. Materials and Methods: Four hundred COVID-19-proven patients were enrolled in this study. Nasal swabs for molecular assay (Real-time PCR) and sputum samples for further microbiological assays were collected. Following a broad-spectrum search, a meta-analysis was performed using StatsDirect software (version 2.7.9) according to the DerSimonian and Laird method applying the random-effects models. Results: Streptococcus spp. (21.5%) and Staphylococcus spp. (16.7%) had the highest prevalence of bacterial coinfection among the COVID-19 patients, while Acinetobacter spp. had the lowest prevalence (4.2%). Among fungal coinfections, Candida albicans was the most prevalent (6.7%), and Aspergillus spp. was the lowest (2%). Males, elderly patients, patients with a history of underlying diseases and drug use, patients who showed acute clinical symptoms, and patients with a prolonged hospital stay had a higher incidence of secondary infections (P-value 0.05). The pooled prevalence for bacterial and fungal coinfections was 33.52% (95% CI: 18.12 to 50.98; I²: 99.4%; P-value: 0.0001). Conclusion: We found that male patients, the elderly, those with a history of underlying disease, and patients with acute clinical manifestations favoring COVID-19 should have higher rates of secondary infection. We suggest designing additional research with a larger target population and diagnostic molecular analyses to depict a more realistic view of the coinfection's status. Keywords: COVID-19; Secondary infection; Nosocomial infection

Reports on tympanic membrane perforation secondary to otomycosis in the world

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نوع پذیرش: پوستر | کد مقاله: G-12896

Abstract: Background: Tympanic membrane perforation (TMP) is an infrequently reported complication of otomycosis. As reported previously, TMP is one of the most misleading complications of otomycosis and can result in an inaccurate diagnosis. Materials and Methods: The literature search included five electronic databases (Web of Science, PubMed/Medline, Scopus, and ScienceDirect), in addition to gray literature, google scholar, World Health Organization (WHO) online libraries, and hand search of reference list of included study. Two independent reviewers scanned titles and abstracts, and afterward included full-texts according to eligibility criteria were extracted. Results: Eleven papers were included in this systematic review that has fulfilled the inclusion criteria. An overview of literature reports in chronological order on TMP secondary to otomycosis. Of note, the most of cases, otomycosis was associated with tympanic membrane perforation (TMP) in Iran jahrom (36.11%), Isfahan (19.6%) followed by China (16.67%), Nepal (15.8%), Pakistan (15.5%), USA (14%), Poland (12.5%), Mazandaran (6.75%), Turkey (3.4%), and India (3%). Conclusion: The diagnosis of TMP is based on a clinical examination by a specialist physician and can be difficult. Nevertheless, we cannot affirm whether perforation is caused by a fungus or a secondary infection in the otitis media. TMP should be considered in patients with otomycosis, as it appears to be relatively common in this population
Keywords: Otomycosis, Epidemiology, Iran, Tympanic membrane perforation



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Molecular identification of *Candida* species isolated from candiduria

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نوع پذیرش: پوستر | کد مقاله: G-39421

Abstract: Background: Candiduria is a debilitating long-term illness affecting a 10–15% of the cases with UTI. This disease is caused mainly by *Candida albicans* and a lesser extent by other species, however candiduria has been considered as more problematic infection for patients, and physicians. Materials and Methods: In this study, we report detailed molecular epidemiological data about the occurrence of pathogenic yeasts in Iranian patients affected by Candiduria. A total of 40 yeast isolates, identified based on phenotypic and restriction analysis of rDNA. Results: In total, specimens from 250 patients with suspected candiduria were examined. Based on the molecular results, among 40 yeast isolates, we identify 28 *C. albicans* (70%), 9 *C. glabrata* (22.5%), 2 *C. tropicalis* (5%), and 1 *C. rugosa* (2.5%) isolates. Conclusion: Although *C. albicans* remains the most common *Candida* species recovered from Candiduria patients, our data show that its prevalence may be slightly overestimated due to the presence of difficult-to-identify closely related yeast. Keywords: *Candida albicans*, Candiduria, rDNA

Molecular Identification Yeasts and Molds Isolated from Patients with Otomycosis

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نوع پذیرش: پوستر | کد مقاله: G-58792

Abstract: Background: Otomycosis is a superficial infection of the external ear caused by fungal pathogens. The present study aimed to evaluate the clinical symptoms of patients with otomycosis and predisposing factors and to identify fungal etiological agents using molecular approaches. Materials and Methods: An otorhinolaryngologist collected specimens from external ear canals of patients with suspected otomycosis based on the patient's history and clinical examinations. The specimens were collected using sterile swabs. Fungi were confirmed in clinical specimens by direct microscopy and culture methods. Fungal isolates were identified based on molecular approaches. Results: In total, specimens from 211 patients with suspected otomycosis were examined. The presence of fungi was confirmed in about 51% of patients based on fungal elements in direct microscopy and culture-positive fungi. *Aspergillus tubingensis* was the most commonly isolated species (52.77%), followed by *Aspergillus niger* (25.92%). Otomycosis due to infection with *Candida* species was observed in 16% of cases. Conclusion: : In our patient population, *A. tubingensis* and *A. niger* were the predominant causative agents of otomycosis. Successful treatment of otomycosis and recurrence prevention depend on accurate identification of predisposing factors and the causative fungal agents. Keywords: Otomycosis, Epidemiology, Iran

Fungal Profile and Antifungal Susceptibility Patterns Among Symptomatic Pediatrics Patients Attending Aboozar Children's Hospital, Ahvaz, Iran

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Abstract: Background: Urinary tract infections (UTIs) have been reported in children with nephrotic syndrome. However, the only causes for the infection reported to date are bacteria, but not many prior reported occurrences of fungi or yeast as causative organisms. Hence, the present study aimed to describe the epidemiology of urinary tract fungal infections in a tertiary care pediatric. Materials and Methods: A single-center cross-sectional study was conducted at the nephrology ward of Aboozar Pediatric Hospital between March 21, 2021, and April 28, 2022. Urine was collected aseptically from children, inoculated onto culture media, and incubated at 37 °C for 18–48 hours. Yeast was identified following standard procedures. Antifungal susceptibility testing was determined by the disk diffusion method according to the CLSI guideline. Descriptive statistics and logistical regressions were used to estimate the crude ratio with a 95% confidence interval. P-value 0.05 was considered significant. Results: Among 68 individuals referred to the mycology lab, the result of direct examination and culture of all patients approved for *C.albicans*. Of these, 38 individuals (55.8%) were male and 30 (44.2%) were female. The patients' age ranges were between one month and an 18-year-old. In the study of infection intensity, the patients were classified into three levels such as few (73.5%), moderate (20.6%), and many (5.9%). In the present study, all the patients were sensitive to Posaconazole. Also, the eagle effect was found in Amphotericin B, Voriconazole, and Fluconazole with frequencies of 91.7%, 91.7%, and 83%, respectively. In addition, just 8.3% of isolates were resistant to Itraconazole. It has not shown resistance in other mentioned medicine. The patients showed an intermediate response to Itraconazole (91.7%), Fluconazole (17%), Voriconazole (8.3%), and Amphotericin B (8.3%). Conclusion: There is a high prevalence of yeast infections in children with suspected UTIs. Also, boys are more likely to get yeast infections and the severity of the infection is higher than girls. The present study demonstrated the importance of diagnosing and selecting the appropriate drug for urinary tract fungal infections in hospitalized children. Keywords: Urinary tract infections, Children, Fungal infections, Yeast

Candiduria in intensive care units patients: Prevalence and antifungal susceptibility pattern

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Background: Candiduria is a urinary tract infection (UTI) that is defined as the presence of *Candida* species in the urine. This infection is a common finding in hospitalized patients. In recent years, resistance to antifungal agents has been raised. Since there are few studies about the sensitivity or resistance of *Candida* species, deciding for physicians is complicated. This study aims to present the prevalence and identification of *Candida* species in the urine samples of intensive care units (ICU) patients and determination of antifungal susceptibilities pattern in a year (March 2021 until February 2022) in Labafinejad educational hospital. **Materials and Methods:** Urine samples (n=80) of ICU patients were obtained by catheterization on admission day and every three days. Data (sex, age, antifungal and antibiotic therapy, underlying diseases and stay in the hospital) were collected from patients. Urine sediments were spread onto a fungal medium and incubated at 37 C for 48h. Then unique colony was cultured in the CHROM agar *Candida* medium and then was evaluated based on color. In vitro antifungal susceptibility test of the *Candida* species against amphotericin B and fluconazole was performed according to the standard CLSI guidelines (M60). **Results:** The prevalence of candiduria was 40% (n:32). Only specimens were considered as candiduria, which have a colony count of $\geq 10^4$ CFU/mL colonies. The commonest predisposing factors were antibiotic therapy (100%) and indwelling urinary catheter (98.3%). The most common species isolated was *C. glabrata* (82%), followed by *C. albicans* (75%), and *C. tropicalis* (4%). In vitro antifungals susceptibility tests have been evaluated. All *Candida* species were sensitive to fluconazole. Only *C. albicans* (28%) and *C. glabrata* (12%) isolates were resistant to amphotericin B. **Conclusion:** According to our findings, the efficacy of fluconazole therapy to eradicate *Candida* species was demonstrated ($p = 0.01$). Resistance in *C. albicans* and *C. glabrata* was due to prior use of amphotericin B. The catheter removal was suggested to decrease infection. The repetition of culture can help to diagnose asymptomatic cases and to reduce the use of antifungals. **Keywords:** Urinary tract infection, Candidiasis, Antifungal drug resistance



چهاردهمین کنفرانس بین المللی آزمایشگاه و بائین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Enhancement of the antifungal effect of green synthesized selenium nanoparticles using *Aspergillus fumigatus*

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Abstract: Background: Green synthesis as a new method of synthesis of nanoparticles with a simple, biocompatible, safe, and economical approach can be an alternative to chemical and physical processes. Fungi can convert some toxic ions into less harmful forms, including nanoparticles. Nanoparticles with a size of 1 to 100 nanometers have unique quantum properties. Today, the problems of drug resistance have been seen in different species of fungi. Selenium nanoparticles (SeNPs) are substances that have been reported to have antifungal properties. The present study aimed to investigate the antifungal effect of biosynthesized SeNPs using *Aspergillus fumigatus*. Material and Methods: For this purpose, SeNPs were biosynthesized with a specific concentration using *A. fumigatus*. The presence of nanoparticles was confirmed by various methods, including UV-Vis, FT-IR, FE-SEM, EDX, XRD, DLS, and Zeta potential. Then, susceptibility determination based on the Minimum Inhibitory Concentration (MIC) test was performed on standard fungal strains treated with SeNPs. Results: After confirming the results of nanoparticle biosynthesis, the MICs for Itraconazole and Amphotericin B against the standard fungal strains were 8 and 4 $\mu\text{g}/\text{mL}$ respectively. In comparison, MIC values for SeNPs-treated samples were reduced to 1 $\mu\text{g}/\text{mL}$ and below. Conclusion: Due to the increasing resistance of opportunistic fungi to target antifungal drugs, the use of biosafety SeNPs even at low concentrations can have favorable inhibitory effects on the growth of fungal pathogens. Keywords: Green synthesis, Selenium nanoparticles, *Aspergillus*, Drug resistance, MIC



چهاردهمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



A systematic review on the significance of mucormycosis diagnosis in Covid-19 patients

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نوع پذیرش: پوستر | کد مقاله: G-12958

Abstract: Mucorales are ubiquitous fungi and their spores are found in every environment. They can cause a potentially fatal opportunistic infection, Rhinocerebral mucormycosis. Covid-19 infection can result in various opportunistic fungal and bacterial infections that are angio-invasive and associated with high rate of morbidity and mortality. Unfortunately, a definite correlation between COVID-19 and elevated mucormycosis infection cases is now clear worldwide. Since early diagnosis of mucormycosis especially in patients with COVID-19 is significant in disease prognosis, this systematic review was conducted to investigate effective diagnostic tests to identify mucormycosis in COVID-19 patients.
Keywords:

A review on the effects of mucormycosis in Covid-19 patients

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نوع پذیرش: پوستر | کد مقاله: G-49325

Abstract: Mucor, a fungus present ubiquitously in the environment, can cause a potentially fatal opportunistic infection, leading to invasion of blood vessels by fungal hyphae, causing infarction and necrosis of a variety of end-organ host tissues and Covid 19 infection can result in various opportunistic infections and that is angio-invasive and is associated with a high rate of morbidity and mortality. Unfortunately, a definite correlation between COVID-19 and elevated mucormycosis infection cases is now clear worldwide. Mucormycosis is not contagious, so it cannot be passed from one. Impaired host defence- SARS-CoV-2 infection impairs cell-mediated immunity and decreases CD4+ and CD8+ cell counts, predisposing fungal infections. Patients with COVID-19 might present with markedly higher levels of inflammatory cytokines (such as interleukin [IL]-2R, IL-6, IL-10, and tumor necrosis factor-alpha), associated with impaired. There have been a variety of complications reported during and post-COVID infection. Recently, there has been an increase in sporadic cases of paranasal sinus mucormycosis in COVID- 19 patients. According to studies The prime susceptible reason for the increase of mucormycosis cases is elevated iron levels in the serum of the COVID survivors and There has been a surge of mucormycosis cases in India in the wake of the second wave of COVID-19 with more than 40000 cases reported. Keywords:

Investigating the effect of linoleic acid conjugated with chitosan coated with zinc oxide nanoparticles in inhibiting the expression of MDR and CDR genes in *Candida albicans* by Real time-PCR technique

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نوع پذیرش: پوستر | کد مقاله: G-39840

Abstract: Background: *Candida albicans* is an opportunistic human fungal pathogen, the fourth most common cause of nosocomial infections, and the leading cause of systemic candidiasis with a mortality rate of 50%. Increase in resistance to antifungal drugs, especially azoles, such as fluconazole, has resulted in the failure of *Candida* infections treatment and hence in the use of naturally occurring nano-derived compounds which have appropriate antifungal effects, lack toxic effects on the human body, and can inhibit drug resistance genes. Materials and Methods: Fluconazole-resistant *Candida albicans* isolates with MDR and CDR drug resistance genes were confirmed with molecular methods. In the first step, RNA was extracted, specific bacterial cDNA was synthesized, and real-time PCR was performed to quantify the expression rates of MDR and CDR genes. In the next stage, *Candida* was exposed to the Minimum Inhibitory Concentration (MIC) of the nano-complex and re-cultured. As in the first stage, RNA extraction, specific bacterial cDNA synthesis, and real-time PCR were performed. The $\Delta\Delta CT$ formula was used to calculate the expression rate of MDR and CDR genes before and after treatment with the nano-complex, and the results were compared Results: A total of 20 samples of *Candida albicans* with MDR and CDR drug resistance genes were isolated from patients with Candidal vaginitis by a gynecologist in health centers of Tehran using a vaginal swab. The samples were examined with real-time PCR in terms of MDR and CDR genes expression before and after exposure to the nano-complex, and the obtained data were analyzed with SPSS. The results showed that CDR and MDR genes expression was reduced as 97.41 and 94.36, respectively, indicating the great impact of this nano-complex in reducing the expression of MDR and CDR drug resistance genes. Conclusion: Given the inhibitory effect of ZnO-conjugated linoleic acid nano-complex on *Candida albicans* growth, which is accomplished through inhibition of the main drug resistance genes of MDR and CDR, this nano-complex is used for the first time in this study to reduce the expression of these drug resistance genes Keywords: *Candida albicans*, Antifungal Resistance, ZNO Nanoparticles, Chitosan, Linoleic Acid

Antifungal susceptibility and evaluation of extracellular enzymes activity in non- albicans Candida isolated from vulvovaginitis

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نوع پذیرش: پوستر | کد مقاله: G-12859

Abstract: Background: Vulvovaginal candidiasis (VVC) is one of the most common superficial fungal infections, and studies show that about 75% of women experience VVC at least once in their lifetime. The objective of this study was to analyse the antifungal susceptibility and the activities of phospholipase and proteinase enzymes as a virulence factors in non- albicans Candida isolated from vulvovaginitis patients. Methods: The study was performed in 100 women suspected of vulvovaginitis. Isolated non-albicans Candida were identified using the ITS-restriction fragment length polymorphism (ITS-RFLP) technique. Antifungal susceptibility testing was performed for fluconazole, posaconazole, voriconazole, and caspofungin according to the CLSI M27-A3 guideline. The production of phospholipase and proteinase enzymes was evaluated in VVC infections. Results: Out of 100 clinical cases, 38 isolates were identified as non-albicans Candida. Candida glabrata (50%) was the most prevalent species in non-albicans Candida, followed by C. tropicalis (18.4%), C. krusei (13.2%), C. parapsilosis (10.5%), and C. guilliermondii (7.9%). Voriconazole was the most effective drug with MIC₉₀=4 µg/mL against non-albicans Candida among four tested antifungals with MIC range between 0.06-8 µg/. Proteinase activity was observed in C. parapsilosis (100%) and phospholipase activity was observed in C. tropicalis and C. krusei (100%). Conclusion: In this review, our results demonstrated that enzymes activity as a virulence factor involved in pathogenesis of non- albicans Candida species and drug susceptibility testing is necessary to choose the appropriate drug. Keywords:



چهاردهمین کنفرانس بین المللی آزمایشگاه و باالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Hospital acquired fungal infection; an important but neglected issue

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Abstract: The Hospital acquired fungal infection is considered as major health challenge in hospital settings especially in immunocompromised and transplant patients. As general fact, this infection is neglected due to lower frequency in compare with bacterial hospital acquired infections. There are some important infection agents which are more common in this setting. The fungal infections are important health issue in immunocompromised and transplant patients due to immune suppression. Immune modulator agents which used for transplant patient by suppressing immune system can leads to opportunistic infections or even iatrogenic infections in hospital settings. In this regards, the most important agent is considered as aspergillosis. The Aspergillosis spp. can leads to cutaneous infections in burn units or systemic infections in ICU unites. Furthermore, candidiasis can induce infections in ICU unites and leads to fungemia in immunocompromised patients or during steroid treatment patients. In this regards, another aspect could be the antibiotic resistance due to the prophylactic treatment in hospitalized patients. Also, by considering the rise in some non-communicable diseases for instance diabetes in Iran, and its effect on immune system and patients care and management. Fungal infections in these patients are major change in future years. The aim of current study is to introduce the most important fungal agents for hospital acquired infections such as aspergillosis, mucormycosis and Candidiasis based on basic mycology aspects, clinical syndromes or manifestations, anti-fungal agents and antibiotic resistance patterns. **Keywords:**

Antifungal effects green synthesized zinc nanoparticles against *Candida albicans*

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نوع پذیرش: پوستر | کد مقاله: G-30867

Abstract: Antifungal effects green synthesized zinc nanoparticles against *Candida albicans* Arezoo Yazdani Baghmaleki¹, Hoda Ataeinezhad¹, Marzieh Rashidipour², Hossein Mahmoudvand²* 1. Student Research Committee, Lorestan University of Medical Sciences, Khorramabad, Iran 2. Razi Herbal Medicines Research Center, Lorestan University of Medical Sciences, Khorramabad, Iran *Email: dmahmodvand@gmail.com, Razi Herbal Medicines Research Center, Lorestan University of Medical Sciences, Khorramabad, Iran Background: *Candida albicans* is the most common etiological agent of diseases caused by yeasts of the genus *Candida*. Considering the resistance of fungi to conventional antifungal drugs has increased and many of these drugs are toxic and expensive, it is necessary to investigate other effective products against these fungi this research aimed to investigate the antifungal effect of zinc nanoparticles synthesized with a lavender extract by microwave method on *C. albicans*. Materials and Methods: In this study, the standard strain of *C. albicans* (ATCC5027) was used. After preparing zinc nanoparticles to investigate the antifungal effects of zinc nanoparticles and nystatin, the microplate method was used to determine MFC and MIC. Descriptive statistics and calculation of central and dispersion indices were used to describe the data. After measuring the normality of the data with the help of the Shapiro-Wilk test, since the distribution of the data was normal, independent t-tests, ANOVA, Tukey's and Dunnett's post hoc were used, and p0.05 was considered as the significance level. Results: The synthesized nanoparticle was shown to be spherical in size from 30 to 80 nm. Based on the findings, the lowest amount of MIC belonged to zinc nanoparticles + nystatin (0.204µg/ml) and the highest amount was related to zinc (8.6µg/ml) nanoparticles. Similarly, the combination of zinc nanoparticles with nystatin (0.250 µg/ml) and zinc nanoparticles alone (10 µg/ml), respectively, were the lowest and highest amount of MFC. Conclusion: The results of this study showed that the combination of zinc nanoparticles + nystatin compared to nystatin alone has a significant antifungal effect on *C. albicans* and can be used in combination with conventional mouthwashes to increase their effectiveness. Keywords: Oral thrush, Oral candidiasis, Nystatin, Zinc nanoparticles, Nanotechnology

Fungal and bacterial co-infections of the respiratory tract among patients with COVID-19 hospitalized in intensive care units

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نوع پذیرش: پوستر | کد مقاله: G-04958

Abstract: Backgrounds: The pandemic of COVID-19 has created a global public health crisis. ICU patients with COVID-19 are prone to infections of bacterial and/or fungal origins due to several risk factors. Consequently, the current study was conducted to evaluate the frequency, demographic characteristics, underlying conditions, and etiologic agents of fungal and bacterial co-infections of the respiratory tract among ICU patients with COVID-19 in Iran. Materials and methods From May to October 2020, sputa and endotracheal aspirates were collected from ICU patients hospitalized with COVID-19 who also were suspected of bacterial and/or fungal co-infections according to inclusion criteria. The etiologic agents of bacterial co-infections were identified using the Vitek 2 identification method. For fungal identification, all samples were analyzed by direct microscopy using KOH 10% and culture. Furthermore, all isolates were subjected to sequencing method. Results A total of 73 lung specimens were obtained from patients who met the inclusion criteria. Of these, in 15 cases (20.54%) fungal and/or bacterial co-infections were confirmed. Males were more infected (73.33%) and all of them were between 49 and 79 years. *Candida albicans* (n = 8, 61.53%) and *Klebsiella pneumoniae* (n = 5, 38.46%) were the most frequent etiologic agents related to fungal and bacterial co-infections, respectively. Pneumonia (n = 15, 100%) and diabetes mellitus (n = 8, 53.33%) were documented as the most prevalent underlying conditions. In the current study, 3 out of 15 patients (20%) died. Conclusion :The frequency of bacterial co-infections of the respiratory tract in ICU patients hospitalized with COVID-19 was relatively high. According to the results, one of the causes of death of these patients could be a secondary infection. Keywords:

Trichophyton indotinae dermatophytosis: A case report and literature review from Iran

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Background: *Trichophyton indotinae* (formerly *T. mentagrophytes* genotype VIII) is a new emerging pathogen, causing recalcitrant dermatophytosis with high level of terbinafine resistance which could make the treatment challenging. This species was first reported from India in 2020, followed by has been reported from Vietnam, Denmark, France and many other countries. Due to the shared morphological features and similar nucleotide sequences of *T. indotinae* with *T. interdigitale* and *T. mentagrophytes*, discrimination of these species is difficult and controversial.

Case presentation: A 55-year-old male patient suspected to tinea cruris and tinea pedis was admitted to Dermatology Clinic at Razi Hospital, a tertiary care center for dermatology in Tehran, Iran. Based on the mycology testing and molecular identification the isolated was identified as *T. indotinae*. And the PCR product was sequenced, the result was analyzed by BLAST (<http://www.ncbi.nlm.nih.gov/BLAST>) which was compatible with *T. indotinae*. Urease test was revealed weakly positive result after 7 and 14 days of incubation which were different from those of *T. interdigitale* and *T. mentagrophytes*. Accordingly, this test could be useful for preliminary identification of *T. indotinae*. The antifungal susceptibility of the isolate to terbinafine, itraconazole and griseofulvin was evaluated according to the Clinical & Laboratory Standards Institute (CLSI) M38 third edition guideline. The Minimum Inhibitory Concentration (MIC) values of terbinafine, itraconazole, and griseofulvin were 8 µg/mL, 0.25 µg/mL, and 2 µg/mL, respectively. The patient was successfully treated by oral itraconazole.

Conclusion: Timely and accurate identification of dermatophyte isolates and antifungal susceptibility testing, especially in cases with extended lesions is recommended. Fortunately, the present case was treated successfully with itraconazole.

Keywords: *Trichophyton indotinae*, *Trichophyton mentagrophytes* type VIII, Dermatophytosis, Terbinafine

In vitro comparative survey of the effect of aqueous and alcoholic extracts of Rosa canina hips on Trichomonas vaginalis and Candida albicans

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نوع پذیرش: پوستر | کد مقاله: G-32968

Abstract: Background and aim: Candida albicans and Trichomonas vaginalis are two common microorganisms in human sexually transmitted diseases. The first choice for the treatment of trichomoniasis and candidiasis is metronidazole and fluconazole respectively. In recent years, the carcinogenicity and resistance of microorganisms to these drugs have been reported. Therefore, it is necessary to find new non-toxic, safe, and efficient compounds to deal with C. albicans and T. vaginalis. Plant extracts are a rich source of active phytochemicals or bionutrients which play an important role in preventing infectious diseases. For this reason, the aim of the present study was to compare the inhibitory effect of the aqueous and alcoholic extracts of the Rosa canina hips on C. albicans and T. vaginalis in laboratory conditions. Methods: T. vaginalis was obtained from Karaj Islamic Azad University strain center and C. albicans ATCC 10231 (PTCC 5027) was obtained from Abusina company. Aqueous and alcoholic extract of Rosa canina hips was prepared using water and 97% ethanol. The growth inhibition of extracts was evaluated using the microdilution method at different concentrations. The statistical analysis was performed by GraphPad statistical software version 9 and the results were compared at a 95% statistical level. Results: Aqueous extracts of Rosa canina hips at 30, 15, 7.5, 3.8, and 1.88 mg/ml of preventing the growth of T. vaginalis by 45, 37, 20, 11, and 2%, respectively at 24 h, while the inhibitory rate was increased to 72, 60, 56, 52, 28% at 48 h. In addition, alcoholic extract at 30, 15, 7.5, 3.8, and 1.88 mg/ml, decreased 55, 47, 33, 21, 4% growth of T. vaginalis at 24 h. Furthermore, the inhibition rates increased significantly within 48 hours. Based on the results, it was determined that the aqueous and alcoholic extracts are not suitable for inhibiting the growth of C. albicans. Conclusion: The results of the study showed that Rosa canina hips which contain various phytochemical compounds can be considered as a potential alternative to chemical drugs in the treatment of T. vaginalis infections but the aqueous and alcoholic extracts didn't show favorable results against C. albicans. Keywords:

Dermatophyte monitoring in an Northwest Iranian training hospital

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نوع پذیرش: پوستر | کد مقاله: G-63208

Abstract: Background: The most common cutaneous fungal infections are caused by dermatophyte fungi including *Microsporum Trichophyton*, and *Epidermophyton* species. To get better perception of dermatophyte distribution in Northwest of Iran, we studied the identification of isolated dermatophytes from human specimens by using the fast and cheap molecular method, PCR based restriction fragment length polymorphism (PCR-RFLP). Materials and Methods: The study samples were collected from clinically suspected cutaneous lesions. All the specimens were transported to Medical Mycology Center, UMS University of Medical Sciences. First of all, a conventional diagnosis was carried out which included microscopic examination and culture on sabouraud dextrose agar medium with antibiotics: chloramphenicol and cycloheximide. All the dermatophyte isolates were then identified at the level of species by the molecular method of PCR-RFLP. Results: From the tested 357 clinical specimens, 30 dermatophytic isolates were identified. The percentage rate of dermatophyte species were *Trichophyton mentagrophytes* (36%), *Microsporum canis* (32%), *Microsporum gypseum* (16%), *Trichophyton rubrum* (4%), and *Epidermophyton floccosum* (12%). Conclusion: By using of PCR-RFLP, a fast and reliable identification of these species is possible. This molecular method provided an opportunity for dermatophyte identification at the species level. Keywords: Dermatophyte, Molecular Epidemiology, RFLP

Candida Monitoring of the cases with a recent Covid-19 in West Azarbayegan

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نوع پذیرش: پوستر | کد مقاله: G-15038

Abstract: Background: Candida yeasts are opportunistic organisms cause variable diseases including pulmonary secondary infection in immunocompromised patients. Most common Candida species in human is *C. albicans*, although other species (Non *albicans* Candida species) have pathogenicity and antifungal drug resistance as well. During the pandemic Covid-19, in a considerable number of involved persons the infection developed into bronchial and lower respiratory tract. Materials and Methods: A screening of Candida colonization and infection in cases with a recent history of Covid-19 was performed during Feb 2019 to Feb 2022. Microscopic direct examinations showed overgrowth of Candida yeasts, basic and differential culture on sabouraud agar and CHROM agar Candida (respectively) confirmed Candida species. Results: During the pandemic Covid-19 in Iran, since February 2020 to Feb 2022, totally, 200 cases with a recent history of Covid-19 and respiratory tract involvement were studied for fungal infections. Among them, 29 (14.4%) had a yeast infection or colonization on the upper or lower respiratory tract. Candida species including *C. albicans* 11 (38%) and non *albicans* Candida 18(62%) were identified. Conclusion: As a fact, the long stay at hospital especially ICUs and Corticosteroid therapies, are predisposing factors for colonization and infection by Candida organisms which are commensally living in oro-pharyngeal tract. Key words: Covid 19, *Candida albicans*, Non *albicans* Candida.

The Important Aspects of General Health Could be Affected by Mycobiome of Oral Cavity

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نوع پذیرش: پوستر | کد مقاله: G-50827

Abstract: Background: The mycobium or population of the fungal flora of the oral cavity is one of the most complex and diverse microbial communities in the human body. For the fungal normal flora, the oral cavity can act as the most important way of entry and they are critical components of health and disease. Because of increasing the chances of oral and systemic mycoses in immune system disorders and the onset of this fungal flora on the process of possible dental caries, fungal microbiota plays an ambiguous role, even in the development of auto immune diseases, inflammatory ulcers and gastrointestinal disorders, the process of developing various types of oral-esophageal cancers and totally in the general health. In the meantime study around the human microbiome and its close relation to different aspects of health has been considered. Materials and Methods: To obtain a comprehensive profile of the fungal mycobiome among 100 individuals in this study, we applied 2 sterile swabs from the gingival groove, saliva and buccal surfaces for sampling. One swab for direct study and the other swab for cultured immediately in Saburo-dextrose agar solid medium. The samples were then incubated for 24 hours for 72 hours at 37 ° C and the growth rate of filamentous/yeast in daily culture medium was evaluated. Classification and sorting was based on the number of colonies produced in each plate. Then each candida suspected colony cultured in chrom agar medium. 24 hours incubation at 37 ° C - after 48 ° C, growth of Candida species based on colony color created according to the descriptions in the brochure were evaluated. In the case of saliva samples, the sample was inoculated on SDA solid culture medium. In addition to using physiological and morphological features, differential biochemical tests of catalase, oxidase and urease were performed to differentiate: Rhodotrolla, Candida and Saccharomyces. Results: Candida species were the most frequently obtained genera, isolated from 83% of all study participants by using differential techniques Candida albicans(42%), Candida glabrata (15%), Candida dubliniensis (10%), Candida tropicalis (6%) , Candida parapsilosis(5%) and Candida krusei (5%) were reported. In the following other fungal genera such as: Rhodotrolla (5%), Geotrichum (3%), Saccharomyces (2%), Aspergillus (1%), and Alternaria (1%), unclassified members (5%) were isolated. Holders of Geotrichum had gastrointestinal disorders such as stomach ulcers and Inflammatory Bowel Disease (IBD). The most important factor of tooth decay (DMFT more than 10) and oral Hyperplasia were reported in people with high population of Candida spp specially, Candida krusei, Candida tropicalis and Candida albicans. Two cases of Plaque Psoriasis and Lupus Erythematosus were detected in Saccharomyces spp and Candida albicans carriers. Two cases with Candida albicans normal flora had a recurrent volvu-vaginal candidiasis. Additionally one case of stomach ulcer was reported in current group. Conclusion: We interpreted demographic characters, oral health status, general health factors and auto-immune disorders regarding isolated fungal flora. Hence it was a novel regional prospective work that identified the mycobiome influences on possible disorders in Iran. Keywords: Mycobiome, General Health Factors, Oral cavity

Geographical distribution of *Cryptococcus neoformans*, pathogenic factors, and antifungal susceptibility profile

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Background: Today, approximately 70 species of *Cryptococcus* have been identified. Some of them can cause disease in humans and animals, and some others are found as saprophytes in the environment. *Cryptococcus neoformans* is one of the most important pathogenic species. It is found in urban and rural areas worldwide, and pigeon droppings are its most important ecological niche. Polysaccharide capsules, melanin production, growth at 37°C, and extracellular enzyme secretion are the main pathogenic factors of organism. Cryptococcal meningitis in immunocompromised patients has worldwide distribution. Although disease has been known in the world for more than three decades, there is little information about the epidemiology, distribution, virulence factors, and antifungal susceptibility of *Cryptococcus* species in Iran.

Materials and Methods: This study was conducted from September 2021 to December 2022. Four hundred and twenty-eight samples of pigeon droppings were collected from 11 different cities (Karaj, Kermanshah, Yasouj, Dezful, Gorgan, Gonbad, Sari, Ilam, Kashan, Shiraz, and Shahrekord) of Iran. Preparation of samples and primary separation were done using Niger seed agar. Identification of virulence factors of *C. neoformans* isolates was done including; capsule determination, melanin production, growth at 37°C, different temperature tolerance, urease activity, and catalase activity. *In vitro* antifungal susceptibility testing was performed for all identified *C. neoformans* strains by broth microdilution method according to the clinical and laboratory standard institute (CLSI) document M27 4th. Minimum inhibitory concentrations of different antifungal agents including; amphotericin B, 5-flucytosine, fluconazole, itraconazole, voriconazole, luliconazole, caspofungin and micafungin were evaluated.

Results: Of 428 samples, 37 (8.6%) were positive for *C. neoformans*. All isolates were able to produce capsules, grow at 37°C, and melanin production (with four exceptions). Extracellular enzymes were observed in all isolates with different ranges. Based on defined ECVs by CLSI M59 guidelines, all isolates were found to be wild-type phenotype (WT) to voriconazole and 5-flucytosine. It was found that



چهاردهمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



100% of the isolates had a non-wild phenotype (non-WT) to amphotericin B and itraconazole, while only 2.7% of the isolates had a non-wild phenotype to fluconazole.

Conclusion: The frequency of *C. neoformans* was 8.6% in the Iranian cities (High frequency, Kermanshah (46%); Low frequency, Shiraz (3%)). All isolates were sensitive to voriconazole and 5-flucytosine.

Keywords: *Cryptococcus neoformans*, Virulence factors, Antifungal susceptibility, Capsule, Melanin



چهاردهمین گنگره بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



The Inflammatory Role of Interleukin-33 in breast cancer and idiopathic granulomatous mastitis

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Abstract: Background: Breast cancer (BC) is the main cause of cancer death in women. Idiopathic granulomatous mastitis (IGM), a rare and chronic disease mimics breast carcinoma clinically, which is related to the high rate of mortality. Immediate and accurate diagnosis decreases its mortality and morbidity rates. Interleukin-33 (IL-33) has an induction role in the network of pro-inflammatory cytokines and is expressed in numerous human tissues. The aim of this study was to investigate the levels of IL-33 in BC, and IGM patients. Material and Methods: In this descriptive- analytical study, 28 patients with BC, and 25 patients with IGM were sampled after obtaining written consent. Histopathological pattern of BC and IGM were confirmed by specialized pathologists. In addition, 25 healthy volunteers with normal screening reports consist of the control group. The serum concentration of IL-33 was measured using enzyme-linked immunosorbent assay (ELISA) according to the kit manufacturer's instructions. Results: The mean age of the participants with BC, IGM, and control groups were 49.1, 37.1, and 36.8 years, respectively. IL-33 assay indicated a significant difference between BC ($p = 0.011$), and IGM ($p = 0.031$) groups compared to the control group, but the comparison levels of IL-33 between the IGM and BC groups didn't show a significant difference. Also, there was no significant difference in all groups by considering age, marriage, BMI, and menopause with the IL-33. Conclusion: IL-33 is a significant factor in IGM and BC patients compared to the control group, but it couldn't be used to diagnose and differentiate BC from IGM. Keywords: Breast cancer, Idiopathic granulomatous mastitis, Interleukin-33

Identification of *Candida* species isolated from blood cultures submitted to the laboratories of Mashhad University Hospitals by PCR- RFLP method

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نوع پذیرش: پوستر | کد مقاله: G-58943

Abstract: Background: *Candida* blood stream infection is the most prevalent clinical manifestation of invasive Candidiasis and is an important factor in mortality in hospitalized patients. Therefore, rapid and definitive identification of *Candida* isolates is necessary for antifungal treatment of these patients. This study was designed to identify *Candida* species isolated from blood culture. Material and Methods: In a one-year period, a total of 9920 blood samples from hospitalized patients at university hospitals in Mashhad, submitted to the Microbiology and Mycology Laboratories, were prospectively studied by BancTec system and 100 positive bloods culture were collected. After passage of blood samples on fungal culture media, the fungal colonies were isolated and purified and finally PCR-RFLP was performed. At the same time, demographic information and patient admissions were obtained in the form of a questionnaire. Results: Of 100 candidemia cases, 40% belonged to male patients and 60% belonged to female patients. Most cases of candidemia were in the age group of 10 years. After determining the species by PCR-RFLP, *Candida albicans* was the most prevalent species with 47%, followed by *Candida parapsilosis* 23 cases (23%), *Candida tropicalis* 9 cases (9%), *Candida glabrata* 8 cases (8%), *Candida krusei* 6 cases (6%), *Candida lusitanae* 4 cases (4%), *Candida kefyr* 2 cases (2%) and *Candida guilliermondii* 1 case (1%). Conclusion: Two species of *Candida* include *Candida albicans* and *Candida parapsilosis* were the most common species causing candidemia in hospitalized patient of Mashhad university hospitals. Key words: PCR-RFLP, candidemia, candida



چهاردهمین کنفرانس بین المللی آزمایشگاه و باالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Investigating the effect of fennel fruit essential oil from different regions of Iran on *Fusarium, flavus* and *Sclerotinia* pathogenic fungi

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نوع پذیرش: پوستر | کد مقاله: G-03254

Abstract: Introduction and purpose: The importance of fennel has long been considered as one of the plant species with health and treatment properties. Today, with the advancement of science and knowledge, the use of fennel and its essential oil in various fields such as health and treatment, pest control and diseases have been considered. The aim of this study was to investigate the effects of fennel essential oil on the growth and inhibition of some pathogenic fungi. Methods: The essential oil of each fennel was evaluated separately in four concentrations of 1ml, 0/1ml, 0/01ml and control to evaluate the effect on the growth of pathogenic fungi such as *Fusarium*, *Flavus* and *Sclerotinia*. Results: Results showed that the effect of fennel essential oil in different areas on the growth of fungi at a concentration of 1 was significant and caused a severe reduction in growth and even lack of growth. Conclusion: According to the obtained results, fennel essential oil of different regions of Iran can be used in concentration 1 to reduce and eliminate pathogenic fungi such as *Flavus*, *Fusarium* and *Sclerotinia*.
Keywords:

Epidemiology, prevalence, and associated factors of oral candidiasis in HIV patients from southwest Iran in post-highly active antiretroviral therapy era

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نوع پذیرش: پوستر | کد مقاله: G-79301

Abstract: Background: Oral candidiasis (OC) is one of the most common opportunistic fungal infections among people living with HIV/AIDS (PLWHA). The prevalence of OC and *Candida* profiles among HIV-infected patients might be changing in the era of Highly Active Antiretroviral Therapy (HAART). This study aimed to identify *Candida* spp., determine OC prevalence and associated risk factors for PLWHA. Materials and methods: Oral candidiasis prevalence was explored in oral swabs of 276 patients who referred for consultation at Behavioral Diseases Counseling Center (BDCC). Clinical symptoms, culture and molecular assays were used for OC detection. In statistical analysis, we assessed sociodemographic characteristics, clinical information and treatment history of some infections. Results: The overall prevalence of OC was 41%. *Candida albicans* (64.6%) was the most common species, followed by *C. glabrata* (26.5%) and *C. dubliniensis* (19.5%). *Candida famata*, *C. africana*, and *C. stellatoidea* as the first fungi isolated from OC in PLWHA from southwest Iran. In 36.3% of patients, mixed cultures of more than one species were observed. Body mass index (BMI) (OR = 0.947; CI = 0.89–0.99; p = 0.045) and CD4 count (OR = 4.365; CI = 1.73–10.98; p = 0.002) were the predictors of OC in the final model of multiple logistic regression analysis. Education level, addiction status, sexual behaviors, chest X-ray, other infections and WHO clinical stage were other important risk factors for OC. Conclusion: Oral candidiasis remains a significant opportunistic infection in post-HAART era among PLWHA. Despite the increasing prevalence of NAC species, *C. albicans* (64.6%) was still the predominant species. Our results showed that low BMI with OC indicates treatment failure (i.e., failure to increase CD4 count or suppress viral load). Also, low CD4 counts in HIV patients show an impaired immune status, and our findings emphasize that OC can be a clinical indicator of HIV infection in individuals who do not know their HIV status or have failed treatment. **KEYWORDS:** oral, candidiasis, HIV, BMI, *Candida* species

Low Level of Antifungal Resistance in Candida Species Recovered from Iranian HIV-Associated Oral Infection

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Abstract: Background: Oral candidiasis (OC) is the most frequent opportunistic infection encountered in approximately 90% of people living with HIV/AIDS (PLWHA) in the primary, asymptomatic, or overt phases of the disease, which is a predictive indicator of immunosuppression and the disease progress. In the present study, molecular epidemiology and antifungal susceptibility pattern of *Candida* spp. isolated from oral *Candida* infection (OCI) of PLWHA was determined following highly active antiretroviral therapy (HAART) treatment. Materials and Methods: 109 *Candida* isolates were collected from 94 PLWHA afflicted with OCI. The susceptibility profiles of *Candida* spp. to six antifungal agents were evaluated using broth microdilution. Results: The prevalence of OCI was 34.06%. The susceptibility profile of *Candida* spp. revealed 100% sensitivity to caspofungin, while 6.4%, 5.4%, 24.5%, and 2.8% of *Candida* isolates showed resistance or non-wild type MICs to fluconazole, itraconazole, posaconazole, and amphotericin B, respectively. It is noteworthy that 15.9% of patients and 3.7% of isolates showed co-infection and multidrug resistance, respectively. Conclusion: Considering that the majority of participants in our study had no previous exposure to antifungals, the overall low resistance obtained in this study to the six tested antifungal agents can confirm that by managing the appropriate antifungal prescription and adhering to the full course of treatment, It is possible to minimize the development of drug resistance among *Candida* isolates. The data indicate the epidemiology of local fungal resistance and support accurate treatment selection using antifungal susceptibility tests. Keywords: HIV, Antifungal, CLSI, *Candida*, Candidiasis

Antifungal effect of silver nanoparticles synthesized by *Prosopis farcta* extract against *Candida* species

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Abstract: Background: antifungal resistant is an increasing problem with the *Candida* species. *Candida* infections may resist antifungal drugs, making them difficult to treat. The occurrence of fungal species resistant to antifungal drugs and also their numerous side effects have persuaded researchers to work on new therapeutic methods. One of the most prominent methods is the production and synthesized of nanoparticles using plants. The purpose of this study was to investigate the antifungal effects of silver nanoparticles (Ag- NPs) synthesized by *Prosopis farcta* extracts against *Candida* species. Materials and Methods: in the present study *Prosopis farcta* used for synthesis of Ag- NPs and antifungal effects of this nanoparticles against six *Candida* species were examined. *Prosopis farcta* leaves were collected from Zabol, Sistan and Baluchestan province. They were dried and powdered. The leaves extract was prepared by taking of powder with distilled water. To synthesize Ag- NPs, the extract combined with silver nitrate solution. After preparation of Ag- NPs, the susceptibility of the *Candida* species to this extract and drugs (fluconazole and clotrimazole) were evaluated by broth microdilution method according to CLSI M27-A3 protocol. Finally, MIC and MFC was determined. Results: synthesized silver nanoparticles by *Prosopis farcta* showed antifungal effects against *Candida* species. *Candida albicans* with MIC= 1.95 µg/ml was the most sensitive species to Ag- NPs. The MICs of Ag- NPs for *Candida glabrata* (ATCC strain), *Candida krusei*, *Candida tropicalis*, *Candida glabrata* (PTCC strain) and *Candida parapsilosis* were 7.8, 15.6, 15.6, 31.2 and 62.5 µg/ml respectively. The MFCs of Ag- NPs for *Candida glabrata* (ATCC strain) and *Candida tropicalis* was 125 µg/ml. *Candida glabrata* (ATCC strain) with MIC= 25×10³ µg/ml was the most sensitive species to *Prosopis farcta* extract alone. This extract had no fungicidal effect on any of the *Candida* species. The MICs of fluconazole and clotrimazole for *Candida albicans* was 8 µg/ml and 0.0625 µg/ml respectively. *Candida glabrata* (2 strain) was resistant to fluconazole. Conclusion: synthesized silver nanoparticles by *Prosopis farcta* extract were more effective on *Candida* species than plant extract alone. *Candida albicans* was the most sensitive species to Ag- NPs. *Prosopis farcta* plant is a good source for the synthesis of silver nanoparticles, so that it showed significant antifungal activity against *Candida* species. Key words: *Prosopis farcta*, silver nanoparticles, *Candida*

The prevalence of *Tinea unguium* among patients referring to the medical laboratory of Bu-Ali Hospital of Zahedan during 2022

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Background: *Tinea unguium* is a common mycosis in many part of the world including Iran and caused by dermatophytes species. The prevalence of this infection varied depending on time, age, sex, occupation, health level and geographical location. The present study was an attempt to investigate the prevalence of *tinea unguium* among patients referring to the laboratory of Bu-Ali Hospital of Zahedan.

Materials and Methods: The present cross-sectional descriptive study was conducted on 24 patients (male: 2, female 22) suspected to be suffering from *tinea unguium* who referred to the medical mycology laboratory of Bu-Ali hospital of Zahedan during 12 months (from January 2021 to January 2022). Samples were taken by scraping the infected nail area with a scalpel. Fungal elements were directly examined using 20% KOH and were cultured in SC and SCC medium.

Results: Dermatophyte and saprophytic fungi were isolated from nail samples in 11 (55%) and 9 (45%) cases respectively. 20 of cases (83.3%) were Of the 20 patients with onychomycosis. 19 females (95%) and 1 male (5%) were positive, which was statistically significant ($P \leq 0.05$).

Conclusion: The findings showed that *tinea unguium* is more prevalent among women than men.

Keywords: Dermatophyte species, Prevalence, *Tinea unguium*



چهاردهمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Molecular discrimination of *Candida* species causing primary and recurrent vulvovaginal candidiasis in Kerman, southeast Iran

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نوع پذیرش: پوستر | کد مقاله: G-45819

Abstract: Background: Vulvovaginal candidiasis (VVC), is a fungal infection that affects almost 75% of all women at least once in their lifetime. Besides, nearly 9% of women experience four or more episodes per year, defined as recurrent VVC (RVVC), which can severely affect women's quality of life. The objective of this study was to molecular discrimination of *Candida* species, causing VVC/ RVVC in Kerman, southeast Iran. Materials and Methods: A cross-sectional investigation was carried out on 119 nonpregnant females suspected of VVC between February 2019 and May 2021. *Candida* species were identified based on the PCR-RFLP method. The discrimination of *C. albicans* complex species was conducted by the partial amplification of the HWP1 gene. Results: Out of 119 subjects, 41 (34.45%) cases were affected by VVC, and 11 (9.2%) cases had RVVC. Among 52 yeast isolates, *C. albicans* was the most species in both VVC (n=17/41) and RVVC (n= 4/11) groups. The overall prevalence of non-*albicans* *Candida* (NAC) species was 59.6% (n = 31). One *C. dubliniensis* and three *C. africana* isolates were identified using HWP1 gene amplification. The most NAC species were *C. tropicalis* and *C. glabrata* in the VVC and RVVC groups. Conclusion: This study demonstrated that the majority of VVC cases were caused by NAC species. Regarding the emergence of the infrequent *Candida* species, which is indistinguishable from conventional methods, developing accurate identification molecular methods should be considered in the clinical setting. In addition, our findings revealed the importance of conducting periodical epidemiological studies to determine changes in species distribution. Keywords: Vulvovaginal candidiasis, *Candida* species, Polymerase chain reaction, Iran.

Antifungal susceptibility pattern of *Candida* species causing primary and recurrent vulvovaginal candidiasis in Kerman, southeast Iran

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Background: Vulvovaginal candidiasis (VVC), is a common type of fungal infection of the inferior genital tract of women worldwide. Recurrent vulvovaginal candidiasis (RVVC) is defined as four or more disease episodes per year. The increased VVC /RVVC incidence and drug resistance pose a serious challenge to public health. We investigated the antifungal susceptibility profiles of 52 *Candida* species isolated from patients with VVC/ RVVC in Kerman, southeast Iran.

Methods: All *Candida* isolates were tested for in vitro susceptibility to Amphotericin B, Fluconazole, Itraconazole, Voriconazole, Posaconazole, and caspofungin according to the Clinical and Laboratory Standards Institute guidelines.

Results: The resistance rate of *Candida* isolates to fluconazole, itraconazole, and voriconazole was 15.38%, 11.5%, and 3.8%, respectively. Amphotericin B and posaconazole had excellent activity against all *Candida* isolates. Significant differences were observed between fluconazole (p-value = 0.007) and caspofungin (p-value = 0.01), in VVC and RVVC groups. Resistance to fluconazole was obtained in 46% (5/11) of RVVC cases but only in 7% (3/41) of VVC cases.

Conclusion: Our results suggested that antifungal susceptibility monitoring should be regularly implemented to help clinicians with appropriate treatment modalities since some species showed a varying rate of resistance to antifungal agents. On the other hand, it is imperative to evaluate the susceptibility profiles of *Candida* species isolated from VVC/RVVC patients for effective treatment of infection.

Keywords: Antifungal susceptibility, Vulvovaginal candidiasis, *Candida*, Iran.

Phenotypic and genotypic characterization of biofilm formation and antifungal susceptibility of oral *Candida* species from diabetic and non-diabetic hemodialysis patients

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نوع پذیرش: پوستر | کد مقاله: G-06759

Abstract: Background: *Candida albicans* is a yeast that can cause oral infections in some circumstances. The hydrolytic enzymes and biofilm production play an important role in the pathogenesis of *Candida* infection. The aim of this study was to identify the *Candida* species, antifungal susceptibility, biofilm formation and characterize their relevant virulence genes in DM and non-DM patients undergoing hemodialysis. Materials and Methods: The conventional and molecular methods were performed to identify *Candida* species. The antifungal susceptibility of amphotericin B, fluconazole, itraconazole, voriconazole, and caspofungin to planktonic forms of *Candida* species was assessed according to CLSI M27-A3/S4. The biofilm formation using the crystal violet and XTT assay, and genotypic characterization of genes were evaluated. Results: The distribution of *Candida* species isolated showed that *C. albicans* complex was the most prevalent species (52.7%), followed by *C. glabrata* (16.5%), *C. tropicalis* (12%), *C. kefyr* (8.8%), *C. parapsilosis* (6.7%), and *C. lusitaniae* (3.3%). The resistance rate of *C. albicans* planktonic cells to fluconazole was 6.3% (MIC greater than or equal to 64 µg/mL) with the susceptible dose dependence of 10.5% (MIC 4 µg/mL). Within the NAC species, only one isolate of *C. glabrata* (MIC greater than or equal to 64 µg/mL) was FLC-resistant. The NAC species produced higher biomass and metabolic activity than *C. albicans* (*P* smaller than 0.05). Statistically significant correlations were found between the biofilm biomass and metabolic activity of biofilm in *C. albicans* and NAC species. Furthermore, there were significant (*p* smaller than 0.05) negative correlations between FLU MICs and biofilm formation. ALS3 and Sap5 were the most common virulence genes identified in oral *Candida* species. Conclusion: These results show the importance of the prevalence of NAC species in hemodialysis patients, investigated the antifungal susceptibility profile, and the understanding of the role of virulence markers in the pathogenesis of *Candida* strains. Keywords: Antifungal susceptibility, *Candida* species, Oral candidiasis, Biofilms

Antifungal effects of thymol loaded chitosan nanocomposite alone and in combined with nystatin against *Candida albicans*, a major cause of oral candidiasis

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نوع پذیرش: پوستر | کد مقاله: G-34762

Abstract: Background: Oral candidiasis is the most common oral infection that affects the oral mucosa. The most common oral thrush is caused by the fungus *Candida albicans*, but it can also be caused by *C. glabrata* or *C. tropicalis*. The aim of this study was to evaluate the antifungal effect of thymol loaded chitosan nanocomposite in comparison with nystatin control drug on *C. albicans*. Methods: Thymol loaded chitosan nanocomposite was synthesized by ionic gel method. The obtained nanocomposite was characterized by scanning electron microscope (SEM), nano-sizer-zetacizer, and Fourier-transform infrared spectroscopy (FTIR). Anti-*Candida* effects thymol loaded chitosan nanocomposite was assessed through the evaluating the the minimum inhibitory concentrations (MICs) and minimum fungicidal concentrations (MFCs) using broth microdilution method, according to the modified M27-A3 protocol on yeasts, proposed by the Clinical and Laboratory Standards Institute (CLSI). Results: Based on the results of SEM analysis, thymol loaded chitosan nanocomposite with synthesized chitosan base show a spherical shape. According to the size of the synthesized nanoparticles, the results showed that the size of nanoparticles varies from 100 to 600 nm, while most nanoparticles were between 200 to 300 nm with an average size of 295 nm. The lowest and in fact the best MIC and MFC were related to the combination of nanoparticles + nystatin with 0.158 and 0.158 $\mu\text{g} / \text{ml}$, respectively. The results showed that the combination of nanoparticles + nystatin in comparison with nystatin group as a control drug showed a significant anti-*Candida* effect. Conclusion: The findings of the present in vitro study showed that thymol loaded chitosan nanocomposite particularly along with nystatin showed promising antifungal effect against *C. albicans* as the main cause of oral candidiasis. Nevertheless, further investigations are required to elucidate the precise mechanism as well as systemic toxicity especially in clinical settings. Key words: Oral candidiasis, nanomedicine, in vitro, treatment

The effects of peracetic acid solution on the treatment of otomycosis in an animal model: a new antifungal drug?

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نوع پذیرش: پوستر | کد مقاله: G-65718

Abstract: Background: Otomycosis is a worldwide ear infection caused by fungus, especially *Candida* and *Aspergillus* species. Peracetic acid (PAA) as an antifungal can represent the proper potential for otomycosis therapy. This study aimed to investigate the therapeutic effects of 1% and 0.01% PAA in the animal model of otomycosis. Methods: Eighteen male Guinea pigs were divided into three groups (n=6). After creating a superficial scratch in the external auditory canal (EAC), the both ears of all animals were inoculated with a suspensions of *Aspergillus niger*, *Aspergillus fumigatus*, and *Candida*. After otomycosis, in each animal groups, 1% or 0.01% PAA were separately poured into the right EAC, while 2% acetic acid, as control, used in the left ear. The assessment of effects was performed by oto-microscopy in days 3, 5, 7, 10 and culture at the end of 10 days post-treatment. Results: None of the animals died or reacted adversely during the therapy. A 10-day treatment with 1% PAA and 2% acetic acid (control) were accompanied with normal oto-microscopy and negative cultures compared to 0.01% PAA. There was not any drug sedimentation or other side effects in EAC or tympanic membrane during treatment with PAA, but white drug sedimentations observed in EAC of the acetic acid group. Conclusion: Our findings confirm that the efficient treatment of otomycosis by 1% PAA in animal model would be beneficial as a novel therapeutic material for otomycosis. Keywords: Otomycosis, Peracetic acid, Acetic acid, Treatment, Guinea pigs



چهاردهمین کنفرانس بین المللی آزمایشگاه و بائین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



A new record of *Scedosporium dehoogii* isolated from paddy field soil from Iran: Phylogeny and antifungal susceptibility profiles

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نوع پذیرش: پوستر | کد مقاله: G-50238

Abstract: Background: *Scedosporium* species are ubiquitous environmental fungi considered emerging agents that trigger disease in humans and animals. The present study aimed to determine *Scedosporium dehoogii* strain genetically from paddy field soil samples using semi-selective media and evaluated the antifungal susceptibility profile. Methods: Three paddy field soil samples were collected during an investigation for the isolation of *Scedosporium* species in Mazandaran province, Iran. Morphological and molecular analyses based on ITS-rDNA sequencing were performed. Furthermore, in vitro antifungal susceptibility testing for conventional drugs and novel imidazole (luliconazole) was performed based on CLSI M38-A3 guidelines. Results: One *Scedosporium dehoogii* was isolated in the paddy field soils. Itraconazole has low activity and luliconazole showed the most antifungal activity against this isolate. Conclusion: Based on the findings, molecular identification was essential for distinguishing the species of *S. dehoogii*. Remarkably, luliconazole has shown potent activity against this strain. Keywords: *Scedosporium dehoogii*, Molecular identification, Morphology characteristic, paddy field soil, Antifungal susceptibility

Epidemiology, Clinical Features, Diagnosis, and Treatment of Cerebral Mucormycosis in Diabetic Patients: A Systematic Review of Case Reports and Case Series

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نوع پذیرش: پوستر | کد مقاله: G-94235

Abstract: Background: Patients with diabetes are known as an important high-risk group for Cerebral Mucormycosis (CM). Method: We conducted a structured search using PubMed/Medline to collect both case reports and case series case (i.e., including at least two patients) on to CM in diabetic patient published between 2000 and March, 2020. Results: Forty-five reports of individual cases and eighteen case series articles were included. India accounted for the largest share of reports with 37.7% and 38.8% of individual cases and case series, respectively. Mortality ranged from 0 to 100% in the case series. The overall mortality in the individual cases was 46.3% and 64.2% of deaths were reported in patients with ketoacidosis diabetes. Facial swelling (53.3%), headache (44.4%), loss of vision (35.5%) and ophthalmoplegia (35.5%) were the most frequently reported clinical symptoms. In all patients except 4 (91.1%), CM was treated surgically; however, in many cases (42%), despite the use of surgery, death occurred. Amphotericin B deoxycholate (AMB) and lipid-based AMB (LAMB) were used as the first lines of treatment for all patients; however, posaconazole, echinocandins, Hyper Baric Oxygen Therapy (HBOT), and deferasirox were used in combination for a number of patients. Posaconazole has been shown to have positive therapeutic effect; however, posaconazole, LAMB, and HBOT are not commonly used in low-income and health-challenged countries. Conclusion: CM is a rapidly progressive infection in diabetic patients and carries immense morbidity despite early diagnosis and treatment. Low-income countries have had the highest number of reports of the disease in recent years, indicating the need to control diabetes in these countries. Keywords:

The effect of beta-carotene on *Candida albicans* pathogenicity

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نوع پذیرش: پوستر | کد مقاله: G-63741

Abstract: *Candida albicans* is a dimorphic fungus that has the morphological conversion from yeast to the hyphae form. Prostaglandin E2 (PGE2) can induce the morphogenesis, germ tube formation, and biofilm formation, so it increases during candida colonization and candida infection. Consequently, PGE2 may be an effective virulence factor in the pathogenesis of *C. albicans*. Non Specific cyclooxygenase (COX) and lipoxygenase (LOX) inhibitors block PGE2 produced by *C. albicans*. Beta-carotene (BC) is an organic compound, inhibiting COX isoenzymes such as COX.1 and COX.2. In the present study, we try to investigate the inhibitory effect of the BC on the expression of genes (OLE2 and FET3) playing the main role in the production of *C. albicans* PGE2. Methods: *C. albicans* standard strain was cultured on the Sabouraud dextrose broth (SDB) medium supplemented with acid arachidonic and *C. albicans* cells were used to prepare the suspension. The antifungal activity of BC (concentrations from 0.1 μ M to 100mM) and expression level of OLE2 and FET3 genes were assessed. Results: the inhibitory effect of beta-carotene was observed in the lowest concentration (0.1 μ M). In addition, we observed the down expression of OLE2 and FET3 genes in BC-susceptible *C. albicans* isolate (mRNA fold change of OLE2 0.855 versus 1.083, P 0.01; mRNA fold change of FET3 0.751 versus 1.096, P 0.001). Conclusion: The effect of beta-carotene on the expression of OLE2 and FET3 genes involving in the biosynthetic pathway of prostaglandin E2 can play a key role in the reduction of *Candida albicans* pathogenicity. Keywords:



چهارمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Toxicity effects of Astragalus maximus extract on serum level of liver and kidney enzymes and hematological paramets in mice

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نوع پذیرش: پوستر | کد مقاله: G-21096

Abstract: Abstract Background: Considering the preventive and therapeutic uses of medicinal herbs, but, any herbal product should be evaluated in terms of toxicological studies before it is used as a medicinal form. Since, no documented study is existing on the toxicity characteristics of Astragalus maximus, here, we aimed to assess the sub-acute toxicity effect of A. maximus chloroform extract (AMCE) by assessing the kidney and liver enzymes, and hematological factors in male Balb/c mice. Materials: The effects of AMCE was investigated by studding the kidney and liver enzymes, and hematological factors followed by the oral treatment of mice with AMCE (0.1, 0.2, 0.4, and 0.8 g/kg) for 28 following days. Results: Lethal dose 50% (LD50) of the AMCE was 2.87 g/kg of body weight. We found that the kidney and liver enzymes has no significant modifications (p0.05). Likewise, blood parameters did now show significant modification (p0.05) in comparison to the control mice. Conclusion: We reported that AMCE at the doses of 0.1-0.8 g/kg had no significant sub-acute toxicity on kidney and liver function in Balb/c mice after 28 days' oral administration; but, supplementary surveys are mandatory to determine other toxicity phases, e.g. genotoxicity. Key words: liver, kidney, hematological, toxicity, herbal medicines

Investigating the antifungal sensitivity of 3,4-dihydropyrimidine-1-(H2)-LH1-pyrrole derivatives on *Candida* species isolated from otomycosis patients

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نوع پذیرش: پوستر | کد مقاله: G-08594

Background: There is an increasing rate of drug resistance to azole among *Candida* species, so, finding new compounds that are effective in laboratory conditions, such as 3,4-dihydropyrimidine derivatives are important. The purpose of this study was to evaluate the antifungal sensitivity of 3,4-di-hydropyrimidine-1-(H2)-L-H1-pyrrole derivatives in *Candida* isolates.

Materials and Methods: Antifungal sensitivity of 102 *Candida* isolates with the origin of otomycosis to dihydropyrimidine derivatives and itraconazole were evaluated by broth microdilution according to CLSI-M27S4 guidelines. The serial dilution range of compounds and antifungal drug was 0.016-16 µg/ml. A concentration of compounds that showed at least 50% growth inhibition compared to the positive control group was considered as the minimum inhibitory concentration (MIC). Statistical analysis was performed in SPSS V16.

Results: Findings showed that 3,4-di-hydropyrimidine-1-(H2)-L-H1-pyrrole derivatives have higher MIC than itraconazole against *Candida* species. Also, comparing the MIC values of 3,4-dihydropyrimidine with each other (P1-P4), P1 derivatives were found with lower MIC values than the other three derivatives and almost all compounds showed more efficacy against *Candida albicans* than other *Candida* species.

Conclusion: Although the antifungal effects of 3,4-dihydropyrimidine-1-(H2)-L-H1-pyrrole derivatives against *Candida* species were lower than itraconazole, but, making structural changes in these compounds can increase their antifungal effects.

Keywords: 3,4-di-hydropyrimidine-1-(H2)-L-H1-pyrrole derivatives, itraconazole, *Candida* species

Case report: Candida Infection in a Co-infected Patient with COVID-19

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نوع پذیرش: پوستر | کد مقاله: G-50894

Abstract: Background: Oropharyngeal candidiasis (OPC) is the commonest problem that predisposes head and neck cancer patients receiving radiotherapy with or without chemotherapy to candida colonization and infection. We report a case of an 83-year-old female with three atherosclerotic plaques characterized as hyperechoic at the distal part of the left common carotid artery. Four segments with irregular surfaces and short papillae, with relatively thick paving units of the oral tongue, were prepared and then pathologically tested. After detailed investigations, squamous cell carcinoma (a common cancer of the oral cavity) was confirmed and she underwent radiotherapy afterward. During the peak of the COVID-19 in early 2021, she was hospitalized for COVID-19 pneumonia. A fissured tongue with white scars that appeared after the COVID-19 recovery might cause swelling, pain, and difficulty in swallowing and speaking. Histologic examination of the tongue sample confirmed the presence of *Candida glabrata*. Material and Methods: Histology examination confirmed the presence of *Candida glabrata* and its antifungal susceptibility was performed against 10 antifungals including caspofungin, nystatin, amphotericin B, tioconazole, voriconazole, itraconazole, econazole, ketoconazole, Clotrimazole, and fluconazole. Results: *Candida glabrata* showed resistance to nystatin and caspofungin but this species was susceptible to the other azoles. Conclusion: The risk of fungal infection seems to be high in patients with severe COVID-19 which mainly affects the oral mucosa, but it is unknown whether they are directly attributed to COVID-19 or other surrounding factors. In addition, the diagnosis of *Candida* species should be considered an important key for the ideal choice of antifungal therapy against this mycosis.

Isolation, diagnosis, and investigation of the frequency of fungal lung colonization in inpatients and outpatients

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نوع پذیرش: پوستر | کد مقاله: G-52147

Abstract: Background: Due to the epidemic of the coronavirus and hospitalization of patients in different departments of the hospital, the rate of exposure to fungal infections such as aspergillosis and candidiasis has increased in patients with immune system defects, cancer patients, and malignancies. This study aimed to survey fungal colonization in inpatients and outpatients. Materials and Methods: During 16 months, inpatients and outpatients referred to Kosar and Sina hospitals in Semnan, Iran were included in the study. All participants who were suspected of pulmonary fungal infection and met the inclusion criteria underwent sputum sample collection. Sputum samples were homogenized with pancreatin 0.5% and then were analyzed by direct microscopic examination with 20% potassium hydroxide (KOH) and culture on sabouraud dextrose agar. The media were inoculated into in at 30°C for 7 days and examined daily for fungal growth. Fungal identification was accomplished by morphological methods at the genus level. Result: Fungal respiratory colonization was confirmed in 66 patients, including 29(44%) males with an age range of (29-93) and 37(56%) females with an age range of (18-71). 55 (83%) cases were hospitalized in the ICU ward and 11 (17 %) cases were outpatients. Most of the referring seasons are in autumn 21 (32%) cases. 64 (97%) cases were positive have Aspergillus and Candida colonization. In direct examination, 63 cases (95%) were positive for yeast forms and only 23(35%) for hyphae forms, 14(22%) of yeast alone, and 27(42%) of (yeast and pseudohyphae), 10(16%) of (hyphae and yeast), also Co-infection (yeast, pseudohyphae, and hyphae) 12(19%) and only 1 case of hyphae alone (1%) were observed. In total, 94 fungal isolates were isolated from 64 positives with fungal colonization, from 55 cases of hospitalized patients who were in ICU, and from 54 positive cases, Aspergillus genus was found in 26(84%), including 5(19%) of sections Flavi, 6(23%) of section Fumigati, 9(35%) of section Nigri, 2(8%) of section Terrei, and 4(15%) of other sections, which requires species determination(sequencing), were also isolated from a total of 11 cases of outpatients from 10 cases(16%) positive for the genus Aspergillus from each section, 1 case(20%) of Flavi, Fumigati, Nigri, Terrei, and other sections were isolated. The other remaining isolates were related to Candida genus, of 63 isolated, 52 (83%) were isolated from 54 hospitalized in ICU, and 11 (17%) were separated from 10 outpatients. Also, Co-infection of Aspergillus genus and Candida genus were observed and reported in 22(33%). Conclusion: Our



چهاردهمین گنگره بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Isolation and In vitro Antifungal Susceptibility testing of *Malassezia pachydermatis* strains from stray and domestic Dogs

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نوع پذیرش: پوستر | کد مقاله: G-12540

Abstract: Background: Dermatitis caused by *Malassezia* spp., one of the most common skin diseases in dogs, requires prolonged therapy and/or high doses of antifungal agents. In the present study, the antifungal susceptibility of *M. pachydermatis* to fluconazole (FLZ), itraconazole (ITZ), ketoconazole (KTZ), nystatin (NYS), and voriconazole (VOR) was evaluated in vitro using CLSI M27-A3 reference broth microdilution. Materials and Methods: Samples were collected from 250 stray and domestic dogs, with or without skin lesions, and cultured using modified Dixon agar. *M. pachydermatis* strains were identified by molecular method. The in vitro antifungal susceptibility of *M. pachydermatis* was determined using the Clinical and Laboratory Standards Institute (CLSI) M27-A3 broth microdilution method with the following antifungal drugs KTZ, MICO, ITZ, TER, FLZ, VOR, and NYS. Results: A total of 37 yeasts were isolated. 64% *Malassezia pachydermatis*, 46% *Candida albicans*, and 78 saprophyte fungal genera (most frequently *Aspergillus niger* 37%, *Aspergillus fumigatus* 21%, *Aspergillus flavus* 11%, *Alternaria* 5%, *Cladosporium* 2%, *Penicillium* 4%). All *M. pachydermatis* strains exhibited high susceptibility to the majority of the tested antifungal agents. *M. pachydermatis* strains were susceptible to ITZ, and KTZ. NYS and FLZ had the highest MIC. Conclusion: *Malassezia pachydermatis* was the most common yeast and *A. niger* was the most saprophyte isolated from stray and domestic Dogs. Keywords: *Malassezia pachydermatis*, Antifungal Susceptibility, stray and domestic Dogs

Chrysosporium crassitunicatum infection in a stray dog: a case report

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نوع پذیرش: پوستر | کد مقاله: G-73028

Abstract: Chrysosporium species include mostly keratinophilic species that live on the remains of feathers, and hair and live in the soil. These fungi are reported as animal pathogens rarely, apart from in reptiles, and only a few species have been involved in mycoses. The aim of this report is to present a rarely seen dermatophytic skin disease caused by Chrysosporium crassitunicatum in a stray dog living in the shelter. Case Presentation: A 1.5-year-old female stray dog, kept in a dog shelter in Mazandaran province, Iran, was presented with chronic dermatophytosis with mild crusting, erythema on the trunk, and mild alopecia. The initial lesion was noticed at age of 6 and a half-year-old exhibited on the trunk as multifocal circular patches of alopecia, mild scaling with minimal pruritus. Skin samples were at first cultured on Mycosel™ Agar, incubated at 27°C, and observed and follow the fungal growth. After ten days, the fungal colonies had a distinct velvety white color, a flat appearance, and elevated slightly raised in the center; the reverse showed a light-yellow pigment. DNA extraction phenol-chloroform. Polymerase chain reaction (PCR) was then performed using universal fungal primers ITS1 and ITS4 to amplify the ITS rDNA region. Morphologically, this isolate was the same as Trichophyton sp. Also, the molecular characteristics were identified by sequence analysis of the internal transcribed spacer (ITS) region. Results of comparative sequence analyses by nucleotide BLAST analysis on the NCBI website showed that the sequences amplified were 99% conserved among strains, including the reference strain of Chrysosporium crassitunicatum. Antifungal agents including terbinafine, itraconazole, miconazole, ketoconazole, griseofulvin, butenafine, luliconazole, and tolnaftate were assessed by the broth microdilution protocol that was recommended by the CLSI-M38-A3. This isolate displayed susceptibility against luliconazole, terbinafine, itraconazole, ketoconazole, butenafine, and tolnaftate (MIC 0.08 µg/ml) and this isolate was less susceptible to miconazole and griseofulvin with (MIC 4 µg/ml). Conclusion: This was the first case of C. crassitunicatum in dogs. this isolate displayed high susceptibility against luliconazole and terbinafine, but this isolate was less susceptible to miconazole. Keywords: Chrysosporium crassitunicatum, Antifungal Susceptibility, Stray Dogs



چهارمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Genotyping of Acanthamoeba from patients in Qazvin, Iran

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نوع پذیرش: پوستر | کد مقاله: G-04175

Abstract: Abstract Background: Free-living amoebae (FLA) such as Acanthamoeba spp., considered as opportunistic and pathogenic protozoans. Human infections with amoebic keratitis, fatal granulomatous encephalitis, and cutaneous acanthamoebiasis are the consequences of Acanthamoeba infection. This study was carried out to identify the presence of Acanthamoeba among contact lens users in Qazvin, Iran. Methods: Totally, 251 nasal and oral swabs were collected from patients with diabetes, AIDS and those under periodic dialysis. Following DNA extraction, PCR and sequencing were conducted to identify the genotypes of the amoeba. Phylogenetic analysis of the identified sequences was performed using MEGA 7 software. Results: One isolate of Acanthamoeba isolated from hemodialysis patients with diabetes background. A strain of Acanthamoeba belonging to the T3 genotype. Conclusion: The result of the present study showed that the clinicians should pay attention to the possible complication of this organism because this amoeba is potentially pathogenic for immunocompromised patients. Keywords: Acanthamoeba, Genotypes, Patients, Qazvin, Iran



چهاردهمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Hydatidosis: traditional and current diagnostic methods

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Abstract

Background: Hydatidosis is an important infectious disease in human being that occurs by the larval stages of cestodes of the genus *Echinococcus*. Our aim was to carry out a narrative review on traditional and new diagnostic methods that are available for routine diagnosis.

Methods and materials: All main databases included in our searches e.g. PubMed, Scopus, and ProQuest. Relevant studies between 2001 - 2020 enrolled in our investigation. Traditional and newly developed methods to identify the parasite were reviewed and clarified our work.

Results: Eligible studies showed that most common methods to detect the Hydatidosis in human being depends on serological techniques and seeking antibodies against *Echinococcus granulosus*. Because human harbors larval stages and we couldn't find sexual stages of parasites in any organ. The best method to detect antibody against parasite is ELISA for IgG4.

Conclusion: Serological methods are non-invasive and can be routinely used in clinical and research laboratories. Molecular tests are used to identify genotypes in human and animals specially to detect in final hosts (canids). Emphasis should be on programs to reduce the reservoir of infection and hence transmission of this disease.

Keyword: Hydatidosis, *Echinococcus*, serology, diagnosis

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Anticancer findings of Antigen B from hydatid cyst fluid of *Echinococcus granulosus* on melanoma cancer cell line

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نوع پذیرش: پوستر | کد مقاله: G-70348

Abstract: Background: Worm parasites, including *Echinococcus granulosus*, contain compounds that exhibit antitumor activity. So, the objective of this study was to evaluate the effects of antigen B extracted from hydatid cyst fluid on melanoma B16F10 cell. Methods: Effects of different concentrations of antigen B on B16F10 and HEK293 cells proliferation were investigated using the MTT assay. Cell cycle analysis to measure cellular DNA content in the G0/G1, S and G2/M was done using Flow cytometry. Annexin-V/PI staining method was used to determine cells apoptotic rate. Furthermore, the mRNA expression of pro-apoptotic gene BAX and anti-apoptotic gene BCL2 was assessed by RT-PCR after exposure to antigen B. Results: The effect of antigen B on HEK293 and B16F10 cells showed that HEK293 cells as a normal cell line is less sensitive than cancer cell line B16F10 to antigen B, and IC50 values in HEK293 and B16F10 cells were 35 ± 4.3 and 15 ± 3.1 μ M, respectively. In both cell lines, the antigen B induced anti-proliferative effect on the cells with increasing cell population at G0/G1, and decreasing the numbers of cells at the S and G2/M phases. Our results also showed antigen B can induce cell apoptosis in both HEK293 and B16F10 cell lines and increased the mRNA expression of BAX and decreased the mRNA expression of BCL2 thereby induction of cell apoptosis. Conclusion: this study confirmed that antigen B inhibits proliferation and promotes apoptosis of HEK293 and B16F10 cells and can raise hopes in the treatment of melanoma cancer. Keywords: Antigen B, *Echinococcus granulosus*, Melanoma, Cancer, Apoptosis



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Anti-cancer activity of hydatid cyst fluid on colon cancer cell line (C26)

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نوع پذیرش: پوستر | کد مقاله: G-62783

Abstract: Background: Colon cancer is the third most common cancer and the fourth leading cause of death from cancer. Some parasites introduce as an antineoplastic agents that can to inhibit the progress of some cancers. The aim of this study was to investigate the effect of crude hydatid cyst fluid (HCF) on clone cancer cell line (C26). Methods: HCF was isolated from hydatid cysts by syringe and at the first its toxicity was obtained by MTT assay. Cell cycle analysis and apoptosis were measured by flow cytometer and also the expression of BAX and BCL2 genes were measured by real time PCR. Results: The amount of apoptosis was increased in B antigen-treated cell lines in comparison with control group. Also the expression of pro-apoptotic gene (BAX) was increased in treated group, while the anti-apoptotic gene (BCL2) expression was decreased in comparison with control group. Cell cycle analysis in the antigen-treated group compared to the other groups showed that the cells were more in the G0/G1 phase as well as in the G2/M phase and fewer cells were in the synthesis phase. Conclusion: Our finding showed that HCF possibly contains active compounds and can limit the growth and development of C26 cell line by reducing or increasing the genes involved in apoptosis and finally the effect on the cell cycle. Keywords: Colon cancer, Hydatid cyst, C26, Apoptosis



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دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Application of medicinal plants in treatment of leishmaniasis: a systematic review study

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نوع پذیرش: پوستر | کد مقاله: G-26483

Abstract: Background: Parasitic diseases including leishmaniasis are the most prevalent infections around the world that have serious risks for the human health. Due to the serious side effects of chemical drugs and their inefficiency in some cases, medicinal plants have been considered for treatment of parasitic diseases, recently. The aim of this systematic review study was investigation and identification of medicinal plants introduced for using in treatment of leishmaniasis throughout the world. Materials and Methods: In order to collect the scientific information and research papers, it was referred to the scientific websites including Google Scholar, PubMed, Magiran, Web of Science and Elsevier. The used keywords are Leishmaniasis, Medicinal Plants and Protozoal Infection. The data were extracted and collected using research papers published over the past 16 years (2006-2022) Results: From 385 collected articles they were selected 43 papers for the present study because of their complete relationship with the main aim of the research. Based on the results of these selected articles, it was cleared that 32 species of plants were investigated for the treatment of leishmaniasis. Conclusion: Based on the results of this systematic review study, it is concluded that the therapeutic effect of 32 different kinds of medicinal plants has been confirmed. Among these plants, three of them had stronger therapeutic effects and fewer side effects, including Rosmarinus Officinalis, Aloe otallensis, and Cephalisipecaacuana. Keywords: Medicinal plants, Leishmaniasis, Parasitic disease, Natural medicines



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The relationship between frequency of Covid-19 and the most universal parasitic infection (Toxoplasma gondii)

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نوع پذیرش: پوستر | کد مقاله: G-73692

Abstract: Background: The covid-19 virus as a respiratory disease pandemic, can cause acute respiratory distress syndrome (ARDS). The disease is now a major health problem worldwide. According to different studies on the inverse relationship between Toxoplasmosis and Covid-19 and the aim of these study is to evaluate of relationship between Covid-19 with Toxoplasmosis infection. Materials and methods: In this cross-sectional descriptive study samples were taken of 360 patients which 50% of individuals were men and 50% were women. One hundred and eighty of them were considered as covid positive group by ELISA kit and 180 of them were as control group. Also, some demographic characteristics such as gender, age range, and occupation were recorded. Data analysis was performed using chi-square, and Fisher's exact tests and the confidence level of 95% was considered. Also, the significance level value was less than 0.05. Results: Of the 180 patients who were positive for anti-Covid antibodies, 26.7% patients were in the age group of 16-30 years, 25.1% of them were self-employed, 31.7% of them had anti- Toxoplasma gondii antibodies. Out of 180 control groups, 21.1% patients had Toxoplasma gondii antibody. The results of the study of sex frequency in 57 people who had both of Covid-19 and toxoplasmosis showed that the infection rates in men and women were 63.2 and 36.8, respectively. Also there is a significant relationship between co-infections of covid-19 and toxoplasmosis with sex (P-value = 0.030) and no significant relationship was observed between co-infections of Covid-19 and toxoplasmosis with age (P-value = 0.213). However, based on the results of Fisher's exact test, a correlation was observed between co-infections of Covid-19 and toxoplasmosis with a significant job (P-value



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Genetic characterization and frequency of *T. gondii* infection in stray cats in Lorestan province, West of Iran

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نوع پذیرش: پوستر | کد مقاله: G-86430

Abstract: Background: Cats as the definitive hosts of *Toxoplasma gondii* play an important role in parasite dispersion and outbreaks. To understand the transmission pattern of this parasite, the distribution of genetic diversity of *T. gondii* in cats is important. The current study aimed to determine the prevalence and genetic diversity of *T. gondii* isolates from stray cats in Lorestan Province, western Iran. Materials and Methods: Fresh stool specimens were collected from 200 cats in Lorestan province, West of Iran during 2016-2017. Formalin-ether concentration technique and the modified acid-fast staining method were used for the recognition of oocysts. The DNA was extracted from the stool by a commercial Genomic Mini Kit (Bioneer, South Korea). PCR-RFLP examination, sequencing, and phylogenetic analysis of the GRA6 target gene were used to determine the genetic characterization of *T. gondii*. Results: All samples were negative by parasitology techniques. Thirteen (6.5%) samples were positive by using the GRA6-PCR assay. The results of PCR-RFLP indicated that all samples were belonging to the type III of *T. gondii* genotype. The phylogenetic tree for GRA6 nucleotide sequences of 2 isolates from current work, with 12 reference strains of *T. gondii* and one strain of a *Hammondia hamondi* as external control indicated a 5% nucleotide difference. Conclusions: According to the results, high sensitivity and specificity, molecular tests are suitable for genotyping and the results of the RFLP technique indicated that type III of *T. gondii* is the most important and predominant genotype in Lorestan Province, western Iran. Keywords: Genetic characterization, *T. gondii*, Stray cats, Lorestan province, PCR-RFLP

Estimation of Burden of Cystic Echinococcosis in Iran Using Disability Adjusted Life Years (DALYs) in 2018

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نوع پذیرش: پوستر | کد مقاله: G-21809

Abstract: Background: Human hydatidosis as a public concern has increased in a number of countries that have reduced control programs for the disease due to lack of resources or policies. We aimed to estimate Disability-Adjusted Life Years (DALYs) for human hydatidosis in Iran in 2018. Materials and Methods: Data were collected from the Center of Communicable Diseases Control, Ministry of Health & Medical Education, Tehran, Iran in 2018. To calculate DALYs, years of life lost due to premature death (YLL) with years of life with disability (YLD) were calculated according to the formula as $DALY = YLL + YLD$. The standard life expectancy lost method (SEYLL) was used to calculate the years lost due to premature death. Results: DALYs for human hydatidosis was calculated as 1210.12 years (YLD equals to 177.12 and YLL equals to 1033) in Iran for the year 2018. It was estimated to be 700.2 years for men and 509.8 years for women. DALYs in men were significantly different from women ($P= 0.001$) so DALYs were more in men than women were. YLD was calculated at 78.228 years in men and 98.892 years in women and in both men and women at 177.12 years. YLD was significantly different in women compared to men ($P=0.001$), so YLD in women was more than in men. Conclusion: We reached considerable indices for hydatidosis in our study. Therefore, disease prevention and control programs in Iran seem necessary by the policy makers. Keywords: Hydatidosis; Burden; Disability-adjusted life years; Human; Iran

Risk Mapping and Spatial Modeling of Human Cystic Echinococcosis in Iran from 2009 to 2018: A GIS-Based Survey

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نوع پذیرش: پوستر | کد مقاله: G-71904

Abstract: Background: Cystic echinococcosis (CE) is one of the most important parasitic infections in subgroup seven common neglected diseases of humans and animals. It is in the list of 18 neglected tropical diseases of the WHO. We aimed to analyze the situation of the disease in Iran using Geographical Information System (GIS) and satellite data analysis. Materials and Methods: The data obtained from the Ministry of Health and Medical Education, Tehran, Iran and other related centers from 2009 to 2018 were analyzed using GIS. Then, the spatial distribution maps of the disease were generated, and the hot spots of the disease in Iran were determined using spatial analysis of ArcGIS10.5 software. Geographically weighted regression (GWR) analysis in ArcGIS10.5 was used to correlate the variables affecting the disease including temperature, relative humidity, normalized different vegetation index (NDVI) and incidence of hydatidosis. Data analysis was performed by Linear regression analysis and SPSS 21 software using descriptive statistics and chi-square test. Results: Zanjan, Khorasan Razavi, North Khorasan, Chaharmahal Bakhtiari, Hamedan, Semnan, and Ardabil provinces were the hot spots of CE. The results of geographical weighted regression analysis showed that in Khorasan Razavi, North Khorasan, Chaharmahal Bakhtiari, Hamedan, Semnan, Ardabil, Zanjan, Qazvin, and Ilam provinces, the highest correlation between temperature, humidity, vegetation density and the incidence of hydatidosis was observed (P0.001). Conclusion: The use of maps could provide reliable estimates of at-risk populations. Climatic factors of temperature, humidity, NDVI had a greater impact on the probability of hydatidosis. These factors can be an indicator used to predict the presence of disease. Environmental and climatic factors were associated with echinococcosis. Keywords : Hydatidosis; Incidence; Environmental variables; Geographical information system; Iran

Spatial modeling of visceral leishmaniasis in Iran from 2010 to 2018

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نوع پذیرش: پوستر | کد مقاله: G-17046

Abstract: Background: Kala-Azar is the most lethal type of leishmaniasis, sporadic in most parts of Iran and prevalent in some provinces. Using the Geographical Information System (GIS) and satellite data analysis, we intended to assess the disease's incidence in Iran. Materials and Methods: Using GIS, data received from the Ministry of Health and Medical Education in Tehran, Iran , and other associated institutions between 2010 and 2018 were evaluated. The disease's geographical distribution maps were then constructed, and the disease's hotspots in Iran were identified using spatial analysis using ArcGIS10.5 software. Geographically weighted regression (GWR) analysis in ArcGIS10.5 was used to link disease-influencing variables such as temperature, relative humidity, normalized difference vegetation index (NDVI), and incidence of visceral leishmaniasis. Linear regression analysis, SPSS 21 software descriptive statistics, and chi-square test were used to analyze the data. Results: This study revealed that the provinces of Ardabil, East Azarbaijan, North Khorasan, and Fars were the hot spots of VL. The provinces of Ardabil, East Azarbaijan, North Khorasan, Fars, Bushehr, Semnan, Sistan, Baluchistan, Esfahan, Chaharmahal Bakhtiari, Qom, Golestan, and Kerman had the highest correlation between temperature, vegetation density, and the incidence of Kala Azar, as determined by geographical weighted regression analysis. Conclusion: The use of maps might give accurate estimates of populations at risk. The probability of the presence of visceral leishmaniasis in an area was more influenced by climatic conditions such as temperature, humidity, and NDVI. These indicators can help as a predictor of the occurrence of disease. Visceral leishmaniasis is linked to environmental and climatic conditions. Keywords: Leishmaniasis Visceral, Incidence; Geographical information system, Environmental variable Iran

Antiparasitic and Hepatic effects of Caffeic acid on laboratory mice infected with hydatid cyst

مهرداد باوقای طوسی^۱، الهه ابراهیم زاده^۲، ©، مهرداد مهری^۳

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۲ دانشیار بخش پاتوبیولوژی دانشکده دامپزشکی دانشگاه فردوسی مشهد
۳ استاد بخش علوم درمانگاهی دانشکده دامپزشکی دانشگاه فردوسی مشهد

نوع پذیرش: پوستر | کد مقاله: G-37491

Abstract: Hydatidosis; is one of the most important zoonotic parasitic diseases, which is caused by the larval stage of *Echinococcus granulosus*. Albendazole is an effective drug on hydatid cysts and has to be applied at high doses for extended periods and adverse side effects are frequently observed. researchers are looking for alternative treatment methods or using Albendazole simultaneously with other drugs. Recently, many efforts have been made to discover new compounds from various kinds of sources such as plants. Caffeic acid is a phenolic compound with antioxidant and antibacterial activity and is present in some food. **Materials and Methods:** Fifty male and female laboratory mice were infected intraperitoneally by injection of 1,500 viable protoscolices. At 4 months post-infection, fifty mice were allocated into the six experimental groups: group 1 (Caffeic acid 50 mg/kg/bw), group 2 (Caffeic acid 25 mg/kg/bw), group 3 (albendazole 200 mg/kg/bw), group 4 (Caffeic acid 50 mg/kg/bw and albendazole 100 mg/kg/bw), group 5 (Caffeic acid 25 mg/kg/bw and albendazole 100 mg/kg/bw), group 6 (control). Animals were treated with Caffeic acid and albendazole every 24 h for 15 days. Treatments were performed by oral administration (by air displacement pipette). At the end of the treatment period, all mice were euthanized and necropsied. Hydatid cysts were examined and blood samples from the heart were collected. **Results:** The results of the present study showed that the total number and weight of cysts were significantly lower in treated groups with Caffeic acid in comparison to the control group ($p < 0.05$). No significant difference was observed in the results of liver enzyme activity and bilirubin concentration in the treatment groups compared to the control group. **Conclusion:** The present study shows that Caffeic acid had an antiparasitic effect in vivo that shows a remarkable reduction in the total number and weight of cysts. **Keywords:**



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How to distinguish *Fasciola hepatica* from the *Fasciola gigantica* species in tissue sections?

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نوع پذیرش: پوستر | کد مقاله: G-92673

Abstract: Background: Reliable differentiation between fasciolid species nowadays relies on molecular techniques mostly using PCR. Implementing nonmolecular techniques in this way can be of interesting laboratory practice regarding its easier feasibility. Methods: *Fasciola* specimens obtained from different parts of Iran were initially differentiated using DNA extraction, RFLP-PCR, and scanning electron microscopy to *F. hepatica* and *F. gigantica*. Aiming to illustrate the capability of tegumental spines morphology, the histopathological technique was performed for the selected specimen while the identified worms were managed blind. Hematoxylin and eosin (H and E) staining were used. Results: Two types of tegumental spines, "pointed" and "molar" shapes were observed in *F. hepatica* and the gigantic species respectively in tissue sections. These findings highlighted the value of detailed morphology. Conclusion: Studying morphological characters of the tegumental spines of *Fasciola* sp can be a remarkable tool in species identification. In addition, observing the other means of taxonomical study such as computer imaging analysis techniques has been also found effective. morphologic and morphometric measurements using detailed parameters of helminths can be introduced as reliable diagnostic tools along with molecular techniques capabilities. Keywords: *Fasciola*, Tissue section, Diagnosis, Tegumental Spine.

Investigating of bacteria and fungi in camel hydatid cysts in Yazd city

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نوع پذیرش: پوستر | کد مقاله: G-90378

Abstract: Introduction: Echinococcus granulosus sensu lato is a member of Platyhelminthes and causes echinococcosis. Hydatid cysts infected with various species of fungi and bacteria can cause bacterial and fungal contamination of animal carcasses. This study was conducted with the aim of investigating the presence of bacteria and fungi in hydatid cysts isolated from camels slaughtered in Yazd slaughterhouse. The genotype of the studied hydatid cysts and its relationship with the rate of bacterial and fungal infection were investigated. The code of ethic in this study was approved IR.SSU.MEDICINE.REC.1398.208. Materials and methods: This is a descriptive-analytical study that was conducted in Yazd city. The number of 26 hydatid cysts isolated from camels was investigated. Hydatid fluid was aspirated from each cyst and cultured for bacterial and fungal detection. Genomic DNA was extracted from the germinal layer and used to determine the genotype. Statistical analyzes were performed using SPSS version 16.0 and chi-square test. Results: Bacterial contamination in camels was 19.2%. Live and dead protoscolices were colorless and red, respectively. The presence of bacteria in hydatid cyst was not significantly related to fertility and survival. The relationship between the involved organs and bacterial infections was not significant. The most common type of bacteria was Escherichia coli. No fungal contamination was observed in hydatid cysts. Statistical analysis did not show a significant relationship between the occurrence of bacteria and genotypes. Conclusion: Due to the presence of bacteria in hydatid cysts isolated from camels and the possibility of bacterial contamination of carcasses and consequently meat, special considerations should be made in slaughterhouses during the separation of infected tissues. Keywords: Camel, Echinococcus granulosus, bacteria, fungi

Bacterial and Fungal Occurrence in Hydatid Cysts from Sheep in Central Iran

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نوع پذیرش: پوستر | کد مقاله: G-46792

Abstract: Introduction: Echinococcus granulosus sensu lato is a member of Platyhelminthes and causes Echinococcosis. Complications of hydatid cyst with fungal and bacterial contamination may cause bacterial and fungal contamination of carcasses. The aim of this study was to investigate the presence of bacteria and fungi in hydatid cysts from sheep slaughtered in Yazd slaughterhouse. The genotype of the studied hydatid cysts and its relationship with the rate of bacterial and fungal infections were investigated. Materials and methods: This study was conducted in Yazd province. Twenty sheep infected with hydatid cyst were examined. Hydatid fluid was aspirated from each cyst and cultured to detect bacteria and fungi. Genomic DNA was extracted from the germinal layer and used to determine the genotype. Statistical analyzes were performed using SPSS version 16.0 and Chi-square test. Results: Bacterial infection in sheep was 30%. The living and dead protoscolices were colorless and red, respectively. There was no statistically significant relationship between the incidence of bacteria and the type of organs involved. The presence of bacteria in hydatid cysts was not significantly associated with fertility and viability. The relationship between the affected limb and bacterial infections was not significant. The most common bacterial species were Staphylococcus saprophyticus and then staphylococcus epidermidis. No fungal infection was observed in hydatid cysts. Statistical analysis did not show a significant relationship between bacterial incidence and genotypes. Phylogenetic analysis showed the most similarity of G1 in Iran with the rest of the world. Conclusion: Hydatid cyst infection is common in sheep. Bacteria isolated from lung hydatid fluid, Yersinia enterocolitica, Shigella .spp, S. saprophyticus and in the liver were S. epidermidis, S. aureus, S. saprophyticus, E. coli. The main route of infection in hepatic hydatid cysts is apparently the bile duct. The effect of bacteria on hydatid cysts seems to be the degeneration of protoscolices in livestock hydatid cysts. The presence of bacterial species in hydatid cysts can lead to the destruction of protoscolices and sterilization of the cyst due to damage to the germinal layer and the entry of bacteria into the cyst. This phenomenon may occur due to bacterial invasion or secretion of bacterial toxins. Evidence suggests that bacteria inside hydatid cysts destroy protoscolices by invading or secreting exotoxins or enzymes. Key Words: Sheep, Echinococcus granulosus, bacteria, fungi



چهاردهمین گنگره بین المللی آزمایشگاه و باالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Survey on prevalence rate of Cryptosporidium infection in stockmen of Boukan city

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نوع پذیرش: پوستر | کد مقاله: G-93852

Abstract: Background: Cryptosporidium is a protozoan that causes an important opportunistic infection in humans and a wide spectrum of different vertebrates. This survey aims to determine the prevalence rate of infection considering some epidemiological factors in stockmen of Boukan city. Materials and Methods: In this cross sectional survey, a total of 200 faecal samples were taken from stockmen of Boukan city and after preparation of direct smear and smear of after centrifuge supernatant, the resulted smears were stained by modified ziehl –neelsen method, then the slides were examined microscopically (400-1000 X). Results: Six out of 200 samples (3%), were diagnosed as being infected to cryptosporidium oocysts. Conclusion: The highest prevalence rate was observed in " 1-7 year " (20.83%), uneducated (8.45%), with presence of clinical signs (26.32) and with consumption of home raised vegetable using animal origin fertilizer (18.52%) groups and no significant statistical difference were observed about the rest of studied parameters.



چهارمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Scolicidal effects of *Pimpinella anisum*, *Commiphora myrrha*, and *Nigella sativa* on protoscolices of hydatid cysts

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نوع پذیرش: پوستر | کد مقاله: G-84167

Abstract: Background: Hydatidosis caused by *Echinococcus* species is a major zoonotic infection that is detrimental to both humans and animal husbandries in many countries. Cystic echinococcosis (CE) affects mainly the intermediate host's viscera, including the liver, lungs, and less frequently, the spleen, kidneys, bone, brain, and other organs. Treatment of hydatid disease is mainly surgical, with medical treatment being reserved as a co-adjuvant treatment. Use of effective scolical agents during surgery of cystic echinococcosis is essential to reduce the recurrence rate. The aim of this study was to evaluate the in vitro scolical effects of methanolic extracts of *Pimpinella anisum*, *Commiphora myrrha*, and *Nigella Sativa* on hydatid cyst protoscolices. Materials and Methods: *Echinococcus granulosus* protoscolices were collected from the liver of sheep infected with the hydatid cyst. Different concentrations (0.1, 0.01, and 0.001) of plant extracts were used in different exposure times (1, 5, 10, and 20 minutes) for viability assay of protoscolices. Results: Among the methanol-extracts tested, *Commiphora myrrha* 0.1% concentrations had very strong scolical effects in 20 min. *Pimpinella anisum* 0.1% had strong scolical effects in 20 min, and *Nigella sativa* 0.1% had scolical effects in 5 min of exposure times and the mortality rate decreased with the lower concentrations. Keywords: Hydatid cyst, *Pimpinella anisum*, *Commiphora myrrha*, *Nigella sativa*, Protoscolical activity



چهاردهمین گنگره بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Acanthamoeba as a silent reservoir/Trojan horse for SARS-COV-2 virus: a lesson from COVID-19

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نوع پذیرش: پوستر | کد مقاله: G-29871

Abstract: Background: Acanthamoeba is ubiquitous free-living protozoan parasite with a wide distribution in nature. It is best known as agent responsible for granulomatous amebic encephalitis (GAE), keratitis, skin infection and rarely lung infection. In addition, Acanthamoeba is also known as a nosocomial infection, has been functioning as reservoirs and or Trojan horse for some pathogenic bacteria, viruses and fungi. Herein, we presented three cases of COVID-19 which Acanthamoeba spp., was detected in urinary and respiratory tracts by culture and PCR approaches. Cases presentation: All patients had admitted to the department of infectious diseases of the Razi Hospital in Qaemshahr city in north of Iran between April and May 2022 during COVID -19 pandemic. First case, a 64-year-old male, suffered from lymphoma. Second Case, a 61-year-old female, with hypothyroid and diabetes. Acanthamoeba was found in the urine of both patients. Nonetheless, in third case, a 70-year-old male, the parasite was found in the culture medium derived from the nasopharyngeal swab. Conclusion: Our findings support this idea that Acanthamoeba spp., possibly could play role as a reservoir/Trojan horse for SARS-COV-2 virus. Thus, increased awareness regarding this issue may be resulted in better outcomes for this potentially fatal infection. Keywords: Acanthamoeba spp., Reservoir, SARS-COV-2 virus, COVID-19 pandemic



چهاردهمین کنفرانس بین المللی آزمایشگاه و بائین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Investigating different diagnostic methods of Trichomoniasis infection in health care center clients

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نوع پذیرش: پوستر | کد مقاله: G-39721

Abstract: Background: Trichomoniasis is one of the most important parasitic infections caused by the parasite *Trichomonas vaginalis* (*T. vaginalis*). Different diagnostic methods used for this infection, and conflicting results reported, and the purpose of this study is to investigate the epidemiological situation and diagnostic methods of the *T. vaginalis* parasite! Materials and Methods: This cross-sectional study that conducted during March 2020 to March 2022 and 216 patients with symptoms of Trichomoniasis, including itching, burning, fetid discharge, and inflammation referred to public and private medical centers in Sari city. After completing the questionnaire, vaginal sample was taken using a sterile swab and were assessed using direct, culture, PCR and nested PCR methods. Results: Out of 216 examined patients, 43 samples were positive using different diagnostic tests. 25 were rural and 18 were urban and all patients were married. The results showed that 7 patients were reported positive using direct test, 28 patients using culture method, 38 patients using PCR method and 43 patients using Nested PCR method. Conclusion: The results of current study showed that due to the increase in the level of hygiene, Trichomoniasis infection is still one of the most common infections and among the diagnostic methods, the Nested PCR method was the most sensitive method. Keywords: Trichomoniasis, *Trichomonas vaginalis*, Epidemiology, Direct smear, Nested PCR

Transcriptome data meta-analysis in *Mus musculus* in order to identification of candidate gene in giardiasis

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نوع پذیرش: پوستر | کد مقاله: G-46278

Abstract: Background: *Giardia lamblia* as one of the important protozoan causes giardiasis, an intestinal disease, with high incidence in developing countries. The disease has clinical signs such steatorrhea, diarrhea, and malabsorption that could be very dangerous in children. In addition, some documents reported the parasite inside the tissue of the liver and pancreas causing cancer in humans. In this study, we analyzed the gene expression profiles of the liver tissue in patients with giardiasis. Materials and Methods: Expression profile arrays of GSE113666, GSE113667, and GSE113679 regarding *Mus musculus* obtained from Gene Expression Omnibus (GEO) were used for meta-analysis using R commands. The candidate genes regarding the liver tissue exchange used for protein-protein interaction (PPI) by Cytoscape and String database, then the results were analyzed for significant pathways using the Kyoto Encyclopedia of Genes and Genomes (KEGG) database and Gene Ontology (GO). Similar genes in *Homo sapiens* were identified using BLAST analysis. The specific primer pair of the most important gene was designed using Primer3 software. The gene expression was carried out on eight people, including three persons, who had giardiasis range from 8 months to 16 years before analysis, and five healthy persons using SYBR Green real-time PCR by $\Delta\Delta Ct$. Results: Meta-analysis and bioinformatics analysis showed that *saa3* was the most important effective gene in liver tissue changes in *Mus musculus*, which was similar to *saa1* in *Homo sapiens*. The gene expression analysis showed no difference between two groups of healthy and diseased people. Conclusion: The results showed that the pathway in *Mus musculus* may have no useful pattern for analysis human gene expression. Therefore, we recommend few other gene expression analyses in people with history of giardiasis. Keywords: *Giardia lamblia*; Liver; Gene Expression

Emerging of rural cutaneous leishmaniasis in Mahalat, Central Iran in 2021

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نوع پذیرش: پوستر | کد مقاله: G-92514

Abstract: Background: Cutaneous leishmaniasis (CL), caused by *Leishmania* spp., is endemic in many parts of Iran. CL is caused by *L. major* and *L. tropica* in Iran, resulting in zoonotic and anthroponotic CL, respectively. Recently, there are some reports of CL from non-endemic area such as the Central Iran. Before 2021, there is no report of indigenous CL in Mahalat but after that some cases were reported by Mahalat Health Center. In this study, we identified the agent of CL reported from Mahalat in 2021. Materials and Methods: All lesion samples (7 cases) were collected from the suspected patients with CL referred to Mahalat Health Center in 2021. After Giemsa staining, direct microscopic observation was carried out to detect the Leishman body. All the samples with Leishman body were used to molecular identification using ITS-1-PCR RFLP. DNA extraction was done using the DNA extraction kit. The extracted DNA was analyzed by Nanodrop instrument. The amplification reaction was done by thermo cycler. The results of amplification and restriction enzyme analysis were assessed using agarose gel electrophoresis with 50 bp DNA ladder. The positive and negative controls were used in all reactions. Results: All samples had a fragment with the size of 300-350 bp in length. The restriction enzyme digestion showed 200 and 127 bp fragments showing *L. major*. Conclusion: The new cases of CL in Mahalat should be considered as an alert of emerging of this important disease. The studied area should be considered for designing the useful programs for control and prevention of ZCL. Keywords: *Leishmania major*; Mahalat; Zoonotic cutaneous leishmaniasis

Seroepidemiological Study of *Toxoplasma gondii* in Type 1 and Type 2 Diabetic Patients and Its Comparison with Healthy Individuals by ELISA Method in Zabol.

مجتبی سرگزئی، منصور دبیرزاده¹ © P

کارمند دانشگاه علوم پزشکی زاهدان (ارائه دهنده) دکتر منصور دبیرزاده (نویسنده مسئول)

نوع پذیرش: پوستر | کد مقاله: G-49716

Abstract: Title: Seroepidemiological Study of *Toxoplasma gondii* in Type 1 and Type 2 Diabetic Patients and Its Comparison with Healthy Individuals by ELISA Method in Zabol. Mojtaba Sargazi¹, Mansour Dabirzadeh^{2*} 1,2 Department of parasitology and mycology, school of medicine, Zabol University of Medical Sciences, Zabol, Iran *Corresponding Author: Department of parasitology, Zabol University of medical Science, Zabol, Iran Email: mdabirzadeh20002000@yahoo.com Postad address: 9819616861 Phone number: 09152800624 Abstract Type 1(T1DM) and type 2(T2DM) Diabetics Miletus are prone to opportunistic infections, including toxoplasmosis, due to an immunodeficiency system. This study aimed to evaluate the serum of people with T2DM and T1DM to determine the titer of anti-Toxoplasma antibodies in patients, and compare it with the control group to determine the relationship between each. Methods: From 810 blood samples from people referring to government laboratories in Zabol city, were performed between October and the end of January 2017. Of these, 360 samples were related to healthy individuals (control), and 360 samples were related to T2DM individuals. Since sampling of T1DM individuals was done by the census, 45 samples belonging to T1DM and the same number as control were collected. Results: In this study, out of 360 samples of T2DM by ELISA method, 216 and 144 samples for IgG, and 9 and 351 for IgM were seropositive and seronegative respectively, and only 9 of these patients had IgG and IgM simultaneously. Among 360 samples of healthy (control) individuals, 173 and 187 samples were seropositive and seronegative for IgG. Out of 360 samples, 1 sample was seropositive for IgM and 359 samples were seronegative for IgM. Among controls, only one case of IgG and IgM was positive at the same time. Among T1DM, out of 45 samples, 20 were seropositive for IgG, 3 were seropositive for IgM and only three were simultaneously IgG and IgM positive. Of the 45 (healthy) controls, 26 had seropositive for IgG and seronegative for IgM, and 100% of T1DM were seronegative for IgM. Conclusion: While there is a relationship between diabetes and *Toxoplasma* infection, this connection is most pronounced in T2DM patients, toxoplasmosis increases and the parasite may invade pancreatic cells Keywords: *Toxoplasma gondii*, Toxoplasmosis, Diabetes

Seroprevalence of *Toxoplasma gondii* in COVID-19 Patients in Guilan province, Iran

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نوع پذیرش: بوستر | کد مقاله: G-28310

Abstract: Background: Immunocompromised patients may be at risk for reactivation of the toxoplasmosis infection; therefore, early diagnosis would be highly desirable in these individuals. This study was designed evaluate the possible association between coronavirus disease 2019 (COVID-19) and latent *Toxoplasma gondii* infection in Guilan province, Iran. Materials and Methods: The study was performed among 50 patients and 50 controls referred to hospitals of Guilan University of Medical Sciences during 2022. Peripheral blood samples were taken for serum separation and were collected into tubes and then kept at -20°C until use. Blood samples were obtained from 50 PCR positive COVID-19 patients. IgG antibody to *Toxoplasma gondii* was detected by a commercial ELISA kit. Accordingly, IgG absorbance levels 9 were considered negative, 9–11 was considered borderline, and 11 was positive. Results: *Toxoplasma* IgG antibody was found in 72% patients with COVID-19 and 70 % of the control group. This difference weren't significant between control and ones with Covid19 (P 0.05). Conclusion: These findings demonstrated that latent *Toxoplasma* infection is prevalent amongst the COVID-19 patients. Toxoplasmosis is currently not considered a risk factor for COVID-19. It also did not find any significant association between chronic toxoplasmosis and COVID-19. Keywords:

Relationship between fetal hemoglobin and various hematological indices in sickle cell disease in Bushehr, Iran

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نوع پذیرش: پوستر | کد مقاله: G-07619

Abstract: Background: Fetal hemoglobin (Hb F, $\alpha_2\gamma_2$) moderate the sickle cell anemia (SCA) phenotype by delaying the polymerization of sickle hemoglobin (Hb S, $\alpha_2\beta_s2$). The study examined the levels of Hb F and its relationship with various hematological indices were evaluated in people with sickle cell disease (SCD) who were referred to a laboratory in Bushehr city. Materials and methods: The present study was a cross-sectional study conducted on sickle cell patients who were referred to Mehr Bushehr Laboratory for hematological tests and hemoglobin electrophoresis. Hemoglobin F level was measured by Sebia capillary electrophoresis and hematological parameters were determined by Sysmex XN-1000 hematology analyzer. All statistical analyses were conducted using SPSS software. Statistical differences were considered significant at a 0.05 significance level, and all data were reported as the mean \pm standard error of mean (SEM). Results: We studied thirty-two patients with sickle cell disease with an average age of 27.31 ± 2.45 years participated in the study. There were 17 (53.1%) females and 15 (46.9%) males for Hb SS and Hb AS groups. The Hb F level of the 32 participants with SCD was 8.05 ± 2.10 . The mean Hb concentration, hematocrit (HCT) and total red blood cell count were 13.28 ± 0.74 , 38.15 ± 1.66 and 4.85 ± 0.15 respectively. Hb F had a positive correlation with MCHC ($r = 0.26$), WBC ($r = 0.39$) and PLT count ($r = 0.18$) and an inverse correlation with RBC count ($r = -0.42$), Hb concentration ($r = -0.69$), HCT ($r = -0.74$), MCV ($r = -0.24$) and MCH ($r = -0.26$). Conclusion: Our study showed that Hb F had an inverse correlation with RBC count, Hb concentration, HCT, MCV and MCH, as well as direct correlation with MCHC, WBC and PLT count. It is also recommended to investigate the level of Hb F and its relationship with hematological indices in other hemoglobinopathies, especially Hb D. Keyword: fetal hemoglobin, sickle cell disease, hematological indices, Bushehr

Effect of Astragalus maximus chloroformic on the Toxoplasma gondii Rh strain

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نوع پذیرش: پوستر | کد مقاله: G-57931

Abstract: Background: To the best of our knowledge, there is no scientific document on anti-Toxoplasma activity of Astragalus spp, so, this study aimed to evaluate the in vitro anti-Toxoplasma effects and cytotoxicity effects of A. maximus chloroformic extract (AMCE) on T. gondii Rh strain. Methods: In vitro effects of different concentrations of AMCE (2-64 $\mu\text{g/mL}$) on tachyzoites were measured by MTT assay for 48 h. In addition, effects of different concentrations of AMCE on infectivity rate and intracellular parasites into Macrophage cells (J774-A1) was evaluated. The Griess reaction assay was used to determine the nitric oxide (NO) produced by treated macrophage cells with AMCE. Results: The mortality rate of the parasites significantly ($p < 0.001$) increased in a dose-dependent manner with IC50 value of 9.85 $\mu\text{g/ml}$. The rate of infection and the mean number of intracellular tachyzoites in macrophage cells was significantly reduced ($P < 0.001$) after exposure of the macrophage cells to AMCE. The amount of NO production in macrophage cells after treatment with the AMCE was increased especially at the concentration of $\frac{1}{2}$ IC50 and IC50 ($p < 0.001$) in comparison with the control group. Conclusion: The findings of the current in vitro investigation as the first step to find new anti-Toxoplasma agents revealed the favorable anti-Toxoplasma effects AMCE, a natural isoflavone, against tachyzoites and intracellular forms of T. gondii. Despite of the accurate anti-Toxoplasma mechanisms of AMCE are not clear; our results showed that triggering the NO production can be considered as the one of the main mechanisms of action of AMCE for controlling and eliminating of T. gondii. However, further surveys are mandatory to assess the efficacy and safety of AMCE in animal model and its accurate mechanisms of action before use in the clinical phase. Key words: toxoplasmosis, natural products, isoflavone, nitric oxide

Anti-giardial and cytotoxic effects of Astragalus baba-alliar chloroform extract against clinical isolates of Giardia lamblia

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نوع پذیرش: پوستر | کد مقاله: G-17023

Abstract: The current chemical drugs for treating giardiasis are associated with some adverse side effects. On the other hand, there are reports of parasite resistance to these synthetic drugs. The aim of this work is to investigate the anti-giardial and cytotoxic effects of Astragalus baba-alliar ethyl acetate (ABEA) on Giardia lamblia. Methods: Anti-giardial activity of different concentrations of ABEA (10, 20, and 40 mg/mL) were determined against cysts and trophozoites of G. lamblia for 15-360 min. Furthermore, the cytotoxic effects of ABEA was assessed on normal human intestine epithelial cell (NCM460) and human colorectal adenocarcinoma cell line (SW480) through MTT ([3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyl tetrazolium bromide]) assay. Results: Based on the obtained results, the highest effect of ABEA was observed at a concentration of 40 mg/ml, so that this concentration, after 120 minutes, completely destroyed Giardia cysts (p0.001). The highest effect of ABEA was observed at a concentration of 40 mg/ml, so that this concentration, after 60 minutes, completely killed G. lamblia trphozoites (p0.001). The 50% cytotoxic concentrations (CC50) value of ABEA against NCM460 and SW480 cells were 2.78 and 1.46 mg/ml, respectively. The results showed that ABEA had lower cytotoxicity on normal cells than cancerous intestinal cells. Conclusion: Based on the obtained results in this study, A. baba-alliar chloroformic extract especially at the concentrations of 20 and 40 mg/mL. The results showed that ethyl acetate extract of A. baba-alliar had lower cytotoxicity on normal cells than cancerous intestinal cells. However, more surveys particularly in animal models and clinical setting are mandatory to explain the exact efficiency and mechanisms of action against G. lamblia infection. Keywords:



چهارمین کنفرانس بین المللی آزمایشگاه و باالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Evaluation of anti-toxoplasma effects of solid lipid nanoparticles containing Moringa oleifera oil in vitro on cell line (Vero cell)

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نوع پذیرش: پوستر | کد مقاله: G-19264

Abstract: Background: Toxoplasmosis is an infection caused by a single-celled parasite called *Toxoplasma gondii*. Which could be lethal in immunocompromised patients. This study aimed to Evaluation of anti-toxoplasma effects of solid lipid nanoparticles containing Moringa oleifera oil in vitro on cell line (Vero cell). Materials and Methods: In order to in vitro assay, the kidney fibroblast from the African green monkey cells (Vero cell), were cultivated in Dulbecco's Modified Eagle Medium (DMEM), and were maintained at 37 °C in 5% CO₂. An MTT assay was employed to evaluate the cell toxicity of the component. Also Anti-intracellular Toxoplasma activity of Mor-SLNs was evaluated in T. gondii-infected Vero cells. Results: The CC50 value for the Mor-SLNs was at the concentrations 10mg/mL. The statistical analysis showed a reduced toxicity of the Mor-SLNs regarding the concentrations (P-value = 0.012). The results showed statistically significant anti-intracellular Toxoplasma activity of Mor-SLNs (P-value = 0.011). The Mor-SLNs showed an increased cell viability regarding log-10 of the Mor-SLNs. Conclusion: Overall, our findings demonstrated that employing SLNs as a carrier for Moringa oleifera can effectively kill T. gondii tachyzoites with acceptable cell toxicity.

Keywords:

Antiparasitic Effects of Astragalus maximus chloroform extract on Giardia lamblia cysts

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نوع پذیرش: پوستر | کد مقاله: G-18625

Abstract: Background: Giardiasis is a worldwide parasitic infection of the small intestine caused by the flagellated protozoan *Giardia lamblia* in humans. Considering that chemical drugs to treat this disease have many side effects and their effect is not certain, therefore, finding a drug with less side effects seems essential in the treatment of this parasitic disease. In this research, we compared the effect of chloroform extract of *Astragalus maximus* plant with the drug metronidazole on *G. lamblia*. Materials and Methods: In this experimental study, stool samples infected with cysts were collected from fresh stools of patients referred to university hospitals in Khorramabad city and were examined to confirm *G. lamblia* infection by direct methods and formalin-ether test with optical microscope. Then the sample was centrifuged at 400 rpm for 10 minutes. The resulting solution was centrifuged at 600 rpm for 10 minutes and the cysts collected in the middle layer were slowly transferred to another tube with a Pasteur pipette and then the cysts were washed three times with distilled water. To determine the viability of cysts, the standard method of vital staining of cysts with 0.1% Eosin was used. Results: The results showed that the concentration of 40 mg/ml after 120 minutes and the concentration of 20 mg/ml after 240 minutes caused 100% destruction of *Giardia* cysts. Among the studied concentrations of the extract, the lowest efficiency was related to the concentration of 10 mg/ml extract, where after 360 minutes of incubation, it was able to destroy all *Giardia lamblia* cysts. The results of MTT assay showed that the chloroform extract of *A. maximus* plant did not show significant cytotoxicity against normal HEK293 cells. The amount of CC50 of chloroform extract of *A. maximus* and metronidazole was 12.3 and 34.2 mg/ml. Conclusion: Considering the proper effect of *A. maximus* plant on *Giardia lamblia* parasite and the many side effects reported from metronidazole drug, this plant can be introduced as a natural anti-giardiasis compound. Keywords: Giardiasis, Metronidazole, *Giardia lamblia*, Herbal plants

Evaluation of anti-toxoplasma effects of solid lipid nanoparticles containing cinnamon oil (Cinnamon Zeylanicum) on Toxoplasma gondii tachyzoite in vitro on cell line (Vero cell)

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نوع پذیرش: پوستر | کد مقاله: G-36748

Abstract: Background: Toxoplasmosis is caused by an obligate intracellular parasite called Toxoplasma gondii, which is able to infect all nucleated cells in the host. Infection with this opportunistic pathogen can lead to death in immunocompromised individuals. The use of solid lipid nanoparticles as carriers for drug delivery can be a suitable alternative to old carriers such as liposomes. This study aimed to synthesize cinnamon oil-loaded solid lipid nanoparticles (CZ-SLNs) and to evaluate the anti-Toxoplasma activity of this component. Materials and Methods: The CZ-SLNs were constructed using double emulsification method. The cell culture method was used to cultivate cell line (Vero cell) in DMEM medium. The MTT assay was employed to evaluate the cell toxicity of the CZ-SLNs. The intracellular anti-toxoplasma activity of CZ-SLNs was evaluated with T. gondii infected Vero cells by MTT assay. Results: The statistical analysis for Cell toxicity assay of CZ-SLN on Vero cell line showed a reduced toxicity of the CZ-SLNs regarding the concentrations (P-value=0/0959). The CC50 value for the CZ-SLNs was at the concentrations 0/1mg/mL. The results showed statistically significant anti-intracellular Toxoplasma activity of CZ-SLN (P-value=0/0881). The CZ-SLNs showed an increased cell viability regarding log-10 of the CZ-SLNs. in the concentration 0/01 mg/mL at least 80% of T. gondii- infected Vero cells remained alive. Conclusion: In this study, our findings indicated that the use of SLN as a carrier for CZ can significantly kill tachyzoites with acceptable cytotoxicity. Overall, our results suggest that nano formulation of natural products can increase efficiency and decrease toxicity of the herbal component such as Cinnamon Zeylanicum. Keywords:

Toxoplasma gondii; as a Master of Reversing Tumor-Associated Immunosuppression

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نوع پذیرش: پوستر | کد مقاله: G-07943

Abstract: During cancer development, normal cells change into cells that do not stop reproducing. The immune system typically destroys transformed cells and detects them to stop cancer from spreading. However, sometimes, conditions can occur that make the removal of tumors ineffective. Immunotherapies that enhance immune functions have become increasingly popular for treating many cancers due to their increased specificity and reduced toxicity compared to conventional chemoradiotherapy. Reversing tumor-associated immunosuppression appears necessary to stimulate effective therapeutic immunity against lethal epithelial tumors. Using pathogenic microorganisms in cancer immunotherapy is not new. To study T1 cell-mediated immunity in intracellular infections, *Toxoplasma gondii* can be used as a model pathogen. *T. gondii* persistently affects most warm-blooded vertebrates. Since the immune system is usually strong, the primary infection is typically subclinical. Despite this, *T. gondii* always infects its host over a long period through latent tissue cysts. *Toxoplasma* cells especially reach and overrun myeloid cells, including monocytes/macrophages and dendritic cells, often active in tumor-elicited immunosuppression. *T. gondii* can regulate innate immune cells by attacking myeloid cells, typically producing powerful TH1 immune responses. *Toxoplasma* secretes a collection of technical molecules during the invasion that takes cellular control from within. The parasite even seizes adjacent cells reached but not invaded when it injects its molecules into cells. For example, *T. gondii* inhibits the activator of transcription 3, and signal transducer (STAT3) regulates the production of interleukin-12 (IL-12) and induces arginase 1 after activating STAT6 by injecting rho-tryptophan (ROP)16 kinase into macrophages. *Toxoplasma* cells release ROP18, a protein that protects the vacuoles that contain intracellular parasites and their host cells against the innate immune attack mechanisms mediated by IFN-activated GTPases, which are produced by interferons (IFN). *T. gondii* secretes additional molecules responsible for manipulating the immune responses and host cells. As an uracil auxotroph (cps) strain, a stable, safe, single-copy variant of *T. gondii* was developed. Both standard and severely immunodeficient mice exhibit an exceptional degree of loss of virulence when uracil auxotrophs invade mammalian cells without uracil. It has been reported that this parasite can inhibit the growth of ovarian, mouse melanoma, pancreatic, and breast cancer in-vitro and in-vivo. These effects mean that the avirulent *T. gondii* strain can be a proper immunotherapeutic mechanism for tumor treatment. To break tumor-associated immunosuppression, we can conclude that *T. gondii*-secreted elements and the CPS strain might cause strongly polarized TH1 host responses that would increase innate immune cells in the tumor microenvironment. Keywords:

Inhibition of K562 Cell Growth by Protoscolex Hydatid Cyst Somatic Antigen

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نوع پذیرش: پوستر | کد مقاله: G-86142

Abstract: Abstract Background: Today, cancer is one of the most important causes of death in the world, and so far, many treatment methods have been used in this field. One of the newest achievements of that science is immunotherapy, which is still conducting many types of research in different cancers and with various antigens. One of the subsets of cancer immunotherapy is its treatment using parasitic antigens. In the present study, the effect of using somatic antigens of protoscolex of Echinococcus granulosus on K562 cancer cells has been interpreted. Materials and Methods: In this experimental study, hydatid cysts' protoscolex antigens were extracted, purified, and added to K562 cancer cells at three concentrations of 0.1, 1, and 2 mg/ml and three times 24, 48, and 72 hours. The number of apoptotic cells was compared to the control flask. It was investigated by the MTT method, the antigen concentration of 2 mg/ml was used as a control sample to investigate its effect on the growth of healthy HFF3 cells, and annexin V and PI tests were also performed to differentiate apoptosis from necrosis. Results: In flasks treated with hydatid cyst protoscolex antigen, all three concentrations significantly reduced the growth of cancer cells compared with the control flask, and concentration 2 of crude antigen significantly caused the death of cancer cells. In addition, more cancer cells underwent apoptosis by increasing the antigen exposure time. On the other hand, flow cytometry results also showed that the amount of apoptosis has increased compared to the control group. Conclusion: Protoscolex hydatid cyst somatic antigens induce programmed cell death in K562 cancer cells while being safe for healthy cells; Therefore, it is suggested to do more research on the anti-cancer and therapeutic properties of the antigens of this parasite. Keywords: Echinococcus granulosus, Cancer, Immunotherapy, K562 cells, Flow cytometry

Echinococcus granulosus as a Promising Therapeutic Agent Against Triple-negative Breast Cancer: Vaccine Development

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نوع پذیرش: پوستر | کد مقاله: G-63820

Abstract: Abstract In 2020, breast cancer in women overtook lung cancer as the most common disease diagnosed with cancer, with an estimated 2.3 million new patients. Surgery, radiation, hormone therapy, and chemotherapy are among the first-line therapeutic choices. However, chemotherapeutic agent's non-selective cytotoxicity has undesirable side effects. Drug resistance also creates a poor prognosis for the course of treatment. Therefore, it is crucial to look for anticancer medications that are more efficient and have fewer adverse effects. It has been shown that glycosylated antigens exist both in the hydatid cyst and in cancers. Carbohydrates have also been demonstrated to play a crucial role in the host's immune response in hydatid cysts. Thus, glycan epitopes could also be chargeable for the majority of cross-reactions between hydatid cysts and cancer. In several studies, it was indicated that sera from breast cancer patients cross-react with a peptide band from the hydatid cyst. So, it is interesting that a peptide molecule from the laminated layer of the hydatid cyst cross-reacts with sera from breast cancer patients. In terms of adaptive immunity, it is thought that antibody-mediated immune responses brought on through Tn antigens in echinococcosis patients are taken into consideration to set off immunity toward cancer development. EgKI-1, Kunitz-type protease inhibitor (PI), is highly expressed in oncosphere form and is a potent leucocyte elastase and chemotaxis inhibitor. EgKI-1, negatively affecting the cell cycle progression, inhibits the expansion and migration of a variety of cancer cells in vitro. Moreover, in several studies, it was revealed that treatment with EgKI-1 significantly inhibited cancer growth in a triple-negative breast carcinoma model. Recently, several studies confirmed the anticancer ability of numerous hydatid fluid antigens, along with AgB, glycolipid, glycoprotein, and 78kDa fractions in breast carcinoma cell lines. The findings of the previous studies indicate that certain Echinococcus granulosus antigens can cause adaptive immunity in opposition to cancer. In addition to the significant inhibitory effect on neutrophil elastase, which performs a crucial role in tumor metastasis, EgKI-1 also results in anticancer impact by immediately inhibiting tumor growth probable via disrupting cell cycle progression. EgKI-1 appears to be a promising healing molecule in opposition to cancer, which can be considered in destiny remedy development. Therefore, this dog tapeworm may offer a few desires as a capability treatment in opposition to a few types of cancer. In conclusion, this canine cestode secretes molecules that could be a promising therapeutic against breast cancer. Keywords: Breast cancer, Cancer therapy, Echinococcus granulosus, Parasite

Pathological evaluation of lesions caused by *Leishmania major* during treatment with bone marrow mesenchymal stem cells in BALB/c mouse model

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نوع پذیرش: پوستر | کد مقاله: G-17384

Abstract: Background: Cutaneous leishmaniasis is one of the endemic and common diseases in many countries of the world, including Iran. The use of glucantim is the most important treatment method for cutaneous leishmaniasis, which has many side effects. The aim of this study is to present a herbal treatment method with the effective ingredient of non-alcoholic garlic extract for cutaneous leishmaniasis. Materials and methods: In this study, female BALB/c mice aged 6-8 weeks were infected with the standard strain of *Leishmania major*. A group of animals received garlic extract (0.6 g/bw/kg) before the appearance of a wound and a group received garlic extract together with the drug glucantim (18mg/kg/bw) and another group received garlic as an ointment (1-2 g/lesion). After 123 days of the treatment period, the size of the wound, the death rate of the animals and the healing process of the wound through the examination of tissue sections of the skin, liver, spleen and lymph nodes were investigated in weeks (2, 4, 6, 8, 10, 12). Result: The size of the lesion decreased in the group receiving garlic extract orally during the treatment compared to the group treated with glucantim and garlic extract by topical method (P-Valu 0.05). The percentage of survival of the mice that received the extract as an ointment was significantly higher than the other treated groups (P-Valu 0.001), according to the pathology findings, there was no edema and severe inflammation in the group that received the extract of garlic. Significant reduction of tissue damage were seen in dermis and hypodermis of the skin. Also, granulomas in the liver, the return of the microscopic structure of the lymph node to the normal state and the regeneration of the white pulp in the spleen were observed. Conclusion: The lesion healing process of cutaneous leishmaniasis in the groups receiving garlic extract orally is significant compared to the group receiving it topically and it has a synergistic effect in the groups receiving the drug glucantim, but the dose of the extract for oral treatment as an effective substance in accelerating the effective treatment process should be further investigated. key words: Cutaneous leishmaniasis, non-alcoholic garlic extract, BALB/c mice

Prevalence of Human Fasciolosis in Iran: a systematic review and meta-analysis

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نوع پذیرش: پوستر | کد مقاله: G-28169

Abstract: Background: Fasciolosis is a worldwide disease predominantly caused by two parasites of the class Trematoda, genus Fasciola, named *F.gigantica* and *F.hepatica*. Both parasites are hermaphroditic, have identical life cycles, and induce equivalent clinical manifestations in humans. Fasciolosis is an acute parasitic zoonosis disease and an emerging public health threat in numerous regions worldwide, including Iran. Humans are secondary hosts and frequently acquire infection by eating watercress or water chestnuts and other freshwater plants, including water lettuce, mint, alfalfa, and parsley. Humans can also get infected by drinking polluted water containing metacercariae. We aspire to contain recent information on the distribution, prevalence, and associated risk factors for *Fasciola* spp. This study aimed to scrutinize the prevalence of fasciolosis in humans through a Meta-analysis and systematic review in Iran. Materials and Methods: The best ways to contain these pathogens must be analyzed to reduce massive destruction. Nine databases (PubMed, Scopus, Google Scholar, Cochrane Library, Magiran, SID, Medline, Embase, and Lilacs) were searched for published articles on human *Fasciola* infections in Iran from January 2000 to August 2022. Fifteen affiliated articles with complete abstracts were included in this study. All data were extracted from interconnected papers and analyzed with R version 4.2.1 artificial intelligence software. Results: According to the statistical analysis, the prevalence of Fasciolosis in Iran has reduced in recent years. The occurrence of animal and human infection advances during wet seasons of the year because of an improved number of snails and more prolonged survival of encysted cercariae. The presence of intermediate parasites with unknown biological characteristics, rising sea levels, increased summer rainfall, and increasing contact between people and impure water have become fundamental risk factors in the prevalence and occurrence of *Fasciola* infection in Iran. The highest prevalence was reported in Northern Iran, particularly Guilan and Mazandaran provinces, with a prevalence of 0.1%, in which Rasht city had the highest infection rate. No statistically significant affiliation between gender and disease prevalence could be noticed. Additionally, in various capitals of Iran, there are no discoveries of the disease. Conclusion: In conclusion, disease control policies are mandatory to facilitate human fasciolosis's economic and public health impression. The high-pooled prevalence estimates of *Fasciola* infection and the scarcity of reported data from databases indicate a vital data gap on fasciolosis distribution in the country. It is suggested that educational programs about anti-parasitic treatments are essential for veterinarians and general practitioners. Regarding the importance of fasciolosis and its endemicity, prevention protocols for animal and human fasciolosis are still crucial in Iran. Keywords: *Fasciola*, Prevalence, Meta-analysis, Public health, Iran



چهاردهمین کنفرانس بین المللی آزمایشگاه و باالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



The Innate Immunity Defence against Gastrointestinal Nematode Parasites; for Future Vaccine Development

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نوع پذیرش: پوستر | کد مقاله: G-94025

Abstract: The abundance of natural parasites accounts for a fifth of people being parasitized by gastrointestinal nematodes. Especially in areas without adequate medical facilities and efficient hygiene standards, people usually come into touch with parasites known nematodes. Infected individuals can suffer severe damage from nematodes, which are well spread. Water, food, soil, or close contact with animals can transmit them. By feeding on host tissues or locating larval stages inside organs, these multicellular pathogens can cause damage to several tissues and organs. It is generally possible to avoid nematodes by improving fundamental hygiene practices, but signs of infection may include mild anemia, abdominal pain, diarrhea, impaired cognitive development, or stunted growth. With drug resistance among gastrointestinal nematodes and host immunity propping up other programs for manipulating them, enhancing adaptive and innate immune responses to these parasitic helminths is of interest. Nevertheless, nematodes co-evolved with their hosts to develop mechanisms that prevented excessive immune responses, which enabled them to continue their lives. It's incredible how many different, often particular, molecules nematodes produce. These molecules affect the microenvironment around them, the density of tissues, and immune system properties. These parasites have different immunomodulatory atoms at different life stages to satisfy each stage's needs. Additionally, nematodes secrete a variety of miRNAs, immunomodulatory proteins, vesicles, and other molecules, called ES (excretory-secretory) products, to weaken the immune system. Some of these parasite molecules are homologous to host molecules through the expression of miRNAs that target host gene expression or mimic host proteins. In this way, parasites can manipulate immune cell function to their advantage. Hosts must orchestrate their immune response to counter these parasite survival strategies. This includes maintaining a balance between immunity against helminths and wound healing without rupturing the immune system to the point of inflaming the body. The innate immune system is now recognized as a critical component in developing an adaptive effector response and a driver of vaccine-induced immunity. This paper will overview current research on the innate barriers and immune mechanisms, cells, and receptors involved in the innate host response to nematode parasites. It will also review the 'nematode-associated molecular patterns' that may be specifically recognized by the host. Keywords:



چهاردهمین کنفرانس بین المللی آزمایشگاه و بائین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Epidemiology of cryptosporidiosis among people living with HIV/AIDS in Iran: a systematic review

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نوع پذیرش: پوستر | کد مقاله: G-91805

Abstract: Background: Patients who have HIV/AIDS are susceptible to opportunistic infections, which include certain gastrointestinal diseases. Cryptosporidium is a single-celled parasite known for infecting these patients. This study aims to investigate the epidemiology of cryptosporidium in HIV/AIDS patients in Iran using systematic reviews. Materials and Methods: Search for systematic for published articles in databases (PubMed and Google scholar) up to 2022 and the recently published abstracts using the following. This systematic review study was conducted according to the Preferred Reporting Items for Systematic Reviews (PRISMA) guidelines (figure 1) Results: Using the data gathered from 12 studies, we analyzed 1376 HIV patients from 9 cities in Iran between 2000 and 2022. We found 197 cases of cryptosporidium among HIV patients. According to this systematic review, the prevalence of cryptosporidium infections among HIV patients is 14.31%. This relatively high prevalence shows that cryptosporidium is one of the most common parasitic intestinal infections among AIDS patients. Cryptosporidium infection causes diarrhea and other intestinal disturbances in patients, and in some cases, it may even be lethal. Conclusion: Immune suppression in AIDS patients increases the risk of opportunistic infections and diarrhea. Therefore, HIV patients should be monitored for intestinal parasites alongside following standard hygiene protocols to reduce complications and mortalities. Keywords: Cryptosporidium, AIDS, HIV, Iran

Trypanosoma cruzi; Future of Colorectal Carcinoma Vaccine Development

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نوع پذیرش: پوستر | کد مقاله: G-97365

Abstract: The most common therapeutic approach for cancer elimination is relatively ineffective due to drug resistance. Cancers of the colon and rectum are the third most common form worldwide. Around 250,000 new intestinal diseases are diagnosed in Europe yearly, corresponding to about 9% of all malignancies. Moreover, in recent years, this disease has experienced an increase in its incidence that has been steady since its onset. There has been a substantial advancement in therapeutic interventions for colorectal cancer over the past few decades. Still, deaths from colorectal cancer remain around 40%, mainly because liver metastases account for a significant portion of the mortality rate. Most chemotherapy drugs used are from a synthetic or natural source but cannot limit the growth of tumor cells. Therefore, understanding the immune response to the tumor and the immunosuppression in its microenvironment has contributed to developing new immunotherapeutic treatment approaches such as anti-cancer vaccines. Vaccines against cancer have attracted much attention in recent years as a possible treatment option. Various studies have found that patients with parasite-infected tumors have exhibited unusual anti-tumor immune responses as a result of cross-reactivity with their immune system. One of the most critical factors in eliciting effective anti-tumor immune responses is the selection of ideal antigens for anti-cancer immunization. In recent years, some parasites, especially intracellular protozoal parasites, have been considered effectors to induce anti-pathogen and anti-tumor immune responses, thus overcoming tumor escape and an active tumor surveillance system. Furthermore, due to the immune system's memory cells, this anti-tumor response lasts for life, preventing tumor relapse and recurrence. One of these protozoal parasites is *Trypanosoma cruzi*, the causative agent of Chagas disease, an acute and chronic disease that affects 12 million people in America each year. There are many challenges in diagnosing, treating, and controlling chronic Chagas disease, and due to the migration of infected people, Chagas is a worldwide disease. Previous studies have shown that the patient's immune system controls the acute infection in most people infected with *T. cruzi*, even without treatment. Infection with *T. cruzi* appears to increase cancer resistance, supported by different experiences. In addition, no colorectal cancer was observed in patients with Chagasian megacolon, suggesting that patients with Chagas disease are protected from colorectal cancer. These antitumor effects may be due to the pro-apoptotic activity of *T. cruzi* components. The Tc52 protein released from *T. cruzi* showed an apoptosis-inducing effect on a human T-cell leukemia cell line when fused to glutathione-S-transferase (GST). Other *T. cruzi* components with proapoptotic activity include a ceramide-containing glycolipid and trans-sialidase. The parasite expressed the tumor antigen, activated T cells, and delayed tumor growth. Because of these properties of *T. cruzi* components and significant immunogenicity, it may be an ideal target for anti-cancer immunization. This review article outlined the mechanism of *T. cruzi*'s anticancer effects with the aim of providing novel strategies for the clinical management of colon and rectal cancers without damaging normal tissues. Keywords: Cancer, Vaccine, Therapy, *Trypanosoma cruzi*

Current Status of Mesenchymal Stem Cell Therapy in Solving the Problem of Parasitic Drug Resistance

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نوع پذیرش: پوستر | کد مقاله: G-78290

Abstract: Anti-parasitic drug resistance is a serious problem for all clinical populations, and there are few treatment choices for influenced individuals. Resistance is due to needless or excessive use of anti-parasitic, or Incorrect use is associated with a lower dose or duration. In both human and veterinary medicine, the over-prescription of broad-spectrum anti-parasitic drugs; multiplies our need for new treatment methods. as raw material for tissue regeneration or as immunomodulatory agents for treating inflammatory illnesses, mesenchymal stromal cells (MSCs) have long been investigated in regenerative medicine. As a potential treatment for anti-parasitic drug resistance, MSCs have shown promise in recent years. There are still unknown mechanisms behind MSCs' anti-parasitic properties. As well as releasing anti-parasitic molecules directly interacting with pathogens, they boost host immunity's anti-parasitic capabilities. MSCs have demonstrated an antifungal, antiviral, and anti-parasitic capacity. In proof-of-concept studies and strong synergistic effects with antimicrobial treatments, it has been shown that bone marrow, dental tissue, adipose tissue, and umbilical cord can be used to obtain mesenchymal stromal cells (MSCs). Malaria and Chagas are two parasitic diseases that have been examined as promising treatment strategies using these cells. Several studies convincingly have shown that through chemotactic mechanisms that are not entirely understood, mesenchymal stromal cells (MSCs) can stimulate the endogenous repair of damaged tissues and modulate immune responses to enter inflammatory sites. By secreting growth factors, cytokines, and chemokines, mesenchymal stem cells advance the repair and regeneration of damaged tissues by paracrine action. These factors can inhibit apoptosis, stimulate proliferation, promote vascularization, modulate the immune response and promote tissue regeneration. The results of several studies reported that MSCs play a role in tissue regeneration and management of inflammation in a paracrine manner, which is observed in parasitic diseases such as *Trypanosoma cruzi* and *Schistosoma japonicum*. In some cases, it may also have a direct impact, such as in the elimination of microorganisms by inducing antimicrobial molecules such as lipocalin 2, in treating pneumonia caused by *Escherichia coli* infection, or by increasing or using activated IFN-gamma. MSCs that induce GTPases and guanylate-binding proteins that exhibit anti-parasitic activity against *Toxoplasma gondii* and *Neospora caninum*. If MSC anti-parasitic properties can translate into reasonable treatment options, they supplant much of the anti-parasitic currently used in animals. This review will investigate the veterinary literature regarding MSCs as anti-parasitic. Although this is an emerging field of study, we will outline possible mechanisms and look at potential synergism in combination therapies and the possible deleterious effects of such an approach. Keywords: Medicine, Antiparasite, Mesenchymal stem cell, Cellular therapy

How does nanotechnology help veterinary medicine solve anthelmintic drug resistance for Zoonotic Helminth infections?

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Abstract: Gastrointestinal nematodes are considered one of the most important factors that threaten the health of humans, as well as causing a lot of economic losses to ranchers all over the world. These parasites lead to a decrease in appetite and, as a result, a reduction in the intake of nutrients; consequently, the water and electrolyte balance of the body is disrupted. On the other hand, protein deficiency, weight gain, and amino acid demands also occur. Weakness, malabsorption, and disturbance in reproduction are other negative consequences of these parasites. Over the last 40 years, pharmacotherapy has become the most popular strategy for controlling helminths. Because no complex management practices are involved, the results are almost immediate, and the cost of an anthelmintic dose is relatively low. Therefore, Control of these parasites is generally through the use of broad-spectrum anthelmintic drugs, which are divided into three main groups; benzimidazoles (BMs), imidazothiazoles (IMs), and macrocyclic lactones (MLs). Although this approach was highly successful for several decades, we are now experiencing ever-increasing levels of anthelmintic resistance in all drug classes, involving virtually all of the most economically important parasites. Anthelmintic resistance occurs when parasites, usually eliminated by a given dose, suddenly survive the treatment. Since resistance is inherited, the surviving worms will pass their resistance alleles to their progeny. The emerging significance of anthelmintic resistance demands an urgent need for the development of reliable, reproducible, and standard methods/assays for its detection. As a result of nanotechnology, new drugs were developed by modifying existing ones. This technology can organize the drug in nano-scale structures (less than 100 nm at least. These nano-delivery structures enhance the potential advantages of anthelmintic drugs, regulating their delivery and kinetics, reaching specific targets, and preventing their systemic spread and side effects. The use of nanomaterials and derived materials can be considered ideal for the diagnosis and treatment of gastrointestinal nematodes. In addition to their ability to enter cells rapidly, they also have a shorter detection time. They are a potent alternative to conventional methods, which are limited by gastrointestinal nematode drug resistance. In this review article, we summarized different types of clinically used nanoparticles and their specificity for therapeutic applications of diseases caused by gastrointestinal nematodes. Keywords: Antihelminth, Drug resistance, Nanotechnology, Nematode



چهاردهمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Investigation of scolicidal effect of CM11 on Hydatid cyst: An Invito assay

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Abstract: Background: In present study, scolicidal effect of CM11 peptide against protoscolices of hydatid cyst was investigated. Materials and methods: The liver hydatid cysts were collected from the slaughtered sheep in the Mashhad abattoir in the summer of 1397. Echinococcus granulosus protoscolices were collected and washed three times with 0.9% normal saline. At first, the percentage of viability of protoscolices was evaluated using Eosin staining. Different concentrations of CM11 peptide (16, 64, 128, and 256 μmol .), along with positive control (Savlon) and negative control group (0.9% normal saline), were used against protoscolices (viability of 90%) for 30, 60, 120 and 240 minutes at a 37°C incubator. Eosin staining was done at the end of the incubation time, and the images were taken with a camera equipped with Tcapture software. Finally, the number of dead and live protoscolices was determined by ImageJ software, and the viability and mortality percent was calculated. All the tests were performed five times. Data analysis was carried out by using sigma stat (version 3.5). P value 0.05 was considered statistically significant. Results: Up to 2 hours, the effect of all concentrations of CM11 peptide on protoscolices was not significant compared to the negative control group. However, after 4 hours of exposure, 128 and 256 μmol of peptide, were significantly decreased the viability of protoscolices (p 0.05). Conclusion: With regard to the results of this study and considering the resistance of the present antiprotoscolics drugs, the CM11 can be used as a relatively effective peptide against protoscolices in future research. Obviously, it is crucial to improve the effective dose and time of this peptide. Concomitant use of this peptide with other effective compounds on protoscolices and structural changes in the peptide will potentially reduce the effective dose and time of action. Keywords: CM11, Hydatid cyst, Invito assay

A large-scale study on the seroprevalence of *Toxoplasma gondii* human infection in Iran

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Background: It is estimated that nearly one-third of the world's human population is infected with *Toxoplasma gondii*. Infection in humans is commonly asymptomatic, though it is multifaceted and can manifest in severe pathological forms in congenital toxoplasmosis and immunocompromised individuals.

Materials and Methods: This study attempted to recognize the seroprevalence of *Toxoplasma* infection in a large number of Iranian residents referred to medical laboratories for toxoplasmosis tests throughout the country. This retrospective cross-sectional study was conducted from 2015 to 2019 on individuals referred to diagnostic laboratories in 26 provinces, and these laboratories sent their samples to the referral centers. Accordingly, data associated with serodiagnosis of toxoplasmosis, age, sex, anti-*Toxoplasma* IgG, and IgM status in Iranian residents were collected from two referral diagnostic laboratories. All individuals had evaluated using the antibody immunocapture-chemiluminescence assay (CLIA) method with the Immulite[®]2000s XPi system.

Results: In this study, the first large-scale assay of *T. gondii* infection in Iran, an overall seroprevalence of 30.4% was among 35047 studied patients detected. The highest IgM seropositivity rate was in the 10-20 years old group. In addition, this study showed a very different prevalence of *Toxoplasma* across the country, highest in the humid areas, such as the Caspian Sea basin in the North, the North West with 48.60%, and the South West of Iran at 10.6%.

Conclusion: Overall, about one-third of Iranian people have been infected with *T. gondii*. Accordingly, two-thirds of the human population is seronegative and susceptible to infection. As so, individuals at high risk should be monitored. Several measures will aid in the prevention and control of *T. gondii* infection. These include health policies targeting the promotion of public educational programs, training courses for childbearing age and pregnant women, an inspection of food production industries, improvement of hygienic standards of abattoirs, and sanitary disposal of viscera.

Keywords: Prevalence, Seroprevalence, *Toxoplasma gondii*, Toxoplasmosis

Toxoplasma genotyping using PCR-RFLP from central Iranian *Ovis aries* slaughtered: Effect of One Health

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Background: Since lamb is one of the main animal proteins in the human diet in most countries, consuming raw or uncooked mutton/lamb and other products of these animals could be a significant potential risk factor for toxoplasmosis in humans. The mean of the total seroprevalence of *Toxoplasma* in sheep studies in the North, South, East, West, and Centre of Iran is about 33.136%, 25.954%, 12.403%, 30.417%, and 27.963 respectively, based on those studies and the mean of the total prevalence of sheep molecular evaluations is 27.258%, 16.798%, 33.368%, 7.04%, and 27.785%, respectively. This study aimed to determine *T. gondii* prevalence and genotypes isolated from slaughtered sheep in Isfahan, central Iran.

Materials and Methods: One hundred twenty tissue samples consisting of the brain, heart, diaphragm, and esophagus were obtained from two high throughput abattoirs of Isfahan Province. The DNA was extracted and analyzed by nested PCR using GRA6 loci. The restriction fragment length polymorphism (RFLP) technique with the *MseI* enzyme was used to classify strains into three major lineages of *T. gondii*.

Results: Our results demonstrate the presence of 49/120 (40.83%) *T. gondii* in sheep tissue samples. Positive samples had *T. gondii* GRA6-DNA (344 bp), including sixteen brains (53.33%), sixteen hearts (53.33%), ten oesophagi (33.33%), and seven diaphragms (23.33%), respectively. In this regard, this is the first time that *T. gondii* genotyping has been reported in sheep tissues by the GRA6-PCR-RFLP technique in Isfahan. Following the electrophoresis of the RFLP products. The resulting genotypes were clonal type I (260 and 90 bp) and type II (180 and 160 bp).

Conclusion: Understanding the population structure of the parasite is necessary for studying the transmission patterns of human toxoplasmosis. The high diversity of *T. gondii* genotypes, including mixed genotypes in sheep and the meat consumed, lamb, is critical for public health. Alarmingly, there could be a higher risk when virulent genotypes exist in meat products. According to our results, *T. gondii* Type I is probably predominant in Isfahan province. Comparative studies should be conducted in other parts of the country and even in other countries. As a result, we will gain a deeper understanding of the animal sources of *T. gondii*-based human infection. Slaughterhouses seem more suitable than farms for sampling since slaughtered animals are processed explicitly for a human food source. These studies comprehensively map the *T. gondii* genotype pattern, which signifies toxoplasmosis control and infection prevention.

Keywords: *Toxoplasma gondii*, Foodborne disease, Zoonotic, Small Ruminant, Livestock

Adaptive immunity against *Echinococcus granulosus*: new challenge in diagnostic development

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Abstract: Despite the lots of efforts that have been put into the research and control of echinococcosis, this disease is still one of the most important diseases in the world. In some places of the world, Cystic echinococcosis (CE) caused by *Echinococcus granulosus* is a reappearing disease in areas where it was not very common already. In an attempt to escape from host immune responses, *E. granulosus* change to a hydatid cyst. Cystic echinococcosis consists of 2 layers: an inner cellular germinal layer (GL) and an outer acellular carbohydrate-rich laminated layer (LL). The cyst contains an additional fibrous layer produced as a result of the host's inflammatory response. GL and LL are essential for stimulating the adaptive immune responses in host-parasite communication by the connection and complex of different effective antigens and molecules. The acellular laminar layer is a carbohydrate-protein link to galactose, galactosamine, and glucosamine as the main ingredient of the polysaccharide part. The germinal layer is made up of a distal cytoplasmic syncytium and a perinuclear layer, including muscle, tegumental, flame, glycogen-storing, cells including lysosomal-like bodies, and immature cells. The fluid contained within the cyst, known as hydatid cyst fluid (HF), gathers various products excreted or secreted by the cellular, germinal layer (GL) of the cyst wall and protoscolex too. Additionally, HF gathers diverse host plasma proteins (mainly albumin and immunoglobulins) that enter the cyst wall by unknown mechanisms. *E. granulosus* metacestode infections are determined by the slowly growing hydatid cysts that may not be recognized for months or years after the primary infection. Immunologists are interested in the stability of these cysts since, once completely formed, they are unaffected by the host's immune responses. Uptake of the biological events that occur during infection is essential to visualize the diversity of immune stimuli to which the host is subjected and to elucidate diagnostic and therapeutic tools. However, several immunomodulatory proteins have been isolated and defined; the signature *E. granulosus* antigens in hydatid cyst fluid are still antigen 5 and antigen B (AgB). In this review, we used the available scientific information and considered how these findings helped better comprehension of the immunology of *E. granulosus* infection. The purpose of this review is to point to the many aspects that consider immune and autoimmune responses to save *E. granulosus* from elimination and to minimize the severity of the pathogenicity of *E. granulosus* in the host. In our opinion, we will have a better diagnosis with immunomodulating molecules and possibly better protection from parasitic infections if we understand the adaptive immune mechanisms of *E. granulosus* infection in an intermediate human host. Otherwise, the diagnosing rate of CE has upgraded due to the application of a new molecular tool for recognizing parasites by using new recombinant antigens and immunogenic peptides. Keywords: Adaptive Immunity, *Echinococcus granulosus*, diagnosis

Prospective analysis of human hydatid cyst among patients with space-occupying lesion or cystic mass

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Abstract: Background: Human hydatid cyst or hydatidosis is one of the most important zoonotic diseases in different geographical areas of the world, including Iran. The current study aimed at the prospective analysis of hydatidosis among patients with space-occupying lesions or cystic masses identified by ultrasonography or computerized tomography (CT) scan referred to the Parasitology and Mycology Department of Fasa University of Medical Sciences in Fasa District in the southwest of Iran. Materials and Methods: Native antigen B prepared from sheep hydatid cyst fluid was used to evaluate anti-hydatid cyst antibodies, using ELISA in the Parasitology Department of Shiraz University of Medical Sciences, Fars province. Sera were collected from 311 patients, and a predesigned questionnaire containing epidemiologic and individual information related to hydatid cyst was filled out for each patient during sample collecting. Cases who underwent surgical removal of cystic lesions were investigated microscopically. Results: Patients in the study were 118 males (37.94%) and 193 (62.06%) females. Anti-hydatid cyst antibodies were detected in 187 (60.12%) of the patients. Although the seroprevalence rate for hydatidosis in females (63.21%) was more than that in males (55.08%), lung hydatidosis was more common than hepatic hydatidosis in males. In pulmonary hydatidosis, most cysts were in the right lower lobes. There was a significant association between the prevalence of hydatidosis and occupation (P 0.05). The most contaminated occupation group was housewives. Conclusion: The high prevalence of hydatidosis among the patients in Fasa District, southwest of Iran reveals more consideration of the masses located in the body organs. Keywords:



چهاردهمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Prevalence of Acanthamoeba spp. in hospital samples from Khomein, Iran

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نوع پذیرش: پوستر | کد مقاله: G-93564

Abstract: Background: Acanthamoeba spp. is one of the most common opportunistic amoebae in nature, which could be finding in most of the environmental sources. Acanthamoeba is considered as the causative agents of amoebic keratitis, granulomatous amoebic encephalitis (GAE). Due to this issue the aim of current study was to detect Acanthamoeba spp. in hospital samples from Khomein of Iran. Materials and Methods: In a cross sectional study, a total of 48 samples were collected from hospital environment of Khomein Iran, Samples are collected from internal medicine, surgery and ICU (no = 48). Samples analyzed for the presence of Acanthamoeba spp. based on molecular methods by PCR amplification. PCR were performed with JDP1 primers for 18S rRNA. Results: By evaluation of all 48 samples collected from internal medicine, surgery and ICU units, we could find 10 samples with positive results for PCR. PCR was performed for 18S rRNA. Conclusion: Acanthamoeba are considered as one of the most prevalent free living amoeba in the dust and soil of hospital environment. This result could be considered as preliminary study which highlights the importance of free living amoeba in hospital sources. Keywords: Acanthamoeba, Hospital environment, PCR



چهاردهمین گنگره بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



A Systematic Review and Meta-analysis on Prevalence of Genotypes of Cystic Echinococcosis in Iranian Animals

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Abstract: Background: Cystic Echinococcosis is one of the public health problems. The disease is caused by Echinococcus granulosus larvae. The Echinococcus granulosus is classified into different genotypes. Two of the most important genotypes for human infection are G1 and G3. The main risk factors for infection are direct contact with dogs. The aim of current study is to determined prevalence of Echinococcus granulosus genotypes in Iran. . Materials and Methods: This systematic review was conducted, using PubMed, Scopus and Web of Sciences databases. Published manuscripts from 2010 to April 14, 2021 are considered in search. We used some relevant keywords for serch for instance Hydatid cyst, cystic echinococcosis, Echinococcus granulosus sensu lato, Animal, Prevalence and Frequency. meta-analysis were performed using Stata software version 14. Results: By including 28 relevant study the prevalence of G1 and G3 genotypes were represented as (P=0.91 (95% CI= 0.84, 0.97)) and (P=0.12 (95% CI=0.07, 0.18). Conclusion: by considering the results of the current study, the G1 and G3 genotypes are considered as most important genotypes and most frequent one was G1. Furtur studies for determining the animal hosts are highly suggested. Keywords: Cystic Echinococcosis, Echinococcus granulosus sensu lato, Genotypes



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دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Diagnosis of Hydatid Cyst Disease Using Gold Nanoparticles (AuNPs)

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نوع پذیرش: پوستر | کد مقاله: G-61945

Abstract: Hydatid cyst disease is a parasitic disease caused by *Echinococcus granulosus* tapeworm. Hydatid disease is a zoonotic infectious disease that causes severe damage to human health and causes a lot of economic losses in the livestock industry. Hydatid cysts are one of the significant parasitic infections in Iran that causes many health problems to humans and are responsible for economic losses because of the condemnation of the slaughtered animal's infected viscera and reducing the quality and quantity of livestock products. Because it can pose a severe threat to people's health, it is essential to discover a fast, economical, and convenient way to detect it to prevent further damage. For effective treatment and prevention of recurrences of hydatid cysts, early and accurate diagnosis of the condition is extremely vital for timely and accurate treatment. Hydatid cysts can be diagnosed in a variety of ways, including immunodiagnostic methods, which are used to identify hydatid cysts. Although these approaches are time-consuming, they do not have a high sensitivity level, so tests like these are difficult to perform, making diagnosis challenging. Due to the advancement of nanotechnology, the development of biosensors for the diagnosis of echinococcosis has become much more accessible in terms of efficiency. Because of nanoparticles' chemical and mechanical properties, nanoparticle-based biosensors are highly desirable in human and veterinary medicine. Microorganisms can be detected more accurately and quickly by new methods based on nanoparticles developed over the past few decades. There have been considerable advances in diagnostics using colorimetric biosensors and gold nanoparticle colorimetric biosensors. Ultimately, GNPs (or AuNPs)-based biosensors are used to detect minimum concentrations of anti-*Echinococcus* IgG in human and animal blood for cystic echinococcosis diagnosis. As biosensors will be increasingly used in situ to control epidemics and pandemics in the future, simple and affordable biosensors will be in high demand. It will be advantageous in areas where strict infrastructure control is not possible or accessible. It is effortless to witness how this proof-of-concept can be efficiently translated into practical settings that enable fast and straightforward on-demand detection of Au-nanoparticles. Keywords: Diagnosis, Hydatid Cyst, Gold Nanoparticles, Nanotechnology



چهاردهمین گنگره بین المللی آزمایشگاه و بائین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Soil contamination with *Toxocara* Spp. eggs in public parks of Boroujerd, west of Iran

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نوع پذیرش: پوستر | کد مقاله: G-63185

Abstract: Background: Toxocariasis is one of the zoonotic helminth diseases caused by the larval stage of intestinal nematodes of dogs and cats, namely *Toxocara canis* and *Toxocara cati*. Human toxocariasis occurs after ingestion of embryonated eggs present in the soil, vegetables, or other contaminated surfaces, as well as via consumption of uncooked paratenic hosts, such as bird meat and giblets. This study aimed to evaluate soil contamination in Borojerd (West of Iran) public parks using microscopy methods. Methods: A total of 100 soil samples were taken from 20 public parks in Boroujerd from December 2021 to August 2022. Fifty samples were taken from 10 parks during cold seasons and 50 samples from another 10 parks during the year's warm seasons. Soil samples were collected from 5 distinct sites in the same area. The samples were treated with saturated zinc sulphate solution, and the floating material was analyzed under a light microscope. Results: Based on the flotation results from 20 examined parks, 3 parks (15%) were contaminated with *Toxocara* spp. eggs, and among 100 soil samples, 7 (7%) were found to be positive for *Toxocara* spp. The frequency of egg numbers in positive samples was between 1 to 6, and the level of contamination during the cold seasons was higher than in the warm seasons, but no significant differences were observed between the different seasons (P0.05). Conclusion: This investigation gives baseline knowledge regarding soil contamination with *Toxocara* spp. eggs in Boroujerd city, parks can be a source of *Toxocara* infection of people and especially children in these areas, and measures should be taken to control the stray cats and dogs. Keywords: *Toxocara* spp., Soil contamination, Public Park, Boroujerd, Iran



چهارمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Protoscolicidal effects of Rheum ribes extract on Echinococcus granulosus protoscoleces

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نوع پذیرش: پوستر | کد مقاله: G-18432

Abstract: Background: Cystic echinococcosis is well-known as a zoonotic infection in humans. Considering various therapeutic and pharmacological effects of Rheum ribes L. in folk and modern medicine, this study was intended to assess the in vitro and ex vivo. protoscolicidal effects R. ribes methanolic extract against Echinococcus granulosus protoscoleces Materials and methods: At first, protoscoleces were obtained from liver of infected sheep and then they were treated with extract at 225-900 mg/mL for 5-60 min in vitro and ex vivo. The eosin exclusion analyze was applied to study the protoscoleces viability. Results: Results showed that extract exhibited the in vitro protoscolicidal effects mainly 900 mg/ml eliminated 100% of protoscoleces, followed by 10 min of treatment. By ex vivo test, the extract required further time to destroyed the protoscoleces than the in vitro; where at 900 mg/mL killed all protoscoleces followed by 15 minutes exposure. Conclusion: We found the promising protoscolicidal activity of R. ribes extract, mainly at 900 mg/ml, which entirely destroyed the parasite after 15 min of treatment. Nevertheless, additional studies are required to confirm these results. Keywords:



چهاردهمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



The role of green synthesized copper nanoparticles for preventing the *Toxoplasma gondii* infection in mice through improving cellular immunity

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نوع پذیرش: پوستر | کد مقاله: G-01273

Abstract: Background: This in vivo survey was intended to evaluate the prophylactic potential of green synthesized copper nanoparticles (CuNPs) by means of Capparis spinosa extract against latent *Toxoplasma gondii* infection prompted T. gondii Tehran strain in mice. Materials and methods: At first, animals were orally received CuNPs (2 and 4 mg/kg/day) for two weeks. One day after treatment, the mice were intraperitoneally infected with T. gondii tissue cysts. The mean numbers of brain tissue cysts and the expression level of some immune cytokines (e.g., IFN- γ , IL-12, and inducible nitric oxide synthase (iNOS)) in tested animals. Results: The particle size of CuNPs was reported 17 and 41 nm. The mean number of T. gondii tissue cysts markedly declined as a dose-dependent manner. The expression level of IFN- γ , IL-12, and iNO was elevated in mice received CuNPs. Conclusion: We found the high efficacy of CuNPs for preventing T. gondii infection in mice. While, the prophylactic potential of CuNPs enhanced cellular immunity and low toxicity, but, additional investigations must be performed to confirm the current results. Keywords:



چهاردهمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Isolation and genotyping of Acanthamoeba from selected hospitalized wards of teaching hospitals of Birjand city

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نوع پذیرش: پوستر | کد مقاله: G-96248

Abstract: Background: Acanthamoeba is the most common and abundant free-living amoeba that exists in the human environment. The aim of this study is the isolation and identification of Acanthamoeba genotypes from environmental sources such as dust and biofilm of chemotherapy and ophthalmology parts of hospitals in Birjand city, using 18S rDNA gene and nucleotide sequencing techniques. Materials and methods: In the present study, 120 samples including dust samples (68) and biofilm (52) samples were taken from different part of Razi and Iranmehr hospitals in Birjand city during 1400-1401. The samples were first cultured and then analyzed molecularly. Results: Out of 120 samples collected from dust and biofilm, 45 samples (37.5%) had positive culture results for Acanthamoeba. The frequency of Acanthamoeba in ophthalmology and chemotherapy departments were (30%) and (42.8%), respectively. In this study, a fragment of the 18S rRNA gene of Acanthamoeba was confirmed in 45 positive cultured samples using the PCR technique. A total of 35 Acanthamoeba culture/PCR positive samples were successfully sequenced. After molecular analyzes on 35 Acanthamoeba samples, T4 (91.4%) and T3 (8.5%) genotypes were identified. Conclusion: A high percentage (37.5%) of Acanthamoeba was present in the dust and biofilm of chemotherapy and ophthalmology parts of hospitals. Due to the pathogenic nature of both Acanthamoeba genotypes isolated from hospital environmental sources, there is a possibility of Acanthamoeba infections in susceptible people, and therefore the necessary information should be given to health officials. Keywords: Acanthamoeba, genotyping, Birjand, biofilm

Evaluation of anti-leishmanial activity of the Loaded Artemisinin in ZnAl-layered double hydroxide nanocarriers against Leishmania major in vitro

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نوع پذیرش: پوستر | کد مقاله: G-61534

Abstract: Background: Artemisinin and its derivatives are effective against leishmaniasis. Because of short half-life of artemisinin, in different studies artemisinin were used 2-4 times per day to could have a better therapeutic effect. ZnAl-Layered double hydroxide (ZnAl-LDH) nanocarriers is a suitable for drug delivery to the organs of the body. LDH with very low toxicity it has applications as nanocarrier in the delivery of drugs to their site of action. In this study, an attempt has been made to evaluate the anti-leishmanial activity of the Loaded Artemisinin in ZnAl-layered double hydroxide nanocarriers against Leishmania major in vitro Materials and Methods: In this study ZnAl-LDH was synthesized and evaluated by advanced chemical analyzes such as SEM, XRD, FT-IR, EDAX and Mapping. Then artemisinin loaded in ZnAl-layered double hydroxide nanocarriers (Art-ZnAl-LDH). To evaluating the effects of Art- ZnAl-LDH against Leishmania major we used in vitro assay (promastigote and amastigote assay and cytotoxicity assay for macrophages). Results: The IC₅₀ for artemisinin and (Art- ZnAl-LDH) was 17 and 20 $\mu\text{g}/\text{mL}$ respectively. The results shows that the toxicity of Art- ZnAl-LDH is less than AmpB and Artemisinin. Conclusion: The results shows that the toxicity of Art- ZnAl-LDH is less than AmpB and Artemisinin. As a result, it seems that this compound can be considered as a candidate for the treatment of cutaneous leishmaniasis. Keywords: Leishmania major, Artemisinin, ZnAl-LDH nanoparticle, in vitro

Molecular identification and frequency of cyst-forming coccidia (Sarcocystis, Toxoplasma gondii, and Neospora caninum) in native slaughtered cattle in Kashan, Central Iran

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¹ no

نوع پذیرش: پوستر | کد مقاله: G-69358

Abstract: Cattle is one of the main sources of food supply chain for humans in most countries. The present study aimed to identify the infection rates for *Toxoplasma gondii*, *Neospora caninum*, and *Sarcocystis* spp. by polymerase chain reaction (PCR) method in native slaughtered cattle in Kashan, central Iran. **Materials and Methods:** Totally, 159 diaphragm, esophagus, and muscle samples (53 samples of each) were collected from native beef cattle from Kashan slaughterhouse, central Iran. The genomic DNA was extracted, and PCR method was used separately for detection of *N. caninum*, *Sarcocystis*, and *T. gondii* species using specific primers. **Finding:** *Sarcocystis* was found in 84.9% of muscles, 83% of esophagus, and 84.9% of diaphragm samples. Mixed infection (*Sarcocystis cruzi*-*Sarcocystis hominis*) was the most common infection, followed by *S. cruzi* and *S. hominis*. *Sarcocystis hirsuta* was not detected in any samples. *T. gondii* was detected only in three (5.7%) out of the 53 muscle tissues samples of cattle. *N. caninum* was found in 18.9% of muscles, 24.5% of esophagus, and 28.3% of diaphragm samples. One of the cattle had coinfection to *Neospora*, *Toxoplasma*, and *Sarcocystis* in muscles simultaneously. There was no statistically significant difference between infection rates and age as well as sex in each organ. **Conclusion:** This study revealed a low prevalence rate of *T. gondii*, but a high prevalence of infection to *N. caninum* and *S. cruzi* or mixed infection of *S. cruzi* with *S. hominis* among slaughtered cattle. Prevention measures such as keeping away dogs from cattle grazing are recommended. **Keywords:**

Parasitological and histopathological features of appendectomy specimens in Fars province, southern Iran: a retrospective study

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نوع پذیرش: پوستر | کد مقاله: G-18542

Abstract: Background: Although the appendix is the most commonly resected and examined intra-abdominal organ, the pathogenesis and etiology of acute nonspecific appendicitis remain enigmatic. This retrospective study aimed to assess the prevalence of parasitic infection in surgically removed appendices and to evaluate the probable associations between the presence of parasites and the occurrence of appendicitis through parasitological and histopathological examinations of the appendectomy specimens. Materials and Methods: This retrospective study was carried out from April 2016 to March 2021 among all patients referred to hospitals affiliated to Shiraz University of Medical Sciences, Fars province, Iran, for appendectomy. Patient information including age, sex, year of appendectomy, and type of appendicitis was collected from the available data of the hospital information system database. In positive cases, all pathology reports were retrospectively evaluated for the presence of the parasite, and its type analytical and descriptive statistics were carried out using SPSS software version 22. Results: A total of 7628 appendectomy materials were evaluated in the present study. Of the total participants, 4528 (59.4 %, 95% CI: 58.2-60.5) were males and 3100 (40.6%, 95% CI: 39.5-41.8) were females. The mean age of participants was 23.87 ± 14.28 years. Overall, *Enterobius vermicularis* was observed in 20 appendectomy specimens. Fourteen of these patients (70%) were less than 20 years old. Conclusion: Our results indicated that *E. vermicularis* is one of the common infectious agents that could be found in the appendix and may increase the risk of appendicitis. Therefore, in terms of appendicitis, clinicians and pathologists must be aware of the possible presence of the parasitic agents, especially, *E. vermicularis* to treat and manage the patients sufficiently. Keywords:



چهارمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



In vitro scolicidal effect of *Urtica dioica* and *Pyrus boissieriana* extracts on protoscolices of hydatid cysts

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نوع پذیرش: پوستر | کد مقاله: G-85307

Abstract: Background: Cystic echinococcosis is one of the most important neglected diseases and a public health concern throughout the world. Currently, novel therapeutic approaches are urgently required due to the poor therapeutic effect of the existing drugs. This study evaluated the scolicidal effects of hydroalcoholic extract of nettle plant (*Urtica dioica*) and chloroformic extract of wild pear (*Pyrus boissieriana*) on protoscolices of hydatid cysts. Materials and Methods: Protoscolices were aseptically aspirated from the livers of sheep naturally infected with hydatid cysts. To assess the scolicidal effect of these herbal extracts various concentrations of both were used in different exposure times. Results: Scolicidal effects of *U. dioica* extracts at a concentration of 80 mg/ml were 81 and 89.33% after 60 and 120 minutes of exposure, respectively. Compared to *U. dioica*, almost the same result was obtained for *P. boissieriana* extracts at a concentration of 80 mg/ml (81.33 and 89 % after 60 and 120 minutes of exposure, respectively), which was significantly different from the negative control group ($p < 0.001$). However, the extract of *U. dioica* exhibited stronger scolicidal effects compared to the extract of *P. boissieriana* in concentrations lower than 40 mg/ml ($p < 0.001$). Conclusion: The present findings have indicated that both extracts of *U. dioica* and *P. boissieriana* are potential scolicidal agents. However, further studies will be needed to evaluate in vivo scolicidal effect of both extracts and possible side effects. Keywords:

Splenic recurrence of pulmonary hydatid cyst: A case report

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نوع پذیرش: پوستر | کد مقاله: G-56193

Abstract: Background: Hydatidosis or cystic echinococcosis (CE) is one of the most significant neglected human zoonoses worldwide caused by Echinococcus granulosus (E. granulosus) larval stages. This near-cosmopolitan disease is considered a substantial public health concern, particularly in developing countries. The definitive host of this disease is dogs and canines, as well as Domestic herbivores which serve as intermediate hosts for the hydatid cysts, ingest the infective ova, resulting in hydatid cyst formation in the liver, lungs, and other organs. Humans are also infected via accidental ingestion of infective ova, shed by the fecal material of definitive hosts. In this study, we report a case of recurrence of splenic hydatidosis in a five-year-old girl living in one of the parts of Shush city in Khuzestan province. Presentation of case: The case is a five-year-old girl who went to the emergency room of Ganjavian Hospital in Dezful with symptoms of weight loss, anorexia, vomiting, and frequent coughing. In the patient's history, there was history of pulmonary hydatidosis and subsequent removal of the right lobe of the lung. In the ultrasound of the patient, the image of a large cyst with a daughter cyst with a diameter of 65 x 75 mm was evident in the spleen. Using a CT scan, the case was confirmed as splenic hydatidosis. Therapeutic intervention was performed by the surgeon by splenectomy to ensure that the disease would not relapse. Results: After surgery, the patient was followed up for 1 year in terms of response to treatment and recurrence of the disease, and no evidence of recurrence was observed. In any case, whether surgical treatment or drug treatment is used, Hydatid cyst recurrence remains frequent. However, education of community members and improvement of health level play a significant role in controlling this dangerous infectious disease. Conclusion: early detection of recurrence is of great importance. The poor sanitary status of environment, as well as the presence of stray dogs in that area, and the close contact of people with them, can potentially provide the basis for cases of hydatidosis. Keywords:

Latent *Toxoplasma gondii* infection and associated risk factors among patients with chronic kidney disease

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نوع پذیرش: پوستر | کد مقاله: G-38965

Abstract: Background: Patients with chronic kidney disease (CKD) are susceptible to acquiring opportunistic parasites. Therefore, the present case-control study attempted to determine the seromolecular prevalence of *T.gondii* infection among patients with CKD under hemodialysis and healthy controls in Mazandaran Province, northern Iran. Materials and Methods: 212 cases with CKD and 200 healthy controls were enrolled in this study. Informed consent as well as a questionnaire were obtained from all subjects. Blood samples were collected from each participant and the serum was screened for anti-*Toxoplasma* antibodies (IgG and IgM). PCR assay was performed using the primer pair targeting the RE of *T. gondii*. Results: Out of 412 participants, 67.92% of patients and 15.5% of control subjects were positive for anti-*Toxoplasma* IgG, but all participants were negative for anti-*Toxoplasma* IgM. Also, considering PCR assays with RE target, the prevalence of *T. gondii* infection was 24.1% in case subjects. The results from the multiple multinomial logistic regression revealed that the seroprevalence of anti-*T. gondii* IgG antibody in patients with CKD was 3.12 times higher than in healthy controls (P 0.001). Also, there was a significant association between seroprevalence of *T. gondii* infection and age, having a cat at home, and level of glomerular filtration rate (GFR) in these patients. Conclusion: Our findings demonstrate a highly significant association between latent *T. gondii* infection and CKD commonly in the GFR 3b and 4 stages and older age. Accordingly, exposure to *T.gondii* could pose a risk to CKD involvement in the older decades of individuals. Thus, regular screening of CKD patients for *T. gondii* infection is highly recommended. Keywords:

The latest state of leishmaniasis in Iran and the Middle East countries

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نوع پذیرش: پوستر | کد مقاله: G-10864

Abstract: Background: Leishmaniasis is one of the most forgotten diseases in the world affecting the poor people in large numbers. At present, 350 million people are at risk and 2 million new cases are reported annually, of which 1.5 million of them are cutaneous leishmaniasis and the rest are related to visceral leishmaniasis. The World Health Organization and Tropical Diseases Research (TDR) division ranks leishmaniasis in the first group of emerging and uncontrolled disease. Methods & Results: Leishmaniasis appears in three form; Cutaneous Leishmaniasis (CL), muco-cutaneous Leishmaniasis (MCL) and Visceral Leishmaniasis (VL). More than 90% of cutaneous leishmaniasis are in Iran, Afghanistan, Nepal, Syria, Saudi Arabia and Peru. Visceral leishmaniasis in terms of geographical conditions divided into five different types; Indian Leishmaniasis, is human disease reservoir type and sand fly of *Phlebotomus argentipes* is vector. African leishmaniasis or Sudanese leishmaniasis is second and common in Sudan and Kenya. Gerbils, otters, dogs and cats are reservoirs and the vector is *Phlebotomus orientalis*. Russian type is the third form and prevalent in Turkmenistan and the Caucasus (Soviet Union). Dogs and foxes are the main reservoirs and *Phlebotomus arkaplensis* is vector of the disease. The American type is the fourth form and infects American countries and dogs and jackals carry the disease and *Phlebotomus intermedius* are vectors of the disease. The fifth is Mediterranean Leishmaniasis also called Middle Eastern type which is common in the Middle East countries among people under the age of 10 and in Iran observe in the provinces of Khuzestan, Fars, Isfahan, Chaharmahal and Bakhtiari, Ardabil and Khorasan and *Phlebotomus major* and *Phlebotomus perniciosus* are vectors of the disease. Conclusion: Forms of cutaneous and visceral leishmaniasis are known as old endemic disease in Iran and are considered as health threat. There are three forms of leishmaniasis (urban, rural, and visceral) in Iran, but all these forms have decreased in recent years due to the implementation of control programs. The number of cases of visceral leishmaniasis in Iran has been very small. In general, it should be said that the condition of leishmaniasis, especially cutaneous leishmaniasis (Salek), is acute in the Middle East region, and this disease is still active and many cases are reported every year from the countries of this region. Considering that the Middle East is located in the dry region of the world, and this point is directly related to the epidemic of leishmaniasis, therefore, it is necessary to carry out measures more seriously to prevent and control the disease in the relevant countries. Keywords: Epidemiological, Leishmaniasis, Middle East, Iran



چهاردهمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



The recent findings on drug against Plasmodium falciparum aminoacyl-tRNA synthetases

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نوع پذیرش: پوستر | کد مقاله: G-28301

Abstract: Abstract Background: Malaria, a disease caused by Plasmodium falciparum, is responsible for more than 450,000 deaths annually with half of the world's population at risk of contracting malaria. The Plasmodium parasite is transmitted to the human host through the bite of an infected Anopheles. Malaria remains a major infectious disease and despite declining incidence, threatens the reappearance of drug-resistant forms. Studies in the last century went in the direction of discovering a drug from the group of antimalarial drugs with the target of stopping protein synthesis. In fact, translation inhibition is a strategy to combat the most virulent human malaria parasite. Since aminoacyl-tRNA synthetases (Pf-aaRSs) from Plasmodium falciparum direct protein translation, the mechanism of action of these drugs must be such that they selectively bind to P. falciparum aminoacyl-tRNA synthetase tyrosine. In this review, we studied molecular mechanisms of ML901 effect on P. falciparum. Methods- In this study, the databases of Scopus, PubMed, and Google Scholar were searched from 2010 to 2022. The key words included in this study were "Plasmodium falciparum" and " Plasmodium falciparum aminoacyl-tRNA synthetases" and " nucleoside sulfamate". Results- In this assay, we found papers introducing some compounds for inhibition of the disease with the target of P. falciparum aminoacyl-tRNA synthetases. One of the study introduced one compounds named ((2R,3S,4R,5R)-5-[4-amino-3-(difluoromethoxy)-1H-pyrazolo[3,4-d]pyrimidin-1-yl]-3,4-dihydroxytetrahydrofuran-2-yl)methylsulfamate (ML901) that had inhibitory effects against Malaria. Aminoacyl (tRNA) synthetases (aaRSs) are attractive drug targets, with both classes I and II being studied as previously unknown targets for Nucleoside sulfamates imitator adenosine 5'-monophosphate. Adenosine 5'-sulfamate hijacks aaRSs. ML901 is a nucleoside sulfamate that captures the aaRS in the malaria parasite and prevents the parasite from translating and multiplying. This drug causes a severe self-destruction in the parasite without harming the host cell. Conclusion- This review study showed that ML901 is one of the most important substances for treatment of malaria. Keywords: Malaria; Plasmodium falciparum; aminoacyl-tRNA synthetases



چهاردهمین گنگره بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Investigation of the population rate of toxoplasmosis in patients with malignancies in Baqaei 2 Hospital, Ahvaz, Southwest Iran

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نوع پذیرش: پوستر | کد مقاله: G-56497

Abstract: One of the most prevalent parasite infections of people, other warm-blooded animals as intermediate hosts, and cats as intermediate and final hosts worldwide is toxoplasmosis, which is classified as a zoonotic illness. Material & methods- Blood was drawn from 90 cancer patients who had been admitted to the hospital and were at various stages of chemotherapy. The anti-toxoplasma antibody titer was then determined using the ELISA method, and the data were analyzed using SPSS version 23 software. Results- In this study, 50(55.6%) were women and 40(44.4%) were men, all samples were negative for IgM antibody titer while 50 samples(55.6%) were positive for IgG antibodies. Conclusion- Cancer patients are at great risk of developing severe toxoplasmosis and its consequences due to the high incidence of T. gondii. Oncologists should therefore view this serious medical condition as a matter that requires immediate attention. Keywords:



چهاردهمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Prevalence of intestinal parasites in food handler and study of genetic diversity of Blastocystis subtypes in samples isolated from Birjand city in 1401

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نوع پذیرش: پوستر | کد مقاله: G-17420

Abstract: Today, despite the great efforts of the World Health Organization, the problem of parasitic diseases continues to increase in developing countries. Parasitic diseases are directly related to the level of public health and the level of awareness of individuals about personal and social health issues. This is especially the jobs that directly or indirectly deal with the nutrition of people in the society, and if the parasitic disease increases in these people, the probability of the spread of this problem in the society will double. This study aims to investigate the prevalence of intestinal parasites in Food vendors and study of genetic diversity of Blastocystis subtypes in samples isolated from Birjand city in 1401

Treatment Failure in Cutaneous Leishmaniasis Patients Referred to the School of Public Health, Tehran University of Medical Sciences during 2008-2017

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نوع پذیرش: پوستر | کد مقاله: G-05978

Abstract: Abstract Background: Cutaneous leishmaniasis (CL) is a vector borne disease predominantly found in tropical and subtropical countries. It is an important infectious disease in the Eastern Mediterranean countries, including Iran. For more than 6 decades, pentavalent antimonials have been used successfully worldwide for the treatment of leishmaniasis, but over the past few years, clinical resistance to these medications has increased. In this study, we evaluated CL patients who did not show any desirable responses to the anti-leishmanial treatment within a 10-year period (2008 to 2017). Methods: This is a retrospective study. All patients from different parts of Iran suspected of having cutaneous leishmaniasis, who were referred to the laboratory of leishmaniasis in the School of Public Health at Tehran University of Medical Sciences (TUMS) from 2008–2017 were parasitological examined. Results: During this period, a total of 1480 suspected CL patients were referred to the laboratory of leishmaniasis. Samples from 655 patients (70.8%) suspected of having CL were positive microscopically. The failure rate in patients treated with anti-leishmaniasis medications for a minimum of three complete treatment periods was 1.83% (12 cases). There was no association between the number and size of skin lesions and patient characteristics. Also, the route of drug administration had no significant effect on the number and size of lesions. Conclusion: In the present study, treatment failure was found in some confirmed CL patients treated with meglumine antimoniate. Over the past few years, it seems that had been increased in resistance to these medications. So, a review of the correct implementation of the treatment protocol and/or a combination therapy may be helpful in preventing an increase in the rate of treatment failure. Key words: Cutaneous leishmaniasis, Anti-Leishmania drug, Treatment failure, Iran.



چهاردهمین گنگره بین المللی آزمایشگاه و بائین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



COVID-19 pandemic: Challenges and approaches in blood transfusions

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نوع پذیرش: پوستر | کد مقاله: G-46317

Abstract: One of the goals of the Iranian Blood Transfusion Organization is to provide adequate healthy blood and reduce the risk of various viral and bacterial transmission infections. With the removal of alternative blood donation, all blood units and blood products are provided through voluntary blood donation in Iran. The Blood Transfusion Organization screens the donated blood according to standard guidelines to ensure blood recipients and physicians of providing healthy and pathogen-free components. With the emergence of novel pathogens, such as the pandemic of the COVID-19 virus, despite Iran's self-sufficiency in blood supply and blood products, the number of blood donors has decreased significantly since there is a lack of comprehensive information on pathophysiology and virus transmission ways. Moreover, the existence of some shortages in screening programs can cause problems. Therefore, this study was performed to review the studies conducted investigating this emerging virus regarding blood transfusions and the supply of blood components worldwide. Keywords:

Investigating the anti-Toxoplasma gondii effect of Punica granatum root extract on tachyzoites stage in vitro

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نوع پذیرش: پوستر | کد مقاله: G-89347

Abstract: Backgrounds: Toxoplasmosis is a parasitic disease with wide spread worldwide. This disease is one of the most common infections between humans and animals such as cattle, sheep, and pigs and its cause is an obligate intracellular protozoan called Toxoplasma gondii (T. gondii). Primethamine and Sulfadiazine are the gold standard in the treatment of toxoplasmic infection, but many side effects of these drugs have been reported. Considering the lack of access to imported drugs and their high cost, it is necessary to conduct research in the field of finding alternative drugs, so the purpose of this study is to investigate the effect of Punica granatum (P. granatum) root bark on T. gondii parasite. Materials and Methods: In this experimental study, the root bark of the pomegranate tree was collected from the rural and plain areas of Mazandaran province and the plant extract was collected using the maceration method. Toxoplasma parasite was purchased from Toxoplasmosis Research Center, Faculty of Health, and University of Tehran and cultured in RPMI medium. One ml of the culture medium containing 5×10^5 tachyzoites was added to the wells of the 96-well plate and 1 ml of plant extracts with concentrations of 250, 500 and 1000 $\mu\text{g/ml}$ were added to the medium. The survival rate was evaluated using vital dyes at time intervals of 1, 6, 12 and 24 hours. Results: In this study, pomegranate root bark extract had 100% lethality at a concentration of 250 $\mu\text{g/ml}$ after 24 hours, and 100% lethality at a concentration of 500 and 1000 $\mu\text{g/ml}$ after 12 and 6 hours. Conclusion: The results of this test have shown that the concentration of pomegranate root bark and the time period have a direct effect on the lethality. So that within 24 hours, all the parasites disappeared. Also, in shorter periods of time, as the concentration of this substance increases, the lethal effect increases. Keywords: Toxoplasma gondii, tachyzoite, P. granatum, antiparasitic effect



The effectiveness of the Hydroxychloroquine on the larval stage of the Echinococcus granulosus

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نوع پذیرش: پوستر | کد مقاله: G-30768

Abstract: Background: Echinocosis is one of the most dangerous parasitic infections in humans and dogs and canines are the main hosts. Hydatid cysts are formed in the human body, mainly in the liver and lungs. The treatment of hydatid cyst is done by Albendazole and Mebendazole. Due to the side effects of chemical drugs and the high cost of preparing these drugs, the need to search for an alternative drug without side effects is strongly felt. Therefore, the aim of this study is to investigate the anti-parasitic effect of the Hydroxychloroquine on the larval stage (protoscolex) of Echinococcus granulosus (E. granulosus) parasite. Materials and method: In this experimental study, to isolate the parasite, the livers of sheep infected with hydatid cysts were collected from the slaughterhouse, and in the laboratory, after sterilization of the cyst surface, the cyst fluid was separated using a 10cc syringe. The Hydroxychloroquine at the concentrations of 200, 400 and 800 µg/ml was prepared and 1ml of cyst fluid is placed in 1ml of a sterile test tube. After 1, 2 and 3 hours, the viability were evaluated using eosin 0.1% staining. Results: In this study, the concentrations of the drug on the larval stage of the E. granulosus parasite were investigated and the results showed that with the increase in time and concentration, the lethality rate also increases and the concentration of 800 µg/ml after 2 hours, the best effectiveness were achieved. Conclusion: The results showed that in addition to the effect of the drug, it can also have an anti-parasitic effect, and in the future, such a drug can be used in the treatment lines of echinococcosis. Key words: E. granulosus, Hydroxychloroquine, Hydatid cyst

Seroepidemiology of toxoplasmosis and its risk factors in women referring to Sabzevar Health Center for Pre-marriage tests in 1400-1401

حسین البیاسی، ©¹ انیس باغی کشتان²

گروه میکروبیولوژی دانشکده پزشکی-دانشگاه علوم پزشکی سبزوار
گمیته تحقیقات دانشجویی-دانشگاه علوم پزشکی سبزوار

نوع پذیرش: پوستر | کد مقاله: G-94851

Abstract: Background: Toxoplasmosis is one of the most common causes of parasitic infections in humans and other warm-blooded vertebrates, which has spread throughout the world. The aim of this study was to investigate the seroepidemiology of toxoplasmosis and its related factors in women referring to Sabzevar Health Center for pre- marriage Tests . Materials and Methods: In this cross-sectional descriptive study, 190 women were randomly selected and after completing the questionnaire, they were examined for the presence of IgG antibodies against *Toxoplasma gondii* by ELISA method and The results were analyzed using SPSS statistical test. Results: This study showed that 171(90%) people were negative and 19(10%) were positive for anti-toxoplasma IgG antibody. The results showed that the positivity of the A test is higher in people with a lower level of education than in people with a higher level of education, and also in people in the age group above 24 years than in the group below 24 years. Also, there was a statistically significant relationship between the consumption of raw vegetables and the positive test. Conclusion: Due to the high prevalence of IgG-negative people in this population, these women are potentially at high risk of acute toxoplasmosis during pregnancy and transmission to their fetuses, so proper education and care is necessary to prevent congenital toxoplasmosis. Keywords:



چهارمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Epidemiologic study of liver trematodes of slaughterhouse livestock in Aleshtar city, lorestan province, Iran. (2015 –18)

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نوع پذیرش: پوستر | کد مقاله: G-27390

Abstract: Background: In recent decades, the health importance of fasciolosis and dicrocoeliasis has increased in different parts of the world. As human cases have been reported from all over the world. So although the disease is common between humans and animals, it is not merely a veterinary problem. Humans play an important role in the transmission of these hepatocytes. This study investigated the epidemiologic study of liver trematodes of slaughterhouse livestock in Aleshtar city, lorestan province, Iran, during 2015 –2018 years. Materials and Methods: This descriptive and retrospective study investigated the infection of liver with Fasciola Hepatica and Dicrocoelium Dendriticum in cows, sheep and goats slaughtered in Aleshtar during 2015 –2018 years. Results: A total of 36,649 head of livestock were slaughtered, including 8,854 heads (24.1%) of cattle and calves, 22,559 heads (61.5%) of sheep and 5,236 heads (14.2%) of goats, of which the prevalence of fasciolosis was 8.4% and dicrocoeliasis was 10.1%. The prevalence of fasciolosis and dicrocoeliasis was 11.7% and 6% in cattle and calves, respectively, in sheep 7% and 11.5% and in goats 8.1% and 10.1%. In all livestock (cattle, sheep and goats), the highest prevalence of liver trematodes was 19.4% in 2015. Also, the highest prevalence of liver trematodes was related to goats in 2017 (30.1%), sheep in 2015 (21.8%) and cattle and calves in 2016 (20.1%), respectively. Conclusion: The prevalence of liver trematodes was high in Aleshtar city, so prevention and control programs should be done more carefully. Slaughter of animals should be done under the supervision of veterinary experts to eliminate the cycle of the disease by removing and destroying the livers infected with trematodes and to reduce the great economic damage. Keywords: Slaughterhouse, Liver Trematodes, Aleshtar, lorestan.Iran

Occurrence of *Metagonimus* sp. (Heterophyidae) in *Anas platyrhynchos* in Iran; A potential reservoir for a zoonotic helminth?

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نوع پذیرش: پوستر | کد مقاله: G-76284

Abstract: Background: Heterophyidae is a family of small trematodes consisting of more than 50 genera of which *Metagonimus* spp, *Haplorchis* spp, and *Heterophyes* spp are important fish-borne trematodes in the small intestine of mammals including humans. According to the data obtained, fish-eating birds also harbor these parasites as reservoirs. The occurrence of heterophyid parasites has been recorded in human and animal hosts in Iran, however, the role of migratory birds in wide- spreading of these parasites is poorly known in Iran. We report a natural occurrence of *Metagonimus* sp in *Anas platyrhynchos* for the first time in Iran, with respect to morphological and taxonomical characters. Materials and Methods: This study was conducted on a hunted *Anas platyrhynchos* purchased from a bird market located in Kiashahr, Guilan province, Iran. After recording the bird's characteristics, the bird was dissected, and the gastrointestinal tract was removed and fixed in 70% ethanol. The sample was transferred to the Helminthology Lab of the Department of Medical Parasitology and Mycology, Tehran University of Medical Sciences, Tehran, Iran. The gastrointestinal tract was dissected and examined in a large Petri dish containing phosphate-buffered saline (PBS) for the presence of any helminths under a stereomicroscope. One trematode was recovered, separated, and preserved in 5% formalin for identification. For morphological identification, the sample was stained with carmine and mounted using Canada balsam. Morphological characteristics of the recovered specimen were drawn carefully using a microscope equipped with a camera lucida and diagnosed as *Metagonimus* sp. The shape and the sizes of the body, ovary and testes, seminal vesicle, seminal receptacle, suckers, and eggs, as well as the ratios of body length to body width, and egg length to egg width, were considered for morphological examination. Result: Based on *Metagonimus*-specific morphological features, our sample was recognized as *Metagonimus* sp. with very small body size (410×260 μm), oral sucker (40×48 μm), pharynx (26×23 μm), ventral sucker (40×38 μm), right testis (70×68 μm), left testis (80×72 μm), seminal vesicle (120×78 μm), and ovary (35×48 μm). Also, operculated eggs were (26×17 μm). Conclusion: From the present study, it is confirmed that *Metagonimus* sp. can be prevalent in the ducks from north of Iran urging investigations on the prevalence of this zoonotic fluke among humans and animals in this region. Keywords: *Metagonimus*, *Anas platyrhynchos*, zoonotic helminth

Prevalence of Toxoplasma Infection in humans living in rural and urban areas of Jolfa district, north-west of Iran

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نوع پذیرش: پوستر | کد مقاله: G-57461

Abstract: Abstract Background: *Toxoplasma gondii*, the causative agent of toxoplasmosis is an obligate zoonotic parasite, distributed throughout the world, and can infect all warm-blooded vertebrates. Its final host is a cat, and it is one of the most common parasitic infections in Iran. The overall seroprevalence rate of toxoplasmosis among the general population in Iran was estimated around 39.3%. In this study, serological prevalence of *Toxoplasma* infection was investigated by determining anti-*Toxoplasma* IgG in the rural and urban areas of Jolfa district, north-west of Iran. Materials and Methods: This cross-sectional study was conducted with 600 human serum samples (including 352 female) which collected from rural and urban areas of Jolfa district, northwest of Iran, during 2018. Anti-*Toxoplasma* IgG test have been performed using Enzyme-linked immunosorbent assay (ELISA) method. Results: The positive levels of anti-*Toxoplasma* antibodies IgG were seen in 270 (45%) humans' serum samples. Considering the sex distribution, the positive IgG tests for *Toxoplasma* infection were seen for 161 (45.7%) and 109 (44%) females and males, respectively. There was a significant relationship between *Toxoplasma gondii* IgG seropositivity and contact with soil ($P = 0.002$), and residential area (urban or rural) ($P = 0.001$). Conclusion: According to the results of the present study, the sero-prevalence of toxoplasmosis is considerably high in Jolfa district, especially in rural inhabitants which needs further attention to the health education of the residents in the area. Keywords: *Toxoplasma* IgG, ELISA, Jolfa

Seroprevalence of fascioliasis among rural and urban inhabitants of Jolfa district, East Azarbijan, North West of Iran

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نوع پذیرش: پوستر | کد مقاله: G-64371

Abstract: Abstract Introduction: Fascioliasis is an infection that is caused by two species of flukes, Fasciola hepatica and F. gigantica. It is prevalent in Iran, especially among the livestock; however, the human infections also occur. The infection may end up with serious complications such as cholangitis; cholelithiasis; cholecystitis; pancreatitis; biliary cirrhosis; and hepatic fibrosis. The aim of the present study was to investigate the seroprevalence of fascioliasis among humans live in rural and urban areas of Jolfa district, North of East-Azarbaijan province, north-west of Iran. Materials and Method: In the present study we used serum samples of previous study on the seroprevalence of cystic echinococcosis during 2018 in rural and urban areas of Jolfa district (Jolfa and 15 villages in the district). Randomly 600 human samples were chosen and included in the study. Anti-Fasciola IgG was detected in the sera using enzyme linked immunosorbent assay (ELISA) according to the kit's instruction. Results: Four (0.7%) out of 600 human sera showed positive levels of anti-Fasciola IgG. Three (0.9%) out of 352 females and one (0.4%) out of 248 males were seropositive for Fasciola spp. Furthermore three (0.8%) out of 366 urban and one (0.4%) out of 234 rural inhabitants were seropositive for Fasciola spp. Conclusion: According to the results of the present study, human fascioliasis occurs in low rates in Jolfa district. However, the infection rate was low, yet even in this frequency level, monitoring and health education regarding fascioliasis seems necessary in the area. Keywords: Fascioliasis, Seroprevalence, Jolfa, Iran



چهاردهمین کنفرانس بین المللی آزمایشگاه و بائین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Investigation of toxoplasmosis serum prevalence in female students of universities in Mazandaran province in 2019-2021

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نوع پذیرش: پوستر | کد مقاله: G-68579

Abstract: Investigation of toxoplasmosis serum prevalence in female students of universities in Mazandaran province in 2019-2021 Maryan Faghih Nasiri¹, Shima Hosseinzadeh¹, Masoumeh Moslemi², Bahman Rahimi Esboei^{3*}, Abozar Ghorbani⁴ 1. Department of Laboratory Sciences, Student research Committee, School of Medicine, Tonekabon branch, Islamic Azad University, Tonekabon, Iran 2. Department of Molecular Biology and Medical Genetics, School of Medicine, Iran University of Medical Sciences, Tehran, Iran. 3. Department of Medical Parasitology, School of Medicine, Tonekabon branch, Islamic Azad University, Tonekabon, Iran 4. Department of Immunology, School of Medicine, Mazandaran University of Medical Science, Sari, Iran *Corresponding Author: Email address: Bahman5164@yahoo.com Full postal address: 4719115875 Phone number: +989112139542. Background: Toxoplasmosis is one of the most important parasitic diseases caused by *Toxoplasma gondii*. Toxoplasmosis usually does not cause symptoms in healthy people, but in people with immunodeficiency, lymphadenitis, swelling of lymph nodes and eye symptoms. Toxoplasmosis during pregnancy can be transmitted to the fetus and cause severe eye complications and even death. The purpose of this study is to investigate the serum prevalence of toxoplasmosis in female university students in Mazandaran province in 2019-2021. Materials and methods: In this cross-sectional descriptive study, 227 blood samples were collected from female students studying in Mazandaran province. The samples were transferred to the research laboratory of Islamic Azad University, Tunkabon branch, and the serum sample was isolated. The serum level of IgG, IgG avidity and IgM was checked using Elisa test and the results were checked using kappa test and SPSS software. Results: Among the 227 examined samples, 13 samples were IgM positive, 96 IgG positive and 7 IgG avidity were in the low avidity range. The samples examined in this study are 125 people (55.06%) in the age range of 21-30 years. Among the investigated samples, 34 people (14.97%) had contact with cats. And 41 people (18.06%) had the habit of consuming raw and uncooked meat. Conclusion: The results have shown that a large number of examined people were negative in terms of anti-toxoplasma antibodies. Only 17 people (48.7%) were positive for toxoplasmosis and they need less care during pregnancy to prevent fetal infection. Key words: Toxoplasmosis, *Toxoplasma gondii*, IgG avidity

Improved serodiagnosis of hydatidosis using gold nanoparticles

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نوع پذیرش: پوستر | کد مقاله: G-79054

Abstract: Cystic echinococcosis or hydatidosis is a chronic zoonotic disease caused by the larval stage of the cestode *Echinococcus granulosus*. In the life cycle of this parasite, domestic and wild carnivores are the definitive hosts, and herbivores such as sheep, goats, and cows are intermediate hosts, and humans are accidental hosts. Ingestion of *Echinococcus granulosus* eggs leads to the formation of cysts in the liver, lungs, and other organs. This disease has a global spread, but it is endemic in some regions such as Australia, South Africa, and the Middle East, and unfortunately, its spread has been reported in many places in Iran. Considering the significant impact of this disease on human and animal health, quick and timely diagnosis plays an important role in its management and treatment. It is not possible to diagnose this disease only with clinical symptoms because these symptoms are common with diseases caused by other liver parasites. By considering the history, identifying the structure of the cyst with imaging methods, and the help of immunological diagnostic tests, the diagnosis can be approached. Immunological tests have been developed to detect antibodies against hydatid cysts in the serum, but the problem is that, firstly, 40% of patients do not show antibodies with different techniques, and secondly, antibodies may be present for a long time after cyst removal or treatment. As a result, we will not be able to distinguish between past and present infections. But cyst antigens are only present in the bloodstream during active infection. Therefore, using methods to mark these cyst antigens (such as radioisotopes, fluorescent compounds, and specific enzymes) can help in diagnosis. In the last decade, nanoparticles have also been used for this purpose. Nanomaterials have a large surface area and provide the possibility of connecting a large number of specific molecules. As a result, they lead to an increase in the detection sensitivity in a small sample volume. Gold nanoparticles are useful as markers for electron microscopy due to their high electron density, and also because of their ability to bind to large molecules such as immunoglobulins, streptoavidin, lectin, protein A, etc. Functionalization of the surface of gold nanoparticles by self-assembled thiolated molecules on the surface of the particles can be done for covalent bonding between the surface of gold nanoparticles and biomolecule. **Keywords:**

Evaluation effects of hydro-alcoholic extracts of *Colchicum autumnale*, Chamomille and *Tanacetum parthenium* on *Leishmania Major* (in vitro)

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نوع پذیرش: پوستر | کد مقاله: G-03415

Abstract: Background: Leishmaniasis is a complex disease with a broad spectrum of clinical features, usually divided into Cutaneous Leishmaniasis (CL), Muco-cutaneous Leishmaniasis (MCL), and Visceral Leishmaniasis (VL). Plant extracts or plant-derived compounds are likely to provide a valuable source of new medicinal agents. In endemic countries, a number of traditional plants are commonly used to treat infectious conditions. Advances in the research of natural products for the treatment of leishmaniasis have been recently reviewed. The aim of this study is to evaluate the leishmanicidal activity of three plants hydro-alcoholic extracts of *Colchicum Autumnale*, Chamomille and *Tanacetum Parthenium* on *Leishmania Major* (MRHO/IR/75/ER) promastigotes with compared to Glucantime, in vitro. Methods: According to the aim of study, extracts of each plant were experimentally provided in concentrations of 800, 400, 200, 100, 50, 25, 12/5, 6/25 and 3/12 mg per ml. Then, these concentrations were inoculated in containing parasites and in terms of the number of parasites at 24, 48 and 72 hours were analyzed. Results: The results showed that all three extracts only in high concentrations makes inactivity of all of *Leishmania* parasite, and decreasing the concentration of the extracts increased the number of parasites alive. Furthermore Glucantime was more effective in reducing the number of *Leishmania* than *Colchicum Autumnale* and the difference was significant. Also more likely Chamomille and *Tanacetum parthenium* had similar impact and the differences were not significant. Conclusion: These three plants extracts significantly are effective on activity of *Leishmania*, although appears to be more studies to demonstrate the effectiveness of these extracts are required. Keywords: *Leishmania major*; *Colchicum autumnale*; Chamomille; *Tanacetum parthenium*



چهارمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Evaluation of Strongyloides Stercoralis risk factors among patients referred to therapeutic centers of Babol

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نوع پذیرش: پوستر | کد مقاله: G-97380

Abstract: Background: Strongyloides stercoralis is one of the neglected helminthic infections and about 30-100 million people are infected around the world. Immunocompromised patients are more vulnerable to this infection. This parasitic infection can be asymptomatic in immunocompetent individuals, but it is potent to be fatal in patient with underlying disease. Therefore, this study was aimed to define involved risk factors in patients with Strongyloides stercoralis infection referred to therapeutic centers of Babol. Materials and Methods: The cross-sectional study was conducted on April 2018 to March 2019 among 43 patients that Strongyloides stercoralis was detected in their stool samples. The S. stercoralis larva in the stool samples were investigated by microscopic examination, and direct techniques such as saline wet mounts and concentration technique were applied. Results: Overall, 55.81% of patients were belonged to rural societies and 44.18% of them were from urban area. Among 43 patients that their stool samples were positive for Strongyloides stercoralis larva, 6 of them (13.95%) were diabetic patients, 8 patients (18.60%) were diagnosed with cancer, 3 patients (6.97%) were detected with heart failure and 2 patients (4.65%) suffered from pneumonia. Conclusion: Strongyloides stercoralis prevalence is highly depended on its geographical distribution and rural communities are more susceptible to this infection. Also, underlying disorders make patients more vulnerable to Strongyloides stercoralis and diabetic patients are more sensitive to this infection. Therefore, it is important to detect different risk factors related to strongyloidiasis to prevent mortality in immunocompromised patients. Key words: Strongyloides Stercoralis, Immunocompromised, risk factor



چهارمین کنفرانس بین المللی آزمایشگاه و باالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



The parasitic infection distribution among patient referred to Therapeutic centers of Babol

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نوع پذیرش: پوستر | کد مقاله: G-26843

Abstract: Introduction: Intestinal parasitic infections are one of the significant concerns in hygiene and health care systems in under-developed and developing countries and their high prevalence is noticeable. These infections are caused by protozoan and helminthes parasites. Among parasitic gastrointestinal infections, protozoan parasitic infections are more common than helminthic infections. The aim of this study was to define the prevalence of protozoan and helminthic infections among patients Referred to therapeutic centers of Babol. Materials: The cross-sectional study was carried out from April 2018 to March 2019. 4454 fecal samples were collected. The probable parasitic infections in the stool samples were investigated by microscopic examination, and direct techniques such as saline and iodine wet mounts and concentration technique were applied. Results: Generally, parasitic infections (both helminthic and protozoan parasites) were detected in 413 samples out of 4454 tested samples which concludes 9.27% of referred samples. Overall, the prevalence of protozoan parasitic infection was higher than helminthic infection. Although *Entamoeba histolytica/ dispar* (2.67%) and *Giardia lamblia* (1/01%) were two most observed protozoan parasites and *Strangyloides stercoralis* larva was the most abundant helminthic parasite among all none-protozoan parasites. Conclusion: Gastrointestinal parasitic infections especially protozoan intestinal parasites are distributed all around the world and are mainly affect people by oral-fecal transmission which highlights the importance of environmental hygiene. Therefore, the understanding of parasitic infections distribution is important to elevate the health levels of the society in under-developed and developing countries. Key words: parasitic infection, protozoa, helminthes



چهاردهمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Diagnosis of Echinococcosis by detecting circulating cell free DNA and miRNA

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نوع پذیرش: پوستر | کد مقاله: G-94260

Abstract: Introduction: Diagnosis of the echinococcosis disease is difficult and usually performed based on clinical findings, imaging and serological test. However, clinical manifestations are not specific and often develop in the later stages of the disease. Immunological and imaging methods have limitations especially in follow up approaches. Areas covered: Detection of cell free DNA (cfDNA) and micro RNA (miRNA) is currently a hot topic for diagnosis of echinococcosis diseases. For detecting of cell free DNA in echinococcosis patient's samples such as sera, there are some studies based on NGS, DNA-deep sequencing and some based on PCR-based methods. There are very few works regarding detection of micro RNA for diagnosis of human echinococcosis Expert opinion: In detection of cell free DNA in patient's samples, next-generation sequencing (NGS) and DNA-deep sequencing, has shown high sensitivity, but are not suitable for routine clinical examination due to expensive and inaccessibility in majority of endemic areas. However, studies based on PCR methods have shown sensitivity of about 20-25%. To improve the sensitivity of these tests, improving DNA extraction method, designing appropriate primers for short length fragment of circulating DNA, using higher volume of serum sample, and application of more sensitive PCR methods is recommended. In field of micro RNA detection, further works are recommended.



چهاردهمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Toxoplasma gondii and Male Reproduction Impairment A new Aspect

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نوع پذیرش: پوستر | کد مقاله: G-04165

Abstract: Background: *Toxoplasma gondii* is an obligate intracellular protozoan that is common between humans and animals and causes toxoplasmosis. It is estimated that about 30% of the world's population is chronically infected with *T. gondii*. This protozoan is capable of causing changes in the male and female reproductive system, and men are more at risk of *T. gondii* than women. Very few studies have been done on the impact of English on the male reproductive system. Genital disease is the cause of 15% of infertility in men. Methods: Research results show that there is a direct relationship between toxoplasma infection and the increase in blood plasma testosterone. Examination of sperm parameters showed that in rats infected with *Toxoplasma*, the number of sperm decreased significantly on days 20 to 60, but no significant difference was observed on day 70 after infection. . During this experiment, it was observed that sperm motility was significantly reduced in rats infected with toxoplasmosis on days 10 to 70 after infection. The greatest decrease in motility was observed on the 20th day after infection. In this experiment, it was observed that the percentage of live sperm decreased significantly in rats infected with toxoplasmosis on days 10 to 60 after infection. But on the 70th day after infection, no significant difference was observed. In order to obtain the morphological percentage, 100 spermatozoa were examined in different microscopic fields and their percentage was calculated. During this experiment, a significant increase in abnormal sperms was observed on days 30, 40 and 50 after infection. The most important source of carbohydrates in seminal plasma is fructose, which is produced by the seminal vesicles and gonads. And it is necessary for sperm motility. Inflammation may cause seminal vesicle breakdown and reduce fructose production. During this experiment, the amount of seminal vesicle fructose showed a significant decrease in rats infected with *Toxoplasma* from days 10-50 after infection, but no significant difference was observed on days 60 and 70 after infection. Conclusion: In a series of studies, an increase in the testosterone hormone and a decrease in it have been reported, which in any case can disrupt the male reproductive system. *Toxoplasma gondii* can also cause changes in sperm parameters including number, motility, morphology and viability. According to this research, the biggest change in sperm parameters is related to viability and motility, and there is no significant change in other parameters. *Toxoplasma* can also reduce the amount of seminal vesicle fructose, which is related to sperm motility. Also, in *Toxoplasma gondii* infection, a decrease in spermatogenic cells is observed in the infected group compared to the control group. Keywords: *Toxoplasma gondii*, Male reproductive system, Infection

Toxocara spp. Eggs in soil of public parks and playgrounds of Jiroft district, Iran: A pilot study

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نوع پذیرش: پوستر | کد مقاله: G-20597

Abstract: Toxocara spp. Eggs in soil of public parks and playgrounds of Jiroft district, Iran: A pilot study
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Introduction Human toxocariasis, a worldwide parasitic disease, is caused by the larval stage of intestinal nematodes of dogs and cats, namely Toxocara canis and Toxocara cati. Human infection mostly occurs by the accidental ingestion of embryonated eggs present in the soil and vegetables. Given the abundance of stray dogs and cats, and that toxocariasis could be a dangerous clinical complication in humans, the present study aimed to evaluate the contamination of soil with Toxocara spp. eggs in public parks and playgrounds of Jiroft using microscopy methods. Methods This cross-sectional study was carried out, as a pilot study during, August–October 2022 in Jiroft, south eastern Iran. A total of 95 soil samples were collected from 19 public parks and playgrounds from different areas (north, south, east, west and center) of Jiroft district. The soil samples were collected randomly from five sites in each park, from a depth of 3 cm. Samples were placed in labelled containers and transported to the laboratory. For detection of Toxocara spp. eggs, the soil samples were dried at room temperature overnight and sifted through 100 µm mesh sieve. The samples were treated with saturated zinc sulphate (Zn₂SO₄) solution (specific gravity 1.8). Briefly, about 2 gr of powdery soil was placed in a test tube and suspended in about 8 ml of 0.05% Tween-20 solution. After centrifugation of the test tube at 800 g for 10 min, the supernatant was removed and the zinc sulphate solution was added up to a level of 1 cm from the top of the tube. The contents of the tube were mixed well and centrifuged at 800 g for 10 min. The tube was then filled to the top with the zinc sulphate solution so that a small convex bubble formed and a coverslip could be placed on the tube. After about 10-15 min, the coverslip from the tube was put on a microscopic slide and examined at a magnification of 100× and 400× for Toxocara spp. eggs. Results Soil analysis showed that 3 parks (15.7%) were contaminated with Toxocara spp. Egg. Taken together, 5.2% (5/95) were positive for Toxocara eggs. Among the positive soil samples, the number of Toxocara eggs recovered varied from 1–4 per each positive soil samples (2 gr). Conclusion Our pilot study revealed a considerable contamination of Toxocara spp. egg in parks and playgrounds of Jiroft district. The potential risk of toxocariasis for human and also growing number of stray dogs in the studied region underlined the need for applying preventive measures and further studies among dogs, cats, and children. Keywords:



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A massive hydatid cyst in liver of a 39-year-old female patient: A case report

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نوع پذیرش: پوستر | کد مقاله: G-84675

Abstract: Background: Hydatid cyst is an infectious disease from Echinococcus granulosus larva in which the parasite can invade different tissues such as liver, spleen, lung, brain and kidney and any other sites. The adult form of these worms lives in intestine of dog, fox, wolf and alike. Case presentation: This case study was performed on a massive hydatid cyst, reported in a 39-year-old woman. She was referred to the clinic with right upper quadrant pain and gastric pressure. MRI revealed that the vast space of the liver had been occupied by the massive cyst in the right lobe of the liver. This cyst was massive and had occupied a large space of the right lobe of the liver. The cyst was removed by surgery. In the pathological examinations of the removed cyst, the patient was diagnosed with hydatid cyst. Conclusion: Hydatid cyst rarely can reach an extremely large size without any changes in antibody hydatid levels. Keywords:

An In-Vivo Study for evaluation the Effect of drug combinant contain morphine, Imiquimod and Nalmefene for treatment Leishmaniasis Caused by Leishmania major in BALB/C Mice

© P¹ دکتر جواد جباری

تهران بیمارستان قلب و عروق شهید رجایی¹

نوع پذیرش: پوستر | کد مقاله: G-48793

Abstract: Leishmaniasis is a health problem of many countries in the world. Common treatments have side effects along with resistance in some cases. Therefore, new and combined drugs or new method for prevention may be effective against leishmaniasis. In previous study we found that morphine with low dose and not in high dose could be effective in infected macrophages with amastigotes of Leishmania major. In this study, we used morphine in two separated mice groups, in one group get the morphine with low dose four times before the challenge with promastogotes of Leishmania major and in other groups get the morphine after the challenge for evaluating the prevention and treatment effect respectively. Ultimately, immunological factors such as cytokine assay, lesion diameter and survival rate were measured. Parasitic load was considered by qPCR among the mice treated and prevented with morphine. In the group, that the mice received morphine with low dose three times before being infected with the parasite, the amount of parasitic load was lower than other groups and the differences was significant. Moreover, no lesions were observed at the injection site. This indicates the protective role of morphine. The results of this research showed that prevention effect of morphine in low dose had better function than treatment role. Imiquimod as opioid growth factor receptor when applied alone and with glucantime or morphine has an enhance treatment role with glucantime and morphine. Keywords: Leishmania major, morphine, prevention, treatment, BALB/c.

Investigating intestinal parasitic infections with emphasis on molecular identification of *Trichostrongylus colubriformis* in people referred to Sari diagnostic laboratories

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Abstract: Background: In the world, especially in developing countries, parasitic infections are considered one of the most common health and economic problems. Infections caused by intestinal parasites have usually chronic courses and if the infected person is not diagnosed and treated, they may be asymptomatic for a long time and transfer the contamination to a healthy person, causing complications such as severe digestive disorders, anemia, malabsorption in children, and physical/mental injuries. One of the nematode that is often found in the digestive system of humans and ruminants is *Trichostrongylus* spp. Human infections mainly occur by eating water and vegetables contaminated with third-stage larvae (filariform) or occasionally through the skin penetration by the larvae. In infected with a low parasite load usually does not show any symptoms, but in severe infections, occur symptoms such as anorexia, nausea, weakness, anemia, allergic manifestations and etc. This study was conducted with the aim of investigating intestinal parasitic infections with emphasis on molecular identification *T. colubriformis* in people referred to Sari diagnostic laboratories. Materials and Methods: Five hundred forty stool samples were collected from medical diagnostic laboratories affiliated to Mazandaran University of Medical Sciences in Sari city. First, all the samples were examined using the direct smear, formalin-ether and trichrome staining. In order to break the cell wall and release DNA, the samples containing *Trichostrongylus* eggs were freeze-thaw and placed in liquid nitrogen and then Bain-Marie at 100 °C. DNA extraction was performed using the instructions of the Favorogen kit. DNA was extracted and amplify Internal transcribed spacer2 (ITS2)-rDNA with using forward (NC1: 5-ACGCTCTGGTTCAGGTTGTT-3) and reverse primers (NC2: 5-TTAGTTTCTTTTCCTCC). PCR was performed and the samples with a sharp band in electrophoresis were sequenced by Sanger method. Then sequences were edited and registered in GenBank, in the end phylogeny tree was drawn with Mega 11 software and determined species of *Trichostrongylus*. Results: The prevalence of parasitic infection in our study population using formalin-ether was 5.4% (29 out of 540). The highest rate of infection was related to *Trichostrongylus* (3%, 16 out of 540), followed by *Giardia* spp. (0.6%, 3/ 540), *Blastocystis* spp. (0.6%, 3 /540), *Entamoeba histolytica* (0.4%, 2/ 540), *Dicrocoelium* spp. (0.4%, 2 /540), *Oxyur* spp. (0.4%, 2 /540), and *Strongyloides* spp. (0.2%, 1/540). The molecular result of the amplification of the ITS2 gene and sequencing were showed that all of PCR positive samples were *T. colubriformis*. Conclusion: Our results showed that the prevalence of intestinal parasites has relatively decreased. However, the prevalence of *Trichostrongylus* parasite was relatively high. Although PCR is recognized as a confirmatory test, it is not recommended for screening. Therefore, PCR technique is suggested along with other diagnostic methods to identify intestinal parasites. Keywords:



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Intestinal microsporidia in HIV+/AIDS and cancer patients in north of Iran; A study with simultaneous microscopic and molecular diagnostic approach

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نوع پذیرش: پوستر | کد مقاله: G-47902

Abstract: The aim of this study was to identify *Enterocytozoon bienewsi* (*E. bienewsi*) and *Encephalitozoon* spp. in fecal samples of HIV + / AIDS and cancer patients undergoing chemotherapy, and comparing the results to healthy individuals in Mazandaran province. Stool samples were collected from 50 HIV + / AIDS patients, 50 cancer patients, and 50 healthy samples referred to medical centers in North of Iran. Stool samples were kept out in 2.5% potassium dichromate at 4°C, and stained by modified trichrome for light microscopy examination. Nested-PCR targeted the small subunit ribosomal RNA (SSU rRNA) gene. To characterize genotypes, the internal transcribed spacer (ITS) was randomly amplified and sequenced. Ten out of 50 samples (20%) of HIV+/AIDS patients, 5/50 samples (10%) of cancer patients, and one of healthy individuals (2%) were microscopically positive. From 50 HIV + / AIDS patients, *E. bienewsi* and *Encephalitozoon* spp., were detected in 10 (20%) and 6 (12%) cases, respectively. Furthermore, among cancer patients 7 (14%) and 2 (4%) cases were *E. bienewsi* and *Encephalitozoon* spp., respectively. Out of 50 samples of healthy individuals, only 3 cases of *E. bienewsi* were observed. The genotypes D and M were detected among positive sample of *E. bienewsi*. *E. bienewsi* and then *Encephalitozoon* spp., are the most common intestinal microsporidia in HIV + / AIDS patients and cancer patients undergoing chemotherapy in Mazandaran province. *E. bienewsi* genotype D seems to be the predominant genotype in Mazandaran province. Keywords:

Toxoplasmosis in patients with chronic hepatitis C and patients with fatty liver

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نوع پذیرش: پوستر | کد مقاله: G-42890

Abstract: *Toxoplasma gondii* can affect the human liver and cause pathological changes such as hepatomegaly, granuloma, hepatitis, necrosis and liver cirrhosis may result to chronic liver disease. Objective: The aim in this study was to determine the rate of toxoplasmosis infection in chronic liver disease patients with HCV positive disease and in fatty liver patients. Materials and Methods: This cross-sectional study was performed on 150 samples prepared from three groups, including individuals with hepatitis C, persons with grade 2 and higher fatty liver disease, and patients without liver complications as a control group during 1397 and 1398. Serum and whole blood were taken from each subject for ELISA and PCR study. *Toxoplasma* IgG kit was used for ELISA test and two pairs of specific primers were used to amplify *T.gondii* GRA6 gene in Nested-PCR. Results: Out of 50 controls, only 3 (6%) showed positive chronic toxoplasmosis. Of 50 patients with HCV +, 21 (42%) and of 50 patients with fatty liver disease showed 17 (34%) infection with chronic toxoplasmosis. This difference in infection ratio was statistically significant (P 0.01). No positive sample was observed in the Nested-PCR test for detecting *T.gondii*. Conclusion: The results of this study indicate an association between chronic toxoplasmosis and patients with hepatitis C and fatty liver. Therefore, toxoplasmosis could be assumed as a predisposing factor for the survival of chronic liver disease. Keywords:

Increased TNF production in Leishmania parasites-stimulated monocytes of BCG vaccinated volunteers

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نوع پذیرش: پوستر | کد مقاله: G-16203

Abstract: Background: Leishmania is a genus of protozoan parasites that is transmitted by the bite of phlebotomine sandflies and give rise to different types of leishmaniasis such as cutaneous leishmaniasis (CL). Bacillus Calmette–Guérin (BCG) is a live attenuated vaccine that was developed against tuberculosis at the beginning of the 20th. Since then, it has been the most used vaccine in the world, with around 130 million children vaccinated every year. Interestingly, however, soon after its introduction in Europe in the 1920s, epidemiological studies reported that BCG vaccination strongly reduced infant mortality, and this could not be explained by a reduction in tuberculosis alone. This reduction in childhood mortality by BCG appeared to be due to the protection against unrelated infectious agents due to trained immunity following BCG vaccination. On the basis of these data, it has been hypothesized that BCG vaccination might be a potent preventive measure against Leishmania infection and/or may reduce leishmaniasis severity. Method: Peripheral blood was obtained from five healthy volunteers and then centrifuged over ficoll then PBMCs (Peripheral blood mononuclear cells) were isolated and resuspended in MACS buffer. Subsequently, CD14+ monocytes were isolated using MACS negative selection monoclonal antibodies and MS columns. The flow-through containing unlabeled cells represented the enriched monocytes. Monocytes were counted and 1×10^5 cells were added to each well on a 96-well plate and stimulated in a 10:1 ratio with live promastigotes as antigen (*L. major* or *L. tropica*) or LPS as positive control or left without stimulation. The plates were kept in CO2 incubator for 48 hours. Then, the supernatants of each well was collected and maintained in -70°C . After first blood sampling all of the volunteers were injected with BCG vaccine and after 6 weeks all of the procedures were repeated. Sandwich ELISA was performed to assay TNF concentration following manufacturer's construction (R&D Systems, USA). Results: TNF level before and after vaccination were compared. Amount of this cytokine significantly increased after vaccination for all of the volunteers with or without stimulation. Furthermore, cells which were treated with live parasites showed a higher level of TNF compared to unstimulated cells. Cells which were treated with *L. tropica* had a higher level of TNF production in comparison to *L. major*. Conclusion: BCG vaccination of healthy human volunteers results in enhanced production of pro-inflammatory cytokines, such as tumor necrosis factor (TNF), when monocytes from these individuals are stimulated ex vivo with unrelated pathogens such as Leishmania parasites. In addition, higher antigenic capacity of *L. tropica* comparing to *L. major* suggests that patients with CL caused by *L. tropica*, might produce more TNF following the disease. Key words: Leishmaniasis; BCG vaccine; TNF



چهاردهمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Investigating the role of monoclonal antibodies in identifying promastigotes and amastigotes of Leishmania parasite

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نوع پذیرش: پوستر | کد مقاله: G-91027

Abstract: Background: Leishmanial diseases constitute a wide spectrum of diseases that lead to death if not treated. In these diseases, in addition to the species and race of the parasite being involved in the formation of different clinical states of the disease, the immune status of the host plays an important role in the type of clinical manifestation of the patient. Among the two important immune systems of the body, cellular immune responses play an important role in controlling this disease. Leishmanias live in vertebrates as amastigotes inside xenophagous cells. The disease is transmitted through the bite of the mosquito vector. Parasites live in the stomach of soil mosquito in the form of flagellated promastigotes, and after developmental stages, they become infectious promastigotes and can infect the vertebrate host. Monoclonal antibodies are one of the pillars of today's new technology. Today, these molecules are used in various diagnostic tests. According to the mentioned materials, the aim of this research is to investigate the role of monoclonal antibodies in identifying promastigotes and amastigotes of Leishmania parasite. Materials and Methods: culture of Leishmania infantum parasite in the form of promastigote, amastigote and preparation of antigen from it in order to stimulate the tested mice, integration of spleen cells of immunized mice with SP2.0 cells and preparation of hybridoma clones, preparation of monoclones from obtained hybridomas and preparation of monoclonal antibody from them. Results: After the production of monoclonal antibody, the screening was done and the most favorable ones were selected to continue the investigation. Monoclonal antibodies with the highest absorption were selected and their effects against promastigote and amastigote forms of L. infantum were investigated. Discussion: Overall, in this research, a specific monoclonal antibody was produced against Leishmania infantum amastigotes and promastigotes. It seems that these antibodies react well against amastigotes and promastigotes of Leishmania infantum and can be used in various tests for research and diagnostic applications. Key words: monoclonal antibodies, promastigotes, amastigotes, Leishmania parasite

A review of the epidemiology, diagnosis, and risk factors of toxoplasmosis in children emphasizing with blood cancer, disabled and healthy children

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نوع پذیرش: پوستر | کد مقاله: G-58423

Abstract: Background: Toxoplasmosis is one of the most common parasitic infections in humans and warm-blooded animals worldwide. According to serum evidence, one-third of the world's population is infected with this parasitic infection. This disease is transmitted through consuming water and food contaminated with oocysts, uncooked meat infected with tissue cysts of this parasite, mother to child, and rarely by organ transplantation. This review study aimed at making an epidemiological comparison between children with cancer/disability and healthy children by assessing serological and molecular findings obtained in different parts of the world. Materials and Methods: Regarding the importance of *Toxoplasma gondii* infection, serological and molecular findings were collected from literature. In this regard, Google Scholar, PubMed, databases in the English language were used without any time limit. Results: Based on the data presented in the studies, contact with cat feces and consumption of raw and uncooked meat are considered as the most common risk factors. Thus, the importance of assessing toxoplasmosis in healthy children and children with cancer becomes more apparent due to more contact with soil, cats, poor personal hygiene, etc. Serological and molecular findings have shown that the prevalence of toxoplasmosis was more in children with cancer/disability than in healthy children. Conclusion: The high prevalence of acute and chronic toxoplasmosis in children with cancer requires special attention, and more studies are needed to clarify the role of toxoplasmosis in children with cancer. Keywords: *Toxoplasma gondii*, Epidemiology, Cancer, healthy, disabled children

Detection of hydatid cyst infection in the sputum smears of pulmonary tuberculosis patients in Ardabil during 2016-2019

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نوع پذیرش: پوستر | کد مقاله: G-83420

Abstract: Title: Detection of hydatid cyst infection in the sputum smears of pulmonary tuberculosis patients in Ardabil during 2014-2019 Soheila Molaei^{1*}, Abdolhossein Dalimi² 1. Department of ... School of University of (Times New Roman, font size 11 italic) 2. Department of parasitology, Faculty of Medical Science, University of Tarbiat Modares *Corresponding Author: Email address: s.molaei@arums.ac.ir, Ardabil University of Medical Sciences, phone number: +453-335347) Background: The main aim of this study was to determine hydatid cyst infection by the molecular method in sputum smears of patients with pulmonary tuberculosis in Ardabil province during 2016-2019. Materials and Methods: This study was a descriptive cross-sectional study that socio-demographic and clinical information of 78 TB positive and 78 TB negative smears were recorded in a checklist designed by the researcher. Firstly, DNA was extracted from smears, then the presence or absence of Mycobacterium tuberculosis was confirmed using specific srRNA 16 primers and tuberculosis complex with IS6110 primers in the smears. Hydatid cyst was determined using nad1 and cox1 genes in samples. Results: In the present study, three samples (3.84%) were positive for hydatid infection that related to smears-positive patients, while none of the negative smears were positive for it. Hydatid-positive cases were seen only in two age groups: 50 to 60 years (two cases) and 60 to 70 years (one case) (P value = .203). There was no significant relationship with gender (P value = 0.150), residence (P value = .347), and education (P value = 0.143). Conclusion: Coexisting pulmonary tuberculosis and hydatid in sputum smears of patients in Ardabil refer to the probability of co-infection of tuberculosis and hydatid parasitic diseases which is an important public problem in this co-endemic area. Looking for risk factors that have an impact on co-infection is extremely important for control, prevention, and good treatment.

The effects of climate change on emerging and reemerging parasitic diseases with a focus on zoonotic filariasis

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نوع پذیرش: پوستر | کد مقاله: G-12790

Abstract: Background: Changes in ecological systems affected by climate change as well as variations in insect spread indicate that insect-borne diseases nowadays have the potential for distributing to different regions even in places where these infections have not been reported before. Mosquito abundance is usually related to high temperature and high precipitation levels as basic factors since mosquito breeding sites and appropriate temperatures for survival are positively affected by these two factors. Over 70 species of mosquitoes of the genera *Aedes*, *Anopheles*, and *Culex* are vectors that transmit canine dirofilariosis infections caused by *Dirofilaria* spp. a group of worldwide-distributed vector-borne diseases. *Dirofilaria immitis* and *Dirofilaria repens* are the best known agents of canine dirofilariosis and may also occasionally infect other animal species, including humans. While *D. immitis* infection, also known as heartworm disease, *D. repens* is less pathogenic, being localized under the skin of the infested animals. *Acanthocheilonema reconditum* (*A. reconditum*), which is transmitted by fleas and lice, is a less pathogenic filarial species. The molting and metamorphosis of infective larvae in the mosquito vector needs a total of 130 degree-days above the 14 °C threshold. The aim of present study was investigation the prevalence of this filarial species in stray dogs from five provinces located in different climate of Iran. Materials and Methods: blood samples were collected from stray dogs (n = 344) from five provinces of Iran including Mazandaran, Gilan and Qazvin in the north, Esfahan in the centre and Lorestan in the west, during December 2016 to December 2018. Genomic DNA was extracted using a commercial kit. All samples were tested for the presence of *Dirofilaria* spp. and *A. reconditum* cytochrome c oxidase subunit 1 (*cox1*) partial sequences using conventional PCR. Exact binomial 95% confidence intervals (CIs) and the Chi-square were established using SPSS version 18. Results: Of the 78 dogs with a positive cPCR result for *D. immitis* (n = 75; 21.8%, 95% CI: 17.5–26.5) and for *A. reconditum* (n = 5; 1.45%, 95% CI: 0.47–3.36), two dogs were co-infected with both parasites and three were only infected with *A. reconditum*. The infection with *D. immitis* was present in all five regions, but *A. reconditum*-infected dogs were from three provinces, i.e. Mazandaran, Gilan and Esfahan. The risk of infection by *D. immitis* was significantly associated with the locality (Chi-square test, $\chi^2 = 77.7$, df = 4, P = 0.0001); that is, dogs in northern provinces (Gilan, Mazandaran and Qazvin) with temperate and Mediterranean climate had a higher chance of the infection than those from the warm and dry provinces of Esfahan and Lorestan. Conclusion: : The trend of positivity for *D. immitis* in different provinces of Iran paralleled that of the climatic and ecological features, with the highest prevalence recorded in Gilan (78.6%) and Mazandaran (50%) in the Caspian region, which could be due to the typical Mediterranean climate all year-round. The low prevalence observed in Esfahan (0.9%), Lorestan (6.9%) and Qazvin (27.3%) could be due to the increase in temperature and decrease in yearly rainfall. Keywords:



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The effects of climate change on emerging and reemerging parasitic diseases with a focus on zoonotic filariasis

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نوع پذیرش: پوستر | کد مقاله: G-31047

Abstract: Background: Changes in ecological systems affected by climate change as well as variations in insect spread indicate that insect-borne diseases nowadays have the potential for distributing to different regions even in places where these infections have not been reported before. Mosquito abundance is usually related to high temperature and high precipitation levels as basic factors since mosquito breeding sites and appropriate temperatures for survival are positively affected by these two factors. Over 70 species of mosquitoes of the genera *Aedes*, *Anopheles*, and *Culex* are vectors that transmit canine dirofilariosis infections caused by *Dirofilaria* spp. a group of worldwide-distributed vector-borne diseases. *Dirofilaria immitis* and *Dirofilaria repens* are the best known agents of canine dirofilariosis and may also occasionally infect other animal species, including humans. While *D. immitis* infection, also known as heartworm disease, *D. repens* is less pathogenic, being localized under the skin of the infested animals. *Acanthocheilonema reconditum* (*A. reconditum*), which is transmitted by fleas



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and lice, is a less pathogenic filarial species. The molting and metamorphosis of infective larvae in the mosquito vector needs a total of 130 degree-days above the 14 °C threshold. The aim of present study was investigation the prevalence of this filarial species in stray dogs from five provinces located in different climate of Iran. Materials and Methods: blood samples were collected from stray dogs (n = 344) from five provinces of Iran including Mazandaran, Gilan and Qazvin in the north, Esfahan in the centre and Lorestan in the west, during December 2016 to December 2018. Genomic DNA was extracted using a commercial kit. All samples were tested for the presence of *Dirofilaria* spp. and *A. reconditum* cytochrome c oxidase subunit 1 (cox1) partial sequences using conventional PCR. Exact binomial 95% confidence intervals (CIs) and the Chi-square were established using SPSS version 18. Results: Of the 78 dogs with a positive cPCR result for *D. immitis* (n = 75; 21.8%, 95% CI: 17.5–26.5) and for *A. reconditum* (n = 5; 1.45%, 95% CI: 0.47–3.36), two dogs were co-infected with both parasites and three were only infected with *A. reconditum*. The infection with *D. immitis* was present in all five regions, but *A. reconditum*-infected dogs were from three provinces, i.e. Mazandaran, Gilan and Esfahan. The risk of infection by *D. immitis* was significantly associated with the locality (Chi-square test, $\chi^2 = 77.7$, df = 4, P = 0.0001); that is, dogs in northern provinces (Gilan, Mazandaran and Qazvin) with temperate and Mediterranean climate had a higher chance of the infection than those from the warm and dry provinces of Esfahan and Lorestan. Conclusion: : The trend of positivity for *D. immitis* in different provinces of Iran paralleled that of the climatic and ecological features, with the highest prevalence recorded in Gilan (78.6%) and Mazandaran (50%) in the Caspian region, which could be due to the typical Mediterranean climate all year-round. The low prevalence observed in Esfahan (0.9%), Lorestan (6.9%) and Qazvin (27.3%) could be due to the increase in temperature and decrease in yearly rainfall.

In vitro and in vivo anti-parasitic activity of Sambucus ebulus and Feijoa sellowiana extracts silver nanoparticles on Toxoplasma gondii tachyzoites

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نوع پذیرش: پوستر | کد مقاله: G-58127

Abstract: Background Current chemical treatments for toxoplasmosis have side effects, researchers are looking for herbal remedies with minimal side effects and the best effectiveness. This study aimed to evaluate the anti-toxoplasmic effects of silver nanoparticles based on Sumbucus ebulus (Ag-NPs -S. ebulus) and Feijoa sellowiana (Ag-NPs -F. sellowiana) fruit extracts, in vitro and in vivo. Methods Vero cells were treated with different concentrations (0.5, 1, 2, 5, 10, 20, 40 µg/mL) of extracts and pyrimethamine as a positive control. Vero cells were infected with T. gondii and treated with extracts. The infection index and intracellular proliferation of T. gondii were evaluated. The survival rate of infected mice with tachyzoites of T. gondii was examined after intraperitoneal injection of the extracts at a dose of 40 mg/kg/day for 5 days after infection. Results The Ag-NPs-S. ebulus and Ag-NPs-F. sellowiana, almost similar to pyrimethamine, reduced proliferation index when compared to untreated group. Also, high toxoplasmicidal activity was observed with Ag-NPs-S. ebulus extract. Mice in the treatment groups of Ag-NPs -S. ebulus and pyrimethamine achieved better results in terms of survival than the others. Conclusion The results indicated that Ag-NPs-F. sellowiana and S. ebulus have a significant growth effect on T. gondii in vitro and in vivo. Ag-NPs -S. ebulus extract has a more lethal effect on the parasite than Ag-NPs-F. sellowiana. It is suggested that in future investigate the induction of Toxoplasma-infected cell apoptosis using nanoparticles. Keywords: Toxoplasma gondii, Treatment, Silver nanoparticles, Sambucus ebulus, Feijoa sellowiana

Effect of *Quercus infectoria* methanolic extract on viability and apoptosis induction in *Trichomonas vaginalis* activities

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نوع پذیرش: پوستر | کد مقاله: G-64812

Abstract: Background: *Trichomonas vaginalis* causing trichomoniasis is one of the most widespread sexually transmitted diseases. Currently, metronidazole considered the preferred medication for the treatment of trichomoniasis; however, it has resulted in some complications. Today, it has been shown that herbal supplies and their derivatives play an important role in exploration of new drugs in order to treat or prevent a broad spectrum of diseases such as infectious diseases. Aim of the present study is to evaluate the in vitro antitrichomonal properties of *Quercus* (Q.) *infectoria* methanolic extract that is ethno-medicinally used in Iran against *T. vaginalis* trophozoites. Methods: One hundred grams of plant materials (aerial parts) were dried and extracted by the means of the method of percolation via methanol (80.0%) for three days at 21°C. In this study, the in vitro anti-*T. vaginalis* activities of the Q. *infectoria* methanolic extract against *T. vaginalis* clinical isolates were assessed by Trypan Blue exclusion assay. The effect of the extract on induced apoptosis in *T. vaginalis* trophozoites was evaluated using the fluorescein isothiocyanate (FITC) Annexin V staining kit. Results: The Q. *infectoria* methanolic extract significantly (P0.001) reduced the viability of trophozoites with the IC50 values 21.3 and 3.4 µg/mL, after 24 and 48 h incubation, respectively. Q. *infectoria* methanolic extract also exhibited significantly (P0.001) the high rate of apoptosis on *T. vaginalis* trophozoite compared with the control group. Conclusion: Results of the study revealed that Q. *infectoria* extract can be considered as a suitable choice for medical studies to treat trichomoniasis. However, additional clinical studies are necessary to evaluate accurate biological effects of this plant on volunteer human subjects. Keywords: Trichomoniasis, herbal medicines, trophozoites, apoptosis

High occurrence of *Toxoplasma gondii* infection among blood donors in Ardabil Province as main focus of zoonotic visceral leishmaniasis, northwestern Iran

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نوع پذیرش: پوستر | کد مقاله: G-36798

Abstract: Background: Toxoplasmosis, as cosmopolitan parasitic disease, is considered as one of the transfusion-transmitted parasites. The true burden of *Toxoplasma gondii* (*T. gondii*) amongst blood donors remains undisclosed around the world. Since there was no evidence on the prevalence of *T. gondii* in blood donors in Ardabil Province, as main focus of zoonotic visceral leishmaniasis (ZVL), northwestern Iran, current research was therefore conducted to estimate the seroprevalence of *T. gondii* and PCR assay among them for the first time. Materials and Methods: In the present study, 462 plasma samples from asymptomatic blood donors of Ardabil Province, northwestern Iran, were tested for IgM and IgG anti-*T. gondii* antibodies levels using ELISA test. Moreover, the buffy coat of all seropositive subjects was screened for *T. gondii* DNA by conventional PCR. Also, the data sheet consisting of characteristic information was registered for all the applicants. Results: Overall, anti-*T. gondii* antibodies were found in 36% (166/462) of asymptomatic blood donors. Anti-*T. gondii* IgM and IgG seroprevalence was 1.5% and 32.5%, respectively. Only nine subjects (2%) were found to be positive for both IgM and IgG. Moreover, *T. gondii* DNA was identified in 18% (30/166) of seropositive donors. The logistic regression analysis showed a significant correlation between *T. gondii* seropositivity and contact with cats, agricultural activities, history of consumption of undercooked meat and being non-educated ($P=0.001$). Conclusions: The high prevalence (about one-third) of anti-*T. gondii* antibodies and possibly active infection using conventional PCR test represents that asymptomatic carriers of *T. gondii* are quite common in the study areas and pose a potential threat to the blood safety and hemovigilance program. Keywords: *Toxoplasma gondii*, seroprevalence, PCR, blood donors, Iran

Study of intestinal Helminthes parasites of Urban Shelter Dogs and pet dogs in central parts of Mazandaran province with Emphasis on phylogenetic characterization of Echinococcus granulosus

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نوع پذیرش: پوستر | کد مقاله: G-41689

Abstract: Background: Helminthes parasites are prevalent in dogs, some of them are zoonoses and some are not. Echinococcus granulosus is one of the zoonotic Helminthes parasites that has always caused a lot of human and financial losses. Based on the close relationship that humans have today with stray dogs as well as domestic dogs, it is necessary to study Helminthes parasites, especially Echinococcus granulosus. Materials and Methods: Stool samples were taken from 78 stray dogs and 32 domestic dogs. Then, the presence of parasite eggs in the feces was confirmed by concentration methods (flotation and sedimentation) and use of optical microscope. DNA was extracted from positive samples, PCR was performed for DNA amplification and sent for sequencing DNA was reproduced Results: In morphological experiments, out of 110 samples, 44 (40%) samples had parasitic infection and 66 (60%) samples were negative. Among the samples containing parasite eggs, 8 samples contained taenia eggs; 2 samples Teniahidatijna, 3 samples Echinococcus granulosus and 3 samples were negative. Conclusion: This study shows this fact that stray dogs play a key role in environmental contamination than house hold dogs. Stray dogs are a potential risk to public health as they are released after treatment. Key words: Helminthes parasites-shelter dog-domestic dog-Mazandaran province-Echinococcus granulosus-phylogenetic



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Antiparasitic effects of root extract of *Astragalus maximus* on hydatid cyst protoscoleces

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نوع پذیرش: پوستر | کد مقاله: G-49735

Abstract: Background: Hydatidosis is very common worldwide, mainly affecting the liver and lungs. There are some effective medications for hydatid disease, but surgery is still the most common form of treatment. Various chemical agents are used to inactivate protoscoleces during surgery, but most of them have serious side effects. Therefore, plant extracts have received more attention as alternatives that have acceptable scoliosis effects and do not have side effects. In this research, the lethal effect of root extract of *Astragalus maximus* on hydatid cyst protoscoleces were examined in vitro and ex vivo. Methods: *A. maximus* extract was prepared by rotary evaporator and maceration method. The protoscoleces collected from the hydatid cyst of sheep liver were placed in the vicinity of the concentrations (112.5-450 $\mu\text{l/mL}$) of the plant extract in in vitro and ex vivo conditions for a period of 5-60 minutes. The survival rate of protoscoleces was evaluated by eosin deprivation test (0.1% eosin staining). Results: In vitro, the lethality rate of protoscoleces after 30 minutes of exposure to a concentration of 450 $\mu\text{l/mL}$ of the plant extract was 100%. In addition, after 60 minutes of exposure to a concentration of 225 $\mu\text{l/mL}$, the scolioticidal activity of the extract of the plant was 100%. In ex vivo conditions, after 30 minutes of exposure to a concentration of 450 $\mu\text{l/mL}$ of plant extract, 100% of protoscoleces were killed. Also, after 60 minutes of exposure to a concentration of 225 $\mu\text{l/mL}$, the scolioticidal activity of the *A. maximus* plant extract was 100%. Conclusion: These findings show that the extract is effective on protoscoleces like the common chemical scolioticidals; Therefore, it can be used as a natural scolioticidal medicine for surgeons during hydatid cyst surgery. Keywords: Hydatid cyst, *Echinococcus granulosus*, extract, *Astragalus*.



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دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Lethal effects of Astragalus maximus Chloroform Extract Against Clinical Isolates of Giardia lamblia

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نوع پذیرش: پوستر | کد مقاله: G-28034

Abstract: Background: At present, chemical drugs such as metronidazole, quinacrine and furazolidone are used to treat giardiasis. Although these drugs are useful in most cases, they are associated with some side. The present investigation was designed to evaluate the antiparasitic effects and cellular mechanisms of Astragalus maximus chloroformic extract against both trophozoites and cysts of Giardia. Methods: The extraction was done based on the maceration method with 70% methanol. The in vitro anti-Giardia effects of various concentrations of A. maximus extract (11.25, 22.5, and 450 mg/mL) were evaluated on cysts and trophozoites of G. lamblia for 15-360 min. In addition, the effects on the plasma membrane permeability and the induction of apoptosis in the trophozoites of G. lamblia were studied. Results: Astragalus maximus extract significantly ($p < 0.0001$) declined the viability of cysts and trophozoites of G. lamblia at concentrations of 22.5 mg/mL and 45 mg/mL, after 120 360 min incubation. The findings revealed that treatment of G. lamblia trophozoites with A. maximus extract increased the permeability of the plasma membrane in a dose dependent response. The extract, especially at the concentration of 10 mg/mL, significantly ($p < 0.001$) induced caspase-3 activation. Conclusion: The present study showed the promising in vitro antiparasitic effects of A. maximus extract against both trophozoites and cysts of G. lamblia by affecting the permeability of the plasma membrane and induction of apoptosis. Further investigations especially in animal models and clinical setting are required to clarify the accurate efficacy and mechanisms against G. lamblia infection. Keywords: apoptosis; giardiasis; extraction; trophozoites; cysts; in vitro.



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دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Usefulness of different CRISPR/Cas9 technologies for tagging and editing in human protozoan parasites

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نوع پذیرش: پوستر | کد مقاله: G-86720

Abstract: Background: Genome editing by CRISPR (clustered regularly interspaced short palindromic repeats)/Cas9 (CRISPR-associated gene 9) system has been applied successfully to several protozoan parasites. In recent years this method has established as a functional method for editing in pathogenic human parasites. To date different ways of tagging and knock out in parasites have been introduced. In *Toxoplasma gondii*, the strategy used in CRISPR gene editing studies involved a unique vector for expression of Cas9 fused to a nuclear localization signal and the green fluorescent protein (Cas9-NLSGFP), and the specific sgRNA driven by *T. gondii* U6 promoter, without DNA donor, to induce DNA repair by non-homologous end joining (NHEJ). There is another report of CRISPR/Cas9-mediated gene knockout in *T. gondii* using a 1-vector strategy for co-expression of Cas9-FLAG-NLS fusion nuclease and a specific sgRNA to target TgLAP gene (leucine aminopeptidase). They achieved gene knockout without antibiotic selection. In *Plasmodium* spp an episomal vector for the expression of Cas9 (plasmid pUF1-Cas9) and a second expression vector carrying the sgRNA sequence and a DNA donor (plasmid pL7) to induce DNA repair by homology directed repair (HDR) were used, as *P. falciparum* lacks NHEJ pathway. In *Plasmodium*, generation of mutant cell lines by gene deletion and C-terminal tagging, allelic replacement, and simultaneous insertion of a point mutation plus a silent shield mutation have also been done. In *Leishmania*, there is a progressive propensity to use different types of CRISPR/Cas9 for gene editing and tagging; one of which has introduced as an easy-to-use technique without need of cloning. Materials & methods: In our lab, we have established a method introduced by Eva Gluenz et al., which comes as a toolkit, protocols for gene deletion, or N- and C-terminal tagging, as well as a website for designing the sgRNA primers and the donor DNA cassette are provided (LeishGEdit). Multiple plasmid vectors with resistance cassettes are available. We applied the method to a kinetoplast gene for KO and C-tagging. For this, *L. major* cell line with an episomal plasmid which expressed Cas9 and T7RNA polymerase was produced, then sgRNA template and donor DNA repairment cassette with resistant marker were PCR-amplified and transfected to *L. major* cell line. Using this toolkit for fast and accurate genome editing, we developed *L. major* parasites with C-terminal tagged kinetoplast gene and also we generate single KO parasites and we are initiating to produce null mutants. Results: We found this method very easier than other methods which were developed for gene editing of *Leishmania* and other parasites. The CRISPR/Cas9 gene tagging using this strategy has been successfully established in the lab and study of the pathogenicity of KO parasites will be performed. Further details of the method will be presented. Conclusions: Several approaches of CRISPR/Cas9 editing have been used in *Leishmania* for reverse genetic manipulation to elucidate gene functions. It is hoped that the establishment of the current approach will help in characterization of the role of kinetoplast genes in the biology or pathogenesis of the parasite. Key words: *Leishmania*; Kinetoplast; CRISPR/Cas9; Tagging

Sporotrichosis cutaneous leishmaniasis; repeating a dilemma

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Background: Leishmaniasis is a complex disease that has plagued this world for centuries. Parasitological examinations (direct microscopy of scraping samples and NNN culture) are less sensitive for chronic and unusual lesions with a long evolutionary period since parasites are few or absent. Therefore, the diagnosis was confirmed using molecular methods for *Leishmania*.

Case Presentation: A 45-year-old healthy man with complete ulcerative involvement of the elbow was referred to the Department of Parasitology and Mycology, School of Medicine, Isfahan University of Medical Sciences. Clinical examinations revealed simultaneous involvement in lymphadenopathy with the picture of sporotrichoid lesions from the elbow site to the armpit. The onset of skin lesions was in the form of a nodular lesion in October 2019. Later, with a gradual increase in size, it became an ulcerative form. Direct microscopic examination confirmed the involvement of cutaneous leishmaniasis. Therefore, due to the second bacterial infection of the lesions, antibiotic treatment with glucantime was prescribed by a dermatologist. Due to the patient's refusal to receive glucantime, the patient was prescribed topical nanoliposomal gel containing 0.4% amphotericin B (Sina Ampholeish™, Exir Nano Sina, Iran). Despite the complete course of treatment with liposomal amphotericin B, the developing lesion was still stable, and the ulcerative lesion had developed at the site of the swollen lymph nodes. At the end of this skin smear treatment regimen, the PCR test and parasite culture in the NNN medium were all positive. Frequent visits to dermatologists and failure to respond to the treatment of CL lesions caused another feature of leishmaniasis, namely social disease, so that the effects of distrust of treatment activities and depression appeared in him and inevitably, at this stage, the patient was referred to a psychologist. Finally, due to the problems during treatment and after psychiatric interventions, the patient agreed to receive glucantime. During this treatment period, the patient received 14 ampoules of glucantime in one step, and due to the lack of proper response with a rest period, the patient received 40 ampoules of glucantime, two daily for 20 days. At the end of this treatment, the effects of tissue re-epithelialization appeared at the lesion site, and the conditions for local healing became apparent.

Conclusion: The case report aims to alert physicians to the possibility of turning a simple illness into a psychiatric problem that results from irresponsible management of the disease-healing process. Cutaneous lesions may occur, including macules, papules, nodules, and ulcers. A differential diagnosis of endemic areas of leishmaniasis is necessary; the importance of parasitological examination combined with PCR leads to the appropriate diagnosis. This case provides evidence to fill the gap in the leishmaniasis guidelines of developing countries like Iran. Of course, all progress requires special political and economic attention in this area. Adequate commitment to multilateral tackling of this socio-health dilemma is critical and requires decisive concerted action across all parties involved.

Keywords: Cutaneous Leishmaniasis, Sporotrichosis, Diagnosis, Pentavalent antimonial, Amphotericin B

A review article on the effect of herbal extracts and essential oils on Demodex spp. parasites

© ¹ آنر سیمین

فارغ التحصیل¹

نوع پذیرش: پوستر | کد مقاله: G-13872

Abstract: The purpose of this article was to study the effect of Demodex parasites on skin and hair, as well as how these parasites work and their effect on human health. Demodex parasites are small arthropods that live on the outer surface of the skin and often have no specific clinical symptoms. The main cause of disease in humans is two types of Demodex mites: 1-Demodex folliculorum 2-Demodex brevis. Demodex is a parasite found on the surface of the human body. Currently, chemical drugs that target Demodex usually have side effects and have a weaker therapeutic effect. On the other hand, research has shown that plant extracts and essential oils such as tea tree oil have acceptable effects on the treatment of Demodex parasites and have less side effects. Therefore, the use of these methods can be a better and more appropriate alternative for the treatment of diseases caused by Demodex. Key words: Demodex, parasites, extracts, essential oils, tea tree oil

In vitro evaluation of the inhibitory effect of prodigiosin pigment from *Serratia marcescens* on *Leishmania major*

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نوع پذیرش: پوستر | کد مقاله: G-95612

Abstract: Background and Aim: Prodigiosin pigment is a red redox compound that is metabolically active and has therapeutic effects on eukaryotic and prokaryotic cells. The opportunistic gram-negative pathogen *Serratia marcescens* produces the prodigiosin pigment. *Leishmania major* is a protozoan that causes cutaneous leishmaniasis and is transmitted by mosquito bites. The main treatment for this infection is the use of 5-valent compounds of anti moan and amphotericin B, which scientists are looking for new ways to treat due to the observed side effects and drug resistance. This study aimed to investigate the effect of prodigiosin pigment extracted from *Serratia marcescens* on *Leishmania major* and also the effect of prodigiosin toxicity on the PC12 cell line. Material and Methods: For this purpose, *Serratia marcescens* RTCC 2281 strain was purchased from Razi Vaccine and Serum Research Institute and Prodigiosin pigment was extracted from this bacterium with the help of Ethyl acetate. The relative purity of the pigment was confirmed by thin-layer chromatography, spectrometry UV-Vis and FTIR. We examined its effect on different concentrations against *Leishmania major* and PC12 cell lines. Results: Prodigiosin pigment at concentrations of 10000 µg/ml in 24 and concentrations of 10000 and 5000 µg/ml in 48 hours respectively 97%, 98.68%, and 97.29% inhibited parasites. its IC₅₀ level in 48 hours was 62.41 µg/ml and CC₅₀ of this pigment was obtained on the cell line 842.4 µg/ml. All experimental steps were performed with three replications and statical results were obtained with the help of GraphPad Prism software version 9. Conclusion: According to the results, this pigment was effective against *Leishmania major* parasite, and its selective index on cells was 13.5 times (13.49), so more and more comprehensive studies to investigate the composition of prodigiosin in vitro and in vivo are suggested. Keywords: Prodigiosin pigment, *Serratia marcescens*, *Leishmania major*, Cell line, IC₅₀

Antiparasitic activity of pyocyanin pigment produced by *Pseudomonas aeruginosa* against *Leishmania major* in vitro

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نوع پذیرش: پوستر | کد مقاله: G-76532

Abstract: Background and Aim: Pyocyanin pigment is a blue redox compound with the metabolic activity that affects both eukaryotic and prokaryotic cells. Pyocyanin is produced only by the opportunistic pathogen *Pseudomonas aeruginosa*, which is a non-fermenting lactose gram-negative bacterium. The purpose of this study is to investigate the effects of pyocyanin pigment extracted from *Pseudomonas aeruginosa* on *Leishmania major* in vitro and also toxic effects on the PC12 cell line. Methods: To perform this test, *Pseudomonas aeruginosa* strain RTCC1474 was purchased from Razi Vaccine and Serum Research Institute, then pyocyanin pigment was extracted from this bacterium by using chloroform. The relative purity of the pigment was confirmed by thin-layer chromatography, spectrometry UV-Vis and FTIR. finally, the effects of different concentrations of this pigment were investigated against *Leishmania major* and PC12 cell lines. Result: In this research, it was found that the lowest concentration of pigment (78 µg/ml) was able to reduce 50% of the *Leishmania major* parasite population in 24 hours and the concentration of 10000 µg/ml was able to eliminate 93.2% of the *Leishmania* parasite in 24 hours. The IC50 of pyocyanin on the *Leishmania* parasite was 66.68 µg/ml in 24 hours and 27.32 µg/ml in 48 hours. Also, the CC50 level of this pigment on the PC12 cell lines after 48 hours was 930 µg/ml and its SI index was 34.04. Statistical results were obtained with the use of GraphPad Prism version 9 software. Conclusion: According to the effects of pyocyanin pigment on bacteria, and fungi and its easy production process, and the results obtained, it was concluded that pyocyanin pigment significantly eliminates *Leishmania* and can be used as a drug for the definitive treatment of leishmaniasis. More complete studies should be done in vitro and in vivo on pyocyanin pigment and its effect on *Leishmania major*. Keywords: pyocyanin pigment, *Pseudomonas aeruginosa*, *Leishmania major*, Cell line, CC50

Comparing Diagnostic Accuracy of Antigen B(AgB) with commercial kit by ELISA Method for Human Cystic Echinococcosis

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نوع پذیرش: پوستر | کد مقاله: G-28637

Abstract: Background: Cystic echinococcosis is one of the most prevalent zoonotic diseases, caused by the larvae of the parasitic worm *Echinococcus granulosus*. The disease has a global geographical distribution. Iran is also recognized as endemic area by the World Health Organization. Generally, the disease is accompanied with a wide range of clinical and para-clinical symptoms and findings, depending on the number, size and location of cysts. Liver and lungs are the most important organs involved. Diagnosis of the disease is essentially based on imaging methods (X-ray, ultrasound, MRI, CT scan) and confirmation by assessing the antibody level in the serum of suspected cases. ELISA test has an acceptable validity for the diagnosis of human hydatidosis compared to other serological methods and can be performed for a large number of samples in epidemiological studies. Also, based on the results of various studies, AgB has a significant accuracy for diagnosing the disease. Therefore, in present study, AgB (prepared in BMSU) and the commercial kit were evaluated and compared for sero-diagnosis of human hydatid cyst. Materials and Methods: Hydatid cyst fluid was extracted from the sheep liver infected with the cyst, and AgB was prepared according to Oriol method. A total of 142 serum samples including 36 patients with pathologically confirmed hydatid cysts, 46 patients with other parasitic diseases and 60 healthy individuals were examined. All samples were also evaluated with a commercial kit. Results: According to the obtained results in present study, the sensitivity, specificity and accuracy of the ELISA using AgB were 86.11, 95.28 and 92.96, respectively. The statistics indices were 77.78, 99.06 and 93.66 using ELISA commercial kit, respectively. Conclusion: The results of the present study indicate a high sensitivity, specificity and accuracy of AgB produced in BMSU. Although the validity of both AgB and commercial kit is approximately equal (92.96 AgB and 93.66% kit) and significant, considering that the antigen of commercial kits have usually not domestic origin, in order to achieve independence and self-sufficiency, the development of production of domestic antigens as well as their application is recommended. Keywords: Accuracy, Antigen B (AgB), Commercial kit, ELISA, Cystic echinococcosis.



چهاردهمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Lethal effects of *Astragalus maximus* Chloroform Extract against Clinical Isolates of *Giardia lamblia*

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نوع پذیرش: پوستر | کد مقاله: G-28034

Abstract: Background: At present, chemical drugs such as metronidazole, quinacrine and furazolidone are used to treat giardiasis. Although these drugs are useful in most cases, they are associated with some side. The present investigation was designed to evaluate the antiparasitic effects and cellular mechanisms of *Astragalus maximus* chloroformic extract against both trophozoites and cysts of *Giardia*. Methods: The extraction was done based on the maceration method with 70% methanol. The in vitro anti-*Giardia* effects of various concentrations of *A. maximus* extract (11.25, 22.5, and 450 mg/mL) were evaluated on cysts and trophozoites of *G. lamblia* for 15-360 min. In addition, the effects on the plasma membrane permeability and the induction of apoptosis in the trophozoites of *G. lamblia* were studied. Results: *Astragalus maximus* extract significantly ($p < 0.0001$) declined the viability of cysts and trophozoites of *G. lamblia* at concentrations of 22.5 mg/mL and 45 mg/mL, after 120-360 min incubation. The findings revealed that treatment of *G. lamblia* trophozoites with *A. maximus* extract increased the permeability of the plasma membrane in a dose dependent response. The extract, especially at the concentration of 10 mg/mL, significantly ($p < 0.001$) induced caspase-3 activation. Conclusion: The present study showed the promising in vitro antiparasitic effects of *A. maximus* extract against both trophozoites and cysts of *G. lamblia* by affecting the permeability of the plasma membrane and induction of apoptosis. Further investigations especially in animal models and clinical setting are required to clarify the accurate efficacy and mechanisms against *G. lamblia* infection. Keywords: apoptosis; giardiasis; extraction; trophozoites; cysts; in vitro.

Usefulness of different CRISPR/Cas9 technologies for tagging and editing in human protozoan parasites

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نوع پذیرش: پوستر | کد مقاله: G-86720

Abstract: Background: Genome editing by CRISPR (clustered regularly interspaced short palindromic repeats)/Cas9 (CRISPR-associated gene 9) system has been applied successfully to several protozoan parasites. In recent years this method has established as a functional method for editing in pathogenic human parasites. To date different ways of tagging and knock out in parasites have been introduced. In *Toxoplasma gondii*, the strategy used in CRISPR gene editing studies involved a unique vector for expression of Cas9 fused to a nuclear localization signal and the green fluorescent protein (Cas9-NLSGFP), and the specific sgRNA driven by *T. gondii* U6 promoter, without DNA donor, to induce DNA repair by non-homologous end joining (NHEJ). There is another report of CRISPR/Cas9-mediated gene knockout in *T. gondii* using a 1-vector strategy for co-expression of Cas9-FLAG-NLS fusion nuclease and a specific sgRNA to target TgLAP gene (leucine aminopeptidase). They achieved gene knockout without antibiotic selection. In *Plasmodium* spp an episomal vector for the expression of Cas9 (plasmid pUF1-Cas9) and a second expression vector carrying the sgRNA sequence and a DNA donor (plasmid pL7) to induce DNA repair by homology directed repair (HDR) were used, as *P. falciparum* lacks NHEJ pathway. In *Plasmodium*, generation of mutant cell lines by gene deletion and C-terminal tagging, allelic replacement, and simultaneous insertion of a point mutation plus a silent shield mutation have also been done. In *Leishmania*, there is a progressive propensity to use different types of CRISPR/Cas9 for gene editing and tagging; one of which has introduced as an easy-to-use technique without need of cloning. Materials & methods: In our lab, we have established a method introduced by Eva Gluenz et al., which comes as a toolkit, protocols for gene deletion, or N- and C-terminal tagging, as well as a website for designing the sgRNA primers and the donor DNA cassette are provided (LeishGEdit). Multiple plasmid vectors with resistance cassettes are available. We applied the method to a kinetoplast gene for KO and C-tagging. For this, *L. major* cell line with an episomal plasmid which expressed Cas9 and T7RNA polymerase was produced, then sgRNA template and donor DNA repairment cassette with resistant marker were PCR-amplified and transfected to *L. major* cell line. Using this toolkit for fast and accurate genome editing, we developed *L. major* parasites with C-terminal tagged kinetoplast gene and also we generate single KO parasites and we are initiating to produce null mutants. Results: We found this method very easier than other methods which were developed for gene editing of *Leishmania* and other parasites. The CRISPR/Cas9 gene tagging using this strategy has been successfully established in the lab and study of the pathogenicity of KO parasites will be performed. Further details of the method will be presented. Conclusions: Several approaches of CRISPR/Cas9 editing have been used in *Leishmania* for reverse genetic manipulation to elucidate gene functions. It is hoped that the establishment of the current approach will help in characterization of the role of kinetoplast genes in the biology or pathogenesis of the parasite. Key words: *Leishmania*; Kinetoplast; CRISPR/Cas9; Tagging

A review article on the effect of herbal extracts and essential oils on Demodex spp. parasites

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فارغ التحصیل¹

نوع پذیرش: پوستر | کد مقاله: G-13872

Abstract: The purpose of this article was to study the effect of Demodex parasites on skin and hair, as well as how these parasites work and their effect on human health. Demodex parasites are small arthropods that live on the outer surface of the skin and often have no specific clinical symptoms. The main cause of disease in humans is two types of Demodex mites: 1-Demodex folliculorum 2-Demodex brevis. Demodex is a parasite found on the surface of the human body. Currently, chemical drugs that target Demodex usually have side effects and have a weaker therapeutic effect. On the other hand, research has shown that plant extracts and essential oils such as tea tree oil have acceptable effects on the treatment of Demodex parasites and have less side effects. Therefore, the use of these methods can be a better and more appropriate alternative for the treatment of diseases caused by Demodex. Key words: Demodex, parasites, extracts, essential oils, tea tree oil

In vitro evaluation of the inhibitory effect of prodigiosin pigment from *Serratia marcescens* on *Leishmania major*

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نوع پذیرش: پوستر | کد مقاله: G-95612

Abstract: Background and Aim: Prodigiosin pigment is a red redox compound that is metabolically active and has therapeutic effects on eukaryotic and prokaryotic cells. The opportunistic gram-negative pathogen *Serratia marcescens* produces the prodigiosin pigment. *Leishmania major* is a protozoan that causes cutaneous leishmaniasis and is transmitted by mosquito bites. The main treatment for this infection is the use of 5-valent compounds of anti moan and amphotericin B, which scientists are looking for new ways to treat due to the observed side effects and drug resistance. This study aimed to investigate the effect of prodigiosin pigment extracted from *Serratia marcescens* on *Leishmania major* and also the effect of prodigiosin toxicity on the PC12 cell line. Material and Methods: For this purpose, *Serratia marcescens* RTCC 2281 strain was purchased from Razi Vaccine and Serum Research Institute and Prodigiosin pigment was extracted from this bacterium with the help of Ethyl acetate. The relative purity of the pigment was confirmed by thin-layer chromatography, spectrometry UV-Vis and FTIR. We examined its effect on different concentrations against *Leishmania major* and PC12 cell lines. Results: Prodigiosin pigment at concentrations of 10000 µg/ml in 24 and concentrations of 10000 and 5000 µg/ml in 48 hours respectively 97%, 98.68%, and 97.29% inhibited parasites. its IC50 level in 48 hours was 62.41 µg/ml and CC50 of this pigment was obtained on the cell line 842.4 µg/ml. All experimental steps were performed with three replications and statical results were obtained with the help of GraphPad Prism software version 9. Conclusion: According to the results, this pigment was effective against *Leishmania major* parasite, and its selective index on cells was 13.5 times (13.49), so more and more comprehensive studies to investigate the composition of prodigiosin in vitro and in vivo are suggested. Keywords: Prodigiosin pigment, *Serratia marcescens*, *Leishmania major*, Cell line, IC50

Evaluation of the anti-leishmanial effect of imatinib nanoparticles on *Leishmania major* in vitro and in vivo

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نوع پذیرش: پوستر | کد مقاله: G-56327

Abstract: * Background: Cutaneous Leishmaniasis is an infectious disease caused by protozoan parasites of the genus *Leishmania*, which are transmitted to mammals by the bite of infected female phlebotomine mosquito. Today, several strategies have been proposed to deal with this disease. Utilizing newly produced drugs is effective and useful because high toxicity and costs, low efficiency and possible anti parasitic resistance of some existing medications. Imatinib is an anti-cancer drug that inhibit the parasite in the host cells and some studies were indicated the effect of Imatinib on CL. Therefore, the aim of this study was evaluating of anti-leishmanial effect of imatinib nanoparticles on *Leishmania major* in vitro and in vivo. Materials and Methods: *Leishmania major* promastigotes (MRHO/IR/75/ER) was prepared from Isfahan University of Medical Sciences (Parasitology and Mycology Department). Chitosan and Imatinib nanoparticles were prepared using emulsion solvent evaporation and inotropic coagulation methods, respectively. The toxic effect of nanoparticles on promastigotes and amastigotes of *Leishmania major* was studied by the MTT method. The *L. major* CL model of Balb/c mice was produced by injection of the cultured metacyclic form of parasite at the base of the tail. Mean diameter of the lesions and the optimal dose of imatinib against were evaluated. Results: Nano-drugs indicated higher lethality on promastigotes and amastigotes of *Leishmania major* by increasing the concentration. The maximum lethality was 100 µg/ml. The mean size of the wound after indicating the last dose (after 3 weeks of treatment) in the negative (placebo) and positive (amphotericin B) control groups was 6.98±3.15 and 1.34±0.3 mm, respectively. The average parasite load in the groups treated with concentrations of 10, 20, 50, 100, and 150 mg of Imatinib was 1.79, 1.72, 1.35, 2.03, and 2.04, respectively. Conclusion: The concentration of 20 and 50 mg of imatinib was capable for preventing the formation of CL. Regarding the anti-leishmanial effects of this nano-drug in vitro and in vivo, it can be a promising alternative drug for multidrug therapy against *Leishmania major*. However, further studies are suggested to evaluate the possible efficacy of different physical forms of imatinib for a greater therapeutic effect on *Leishmania major* in mice and humans. Keywords: Cutaneous leishmaniasis, Nanoparticle, Chitosan, Imatinib.



چهاردهمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Phylogenetic analysis of avian schistosome *Trichobilharzia regenti* (Schistosomatidae, Digenea) from naturally infected hosts in northern Iran

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آدرس دبیرخانه:
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چهارمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



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نوع پذیرش: پوستر | کد مقاله: G-52836

Abstract: Background: *Trichobilharzia regenti* (T. regenti) is one of the species that belong to the avian schistosomatid flukes and causes human cercarial dermatitis (HCD) in areas of aquaculture in northern Iran. Understanding the phylogenetic relationships and genetic diversity of this thread-like fluke will lead to a deeper understanding of avian schistosomiasis epidemiology and more effective HCD control in this region. Methods: In the present study, adult or egg of *Trichobilharzia* isolated from aquatic birds as well as schistosomes cercariae isolated from aquatic snails in Mazandaran Province, northern Iran, belonged to the authors' previous research were examined. Molecular studies and phylogenetic analysis were carried out on these schistosomes samples. Results: The phylogenetic analysis of the ITS1 and COX1 genes in isolated schistosomes revealed that all samples belong to the T. regenti clade. Remarkably, based on phylogenetic results, these schistosomes samples from *Anas platyrhynchos domesticus*, *A. platyrhynchos*, *Spatula clypeata* and *Lymnaea stagnalis* grouped together with previously sequenced samples from Iran (*Trichobilharzia* cf. *regenti*). Regarding the COX1 and ITS1 genes, phylogenetic tree and haplotypic network of ITS1 gene did not show distinct clusters. Conclusion: Due to the isolation and genotyping of furkocercariae isolated from *L. stagnalis* and its consistency with isolated new genotype from ducks, for the first time in Iran, the puzzle of the disease in Mazandaran Province was completed and the role of *L. stagnalis* snails in the transmission of the disease was approved. Keywords:

Berberine improves inhibitory avoidance memory consolidation and reconsolidation impairment of *Toxoplasma gondii* infection and ketamine-induced schizophrenia rat model

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چهارمین گنگره بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



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نوع پذیرش: پوستر | کد مقاله: G-68432

Abstract: Background: Memory impairment caused by *T. gondii* infection has been documented. Beberine (BRB) is well known for its enhancing effects on memory and has shown promising results, but the effect of BRB in *T. gondii* infection and schizophrenia-induced consolidation and reconsolidation memory impairment is still unclear. Here, we examined the BRB effect on the inhibitory avoidance (IA) memory consolidation and reconsolidation impairment induced by *T. gondii* infection, and ketamine as a pharmacological model of schizophrenia. Also, the brain-derived neurotrophic factor (BDNF) expression in the medial prefrontal cortex (mPFC) and hippocampus was analyzed. Methods: Rats were infected with *T. gondii* RH strain or received ketamine (30 mg/kg/day) intraperitoneally (i.p) for at least five consecutive days (as the model of schizophrenia), then administrated with BRB orally (25 mg/kg, i.p/day) for three days. Finally, the IA memory retention test 48 post conditioning and BDNF measurement were examined. Results: Results indicated IA memory impairment in *T. gondii*-infected animals since lower step through latency (STL) was observed than control animals. We found significant elevations in STL and decrease in total time spent in dark area following BRB administration in infected and ketamine treated rats, indicating improvement in consolidation and reconsolidation memory. Moreover, BDNF levels were reduced in the hippocampus and mPFC regions of both *T. gondii*-infected and ketamine-induced groups, which remarkably enhanced after BRB treatment. Furthermore, we found that BDNF levels in IA-related brain regions were notably changed in the ketamine base group against rats infected with *T. gondii*. Conclusion: Taken together, BRB may be a useful preclinical treatment for improving memory impairment through BDNF expression in PFC and hippocampus; therefore, BRB is suggesting for memory disturbances induced by *T. gondii* infection. Keywords: *Toxoplasma gondii*; Schizophrenia rat model; Inhibitory Avoidance Memory; consolidation; reconsolidation; Berberine

Toxoplasma infection in patients with myocardial infarction

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نوع پذیرش: پوستر | کد مقاله: G-37208



چهاردهمین گنگره بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Abstract: Background: *Toxoplasma gondii* is a widespread protozoan parasite that infects one third of the global human population. Very little information is known about the impact of *T. gondii* on patients with heart disease. The aim of the present study was to determine the association between *T. gondii* exposure and patients suffering from myocardial infarction. Materials and Methods: The infection rate of anti-*Toxoplasma* IgG antibodies in 86 patients with myocardial infarction (troponin T positive) and 86 age and gender-matched controls (troponin T negative) was examined using enzyme-linked immunoassays. The DNA extraction was performed on separated buffy coats of serologically positive blood samples (32 samples with high titer of anti-*Toxoplasma* IgG). The GRA6 gene of *T. gondii* was amplified using PCR. The existence of polymorphic restriction sites for endonuclease MseI was used with the PCR-RFLP method and the bases of GRA6 gene were sequenced to determine the type of strains (I, II and III). Results: A positive anti-*Toxoplasma* IgG level was found in 61.6% of the myocardial infarction samples and in 24.4% of the healthy controls (P- value 0.05). The PCR results showed that only 3 of the anti-*Toxoplasma* IgG positive patients were found to be positive with GRA6 gene for *T. gondii*. The PCR-RFLP results showed that 2 of the 3 positive sample had 75bp and 623 bp DNA fragments belonging to type II genotype. The sequencing result confirmed the genotype II of *T. gondii*. *Toxoplasma* infection should be considered in myocardial infarction cases. Conclusion: The results of this study showed that *T. gondii* infection was significantly higher in patients with myocardial infarction than in healthy controls. This means that patients with *Toxoplasma* infection may be at increased risk for heart attacks due to the presence of cysts in the heart muscle. Keywords: *Toxoplasma gondii*, IgG level, Myocardial infarction

Evaluation of the 11-Year Trend of Cutaneous Leishmaniasis in Six Main Foci of the Disease in Isfahan Province during the Years 2008 to 2018

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چهاردهمین گنگره بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



نوع پذیرش: پوستر | کد مقاله: G-60428

Abstract: Background: Leishmaniasis is one of the endemic diseases in Iran and Isfahan province. This study was conducted to investigate the trend of cutaneous leishmaniasis in 6 main centers of Isfahan province during the years 2007 to 2018. Materials and Methods: This research is a cross-sectional descriptive-analytical study that was conducted based on the data available in the Zoonosis Diseases Unit located in the Isfahan Health Vice-Chancellor. The data related to the new cases of cutaneous leishmaniasis that were reported by the detection laboratories as well as the data related to the control measures and the fights against the reservoir were collected. The trend of disease incidence was analyzed separately by foci, year and the relationship between disease incidence and control measures. Results: The results showed that during this 11-year period, the incidence of leishmaniasis is decreasing, but some centers, such as the number 1 Isfahan region, have had severe fluctuations in some years. The relationship between the average incidence of the disease and the total number of poisons consumed using the Pearson Correlation statistical test was linear and significant. In other words, in the centers where the highest amount of poison has been consumed, the incidence rate of leishmaniasis is also reported to be higher. Conclusion: Considering the fluctuations of the disease in some years, and the number 1 Isfahan region has the highest rate of incidence despite the highest amount of poisons consumed compared to the Shahinshahr region, the effectiveness of this type of intervention in the long term is doubtful. Keywords: Cutaneous leishmaniasis, Incidence, Isfahan, Pest control, Trends

آدرس دبیرخانه:

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The importance of using nanoparticles in the treatment of hydatid cyst

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نوع پذیرش: پوستر | کد مقاله: G-93762

Abstract: Background: Cystic echinococcosis (CE) is one of the common human and animal diseases seen in wild animals and humans and domestic animals. This hydatid disease is caused by a tissue attack by a tapeworm called *Echinococcus granulosus*. The dominant species of this parasite is *E. granulosus*, which creates cysts in the liver and lungs of animals and humans, so it is a threat to humans and domestic animals. The final host of this parasite is the dog, in which the adult tapeworms attach to the intestinal epithelium and sexual reproduction takes place and causes the development of eggs. These eggs are brought out with the feces, which contain an oncosphere that The host forms are swallowed, and these oncosphere released from the egg penetrate the intestinal mucosa. This cyst has been seen in developing countries such as the Middle East which is considered a threat to human health. A number of studies have shown that nanoparticles of silver nanoparticles (AgNps), gold nanoparticles (AuNps), chitosan and other metal oxides have an inhibitory effect on *Leishmania*, *Toxoplasma*, *Plasmodium* and *Giardia* parasites. Silver nanoparticles have seen the greatest impact due to contact with the environment. The higher the surface-to-volume ratio in nanoparticles, the more unique properties they exhibit. When surgery is performed, the cyst is under pressure and there is a possibility of rupture, so the presence of scolocidal substances such as Hypertonic saline, silver nitrate, and formaldehyde is necessary. Materials and Methods: The PubMed, Google Scholar and Scopus databases were searched for the purpose of finding studies and twenty articles were studied. Results: Albendazole and Mebendazole are common drugs in the chromatography method, but their concentration is not enough to treat cyst disease because the cyst wall is thick. Formalin is one of the first scolocidal agents, but we do not use it because it is toxic. Today, hypertonic saline is often used, but it has side effects of intracranial bleeding, neurological side effects, and hypernatomy. Conclusion: In a study, Anderson and Loveless were able to eliminate *E. granulosus* protoscolices at different temperatures, and the duration of their death was 16 days at 20°C, 8 days at 30°C, 4 days at 40°C, and two hours at 50°C degrees were reported. This study shows that temperatures above 40 degrees cause destruction. In another study, non-toxic AuNPs were introduced as a new scolocidal agent. This nanoparticle produces heat under the effect of laser radiation and in this way destroys protoscolices and causes cell destruction. Keywords: *Echinococcus granulosus*, Hydatid cyst, Nanoparticles

A survey of intestinal parasitic infection among primary school children in Khalil Shahr, East of Mazandaran Province

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نوع پذیرش: پوستر | کد مقاله: G-05278

Abstract: Background: High prevalence of parasitic infections can be the result of the subclinical infections. Some regular and ongoing epidemiological studies are needed to combat and control these infections. Parasitic infections are common among children in schools. The aim of this study was to investigate infections in primary school students of Khalil Shahr in east of Mazandaran province, north. Materials and Methods: In this descriptive cross-sectional study, stool specimens from 500 students (7-12 years old) were collected from six elementary schools of Khalil Shahr from April 2019 to May 2020. The specimens were examined for wet and parasitic expansion of parasite test (Ferm ether) and staining of trichrome and acid fasts in terms of contamination with intestinal parasites. The data collection tool was a questionnaire containing demographic data of the students, parents' education and their occupations. Data were analyzed by t-test and chi-square test (p 0.05). Results: Overall, 11 students (2.2%) were found to be infected by intestinal parasites. The prevalence of intestinal protozoa was 1.8% in blastocystis hominis and 0.2% in giardia lamblia. Other parasitic infections such as Entamoeba histolytica, oxyur, Hymenolepis nana, and Entamoeba coli were not observed in this study. There was a significant relationship between the prevalence of parasites with household size and raw vegetables consumption (p 0.05). However, there was no significant relationship with sex, occupation and education of mothers (p 0.05). Conclusion: The results of this study indicate that the prevalence of parasitic infections in primary schools is low and shows a significant decrease in comparison with other studies in the province and country. This can be due to improved quality of life and access to health services, and the promotion of health literacy and parenting and education awareness. It is also recommended that students and parents be identified and treated to reduce intestinal parasitic infections, in particular Giardia and Blastocystis, as a priority for prevention and control programs in the province. Keywords:



چهاردهمین گنگره بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



The effect of anti-parasitic drugs in COVID-19 treatment: A systematic review

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نوع پذیرش: پوستر | کد مقاله: G-73829

Abstract: Background: Novel COVID-19 is a public health emergency that poses a serious threat to people worldwide. Given the virus spreading so quickly, novel antiviral medications are desperately needed. Repurposing existing drugs is the first strategy. Anti-parasitic drugs including Chloroquine (CQ), Hydroxychloroquine (HCQ), and Ivermectin (IVM) were among the first to be considered as a potential treatment option for this disease. It recently demonstrated anti-parasitic drugs in vitro, and in vivo, and now over 420 clinical trials have been registered worldwide to test their effectiveness in COVID-19 patients. This systematic review aims to collect data on the efficacy or non-efficacy of reported COVID-19 treatment for the use of these drugs as a probably repurposed medication. Materials and Methods: Data was extracted from in vitro, in vivo, randomized trials of COVID-19 treatment trials identified through systematic searches of PubMed, Google Scholar, Scopus, and clinical trial registries. The primary outcome of this study is the frequency of positive or negative effects. Results: Overall, 8 in vitro and in vivo studies, and 48 trials containing results investigating CQ, HCQ, ivermectin, Nitazoxanid, and Niclozamid for COVID-19 have been registered. In vitro, and in vivo studies of animal models revealed a broad range of antiviral effects of CQ, HCQ, and IVM, however, clinical trials are necessary to appraise the potential efficacy of these drugs in clinical settings. Conclusion: We reviewed systematically the prophylactic or therapeutic effects of some FDA-approved antiprotozoal and antihelminthic drugs on COVID-19. Despite in vitro and in vivo success of these drugs, it seems that there still is not any confirmed therapeutic agent for COVID-19. Keywords: Anti-parasitic Drugs, COVID-19, SARS-CoV-2, Efficacy

Investigation of cryptosporidium infection in lambs in Quchan city, Khorasan Razavi

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نوع پذیرش: پوستر | کد مقاله: G-09371

Abstract: Background :Cryptosporidiosis is a zoonotic disease and causes diarrhea syndrome in newborn lambs and calves. This disease is caused by an intracellular and extracellular parasite called Cryptosporidium. This parasite is transmitted via fecal-oral route. Complications of this disease in ruminants are: diarrhea, reduced growth, abdominal pain, lethargy. This protozoan has oocysts that are resistant to adverse environmental conditions and an effective drug that can be effective on the protozoan is not available. Materials and Methods :The aim of this study was to determine the infection with cryptosporidium in lambs in the suburbs of Quchan city. In this research, 202 fecal samples were collected from some villages of Quchan city from lambs aged 5 to 90 days during the winter season of 2022 to mid-summer of 2022. Fecal samples were mixed with the same volume of 2.5% potassium dichromate and transferred to the parasitology laboratory. At the same time, the risk factors include age, sex, breed, rectal temperature, fecal consistency, eating colostrum at birth, type of sheep farming, presence of other animals, type of corral, type of bedding, type of water trough and herd size were gathered in special registration questionnaires. Fecal smear was prepared and stained by Zeihl-Nelson method. The samples were observed with 40X and 100X light microscope. In the current research, the intensity of pollution in the expansions was determined based on the method of Ahamed et al. (2015). Results: Out of 202 fecal samples, 20 positive samples (9.9%) were reported. The lowest intensity of infection (1+) was in 11 samples (55%) and the average intensity of infection (2+) was in 9 samples (45%). In this study, high intensity contamination (3+) was not found. Conclusion: In the present study, no significant relationship was found between the frequency of cryptosporidium infection and risk factors such as age, gender, race, body temperature, fecal consistency, type of sheep farming, herd size, type of corral, type of bedding and type of water consumed



چهاردهمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Retraining over the principles and mechanisms involved in the occurrence of false results from urine drug screening tests: Adulteration and strategies to defeat

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نوع پذیرش: پوستر | کد مقاله: G-95246

Abstract: Screening tests (UDSTs) for the diagnosis of psychoactive drugs can identify drug abuse, improve workplace safety, ensure community health, and play a critical role in therapeutic drug monitoring. Nonetheless, correct interpretation of the results of these tests requires a full awareness of the principles of testing methods, drug kinetics, and various leading causes of false results. Among the advantages of these screening tests (based on the immunoassay technique), we can refer to their high sensitivity in the detection of psychoactive substances, convenience, and cost-effectiveness. Therefore, these kinds of urine drug screening are recommended as the first line of detection in all reliable related guidelines. This method can reliably detect common drug abuse, such as opiates/opioids, amphetamine/methamphetamine, cocaine, cannabinoids, phencyclidine, barbiturates, and benzodiazepines, with high sensitivity. Although the immunoassay technique is sensitive to the presence of drugs/drug metabolites and has relatively good specificity, false negative and positive results may occur in some cases. Therefore, careful attention to proper sample collection methods and tests to determine the integrity nature of the urine sample can identify a wide range of abusers' attempts to produce false negative/positive test results. Finally, unexpected positive test results should be checked with confirmatory methods, such as gas chromatography/mass spectrometry. Keywords:

Melittin as a safe compound to mice immune system

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نوع پذیرش: پوستر | کد مقاله: G-09571

Abstract: Background: Maintenance of a well-functioning immune system is a vital requirement to protect human body against pathogens/cancers. Natural compounds have long been used because of their benefits for the immune system. One of which is bee venom that contains a peptide called melittin having antimicrobial and anticancer effects. Since a limited number of studies regarding the effects of melittin on the immune system have been carried out, we aimed to evaluate BALB/c mice immune system parameters with regard to whether it can enhance or suppress the immune system. Methods: Female BALB /c mice were treated intraperitoneally for 14 days (5 doses per week) with 0.75 and 1.5 mg/kg doses of melittin. The negative control group received normal saline whereas the positive control group received Cyclophosphamide (20 mg/kg). Immunological parameters such as hematological parameters, delayed-type hypersensitivity (DTH), hemagglutination titer (HA), spleen cellularity, splenocytes proliferation, as well as spleen and bone marrow histopathological assessment were evaluated. Results: Our results showed that melittin has no gross pathological effect on the spleen and bone marrow. It was also demonstrated that melittin has no any significant effect on hematological parameters. Melittin did not cause any significant changes to proliferation response of splenocytes to PHA and LPS, spleen cellularity, DTH response, as well as the production of anti-SRBC antibodies. Conclusion: The results showed that melitin at 0.75 and 1.5 mg/kg doses could not induce significant changes on immune parameters. Based on our results, melittin was found to be safe for the mice immune system. Keywords:

Laboratory findings lead to accurate clinical diagnosis of Aluminum phosphide intoxication: preclinical results

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نوع پذیرش: پوستر | کد مقاله: G-57091

Abstract: Laboratory findings lead to accurate clinical diagnosis of Aluminum phosphide intoxication: preclinical results Shima Zeynali-Mogaddam¹, Fatemeh Hashtarkhani¹, Fatemeh Jafari¹, Hamid Soraya¹, Hassan Malekinejad¹, * 1. Department of Pharmacology & Toxicology, School of Pharmacy, Urmia University of Medical Sciences, Urmia, IRAN. *Corresponding Author: malekinejad.h@umsu.ac.ir, +9891414965558 Background: Aluminum phosphide (ALP) or “Rice Tablet” is among the widely used pesticides in Asia due to its availability and effectiveness. It causes acute and subacute poisoning and high mortality rates in humans and animals. Although ALP-induced toxicity has been diagnosed based on both laboratory and clinical findings, however there are no confirmed laboratory differences between two models of intoxication. Hence, this study aimed to clarify some differences between two models. Materials and Methods: The current study was performed on healthy, male and adult Wistar rats weighing between 200 – 220 g (n=5). The animals were grouped and nominated as: control, acute and sub-acute groups. The acute and sub-acute forms of ALP poisoning were induced by administration of 12.5 mg/kg, orally, single dose, and/or 2 mg/kg, orally for 7 consecutive days, respectively. Three h after the last ALP-exposure the heart rates were examined in all groups. The myeloperoxidase (MPO) activity and serum level of CK-MB were determined. The nitric oxide content of heart tissue also was measured according to the Griese method. Results: results are indicating that although the acute ALP intoxication elevated the heart rate (270 ± 8 vs 325 ± 18), the sub-acute poisoning resulted in a remarkable reduction of heart rate (275 ± 6 vs 228 ± 7) compared to the control groups. We found that both models of ALP intoxication increased the MPO activity significantly (p0.05). Moreover, serum level of CK-MB and cardiac content of NO were elevated 2 and 3 fold after acute and subacute ALP poisoning, respectively. Conclusion: our results suggest that all proposed biomarkers of heart rate, serum levels MPO, CK-MB along with cardiac NO content could help in the accurate diagnosis of ALP intoxication. Key Words: Aluminum phosphide; Acute intoxication; Subacute poisoning; Accurate diagnosis.

Evaluation of cytotoxic effects of cell wall compounds extracted from *Candida albicans* on K569 cancer line

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نوع پذیرش: پوستر | کد مقاله: G-34859

Abstract: Background: Cancer is one of the most common cause of death in the world and leukemia as a blood lineage malignancy plays a key role and place in 5 rank in terms of cancer incidence. One of the hypothesis for induction of neoplasm is impairment of apoptosis. The aim of this study is the evaluation of cytotoxicity effect of *Candida albicans* cell wall extract on K569 cancer line. Materials and Methods: K562 cancer cell line and *Candida albicans* were cultured and the compounds extracted from the yeast wall were prepared. Different concentrations (100, 200, 500, 1000 Mg/ml) of the extracted compounds were prepared and cultured simultaneously with the cancer cell line for three times (24, 48, 72 h). To investigate the process of apoptosis, MTT and flow cytometry tests were performed and SPSS 25 was used for data analysis. Results: The average lethality percentage of k562 cells in all concentrations decreased over time. In addition, the average lethality percentage of k562 cells at 24, 48 and 72 h after the intervention was the highest at the concentration of 1000 and then at the concentration of 500 and similarly at the concentrations of 200 and 100 Mg/ml. In other words, with the decrease in concentration, the average lethality percentage of k562 cells decreased. Also, the highest level of cytotoxicity was observed in the first 24 h. Flow cytometry results showed that cell death was due to apoptosis and not necrosis, so that the IC50 in the first 24 hours was reported as 12500 Mg/ml. Conclusion: Our results showed that *Candida albicans* cell wall extract has anti-tumor properties and induces apoptosis in K561 cancer strain, and its cytotoxic effect has a direct relationship with concentration and an inverse relationship with time. Keywords: Cytotoxic effect, *Candida albicans*, K569 cancer line, Apoptosis

Investigation of clinical symptoms of snakebite in children admitted to Abuzar Ahvaz Hospital during 2016-2018

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نوع پذیرش: پوستر | کد مقاله: G-83245

Abstract: Background: Due to the diversity of snakes in Iran, understanding the demographic characteristics of patients can be effective in better treatment. The aim of this study was to determine the clinical symptoms of snake bites in children admitted to Abuzar Hospital in Ahvaz during 2016-2018. Materials and Methods: The present study was descriptive-analytical and retrospective. Number of 145 snakebites children referred to Abuzar Hospital were selected by census and examined. The clarified was extracted from the analyzed using SPSS software version 22. Results: The mean age of snakebite children was 10.73 ± 3.41 years, 92(63.4%) were male children. The mean of antivenom intake in bitten children was 4.93 ± 1.44 , the mean BUN 13.70 ± 4.01 and the mean creatinine 0.68 ± 0.14 . The mean duration of hospitalization 4.05 ± 2.13 days and the mean duration of onset of symptoms after the bite in patients was 94.34 ± 109.31 hours. The mean of coagulation problems in the first stage in patients was 2.76 ± 1.91 and 82(56.6%) of snake bred children received FFP blood product. the first symptom after a bite in 60 snakebite children (41.4%) was pain. Number of 4 patients (2.8%) were hospitalized for two days and 2(1.4%) were admitted to the intensive care unit for three days. Location 49(33.8%) of the snakebite children was Ahvaz and none of the snakebite children had died. Conclusion: According to the results of this study and understanding the epidemiology of snakebite in the khozestan province; It is possible to play an effective role in preventing snake bites and other causes by educating all health care workers and physicians as well as raising public awareness in the community. Keywords: Clinical symptoms, snakebite, child.



چهاردهمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Determination of the frequency of clinical signs of opium and opioid poisoning in patients referred to Razi Hospital in Ahvaz during 2020-2018

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نوع پذیرش: پوستر | کد مقاله: G-07698

Abstract: Background: Opium poisoning is one of the most common reason of poisoning all around the world and lots of people will be hospitalized because of it each year. However nowadays opioids will use in medicin. The main goal of this study is the evaluation of the frequency of clinical signs of poisoning with opium and opioids in Ahvaz Razi hospital between the years of 2018-2020. Materials and Methods: During this descriptive-analytic study records of all the patients that hospitalized between the years of 2018-2020 in Ahvaz Razi hospital are counted and cases are found. The variances of this study are: age, sex, marriage, location, time of refer, needing ICU, needing intubation, using other drugs, needing Anti dote and dose of it, death, time of hospitalization, first symptom, type of opium and ethiology of poisoning. We earned the informations from the patient's files and evaluated the results by SPSS 22. Results: The results showed that 91.8% of patients were males, 53.5% were between the age of 26 to 40. Tramadol was the most common drug (38.3%). LOC was the most common symptom (55.6%). 57.2% of patients needed ICU admission and 19.3% needed intubation. The mortality of patient was 10.7%. the most common ethiology of poisoning was overdose (85.2%). 65% needed anti dot, 58.6% were single, 84.8% lived in town, 77% were refered to hospital in less than 6 hours and 40.3% were hospitalized between 24 to 48 hours. Conclusion: Our findings show that men and singles are more likely to be intoxicated with opioids and the most important cause of poisoning was tramadol. Base on this study these is relation between the type of opium and age, type of opium and sex, type of opium and first symptom, type of opium and needing antidote. Key words: opium, opioid, naloxan, Razi hospital.

Venoms, the potential candidate for the effective control of diabetes

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G-82341 نوع پذیرش: پوستر | کد مقاله:

Abstract: Background: Diabetes (type 1 & type 2), is a chronic disease that occurs due to impaired insulin production and function which in turn lead to increased blood glucose level and several complications. Due to the side effects of current medications used for treating this disease, high cost, and permanent use, it seems necessary to achieve new therapeutic agents with better conditions. Venom as a part of the vital system of venomous creatures is a pharmacologically active compound with great potential to cure diseases. Here we have a complete review of the history and effect of different venoms on the management of blood glucose levels around the world. Materials and Methods: International online databases were searched singularly and the validity, accuracy, and clarity of many published documents were evaluated and classified based on year of publication, type of venom, method of experiment, and effect. Results: Since the first related study in 1930, many studies have been conducted on the effect of venoms on the blood glucose level of different animals. The first study was about ninety years ago, Epstein reported that *Naja flava* increases the level of blood glucose in rabbits. Seventeen years later, Grasset reported the same results. After that, Muhammad and his colleagues reported the raising effects of Egyptian scorpion, bee, and *Echis carinatus* venoms on rabbits' blood glucose. In 1959, Muhammad also reported that the hypoglycemic effect of the lethal doses of the venom of the *Walterinnesia aegyptia* did not occur in alloxan-induced diabetic rats after pancreatectomy. Mabez in 1968 reported that injection of the lethal dose of cobra venom did not alter blood glucose levels in healthy rats and even had no effect on the concentration of glucose, glycogen, and lactate in the liver and muscles. Two years later, another study reported that injection of a lethal dose of the Egyptian cobra venom increased the level of blood glucose in dogs during glucose tolerance. In 2011, Ivas showed that bee venom non-significantly and transiently increased blood glucose in rabbits. In contrast, Roudbari in 2012, reported that the venom of *Anderoctonus crassicauda* significantly decreased the blood glucose levels in alloxan-induced diabetic rats. In 2012, Mousavi showed that bee (*Apis mellifera*) venom significantly decrease blood glucose, triglyceride, and cholesterol level while serum insulin levels were significantly increased. In 2019, Abdel-Rahman showed that the venom of *Scorpio maurus palmatus* in alloxan-induced diabetic mice reduced the level of blood glucose. Finally, in 2022, Fathi et al., reported the significant decreasing effect of the Persian cobra, *naja naja oxiana* venom on blood glucose levels of experimental diabetic male rats (research. continue). Conclusion: Based on these data, we concluded that venoms can be a potential candidate for the effective control of diabetes. Keywords: Diabetes, Venom, Blood glucose, venomous creatures

Cardiovascular complications following acute methadone poisoning with respect to addiction to methadone

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G-39051 نوع پذیرش: بوستر | کد مقاله:

Abstract: Background: Methadone is one of the synthetic opioids used in the treatment of moderate to severe pain and for opioid addiction. Increased use of methadone has resulted in an increased prevalence of its toxicity, one aspect of which is cardiotoxicity. In this paper, we reviewed the effects of acute methadone poisoning on the cardiovascular system. Methods and Materials In this retrospective study, information related to all the people who went to Al-Zahra and Khorshid hospitals in Isfahan with complaints of poisoning between July and March 2019 were obtained from the hospital archives and analyzed. Patients were studied in two groups with and without long-term history of methadone use. Results: Using the findings, there was no significant difference between the two groups in the mean QT corrected, QRS duration, and PR interval at any of the three times zero, 12, and 24 hours after admission (P0.05). The results indicated that the QT dispersion at the beginning of admission (P=0.81) and 12 hours after admission (0.93) was not significantly different between the two groups, but at the discharge, QT dispersion was significantly lower in the group with the long-term use of methadone (P=0.04). Conclusions: It seems that among the cardiovascular influencing factors, only the QT dispersion was different in patients with and without a long-term using of methadone. Cardiovascular events caused by methadone toxicity are among the factors affecting the mortality of patients, which indicates the necessity of managing methadone use in patients.

Misjudgment in the case of a 25-year-old woman with a positive urine test for amphetamine

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G-09157 نوع پذیرش: پوستر | کد مقاله:

Abstract: Background: Urine screen test has publicized in place of clinical especially in toxicology ward and emergency setting and other purposing such as entry Olympic Games of athletes, Issuance and renewal of driver's license, matrimony, Entering the profession of judgment and advocacy and in Forensic Science. It tracks some drugs, substances or their metabolites in urine. in many countries it detect opioid, cannabinoid, amphetamine etc. The biggest test problem is false positives and false negative results. Case presentation: A lethargic 25 years old woman (GCS:12) has brought to emergency room. She did not reply accurate to question of medical staff. Her vital sign was: PR:86 BP:140/85 RR:15 T:38 O2SAT:96% BS:92 Pupil: a little mydriasis skin: N Because of Loss of consciousness, unknown history and not having a companion, requested a Consultation with clinical toxicology fellowship, and then Serum level of acetaminophen and phenobarbital and urine screen test was requested. after 6 hours and receiving a liter of saline sugar serum, she got better and alert. Tox urine test was positive for amphetamine and negative for other substance specially BZD. according to the patient's consciousness, Overcrowding in the emergency room and patient impatience, she gave personal consent and left the hospital. She took the summary note of the case and due to her unfamiliarity with medical terminology, she did not ask the doctor for an explanation about the contents of the case, including the result of a positive urine test for amphetamine. She worked in an important government office and submitted the case summary sheet to superior to explain her absence from work. As soon as the boss saw the positive result of amphetamine in the summary of the employee's file, the security department is notified and an order is issued to temporarily suspend her from work. As a matter of fact she had gone to doctor and was prescribed her pseudoephedrine for congestion of nose and therefore the test was positive (false positive) for amphetamine. Conclusion: The tip we learn from this case is that the doctor should have informed the patient of the test results before leaving the hospital with personal consent and asked the patient about the history of taking other drugs such as ranitidine and pseudoephedrine, and along with that Non-experts should not comment on the patient's tests and debate this issue in the medical commission. The final result is that: (clinical + paraclinic + history taking from the patient or people around) are all together for diagnosis and treatment. one of them alone especially toxicology urine test because of false positive and false negative is not of much use in treating patient. Keywords: false positive, amphetamine, urine tox screen

Investigating the effects of ellagic acid on thioacetamide-induced acute liver damage and subsequent encephalopathy in rats

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G-67294 نوع پذیرش: پوستر | کد مقاله:

Abstract: Background: Liver damage caused by foreign substances and drugs is one of the main causes of liver failure, which can eventually cause disruption in the vital functions of other organs and lead to death if not properly treated. In this study, the effects of ellagic acid administration in the liver damage model caused by thioacetamide in rats were investigated. Materials and Methods: In this experimental study, 60 Wistar rats with a weight of about 200-250 grams were randomly used in 6 groups for in vivo investigation. All laboratory protocols were carried out based on the standard principles of animal welfare ethics. Liver damage and induction of oxidative stress were caused by administration of 100 mg/kg thioacetamide for 3 consecutive days. Different doses of ellagic acid (10, 25, and 50 mg/kg) were administered to the sick mice daily by injection in three experimental groups (n = 10). At the end of the intervention period, the liver damage caused by thioacetamide was investigated by examining serum biochemical factors (ALT, AST, LDH and Bilirubin). In addition, the amount of reactive oxygen species, glutathione, ammonium ion, antioxidant capacity, lipid peroxidation and histopathological changes in liver tissue were evaluated. One-way analysis of variance and Tukey's post hoc test were used for statistical analysis. Results: Thioacetamide caused liver damage in mice, which showed itself as a significant increase in liver damage biomarkers such as ALT, AST and LDH (P0.05). The amount of ammonium ion in the plasma, as a key effective factor in hepatic encephalopathy, was greatly increased in animals receiving thioacetamide (P0.05). On the other hand, significant amounts of lipid peroxidation and reduction in liver glutathione reserves were observed in the group that received only thioacetamide (P0.05). Liver histopathological changes including portal tract inflammation, necrosis, ballooning degeneration and changes in fat also confirmed the aforementioned criteria of liver damage. Administration of ellagic acid in different doses significantly reduced liver damage and plasma ammonium concentration (P0.05). Keywords: liver damage, plasma ammonium, liver failure, ellagic acid, liver protection

The significance of thymoquinone administration on liver toxicity of diazinon and cholinesterase activity; a recommendation for prophylaxis among individuals at risk

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G-65742 نوع پذیرش: پوستر | کد مقاله:

Abstract: Background: Diazinon (DZN), a widely used chemical herbicide for controlling agricultural pests, is an important organophosphorus pesticide and an environmental pollutant which induces toxic effects on living organisms during long-term exposure. Thymoquinone (TQ) is a phytochemical bioactive compound with antioxidant and anti-inflammatory properties. We aimed to evaluate the protective effects of TQ against DZN-induced hepatotoxicity through alleviating oxidative stress and enhancing cholinesterase (ChE) enzyme activity. Materials and Methods: Rats were randomly divided into six groups (n=8); a negative control group receiving corn oil; a group only receiving DZN (20 mg/kg/day); a group treated with TQ (10 mg/kg/day), and three treatment groups as TQ + DZN, receiving different doses of TQ (2.5, 5, and 10 mg/kg/day). All experimental animals were orally treated for 28 consecutive days. The levels of superoxide dismutase (SOD), glutathione (GSH), malondialdehyde (MDA), alanine transaminase (ALT), aspartate aminotransferase (AST), alkaline phosphatase (ALP), and lactic acid dehydrogenase (LDH) were determined. In addition, ChE activity and histopathological changes were evaluated. Results: The results showed that DZN decreased GSH level (p0.01) and SOD activity (p0.01) in parallel to an increase in MDA level (p0.01) and increased the activity of AST, ALT, ALP, and LDH (p0.01) in comparison to the negative control group. Our findings demonstrated that TQ administration could diminish hepatotoxicity and reduce oxidative damage in DZN-treated rats, which could be linked to its antioxidant and free radical scavenging properties. It was also observed that TQ 10 mg/kg remarkably increased the activity of acetylcholinesterase, butyrylcholinesterase, and SOD enzymes, elevated GSH, decreased MDA, and reduced pathological alternations of the liver induced by DZN. Conclusion: Thymoquinone 10 mg/kg increased the activity of plasma and blood cholinesterases and reduced DZN-induced alternations of the liver. Improvement of butyryl- and acetylcholinesterase activity suggests that maybe TQ supplement could be beneficial as pre-exposure prophylaxis among farm workers spraying pesticides. Keywords: Thymoquinone, Diazinon, Supplement therapy, Antioxidant, Hepatotoxicity, Cholinesterase

Modulatory effect of opioid administration on the activity of cholinesterase enzyme: A systematic review of mice/rat models

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G-54073 نوع پذیرش: پوستر | کد مقاله:

Abstract: Objective: We aimed to review the literature to find the specific effect of opioids on the activity of cholinesterase (ChE) enzyme which plays a substantial role in the functioning of cholinergic system. Method: Literature search was performed by two independent reviewers in order to find relevant articles about the changes in the activity of ChE in mice or rat following opioid administration. Results: Based on findings from literature review, opioid administration is able to induce cholinergic modulation via decreasing or increasing the activity of ChE enzyme. However, the degree of variation of ChE in various brain regions is different. No gender differences was reported in the effect of opioids on ChE activity. Although chronic opioid administration may decrease enzyme function, ChE activity might be unchanged following opioid withdrawal using naloxone or the development of tolerance. Opioid type affect whether or not naloxone can reverse the changes of ChE. Direct inhibitory action of morphine and the other opioid ligands believed responsible for the decrease in the ChE activity. Moreover, the potency of codeine to induce allosteric enhancement of acetylcholine receptor signaling might be involved in the cholinergic modulation of codeine and other opioids. Conclusion: Animal studies on rat and mice showed that opioids may change the activity of ChE. These changes can pertain an increase or decrease in enzyme activity; as there might be no change. The type of opioid used may have an effect on the cholinergic modulation. It is beneficial to conduct cross-sectional and cohort studies on addicted individuals, especially opium abusers, to find the precise association of opioids with alterations in human acetyl cholinesterase or butyrylcholinesterase. Simulation studies can also examine the structure-function relationships and provide important details to better understand the mechanism of action of opioid compounds on ChE activity. In addition, understanding how opioids impact ChE activity may help perform proper interventions for drug abstinence. Keywords: Opioids, cholinesterase, modulation, enzyme activity, acetyl cholinesterase

Inhaled simvastatin-loaded PLGA nanoparticles is a new hope in the treatment of paraquat poisoning.

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G-52934 نوع پذیرش: پوستر | کد مقاله:

Abstract: Objective: Pulmonary fibrosis is an important complication of subacute paraquat (PQ) poisoning. Here, we reported a novel nanotherapeutic platform for PQ-induced pulmonary fibrosis in animal inhalation models using simvastatin (SV)-loaded into poly(lactic-co-glycolic acid) (PLGA) nanoparticles (NPs). Methods and Materials: Eight inhalations of normal saline, PQ (24 mg/kg), PQ plus SV (20 mg/kg), PQ plus SV-loaded PLGA NPs at doses of 5, 10, or 20 mg/kg or PQ plus PLGA NPs were given to rats. After the end of the treatment period, inflammatory factors and creatine phosphokinase as well as lung pathological changes and tracheal responsiveness were evaluated. Results: Inhalation of SV-loaded PLGA NPs could significantly prevent the progression of PQ-induced pulmonary fibrosis, especially at a dose of 10 mg through decreasing the serum level of inflammatory factors as well as contractile responses ($p < 0.001$) compared to PQ group. Pathological findings also confirmed the results. However, inhalation of non-formulated SV could not prevent tissue damage and fibrosis in comparison with SV-loaded PLGA NPs. Conclusion: Taken together, the present work provides us with an idea about the pulmonary delivery of PLGA-SV NPs using nebulizer for the treatment of PQ poisoning. However, the efficacy of this formulation in human beings and clinical use needs to be more investigated. Keywords:

Doxorubicin and nanoliposome doxorubicin induce liver cells senescence by enhancing genotoxicity and the accumulation of inflammatory factors and activation of P53 in male Wistar rats

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G-57306 نوع پذیرش: پوستر | کد مقاله:

Abstract: Background: The cellular senescence phenomenon is considered as a tumor-suppressing mechanism that can arrest the proliferation of cancer cells, and prevent abnormal proliferation by activating cell cycle regulatory pathways. Doxorubicin as an anti-neoplastic drug has been used for the treatment of malignancies for a long time, but its clinical utility is limited due to irreversible effects in off-target cells/tissues. Thereby, the encapsulation of plain drugs in a vehicle may decrease the systemic side effects while increasing their permeability and availability in target cells. Here, we aimed to assess and compare the effects of doxorubicin and nanoliposome doxorubicin on the induction of cellular senescence via assessment of genomic damage, the function of P53 as well as senescence-associated inflammatory markers and liver pathologies in the liver tissue. Materials and Methods: The study groups included doxorubicin (0.75, 0.5, 0.1 mg/kg/BW), nanoliposome doxorubicin groups (0.1, 0.05, 0.025 mg/kg/BW), and an untreated control group. Real-Time PCR was used for P53 expression. Results: Data revealed that the highest dose of nanoliposome doxorubicin (0.1 mg/kg/BW) can significantly induce senescence throughout the increasing the level of genotoxic damage and P53 expression pattern and regulation of senescence-associated the inflammatory markers tumor necrosis factor- α (TNF- α), NF- κ B compared with a similar dose of doxorubicin, in which the obtained results were further confirmed by histopathological assessments of the liver. Conclusion: In conclusion, this study provides adequate evidence about the improved therapeutic efficacy of nanoliposome doxorubicin compared with doxorubicin via induction of senescence by enhancing in vivo genotoxicity, P53 expression, inflammatory markers, and hepatotoxicity in male Wistar rats. Keywords: Senescence, Doxorubicin, Nanoliposome, genotoxicity, hepatotoxicity

Occult Hepatitis B Infection among Hemodialysis patient in Tabriz.

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نوع پذیرش: پوستر | کد مقاله: G-61279

Abstract: Background: Hepatitis B is a viral infection that attacks the liver and can cause both acute and chronic disease. Occult Hepatitis B Infection refers to the presence of HBV DNA, at low levels of serum in individuals who were reported negative for hepatitis B surface antigen (HBsAg). The objective of this study is to determine the prevalence of OBI in HD patients in Tabriz Province, northwest of Iran, Materials and Methods: blood samples were drawn from 118 HBsAg-negative patients undergoing HD treatment. Serum was assessed for HBV serological markers (HBsAg and Anti-HBc) by the ELISA method. The specific primers by nested polymerase chain reaction have been utilized to examine HBV DNA plus direct sequencing of surface genes to characterize the viral genotype and S gene mutations. Finally followed by Real-time PCR, the quantity of viral load in OBI-positive patients was determined. Results: A total of 118 HD patients were included (63.6% were male and 36.4% female), with an overall mean age of 60.8 ± 12.8 years old. Prevalence of Anti-HBc in the study population was 26.3% (31/118). Five patients (4.2%) were positive for HBV DNA and labeled OBI-positive; their plasma HBV-DNA load was less than 100 IU/ml. Following the phylogenetic analysis, the samples with OBI roughly belonged to genotype D, subtype ayw2 and only two had mutations within the S 'gene's major hydrophilic region (MHR), this study reports the prevalence of OBI in the HBsAg-negative HD patients being at a rate of 4.2%. Conclusion: Based on our findings and prior research, OBI should be considered a potential cause of HBV infection in HD patients. It is suggested HBV serologic screening approaches need to be renewed to cover nucleic acid testing for hemodialysis and even all high-risk groups by and far associated with it (i.e. blood and organ donors). Keywords: Hepatitis

Severity and prevalence of COVID-19 infection among patients with respiratory symptoms and history of four doses of vaccination

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G-50864 نوع پذیرش: پوستر | کد مقاله:

Abstract: Acute respiratory infection (ARI) is a severe infection that affects a person's respiratory system and causes breathing problems. Coronaviridae is one of the viral families that cause respiratory infections in birds and mammals. The efficiency of vaccination against COVID-19 infection is undeniable so this study aimed to evaluate the symptoms of SARS-CoV-2 in people who received four doses of the Sinopharm vaccine. This study evaluated the prevalence and severity of COVID-19 infection in vaccinated people with four doses of sinopharm vaccine. All samples were collected from patients with respiratory symptoms who were referred to Besat hospital, Tehran, Iran. From 290 patients with respiratory symptoms, 109 patients were positive for COVID-19 infection with a history of four doses of Sinopharm vaccine and the most common clinical symptom of infection were cough, runny nose, and fever but the hospitalization rate was very low. Although vaccination can't prevent infection with SARS-CoV-2, but against COVID-19 infection seems to be beneficial in reducing symptoms and hospitalization rate, especially if they have received a forth booster dose. Keywords:

Neutropenia in patients following COVID-19 infection

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G-67892 نوع پذیرش: پوستر | کد مقاله:

Abstract: Background: Coronavirus disease 2019 (COVID-19) has become a worldwide concern after its global proliferation in 2019, and it has received all medical attention due to its fundamental impacts on the body. As a result, hematologic dysfunction with alterations in hematological parameters is likely. This research aimed to look at the neutrophil and lymphocyte absolute counts and observe their changes in people exposed to the severe acute respiratory syndrome coronavirus (SARS-CoV-2). Materials and methods: the investigation was designed as a cross-sectional study using a Real-time PCR in Tehran, Iran. Children and adults of all genders were included. Hematologic parameters and laboratory data were examined to compare with normal people. Results: Only 10 of the 149 confirmed cases were symptomatic with fever and cough as the most prevalent symptoms. There was statistically significant neutropenia and lymphocytosis in the patients' hematological parameters following SARS-CoV-2 infection. Conclusion: Neutropenia and lymphocytosis may be linked to SARS-CoV-2 infection and serve as a possible diagnostic sign. Keywords:



چهاردهمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



High rate of myalgia and diarrhea in elderly following COVID-19 infection

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G-09148 نوع پذیرش: پوستر | کد مقاله:

Abstract: Background: In humans, viruses cause respiratory infections that are usually mild, including the common cold, or sometimes it can be fatal. The outbreak of coronavirus disease 2019 (COVID-19) occurred in Wuhan, China was more expansive than initially estimated, with cases now confirmed in several countries. Therefore, it is crucial to determine the clinical symptoms of COVID-19 in different age groups. Methods: This study evaluated the presence of SARS-CoV-2 infection in 219 throat and nasal swab samples using Real-time PCR. All samples were collected from people with respiratory symptoms who went to the grand bazaar. Results: Of 219 patients examined, 19 (8.6%) positive cases out of 219 for SARS-CoV-2 were found by using Real-time PCR. Among these 19 positive cases of SARS-CoV-2, 6 (2.7%) were under 5, 3 (1.3%) were between 5-18, 4 (1.8%) were between 18-50 and 6 (2.7%) were over 50 years old respectively. Most common symptoms in positive group was cough and despite other age groups, in patients over 50 years old, myalgia and diarrhea was common. Conclusion: It seems that SARS-CoV-2 symptoms can vary in different age groups but unlike other age groups, in elderly, uncommon symptoms like myalgia and diarrhea seems is seen following COVID-19 infection.

Parents anxiety, stress and depression during the outbreak of COVID-19 and their relation with parents view about their children health-related quality of life

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G-05946 نوع پذیرش: پوستر | کد مقاله:

Abstract: Introduction The disease of COVID-19 can affect the mental health of parents and their children. Children are one of the most vulnerable people in the society who should be taken care of during crises like the COVID-19 epidemic. The aim of this study was to determine the parents anxiety, stress and depression and their relation with parents view about their children health-related quality of life during the outbreak of COVID-19. Methods: This cross-sectional study included 396 parents having children aged 6-18 years old in Rafsanjan, Iran. We used online questionnaire includ demographic information questionnaire, Depression, Anxiety, Stress Scale (DASS-21), questions related to the coronavirus disease and Children Health-Related Quality of Life (CHQoL) to collect data, as well as SPSS25 and descriptive and inferential statistics to analyze data. Results: The present study showed that 28.3% participants had intense/very intense anxiety, 18.4% had intense/very intense stress and 17.1% had intense/very intense depression. A negative significant correlation was found between anxiety ($r = 0.395$), stress ($r = 0.421$), depression ($r = 0.465$) parents with CHQoL ($p 0.001$). Multiple regression models shown, depression and anxiety parents predict 22% of the variance of CHQoL, with depression being the best predictor ($p 0.001$). Conclusion The present study showed that parents have high levels of anxiety, stress and depression due to COVID-19 disease. Paying attention to factors affecting parents' anxiety, stress and depression can play an important role in promoting children's health and preventing the aggravation of psychological problems caused by the COVID-19, so it is suggested that health managers take effective additional measures to reduce parents' anxiety. Key words Anxiety, Stress, Depression, Covid-19, Children, Health, Quality of Life

Diagnostic accuracy of CRISPR in COVID-19 Diagnosis: a meta-analysis

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G-02968 نوع پذیرش: پوستر | کد مقاله:

Abstract: Background: To assess CRISPR-Cas technology's diagnostic precision in COVID-19 patients. Materials and Methods: The Quality Assessment of Diagnostic Accuracy Studies (QUADAS)-2 tool was used to gather and analyze data. A bivariate model was utilized for pooling, and subgroup analysis was done to investigate heterogeneity. The reference standard is specified as RT-qPCR. Results: For assessment of CRISPR technology's precision in diagnosing SARS-CoV-2, 2590 samples from 30 papers were taken. CRISPR technology's combined sensitivity and specificity were 0.98 (95% confidence interval: 0.95-0.99) and 1.0 (95% confidence interval: 0.98-1.00), respectively. Accuracy may be impacted by high risks of patient selection bias and uncertain hazards of index test bias. Due to its active editing properties, subgroup analysis demonstrated that CRISPR-Cas12 is appropriate for molecular diagnostics. For pre-amplification and fluorescence detection, RT-LAMP and RT-RPA are often employed to output findings quantitatively. In our study, nasopharyngeal swabs and dual genes function exceptionally well. Conclusion: The findings of all investigations indicated that CRISPR technology is an effective molecular technique for identifying SARS-CoV-2. It is important to develop standardized procedures considering comparable sample material, patient selection, operational procedures, and operators. Keywords:



چهاردهمین گنگره بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Interactions between SARS coronavirus 2 papain-like protease and immune system: A potential drug target for the treatment of COVID-19

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نوع پذیرش: پوستر | کد مقاله: G-42137

Abstract: Background: Coronaviruses (CoVs) are a large family of respiratory viruses which can cause mild to moderate upper respiratory tract infections. Recently, new coronavirus named as Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) has been identified which is a major threat to public health. Innate immune responses play a vital role in a host's defence against viruses. Interestingly, CoVs have evolved elaborate strategies to evade the complex system of sensors and signalling molecules to suppress host immunity. SARS-CoV-2 papain-like protease (PLpro), as an important coronavirus enzyme, regulates viral spread and innate immune responses. Materials and Methods: In this review, the aim was to survey of the interactions between PLpro of SCoV-2 and IFN response. For these purposes, keywords were searched in popular databases including PubMed, Google Scholar, Science Direct and Scopus. Results: CoV-2 PLpro is multifunctional enzyme with deubiquitinating (DUB) and deISGylating activity. The PLpro can interact with key regulators in signalling pathways such as STING, NF- κ B, cytokine production, MAPK and TGF- β and hijack those to block the immune responses. Conclusion: A majority of the newly reported studies showed that PLpro, which controls replication of the SCoV-2, has been identified as a potential drug target for the treatment. Keywords: Severe acute respiratory syndrome coronavirus 2, papain-like protease, immune system

Prevalence of human herpesvirus 8 infection in patients undergoing hemodialysis using nested-PCR Human herpesvirus 8 Hemodialysis patients Nested-PCR

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G-94056 نوع پذیرش: پوستر | کد مقاله:

Abstract: Background: Human herpesvirus 8 (HHV-8), also known as Kaposi's sarcoma-associated herpesvirus, is one of the oncogenic viruses. In recent years, HHV-8 has attracted more attention because it is linked to the development of several lymphoproliferative disorders including Kaposi's sarcoma (KS), multicentric Castleman's disease, plasmablastic lymphoma and primary effusion lymphoma. During latent infection, some viral genes are expressed which helps the virus escape from the host's immune system resulting in persistent viral infection. Since immunosuppression is considered to be a predisposing factor for KS development, HHV-8 has remarkable clinical significance for immunosuppressive subjects. Transmission by blood transfusion is a risk factor for HHV-8 infection. Since hemodialysis (HD) patients require frequent blood transfusions, they are prone to HHV-8 acquisition. Materials and Methods: In this study, blood samples of 89 patients undergoing hemodialysis were collected. DNA was extracted from peripheral blood mononuclear cells and HHV-8 DNA was evaluated by nested-PCR. Results: Of total 89 patients, 51 (57.3%) were males and 38 (42.7%) were females. The patients' age ranged from 24 to 90 years and the mean age was (57.5±1.4) years. HHV-8 DNA was found in 9 of 89 (10.1%) peripheral blood mononuclear cell samples, 8/51 (15.7%) in males and 1/38 (2.6%) in females (P=0.07). All patients who were positive for HHV8-DNA were more than 50 years old. Conclusion: This study shows high prevalence of HHV-8. Since hemodialysis patients are candidates for kidney transplantation and due to the possibility of HHV8-reactivation and its serious complications in immunocompromised patients, routine screening for detection of the virus should be implemented for all hemodialysis patients. Keywords: Human herpesvirus 8, Hemodialysis patients, Nested-PCR



چهاردهمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Study on the Prevalence of Occult Hepatitis B Virus Infection in Patients Undergoing Hemodialysis

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نوع پذیرش: پوستر | کد مقاله: G-08654

Abstract: Background: occult hepatitis B (OBI) is a major challenging clinical entity characterized by the absence of hepatitis B surface antigen (HBsAg). The persistence of OBI may progress to fibrosis, cirrhosis, and hepatocellular carcinoma. This study was aimed to investigate the prevalence of OBI among HD patients. Materials and Methods: In the present cross-sectional study, 89 sera samples of hemodialysis individuals were tested for HBsAg and HBe-IgG by Enzyme-linked Immunosorbent Assay (ELISA). In addition, the HBV DNA was tested in sera and peripheral blood mononuclear cell (PBMC) samples by nested-PCR. Results: Out of 89 patients, 51 (57.3%) were males, and 38 (42.7%) females. The ages ranged from 24 to 90 years (with a mean of 57.5 ± 1.37 years). All the sera samples had normal levels of Aspartate Aminotransferase (AST) and Alanine Transaminase (ALT) but had high levels of Creatinine (Cr) (6.9 ± 2.17) and Blood Urea Nitrogen (BUN) (61.83 ± 2.03). 2/89 (2.2%) sera samples were positive for both HBsAg and HBe-IgG test; in addition, HBV DNA was detected in both sera and their PBMC samples. The sera of 15/89 (16.85%) were only positive for the HBe-IgG test, including 10/51 (19.6%) males and 5/38 (13.2%) females ($P=0.5$). The high 16.85% prevalence OBI has been found among HD patients. Conclusion: To manage OBI infection, screening of HBV DNA should be implemented for HD patients by sensitive molecular means such as nested-PCR and real-time PCR. Keywords: Occult hepatitis B, Hemodialysis, Enzyme-linked immunosorbent assay (ELISA), Nested polymerase chain reaction (Nested-PCR)



چهاردهمین کنفرانس بین المللی آزمایشگاه و باالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Syncytia formation in the pathogenesis of SARS-CoV-2 infection: Lessons from viral infections

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Abstract: It is well known that a wide variety of enveloped viruses cause It is well known that a wide variety of enveloped viruses induce multinucleated cells (syncytia) formation by membrane fusion events underlying viral entry. Theoretically, these syncytia support the replication of the virus and evade the host's immune system. Syncytia are formed when cells fuse. The syncytia reaction is induced by the interaction of a viral spike protein (S) on the surface of an infected cell, with its receptors on neighboring cells. There are some Interferon-Stimulated Genes (ISGs) that modify the membrane so that it will be unfavorable for fusion. Several viral families are capable of forming syncytia in infected cells and neighboring uninfected cells. Up to now, naturally occurring fusogenic viruses such as Newcastle Disease Virus (NDV), Sendai Virus (SV), Respiratory Syncytial Virus (RSV), and Measles have been studied. In addition to these viruses, some other viral families like retroviruses can induce membrane fusion between viral particles and cellular membranes without causing syncytia formation. The SARS-CoV-2 virus is rapidly evolving, and its S protein has undergone many mutations that have significant effects on S function and syncytia formation. The fusion process is facilitated by a class of specialized proteins known as fusogenic, which helps overcome natural repulsive forces and energetic barriers that act to keep cellular plasma membranes apart. In addition, the membrane of enveloped viruses must fuse with cellular membranes to deliver vital contents into the cytoplasm, beginning the viral replication cycle. In conclusion syncytia may contribute to pathology by promoting viral dissemination, cytopathic, immune evasion, and inflammatory responses. In comparison with other causes of acute respiratory syndrome, Coronavirus Disease 2019 (COVID-19) is particularly severe for lung thrombosis and the virus causes an increase in syncytia formation. Keywords:

The detection of common cold viral agent genomes in SARS-CoV-2 infected individuals

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نوع پذیرش: پوستر | کد مقاله: G-60187

Abstract: Background: In this study, we collected swab samples from Iranian patients who had contracted the coronavirus disease 2019 (COVID-19) pandemic-related severe acute respiratory syndrome 2 (SARS-CoV-2) and then evaluated them for the presence of common cold viral agents like non-SARS-CoVs (HCoV-OC43 and HCoV-229E), rhinoviruses, and adenoviruses. The COVID-19 pandemic, driven by SARS-CoV-2, is a significant concern for worldwide population health. We still have a limited understanding of the co-circulation of occasionally targeted respiratory viruses and their impact on illnesses during the COVID-19 pandemic. A good understanding of coinfections and how they impact their hosts may assist in more efficiently and precisely detecting viral infections, which might improve clinical outcomes and reduce the need for antibiotics and treatment sessions. Methods: From March 21, 2021, to April 18, 2022, a total of 209 Iranian patients were examined using the Multiplex PCR and Conventional PCR procedures, including 95 (45%) SARS-CoV-2 positive and 115 (55%) negative samples (either symptomatic or asymptomatic). Results: Rhinovirus RNA presence was confirmed in Six Covid-19-infected research participants (2.87%) and 12 (5.74%) SARS-CoV-2-negative samples. HCoV-OC43 and adenoviruses were found in two (0.95%) and one (0.47%) sample, respectively. In neither positive nor negative test subjects, HCoV-229E has been detected in any sample. Conclusion: We conducted these experiments to characterize the coinfection rate in SARS-CoV-2 patients as well as the frequency of viral respiratory cold agents in the pandemic era. In the current study, we evaluated the presence of common cold viral agent genomes such as non-SARS-CoVs (HCoV-OC43 and HCoV-229E), rhinoviruses, and adenoviruses in COVID-19 patients over a year. Although these viruses are known to give people cold symptoms, detecting them along with other respiratory viruses, even in a small proportion, should be taken into consideration, especially in SARS-CoV-2 infected patients, as it may cause worsening symptoms and put the patient in a life-threatening situation. Based on the articles' findings, it is advised that COVID-19 patients should be screened and monitored for coinfection, especially if they were diagnosed during the pandemic, to improve treatment plans and outcomes. Keywords: COVID-19, SARS-CoV-2, Co-infection, Rhinovirus, non-SARS-CoV-2 coronaviruses

Assessment of CH50 and C4 complement protein changes in COVID-19 patients

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G-43250 نوع پذیرش: پوستر | کد مقاله:

Abstract: Background: The new corona virus (SARS-Covid 2), which is known as the Covid-19 disease, originated in China at the end of 2019 and has spread from there to all continents of the world. It is accompanied by symptoms such as cough, fever, headache and muscle pains and rarely digestive disorders, but on the other hand, the new corona virus sometimes causes serious lung damage and death. The pathogenesis of SARS-CoV-2 infection can be better understood if the details of complement activation in COVID-19 infection and different severities of infection are clarified. As a result, this study was conducted with the aim of investigating the changes of CH50 and complement C4 protein in patients with COVID-19. Materials and Methods: From April to June 1401, a total of 100 serum samples from Covid-positive people were prepared in Imam Khomeini Hospital. The ELISA test was performed in terms of examining the level of changes in CH50 and complement C4 protein in patients with COVID-19. The data was statistically analyzed by SpSS software. Results: The average age of patients is in the age range of 17 to 79 years. In Covid-positive people, in terms of symptoms, patients had more fever, diarrhea and muscle pain. In the comparison of the relationship between the disease symptoms and the reported rate of C4 and CH50 increase in cough and rhinitis, a significant difference was reported ($p < 0.001$). The average level of C4 and CH50 in covid positive patients was 92.4%. Based on the t-test, a significant difference was reported between the serum levels of C4 and CH50 and Covid-19 ($p < 0.001$). Conclusion: The results showed that CH50 and complement C4 protein were increased in patients with COVID-19 and complement activation is associated with disease severity. Evaluation of markers of complement activation may have prognostic value as a tool to monitor disease severity. In addition, inhibition of C4 activation could serve as a therapeutic strategy for COVID-19. Keywords:



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Investigating the diagnostic value of CRP and ESR in the diagnosis of corona disease compared to the Real Time PCR method

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Abstract: Background: SARS-Cov2 infection is one of the most important emerging diseases in the current century, which has caused the biggest pandemic in the world. Various methods have been used to diagnose the disease, including clinical diagnosis based on symptoms and serological and molecular methods to diagnose this disease. In addition to these methods, non-specific methods such as CRP and ESR have also been used in diagnosis, but the sensitivity and specificity of these methods have not yet been determined. The purpose of this study is to investigate the diagnostic value of CRP and ESR in the diagnosis of SARS-Cov2 infection compared to the Real Time PCR method. Materials and methods: In this research study comparing the methods, the files of 527 patients with SARS-Cov2 infection who referred to medical centers in Mazandaran province during the years of the corona pandemic and were examined using CRP, PCR and Real Time PCR diagnostic tests were examined. Also, 500 patients with corona, in whom the Real Time PCR test was negative, were used as a control group. The results of the tests have been evaluated using the Kappa test. Results: In this study, among the 527 examined patients who were reported positive using Real Time PCR method, 328 (72.48%) and 289 (54.83%) were reported positive using CRP and ESR diagnostic tests, respectively. Also, in patients who were negative in terms of Real Time PCR test, 274 (51.99%) and 257 (48.76%) were reported positive using CRP and ESR diagnostic tests, respectively. The results of the Kappa test showed that the agreement coefficient of CRP and ESR diagnostic tests was reported as 0.72 and 0.69, respectively. Conclusion: The results of this study showed that CRP and ESR diagnostic tests are confirmatory and non-specific tests for the diagnosis of SARS-Cov2 infection, which can be used as alternative tests in emergency situations. Keywords: SARS-Cov2 infection, PCR, ESR, CRP, Real Time PCR



Detection of crAssphage in surface water samples of Mazandaran province, Iran

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نوع پذیرش: پوستر | کد مقاله: G-63915

Abstract: Background: Humans may contract numerous diseases as a result of water contamination, which also threatens the environment. According to recent research, bacteriophages that can infect enteric bacteria make a promising candidate for use as fecal indicators since they highly correlate with human viruses in aquatic habitats that are seen in nature. Tracking of a contamination source can be successfully performed utilizing crAssphage, as an appropriate marker of fecal pollution in environmental investigations. In this study, we checked whether crAssphage was present in the water of three significant rivers in Mazandaran, Iran. Materials and Methods: 15 samples from 3 Rivers in the province of Mazandaran were gathered for a four-month period (from July to October 2022). Four-liter sterilized plastic carboys were used to collect samples, which were then delivered to the lab at 4°C. The polyethylene precipitation procedure was used to further concentrate the viruses after filtration and elution with NaOH. Viral DNA was extracted and real-time PCR was used to detect crAssphage in the river samples. Results: In total, the crAssphage genome was detected in 10 of the 15 samples, making up 66.6% of the river samples positive for this contamination marker. For positive samples, CT values ranging from 28.72 to 39.86 were observed. Conclusion: The health risk to those who use downstream water for irrigation or recreation is highlighted by the detection of crAssphage as a fecal indicator in urban rivers in Mazandaran, Iran. It is essential to take action to monitor the quality of the water since acute gastrointestinal diseases can have a significant negative public health and economic impact on society. The existence of this bacteriophage as an MST marker can also be employed as a surveillance tool for an early warning system that aids in managing enteric virus outbreaks. Keywords:

Human monkeypox disease from an epidemiologic to clinical point of view: A systematic review and meta-analysis

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Abstract: Introduction: Human monkeypox (HMPX) is a zoonotic infectious disease caused by the monkeypox virus, a member of the Poxviridae family. The HMPX became the most concerning Poxviridae genus after the eradication of smallpox in 1980, causing 300-500 million fatalities. Since then, most cases have been sporadic and diagnosed in African countries for many years. In early May 2022, an increasing number of monkeypox cases were reported in non-endemic regions of the world. This concurrent high incidence of HMPX cases in widely disparate geographical regions raised World Health Organization (WHO) concerns. Currently, the WHO emergency committee has called on scientists worldwide to collaborate on HMPX to better understand the disease and prevent further harm. Here, we provide a comprehensive systematic review and meta-analysis of HMPX-confirmed patients introduced in recent 10 years in peer-reviewed publications from demographic, epidemiologic, and clinical perspectives. Methods: A systematic search was performed for relevant studies published between 2012 to May 2022 using Pubmed/Medline, Embase, and Scopus. Articles containing the following keywords in titles or abstracts were selected for further screening: "Monkeypox" OR "Monkeypox virus". Results: Out of 1157 articles, 29 meet the inclusion criteria and 9 cross-sectional studies were included for meta-analysis. Overall, 61.64% were primary cases (animal-to-human transmission) and 38.35% were secondary cases (human-to-human transmission). The West African clade was the most common clade of the monkeypox virus and most of the cases were reported from Africa, especially Nigeria. The male gender was dominant (59.8%, CI 54.6-64.8, I2: 80.28%), and the mean age of confirmed cases was 23.03 years (5.77-38, SD: 9.42). The most frequent clinical manifestations of MPX were skin rash (98.8%, CI 94.3-99.8, I2: 68.80%) and fever (96.8%, CI 83.9-99.4, I2: 88.34%). The pooled frequency of lymphadenopathy was 76.2% (CI 60.1-87.2, I2: 97.81%). The most frequent rash locations were the head and neck (98.0%, CI 96.2-99.0, I2: 45.18%), trunk (95.4%, CI 80.9-99.0, I2: 95.54%), upper limb (95.0%, CI 81.2-98.8, I2: 95.27%), and lower limb (90.5%, CI 66.8-97.8, I2: 95.04%). The involvement of palms and/or soles was reported in 89.1% (CI 69.0-96.8, I2: 98.30%) and 78.6% (CI 60.7-89.8, I2: 98.04%) of the patients, respectively. Oropharyngeal (55.9%, CI 52.7-58.9, I2: 54.49%) and genital (40.0%, CI 27.0-54.6, I2: 92.92%) involvement were rather less common according to our meta-analysis. Conclusion: In the current outbreak, due to the sudden increase of patients, especially in non-endemic areas of the disease, there are speculations about the possibility of changes in the pathogenic characteristics of the virus. Therefore, our study could be a basis for current investigations to recognize and compare the different aspects of the previous MPX outbreaks with the ongoing ones. In the current global emergency, first-line medical practitioners, as well as public health policymakers, should be aware of the previously identified characteristics of the disease, especially clinical manifestations and epidemiological features to make appropriate decisions and measures for controlling the outbreak. Keywords: Monkeypox, outbreak, rash, lymphadenopathy, mortality



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The polymorphisms (rs11568821 and rs41386349) in Programmed Cell Death-1 (PD-1) gene is associated with Risk of HTLV-1 infection in northeast Iran

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G-61592 نوع پذیرش: پوستر | کد مقاله:

Abstract: Background: Human T lymphotropic virus type-1 (HTLV-1) infects approximately 5-10 million individuals and mainly infect CD4+ T cells. HTLV-1 associated with immunosuppression. During chronic infection, the expression of programmed cell death -1(PD-1) protein increases and causes exhausted phenotype in T cells. In this research, association between Intron 4 of the PD-1 gene polymorphisms, with susceptibility to HTLV-1 infection in Iran's population studied. Materials and Methods: The rs11568821 and rs41386349 polymorphisms of PD-1 gene were genotyped by Polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP) method in 81 asymptomatic carriers and 162 healthy controls. Results: It was found that mutant allele of rs41386349 and rs11568821 increases the risk of HTLV-1infection significantly ($p=0.000$ and $p=0.019$ respectively). Also the GA+AA of rs11568821 and CT+TT of rs41386349 polymorphism are significantly higher in asymptomatic carriers compared to the wild genotype ($p=0.024$ and $p=0.000$ respectively). Conclusion: Our results suggest that the rs11568821 and rs41386349 polymorphisms of PD-1 gene can play important role in HTLV-1 infection.



چهاردهمین کنفرانس بین المللی آزمایشگاه و بالین

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High prevalence of coronavirus NL63 in SARS-CoV-2 negative COVID-19 suspected patients

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نوع پذیرش: پوستر | کد مقاله: G-64357

Abstract: Background: From the beginning of the Covid-19 pandemic in the world, we had seven waves of the disease in Iran. Materials and Methods: In last months, along with the decrease in the number of positive cases of Covid-19 after third wave of the disease in North Khorasan, because of the patients' symptoms, we examined a panel of respiratory viruses in 10 Covid-19 suspected SARS-CoV-2 negative patients. The studied viruses were included influenza A virus, Coronaviridae (229E, HKU1, NL63, OC43), rhinoviruses, metapneumovirus, bocavirus, RSV, and parainfluenza virus. Results: Interestingly, 126 out of 600 samples were positive for the presence of coronavirus NL63. It should be noted that 28 samples were positive for influenza A virus. Totally 191 cases were positive for other respiratory viruses and 409 cases were negative. These negative samples may need to be evaluated for a wider range of viruses as well as respiratory bacteria. Conclusion: In some previous papers, researchers mentioned a similar mechanism of cell entrance for coronavirus NL63 and SARS-CoV. They found that both of these viruses using the ACE-2 receptor (3, 4). One of the reasons for the decline in Covid-19 positives in recent days may be the winning of coronavirus NL63 over SARS-CoV-2 in connection with the ACE-2 receptors. Of course, this is a primary hypothesis and needs to be thoroughly evaluated in various aspects. To prove the role of this virus, more samples should be evaluated, and also other intervention factors should be eliminated. Keywords: Coronavirus NL63, SARS-CoV-2, Influenza A virus, Co-infection.



چهاردهمین کنفرانس بین المللی آزمایشگاه و بالین

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The Re-emergence of Human Monkeypox and the Risk of its Re-epidemic

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G-12507 نوع پذیرش: پوستر | کد مقاله:

Abstract: Background: Monkeypox virus (also known as mpox) is a common disease between humans and animals and belongs to the poxviridae family and Orthopoxvirus genus. This genus of the virus is the genus of many other smallpox viruses such as vaccinia, cow pox and camel pox. The monkeypox virus emerged in 1958 in an Asian monkey at a polio vaccine research center in Copenhagen, Denmark. In 1960 and 1968, other cases of this virus were reported in the United States and the Netherlands, but there were no reports of human infection. Monkeypox virus in humans was reported in 1970 in the Democratic Republic of the Congo (former Zaire). The infected case was a 9-month-old boy; this baby contracted this virus in an area where smallpox had been eradicated before. In May 2022, new cases of human monkeypox virus infection were reported in the United Kingdom, Portugal and the Netherlands. Most of these infected cases were men who had sex with other men. This reappearance has caused concern and the possibility of a virus re-epidemic in the world after covid-19. Method: In this study, we have examined the reported cases of infection with this virus in the countries that have officially announced it and have described how this virus reappears and the risk of its spread again, in addition we have also offered ways to control and prevent this virus. Results: In the recent outbreak of human monkeypox in 2022, different clinical features emerged from previous cases; For example, the possibility of transmission of this virus through sexual contact was raised, although the proof of this claim requires more research on a higher statistical population. The reported cases of human infection with this virus in 2022 have increased much more compared to previous years. This virus is more common in young children and people with acquired immunodeficiency diseases such as AIDS, as well as men who have high-risk sex with other men. The re-emergence of this virus in 2022 should be considered so that another epidemic like Covid-19 does not occur again. Conclusion: It seems that the gradual decrease of immunity against the smallpox virus is one of the most important reasons for the increase of monkeypox in humans. The symptoms of this disease overlap with the symptoms of other diseases and all sufferers may not notice these symptoms, so people should increase their awareness of the symptoms and continue to take care of themselves to prevent or control this disease. It seems that this continuation of self-care and clinical follow-up of possible skin lesions that may appear anywhere on the body, as well as the completion of vaccination, can be effective in controlling and preventing the widespread spread of this disease. On the other hand, according to recent findings that confirm the possibility of transmission of this virus through sex, high-risk sex should also be avoided. Keywords:

Study the presence of the BK virus large T antigen gene in cancerous and non-cancerous prostate tissues

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G-13569 نوع پذیرش: پوستر | کد مقاله:

Abstract: Background: A double-stranded DNA virus called Human Polyomavirus BK (BKV), which is a member of the Polyomaviridae family, is most likely responsible for the development of prostate cancer (PCa). Early-life BK virus infection is common, and over 90% of people have serum antibodies to this virus. The carcinogenic features of the large T and small T antigens of this virus interfere with the control of the cell cycle. Given the evidence that is available and the virus's location in the urogenital tissue, it appears that this virus is a significant contributor to the establishment of prostate malignancy. As a result, we intend to find out how common this virus is in both malignant and benign prostate tissues in our study. Methods: 49 paraffin-embedded PCa specimens and 49 paraffin-embedded benign prostatic hyperplasia (BPH) specimens were selected as case subjects and control subjects, respectively. The Ministry of Health-approved DNA extraction kit was used, and Nested PCR was used to determine whether the virus's large T gene was present. Results: In our study, the median age of PCa patients was 73.49 years and that of BPH patients was 69.92 years. The BK virus large T antigen gene detected by nested PCR was identified in 53.1% (26/49) of PCa patients and 14.3% (7/49) of BPH patients respectively (P = 0.0001). Conclusion: The BK virus large T antigen gene in samples from PCa patients was significantly higher than in prostate tissue samples from BPH patients. Although these results demonstrate the presence of the virus in cancer specimens, they do not confirm or refute the role of BK virus infection as a cofactor in prostate cancer development. Further studies with serological and in vitro studies are proposed for future studies. Keywords: Human Polyomavirus BK, Prostate cancer, Benign prostatic hyperplasia, large T antigen



چهاردهمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Oncolytic viruses and pancreatic cancer

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G-09746 نوع پذیرش: پوسنتر | کد مقاله:

Abstract: Abstract Background Today, the pancreatic cancer prognosis is poor and genetic technology is developing to treat various types of cancers. Scientists are actively looking for a new technique to design a therapeutic strategy to treat pancreatic cancer. Several oncolytic viruses are known to be valuable tools for pancreatic cancer treatment. Recent Studies demonstrate their effectiveness and safety in various administration routes such as direct intratumoral, intracutaneous, intravascular, and other routes. Method In this study, all studies conducted in the past 20 years have been reviewed. Reputable scientific databases including Irandoc, Scopus, Google Scholar and PubMed, are searched for the keywords of Pancreatic cancer, oncolytic, viruses and treatment and the latest information about them is obtained. Results Engineering the oncolytic viruses' genome and insertion of intended transgenes including cytokines or shRNAs, has caused promising promotions in pancreatic cancer treatment. Some oncolytic viruses inhibit tumors directly and some through activation of immune responses. Conclusion This approach showed some signs of success in efficiency like immune system activation in the tumor environment, effective virus targeting in the tumor cells by systemic administration, and enhanced patient survival in comparison with the control group. But of course, until now, using these oncolytic viruses alone has not been effective in elimination of tumors.

NSP6 mutation in SARS-CoV-2 variants and potential effects on autophagy and pathogenesis

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G-65240 نوع پذیرش: پوستر | کد مقاله:

Abstract: Background: The recent 2019 viral pandemic that caused by Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) resulted in developing pneumonia and may progress to acute respiratory distress syndrome characterized by a rapid onset of widespread inflammation in the lungs and is associated with a significant mortality (1). By analyzing SARS-CoV-2 genome we figure out there are multiple proteins such as non-structure protein (NSPs) associated with viral replication and possibly pathogenicity (2). Particularly NSP6 that acts as a connector in viral replication can also effect Autophagy pathways. It seems to be autophagy activation in the process of early infection is related to severity of symptoms and its overexpression can result in cytokine activation (3). Understanding these mechanisms through viral variants can help us for pharmacological rectification of autophagy flux and therapeutic exploitation. In the current study we tried to highlight these differences in NSP6 sequence between variants by phylogenetic evaluation and epitope mapping. Materials and Methods: all sequences obtained from National Center for Biotechnology Information (NCBI) or global influenza surveillance responses system (GSAID) databases. The sequences translation, alignment, phylogenetic evaluation were performed in CLC Work bench. B cell epitopes evaluated by ABCpred while Value 0.5 is considered as threshold and 16 amino acids for length (4). The phylogenetic analysis performed by neighbor joining method and 1000 bootstrap. Results: the phylogenetic evaluation represents Alpha and Omicron variants in a different branch in compare with other variants or reference sequence. Furthermore, suggested B cell epitopes represents a completely different peptides due to mutations in Alpha and Omicron variants (Figure 1 and 2). Conclusion: NSP6 epitope mapping in SARS-CoV-2 is a useful tool to understanding the relationship between the mutation, autophagy activation and pathogenesis of virus so we can use it in future in vitro studies. The divergence between Alpha and Omicron variants in compare with other sequences in NSP6 could highlight the importance of autophagy in alteration of these variants in clinical or biological features of variants. Keywords: SARS-CoV-2, NSP6, SARS-CoV-2 variants, Epitope Mapping



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Innate immune sensors for detecting nucleic acids during infection

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G-49652 نوع پذیرش: پوسنتر | کد مقاله:

Abstract: Innate immune receptors detect nucleic acids, such as viruses, and initiate an immune response by secreting interferon (IFN) and regulating IFN-stimulated genes (ISG). In autoimmune conditions, expression of ISGs is upregulated, showing the activation of nucleic acid sensory pathways. However, the nucleus-localized innate sensors are recently found to detect pathogenic nucleic acids for initiating innate response, demonstrating a complicated crosstalk with cytoplasmic sensors and signaling molecules to form an elaborate tiered innate signaling network between nucleus and cytoplasm. To sustain immune homeostasis, these innate immune sensors develop different strategies for discriminating between self or non-self-nucleic acid. We reviewed all the sensors involved in the innate immune system in the present study. A better understanding of these sensors can lead to new treatments for infections, cancer, and autoimmune and inflammatory disorders. **Keywords:**



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Monkeypox virus diagnosis and laboratory testing

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Abstract: The multi-country outbreak of monkeypox virus (MPXV) infection, while the coronavirus disease 2019 pandemic is still an ongoing issue, has caused a new challenge. The re-emergence of MPXV and the rising incidence in non-endemic countries is turning into an upcoming threat to global health. Hence, rapid identification of the virus with appropriate methodology with the lowest false results plays a critical role in estimating the global extent of the crisis and providing preventive measures. This review summarised the main applicable strategies for primary detection and confirmation of MPXV and highlighted available data in biosafety, requirements, standard operating procedures, specimen collection, transportation and storage of clinical samples, and waste disposal of the viral agent. Also, various assays including molecular techniques, immunoassays, histopathological methods, electron microscopy, genomic sequencing, and cell culture have been illustrated. Moreover, we reflected on current knowledge of the advantages and disadvantages of each approach. Keywords:



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Epstein-Barr Virus EBNA-1 variants; A possible virological marker for Multiple sclerosis pathogenesis

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G-85690 نوع پذیرش: پوستر | کد مقاله:

Abstract: MS (Multiple sclerosis) is an autoimmune disease of the central nervous system believed to be initiated and mediated by autoreactive T cells. Two of the strongest implied associations include vitamin D deficiency and Epstein-Barr Virus (EBV), the most common cause of infectious mononucleosis (1). Antibodies to Epstein-Barr virus nuclear antigen 1 (EBNA1) are increased in MS patients, which suggests a differential immune response between MS patients and unaffected individuals. EBNA1 is expressed in all EBV-infected cells. Throughout the viral life cycle, it plays a central role in maintenance of the viral genome and transcription regulation and it been reported that The glycine-alanine rich (GAR) region is one of the keys to the autoimmune response from patients (2). understanding EBNA1 mutations and expression of different proteins can help us to determine the course of action and progression of this disease and it also can play a significant role in medical treatments and prevention. The EBNA-1 protein links the EBV genome to the cell mitotic chromosome and nuclear localization. There are limited studies for EBNA-1 variants in autoimmune diseases. The EBNA-1 demonstrates a range of variations in the evaluated clinical samples and could be divided into two major types, prototype (P) and variant (V) based on the amino acid number 487. Furthermore, these types can be divided into different variants. P types are including P-ala (for instance in B95 strain) and P-thr (e.g. Mutu) for P types and V types are including V-val (e.g. Akata), V-leu and V-pro as V types. These variants can alter the virus biology either. For instance, V-val variant in comparison with the other types represents more proliferation and cell survival. Conducted study by Varvatsi et al. represents that, some alleles in EBV genome in EBNA-1, EBNA-3 and LMP-1 seems to be associated to MS in compare with healthy controls (3). In addition, association between the EBNA-1 and HLA-DR15 (A major host factor for MS development) highlights the importance of EBNA-1 amino acid sequence in interaction with immune system and possibly induction of MS (4). Understanding the mechanism of any autoimmune disease is a complicated task to achieve and yet by knowing key factors or trigger factors can help us a lot so the mechanism of EBV infection and understanding its genome specially EBNA1 in MS. Keywords: Multiple sclerosis, Epstein-Barr Virus, EBNA1 mutation



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Assessment of Variations in RBD domain within spike protein of SARS-COV2 during different waves in South Khorasan, East of Iran

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نوع پذیرش: پوستر | کد مقاله: G-47186

Abstract: Background: Genomic analysis of SARS-COV2 have shown a lot of variation in all around the viral genome. So, according to lack of these data from Iran as well as the region of study we aimed to investigate the polymorphic variation of S gene in COVID-19 samples of South Khorasan province. Method: The sampling was performed from January 2021 to March 2022. Cases with confirmed positive PCR result were selected based on severity and symptoms; next, divided to mild, moderated and sever groups. Demographic, clinical and virological examinations data were recorded. Nasopharyngeal samples were given and RNA extracted and forwarded for synthesis of cDNA. Using an in-house PCR assay Partial amplification of S gene was performed for sequencing of RBD region. The sequenced were analyzed in the biological software including Bioedit, Mega7, CLC and online tools such as NCBI and Nextclade databanks. Statistical analysis was performed in the SPSS version 22. Result: In overall there were 272 RNA samples with a confirmed positive PCR test. The PCR product of 142 samples were sequenced to determine RBD region. Among which 71 samples (50%) were male, and the rest were female. The mean age of participants were 45.7 ± 20.9 years. Mutations were mostly accumulated in the RBD and especially RBM motif. The mean numbers of mutations per sample was 5.1 ± 3.4 . Result of analysis in nextclade showed that 39.9% samples are belonged to the clade Rec, and then followed by clades alpha, 20A, 19A and omicron. 19A was distributed in all times and months. Clades delta, 20A and Rec were significantly associated with the ICU admission and death rate. Viral load was significantly lower in death group rather than comparison group. The well-known D614G mutation is now completely established among the current circulating variants. Conclusion: The result of this study demonstrated a lot of mutations accumulated in the RBD region and RBM motif in the spike protein of SARS-COV2. So, these huge numbers of established variants require next studies for continuous sequencing and following of SARS-COV2 genome in specific S gene. Keywords: corona virus, COVID, COVID-19, spike, mutation, genotype, variant, clade, South Khorasan, Birjand

Overall status of env gene expression of human endogenous retroviruses K18 (HERV K18) and plausible association with vitamin D level in systemic lupus erythematosus and healthy controls

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نوع پذیرش: پوستر | کد مقاله: G-36145

Abstract: Background and Objective: Systemic lupus erythematosus (SLE) is a chronic inflammatory and autoimmune disease that is caused by dysfunction of B and T lymphocytes, macrophages, and dendritic cells that as a result, antibody production is disrupted. Different risk factors is thought to play an important role in disease pathogenesis including human endogenous retroviruses (HERVs) and vitamin D. As such, the present study aimed to evaluate the expression level of HERV-K18 envelope gene and its possible association with the plasma level of vitamin D in 20 SLE patients and 15 healthy controls. Method: Plasma and PBMCs were separated from fresh whole blood. To measure HERV K18 gene expression in PBMCs, real time pcr method were employed. Vitamin D levels were also measured in plasma by ELISA. Results: Among the SLE patients, one patient was male and the remaining were female, and in healthy controls, there were 4 males and 11 females. With regards to the expression level of HERV-K18 env gene in PBMC, no significant differences were observed between case and control groups. Although the plasma level of the inactive form of vitamin D was not statistically significant, the average plasma level of the inactive form of vitamin D was lower in healthy controls than in SLE patients. According to the age, the result of expression level of HERV-K18 env gene was shown that the highest level of gene expression was found in the lowest age group of SLE patients and age group of 31-35 of healthy controls. However, statistically no significant differences were observed. The plasma level of the inactive form of vitamin D in both groups indicated that the highest level of vitamin D was found in the lowest age group although the observed differences was not statistically significant. Conclusion: While a positive relationship was observed between the expression level of HERV-K18 env gene and the plasma level of vitamin D, it was not statistically significant in both groups. Key words: Systemic lupus erythematosus, Vitamin D, Human endogenous retrovirus envelope gene, HERV K18 env.



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Investigating the Real Time PCR method in the diagnosis of corona disease and its relationship with the severity of clinical symptoms

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G-83702 نوع پذیرش: پوستر | کد مقاله:

Abstract: Background: Corona virus (Coronaviruses) is one of the most important newly emerging respiratory diseases that cause disease by causing respiratory tract infection in birds and mammals. These viruses can cause some types of common cold to more severe diseases such as SARS, MERS and Covid-19. Various diagnostic methods have been used to diagnose this disease, and Real Time PCR method has been the most sensitive method to diagnose this disease. The purpose of this study is to investigate the prevalence of corona disease in patients referred to hospitals and private centers for the diagnosis of corona disease in Amol city of Mazandaran province. Materials and Methods: In this cross-sectional descriptive study, the files of 76,447 patients with suspected corona and symptoms including: fatigue, weakness, headache, fever, chills, and cough were examined in the laboratories of public and private corona disease diagnosis centers in Amol city during 2018 to 2019. The results were analyzed using T-test and ANOVA statistical test. Results: Out of 76,447 examined patients, 20,471 negative PCR tests were taken, of which 8,431 people had a positive PCR test. Also, in this study, out of 55976 rapid tests, 8797 tests were positive. Of course, all this information is only related to the outpatient department, and there was a direct relationship between the severity of disease symptoms and the result of molecular tests. Conclusion: The results of this study have shown that the city of Amol city has been one of the most dangerous areas for the corona disease, with a high number of positive cases reported. It is also known that molecular tests have high sensitivity for diagnosing corona disease. Keywords: Corona, acute respiratory disease, Real Time PCR, Rapid test

A descriptive cross-sectional study of the potential role of medicinal plants in the treatment of COVID-19

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G-90872 نوع پذیرش: پوستر | کد مقاله:

Abstract: Background: Coronavirus disease (COVID-19) is an infectious disease caused by the SARS-CoV-2 virus, which is the cause of death in thousands of people with the mild to moderate respiratory illness and recover without requiring special treatment. The aim of this study was to investigate the effect of the most common medicinal plants on the relief of general symptoms in patients with COVID-19 in northern Iran. Materials and Methods: In this descriptive study, a Google Form online questionnaire created by researcher were used to collect data. 123 patients were included in current study including 56.6% male and 43.4% female with positive Covid-19 test, respiratory symptoms, fever, and nausea. The data were analyzed using T-test and SPSS software. Results: There are 5 plants with antiviral effects on coronavirus, of which Thyme, Cinnamon, Ginger, Mint, and Marshmallow plant were the most effective in strengthening the immune system and reducing symptoms, with 83.1, 56.1, 49.3, 48.8, and 47.6%, respectively. 95.6% of patients reported no side effects and 4.4% reported some side effects. In 74.6% of cases, family members consumed medicinal plants. Above all, 22.1% of patients reported that the effectiveness of medicinal plants in treating corona and reducing the severity of the disease was very good, 39.8% good, 23% average, 8% poor, and 7.1% ineffective. Conclusion: The medicinal plants administered in this study significantly improved pulmonary symptoms and shortened the course of treatment of COVID -19 infection. Keywords:

High plasma level of angiotensin II, raise an alarm for COVID-19 patients with hypertension.

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نوع پذیرش: پوستر | کد مقاله: G-08431

Abstract: Background: As the crisis of the COVID-19 for the high-risk groups and considering the factors influencing deterioration, complications, and mortality, attentive to high-risk groups is particularly important. Including these groups are people with high blood pressure (HTN) and diabetes. So far, studies with different results have been reported on the relationship between angiotensin II (ANG II) levels and the severity of the Covid-19. This study aims to investigate the correlation between ANG II level and the disease severity and clinical Course in Covid-19 patients. Materials and Methods: A cross-sectional study was conducted on 50 COVID-19 patients (mean age 59.1 ± 20) admitted to Sinai Hospital in Hamedan. Blood samples were taken in two stages, measured plasma ANG II level using ELISA kit. Outcome of the patients was followed, and the data was collected in the questionnaire. Quantitative comparison was analyzed with paired t-test and qualitative comparison with chi-square test. The correlation of variables was checked with Pearson test. P0.05 was considered significant. Results: (44%) 22 patients had HTN, (16%) 8 patients had cardiovascular disease (CHD), (10%) 5 diabetic patients. 21 patients (42%) were female, and 29 patients (58%) were male. Their average age was 59.1 ± 20 . Regardless of the type of underlying disease, 82% of patients had an oxygen level below 90, of which 68% were intubated. The most intubation and low oxygen levels were in HTN and CHD patients, among which 2 deaths were observed. Primary and secondary investigation of ANG II level in COVID-19 patients showed that its level was significantly higher during the illness compared to the full recovery of the same patients and decreased during recovery. Conclusion: The ANG II level is related to the severity of the disease in the early stages of 2019-nCoV infection, therefore, possibly HTN or other diseases that affect the level of angiotensin2 in the blood can increase the severity of the disease. Increased ANG II levels in plasma of HTN patients, can be considered as an important biomarker to identify complications or prognosis of this disease. Future treatment options should focus on blocking the inflammatory properties of ANG II in COVID-19, especially people with HTN. Keywords: ACE2, Angiotensin II, COVID-19, Hypertension



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Human endogenous retrovirus interaction with multiple sclerosis disease progression

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G-23574 نوع پذیرش: پوستر | کد مقاله:

Abstract: Background: Multiple sclerosis (MS) is an inflammatory autoimmune disease of the central nervous system that interferes with the myelination process. Autoimmunity and disease progression may be triggered by complex interactions between various "environmental or infectious" factors. The link between viral infections, particularly human endogenous retrovirus (HERV), and MS is a potential cause that is not fully understood. This study aims to review the existing data on HERV infection and the progression of multiple sclerosis. Materials and Methods: For this study, the keywords "Multiple sclerosis", "Human endogenous retrovirus", and "central nervous system" in the databases PubMed, Google Scholar, Sid, and MagIran between 2016 and 2022 were searched and 14 articles chosen, studied, and analyzed. Results: Multiple sclerosis-associated retroviruses (MSRV) have been identified in the leptomeningeal cells of MS patients as a retrovirus-like element associated with reverse transcriptase (RT) activity. Even though there are mechanisms to suppress their expression, HERVs are expressed in the human CNS. HERV gene expression can be activated by environmental stimuli, including viral infections like influenza virus, Epstein-Barr virus, and herpes simplex virus type 1. Toll-like receptor 4 (TLR4) is activated at the brain's surface by the MSRV coat protein, specifically in oligodendroglial progenitor cells and macrophages, triggering immune cascades and ultimately leading to the downregulation of myelin protein expression. MS patients have inflammatory reactions in response to the HERV-K18 envelope gene (env), which acts as a superantigen. Conclusion: There is a significant expression of human endogenous retroviruses during the course of MS, indicating a link between HERV and MS and that this virus can play a role in the development of MS by causing inflammation. Therefore, strategies for reducing inflammatory processes in MS patients' demyelinated areas may be achieved through efforts to modulate the expression of human endogenous retroviruses. Keywords: Multiple Sclerosis, Human Endogenous Retrovirus, Central Nervous System



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A Multiple-Center, Retrospective Study of Characteristics and Outcomes of Hospitalized COVID-19 Patients with Cardiovascular Disease in North Iran

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G-16578 نوع پذیرش: پوستر | کد مقاله:

Abstract: BACKGROUND: In this retrospective study, we investigated the outcomes and demographic characteristics of COVID-19 patients with and without a history of CVD. MATERIALS and METHODS: This large retrospective, multicenter study was performed on inpatients with suspected COVID-19 pneumonia who were admitted across four hospitals in Babol, Northern Iran. Demographic data, clinical data, and cycle threshold value (Ct) results of Real Time PCR were obtained. Then, participants were divided into two groups: (1) cases with CVDs, (2) cases without CVDs. RESULTS: A total of 11097 suspected COVID-19 cases with a mean \pm SD age of 53 ± 25.3 (range: 0 to 99) years were involved in the present study. Out of whom 4599 (41.4%) had a positive RT-PCR result. Of those, 1558 (33.9%) had underlying CVD. Patients with CVD had significantly more comorbidities such as hypertension, kidney disease, and diabetes. Moreover, 187 (12%) and 281 (9.2%) of patients with and without CVD died, respectively. Also, mortality rate was significantly high among the three groups of Ct value in patients with CVD, with the highest mortality in those with Ct between 10 and 20 (Group A = 19.9%). CONCLUSION: In summary, our results highlight that CVD is a major risk factor for hospitalization and the severe consequences of COVID-19. Death in CVD group is significantly higher compared to non-CVD. In addition, the results show that age-related diseases can be a serious risk factor for the severe consequences of COVID-19. KEYWORDS: COVID-19, cardiac disease, SARS-CoV-2, cardiovascular disease, Iran



چهاردهمین گنگره بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



A Review on Herbal Secondary Metabolites against COVID-19 Focusing on the Genetic Variants of SARS-CoV-2

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G-04761 نوع پذیرش: پوستر | کد مقاله:

Abstract: Background: An outbreak of the new coronavirus disease 2019 (COVID-19) was reported in Wuhan, China, in December 2019, subsequently affecting countries worldwide and causing a pandemic. Although several vaccines, such as mRNA vaccines, inactivated vaccines, and adenovirus vaccines, have been licensed in several countries, the danger of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) variants persists. To date, Alpha (B.1.1.7), Beta (B.1.351, B.1.351.2, B.1.351.3), Delta (B.1.617.2, AY.1, AY.2, AY.3), Gamma (P.1, P.1.1, P.1.2), and Iota (B.1.526) circulating in the United States, Kappa (B.1.617.1) in India, Lambda (C.37) in Peru and Mu (B.1.621) in Colombia are considered the variants of concern and interest. Materials and Methods: Data were collected through the end of August 2021 by searching PubMed, Scopus, and Google Scholar databases. There were findings from in silico, in vitro cell-based, and non-cell-based investigations. Results: Our study has discovered several secondary plant metabolites that interfere with critical components of coronavirus pathogenesis and reproduction to have antiviral efficacy against coronaviruses. According to the present review, some PSMs are promising anti-COVID19 agents, which can block essential proteins, e.g., PLpro, Mpro, ACE2, and RdRp. Among them, green tea beverage (GTB) or its principal ingredient, epigallocatechin gallate (EGCG), bis-benzylisoquinoline alkaloids, and neferine as coronavirus entry inhibitors are highly effective in inhibiting infection of the new variants. Conclusions: More studies are still needed to prevent or evaluate COVID-19 virus infection with appropriate herbal metabolites or natural medicines. However, medicinal plants only work best in combination with modern medical treatment, assistive devices (such as ventilators), and intensive care. Research must continue quickly to find effective PSM compounds to treat the infection. Keywords: COVID-19 Pandemic, Natural Products, Herbal Medicines, SARS-CoV-2 Variant

Prevalence and the association between SARS-CoV-2 cycle threshold, comorbidity and outcomes in population of North of Iran (2020-2021)

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نوع پذیرش: پوستر | کد مقاله: G-32407

Abstract: Background: The present study aimed to investigate the one-year prevalence of SARS-CoV-2, common comorbidities and demographic information among negative- and positive rRT-PCR in health care workers (HCW), hospitalized and outpatients. Also, the association between SARS-CoV-2 cycle threshold (Ct) and the outcomes of patients were analyzed in Babol, northern Iran. Materials and Methods: This large retrospective cross-sectional study was performed between March 2020 and March 2021. The records of 19232 hospitalized, outpatients and HCW suspected to COVID-19 were collected from teaching hospitals in the North of Iran. Results: Out of the 19232 suspected to COVID-19 patients, 7251 (37.7%) had a positive rRT-PCR result; 652 (9%), 4599 (63.4%) and 2000 (27.6%) of those were categorized as HCW, hospitalized and outpatients, respectively. Moreover, between the hospitalized and the outpatient group, 10.2 and 0.8% cases died, whereas no death cases were reported in the HCW. Furthermore, it seems that death rate was significantly different between the three groups of Ct value, the highest mortality in those with Ct between 21 and 30 (group B=7.6%) and the lowest in the group with the highest Ct (between 31 and 40 = 5.5%) (p0.001). Conclusion: In summary, 37.7% of cases were positive for SARS-CoV-2; of which, 63.4, 27.6 and 9% were hospitalized, outpatients and HCW, respectively. With regard to the mortality rate in hospitalized patients and the significant association with Ct under 20 and 30, it seems that the early detection and the initial quantification of SARS-CoV-2 in the first week of the conflict and therapeutic considerations to reduce the relative load can reduce the mortality rate. Keywords: COVID-19, Hospitalized, Health care worker, Outpatient, Cycle threshold (Ct)

Association between SARS-CoV-2 RT-PCR Ct Values with Demographic Data: A Epidemiological Characteristics of COVID-19 Patients in the North of Iran

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نوع پذیرش: پوستر | کد مقاله: G-80524

Abstract: Background: To avoid worsening from mild, moderate, and severe diseases and to reduce mortality, it is necessary to identify the subpopulation that is more vulnerable to the development of COVID-19 unfavorable consequences. This study aims to investigate the demographic information, prevalence rates of common comorbidities among negative and positive real-time reverse transcriptase polymerase chain reaction (rRT-PCR) patients, and the association between SARS-CoV-2 cycle threshold (Ct) at hospital admission, demographic data, and outcomes of the patients in a large population in Northern Iran. Materials and Methods: This large retrospective cross-sectional study was performed from 7 March to 20 December 2020. Demographic data, including gender, age, underlying diseases, clinical outcomes, and Ct values, were obtained from 8,318 cases suspected of COVID-19, who were admitted to four teaching hospitals affiliated to Babol University of Medical Sciences (MUBABOL), in the north of Iran Results: Since 7 March 2020, the data were collected from 8,318 cases suspected of COVID-19 (48.5% female and 51.5% male) with a mean age of 53 ± 25.3 years. Among 8,318 suspected COVID-19 patients, 3,250 (39.1%) had a positive RT-PCR result; 1,632 (50.2%) patients were male and 335 (10.3%) patients died during their hospital stay. The distribution of positive rRT-PCR revealed that most patients (464(75.7%)) had a Ct between 21 and 30 (Group B). Conclusion: Elderly patients, lower Ct, patients having at least one comorbidity, and male cases were significantly associated with increased risk for COVID-19-related mortality. Moreover, mortality was significantly higher in patients with diabetes, kidney disease, and respiratory disease Keywords: COVID-19, Cycle threshold, Iran, SARS-COV-2

Evaluation of correlation between covid-19 and telogen effluvium hair loss pattern: A Systematic Review

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Background:

The coronavirus disease 2019 (COVID-19) has caused several dermatological disorders including hair loss (HL). Telogen effluvium (TE), is a type of diffuse hair loss that occurs commonly 2-3 months after a stressful event that causes hair loss and continues for several months. This issue could be related to post-Covid-19 infection. Since the mechanism of covid-19 in TE is not fully known, this study was conducted to investigate this mechanism.

Materials and Methods:

In this systematic review, the desired information was searched from Google Scholar and PubMed databases with keywords "COVID-19", "Telogen effluvium", "Hair loss", "TE", "SARS-CoV-2," and their combinations for the period of 2021-2022. Titles and Abstracts were screened for appropriateness using predetermined inclusion and exclusion criteria.

Results:

According to this study, the negative effect of proinflammatory cytokines and stress hormones on the normal metabolism of proteoglycan and reduced anagenic expression of proteoglycans is one of the mediating mechanisms linking HL to COVID-19. In patients with COVID-19, hair follicles are directly damaged by thromboembolism and cytokines, so the pathogenesis of TE caused by COVID-19 may be more severe than conventional TE. Psychological stress, systemic inflammation, and oxidative stress are the factors of HL and TE in covid-19 patients. TE has two types, acute and chronic, and its chronic type can be intermittent. The amount of hair loss in the patient is more related to the severity of the covid-19 disease and underlying inflammation and less related to the patient's hormonal status. The prevalence of TE is significantly higher in women. Identifying covid-19 as the cause of telogen effluvium helps the patient to get rid of unnecessary stress by getting counseling because psychological support is the most important factor in the resolution of the complication.

Conclusion:

Telogen effluvium is one of the complications after the covid-19 disease, which usually improves without treatment and by eliminating psychological stress and managing systemic complications.

Keywords: COVID-19, Telogen effluvium, Hair loss, TE, SARS-CoV-2

Clinical performance of rapid antigen tests in comparison to RT-PCR for SARS-COV-2 diagnosis in the Omicron variant: a systematic review and meta-analysis

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G-89076 نوع پذیرش: پوستر | کد مقاله:

Abstract: Background: Omicron variant of concern appearance raised awareness about immunological products such as antigen detection kits and vaccines, because of numerous mutations in different genes. Rapid antigen test (RAT) kits which are commonly used for Covid-19 diagnosis are likely to fail in Omicron detection. Many studies assessed RATs clinical performance presenting controversial results. In this systematic review and meta-analysis, we investigated whether Omicron affected the RAT performance significantly in comparison to PCR. Materials and Methods: We registered this systematic review and meta-analysis in the international prospective register for systematic reviews (PROSPERO), with the registration number CRD4202235510. We searched Web of Science, Scopus, Embase, as well as PubMed systematically on August 26th, 2022. The search strategy briefly included “B.1.1.529”, “Omicron”, “lateral flow test”, and “rapid antigen test” keywords. We included English articles that assess the clinical performance of RATs for detecting SARS-CoV-2, in comparison to RT-PCR in patients infected with the Omicron. We just included the papers that used a valuable method for viral genotyping in order to measure the kit’s performance in the Omicron variant exactly. Two persons screened the article independently. We assessed the eligibility of the included studies using the Joanna Briggs Institute (JBI) checklist. All four indexes (TP, FP, TN, and FN) were extracted from each included study to have standard two-by-two tables. Diagnostic sensitivity and specificity with a 95% confidence interval were calculated. For determining the pooled sensitivity and specificity, we conducted a random effects model using R software V.4.1.3. Results: We included 18 eligible articles presenting adequate data about RATs performance among the Omicron variant, including 1268 positive RT-PCR patients, and 4406 negative RT-PCR cases. The diagnostic specificity of RAT kits ranged between 0.624 and 1.000. The pooled specificity of RATs was 1.000 (0.997-1.000). Furthermore, the range of sensitivity was between 0.222 and 1.000. The pooled sensitivity was 0.671 (0.595-0.721), unveiling a significant reduction from WHO and FDA authorization indexes. The FDA-approved RAT kits represented a better clinical performance rather than the WHO-approved, with a sensitivity of 0.728 (0.620-0.815). The most commonly used sample in Covid-19 rapid antigen tests was the nasopharyngeal swabs showing a pooled sensitivity of 0.673 (0.617-0.724). The next prevalent specimen was nasal swabs, which presented a pooled sensitivity of 0.803 (0.700-0.877), higher than all others. The sensitivity reduced remarkably following the CT-value increase. The pooled sensitivity of samples with CT₂₅ and CT₂₅ is 0.108 (0.048-0.227) and 0.903 (0.819-0.951) respectively (P<0.01). In addition, the sensitivity in symptomatic patients and asymptomatic ones is significantly different. The sensitivity in



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symptomatic (0.875) patients is higher than in asymptomatic (0.614). Conclusion: Rapid antigen tests present defective performance for Covid-19 detection in the Omicron variant, especially in specimens with low viral loads.

Keywords: Covid-19, Omicron, B.1.1.529, Rapid antigen test, RT-PCR

آدرس دبیرخانه:

تهران، خیابان کارگر شمالی، رویروی مرکز قلب تهران،
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The Synergistic Effect of Lasota Virus and Dactinomycin on Lung Cancer

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G-42930 نوع پذیرش: پوستر | کد مقاله:

Abstract: Background: Lung cancer is the most common cause of cancer incidence and death in men, while it is the third most common cause of cancer and the second most common cause of cancer death in women. Lung cancer begins in the lungs and develops after genetic damage to DNA and epigenetic change. Recent studies support this idea that two or more therapies can result in a synergistic therapeutic outcome to improve cancer treatments. The simultaneous use of chemotherapy and viral therapy is suitable method for cancer treatment. The use of viruses is an effective option in the treatment of cancer, for example the Lasota virus. Multiple studies have shown Lasota(NDV) has oncolytic potential due to its propensity to infect and replicate in human cancer cells while sparing normal cells. In addition to its direct lytic effects, the virus triggers both innate and adaptive immune responses. Dactinomycin works by damaging the cancer cell's DNA, inhibits transcription, and used in the treatment of various cancers. Combined treatments, especially the simultaneous effect of drugs and viruses can have better treatment. Materials and Methods: Lasota (Razi Vaccine and Serum Research Institute) was grown in 9 days' embryonic eggs at allantoic fluids to 13 days. On the 13th day, allantoic fluid was collected and the titer was determined by Hemagglutination (HA) test with 0.5% chicken RBC. A549 cell line was used as Lung cancer cells, cultured in DMEM-high glucose supplemented with 10%FBS. 104 cells/100 μ l were seeded in 96-well plates and after the cells reached 70% confluence, the wells were treated by Lasota, Dactinomycin (as chemotherapeutic drug), and Lasota plus Dactinomycin. After 24h, the morphology, viability (by MTT and trypan blue staining), and apoptosis (by Acridine Orange/Ethidium Bromide staining) were analyzed. Results: Although Dactinomycin and Lasota were individually capable of suppressing lung cancer cell growth, their simultaneous treatment was capable of enhancing the ability to repress the cell viability. Dual AO /EtBr staining showed fluorescent color for viable cells that have green chromatin with organized structures was predominantly green. They have normal nuclei staining, but early to late apoptotic (even dead) cells in treated groups showed orange to red fluorescence. The MTT test also showed that the drug and virus were more effective when used together than when used alone. Conclusion: Simultaneous use of Dactinomycin and Lasota showed the synergistic cytotoxic effect on cell viability. Thus, the concept of exploiting concomitant and hybrid therapy could serve as a potential therapeutic remedy for lung cancer apoptosis. It can also reduce side effects by using targeted therapy by the virus according to its characteristics for the target cell. Keywords: Lung cancer, Dactinomycin, Lasota, apoptosis, cell viability



چهاردهمین کنفرانس بین المللی آزمایشگاه و باالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Increased risk of COVID-19 mortality rate in IFITM3 rs6598045 G allele carriers infected by SARS-CoV-2 delta variant

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G-12795 نوع پذیرش: پوستر | کد مقاله:

Abstract: Background: The interferon-induced transmembrane-protein 3 (IFITM3) is a vital component of the immune system's defense against viral infection. Variants in the IFITM3 gene have been linked to changes in expression and the risk of severe Coronavirus disease 2019 (COVID-19). This study aimed to investigate whether IFITM3 rs6598045, quantitative polymerase chain reaction (qPCR) cycle threshold (Ct) values, and severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) variants are associated with an increased mortality rate of COVID-19. Methods: The genotyping of IFITM3 rs6598045 polymorphism was analyzed using the amplification refractory mutation system-polymerase chain reaction in 1342 recovered and 1149 deceased patients positive for SARS-CoV-2. Results: In this study, IFITM3 rs6598045 G allele as minor allele frequency was significantly more common in the deceased patients than in the recovered ones. Furthermore, the highest mortality rates were observed in Delta variant and lowest qPCR Ct values. COVID-19 mortality was associated with IFITM3 rs6598045 GG and AG in Delta variant and IFITM3 rs6598045 AG in Alpha variant. A statistically significant difference was observed in the qPCR Ct values between individuals with GG and AG genotypes and those with an AA genotype. Conclusion: A possible correlation was observed between the mortality rate of COVID-19, the G allele of IFITM3 rs6598045, and SARS-CoV-2 variants. However, large-scale research is still required to validate our results. Keywords: Interferon-induced transmembrane protein 3, Coronavirus disease 2019, Severe acute respiratory syndrome coronavirus 2 variants, qPCR Ct values

Seroprevalence of West Nile Virus in Regular Blood Donors Referred to the Blood Bank of Kurdistan Province, Iran

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G-30217 نوع پذیرش: پوستر | کد مقاله:

Abstract: Introduction: West Nile virus is an infection that is most commonly caused by infected mosquito bites, however, blood transfusions, organ transplants, breast feeding, pregnant mother to the fetus transmission, and occupational transmission among laboratory and medical staff are also the less common routes of infection. Given the endemic nature of this virus in the Middle East, the aim of this study was to investigate the presence of this virus in regular blood donors, as the reliable source of blood supply needed for patients in hospitals. Materials and methods: In this descriptive analytical study, venous blood samples were collected from 259 regular blood donors referring to Blood Transfusion Organization of Kurdistan. After separating blood serum, the amount of IgM and IgG antibodies against West Nile virus was measured via ELISA test. Results: Concerning antibody, IgG and IgM against West Nile virus were positive in 14 patients (5.4%) and 3 patients (1.2%), respectively. Seropositive IgG levels were observed in 11 patients over 40 years of age (12.5%) while they were observed only in 3 patients under 40 years of age (1.8%) and the difference was statistically significant (OR = 7.95; 95% CI: 2.16 to 29.32; p 0.01). Conclusion: Given the value of blood and blood products obtained from regular blood donors for therapeutic purposes and the significant prevalence of the virus and considering the presence of cases with positive IgM, it seems necessary to screen blood donors in blood transfusion centers in the western parts of Iran. Keywords:

State-of-the-art cerium nanoparticles as promising agents against human viral infections

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G-18507 نوع پذیرش: پوستر | کد مقاله:

Abstract: Background: The world is faces a significant global health challenge in the form of viral infections, particularly the emergence of viral strains that are resistant to effective antiviral therapies. This underscores the urgent need for the development of effective and safe antiviral agents. Nanoscale materials are now being used as novel antiviral agents. Cerium nanoparticles have unique chemical and physical properties that make them particularly promising for viral infections. Methods: The review article mainly focuses on the biomedical applications of nanoceria, including its antiviral, antioxidant, antibacterial, anticancer, drug and gene delivery, antidiabetic, and tissue regenerative properties. Results: Nanoceria (CeNPs) have been found to possess potent antiviral properties against various viruses. Metal and metal oxide nanoparticles have attracted much attention in combating viral infections because they are active via multimodal mechanisms of action, e.g., by hindering viral binding to host cells, binding directly to the viral surface, or even interacting with the viral genome. Lipid nanoparticles (LNPs) represent another option for antiviral infection because of their biocompatibility, ease of manufacture, relative safety, superior payload, and protection of encapsulated RNAs. On the other hand, the application of this type of NPs in viral infections has some limitations such as reproducible and large-scale synthesis procedures, microbiological and physicochemical stability, active targeting strategies, sufficiently loaded drug for human dosing, and cost-benefit analysis. CeO₂-NPs are effective against pathologies caused by chronic oxidative stress and inflammation. CeNPs can protect cells from radiation and cellular damage caused by agents, as well as in pathological conditions such as brain or heart ischemia, retinal neurodegeneration, or neurological diseases. The usefulness of nanoceria is due to its inherent property of exhibiting different oxidation states, which enables it to act as an excellent antioxidant and protect healthy cells from oxidative stress. CeNPs can be used as an anti-inflammatory factor and protect the cell due to their ability to suppress inflammation, scavenge reactive oxygen species, and decrease cytokine levels in vitro and in vivo. CeNPs have a number of chemical and physical properties that make them particularly promising for medical applications. Conclusion: The physical properties of CeNPs play a crucial role in their antioxidant properties. Despite several reports on antiviral activities of nanoceria, little research has been conducted on their antiviral applications. Therefore, researchers should further investigate the use of nanoceria. Keywords:

Seroprevalence of SARS-COV-2 antibodies among the medical staff of Dezful Ganjavian Hospital

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G-04952 نوع پذیرش: پوستر | کد مقاله:

Abstract: Background: Infection with SARS-COV 2, belonging to the Coronaviridae family, caused the covid-19 pandemic. Considering the pivotal role of the medical staff in the fight against the Covid-19, they are one of the groups at risk of the disease and suffer severe physical and mental injuries. In addition, medical staff can potentially be important as asymptomatic carriers in the spread of disease in the workplace and the community. Seroepidemiological studies on the medical staff in terms of the presence of anti-COVID-19 antibodies, in one hand can be a suitable criterion for finding asymptomatic carriers, and in another hand, can be used to evaluate the immunity of the infected medical staff and determination of the time of their return to the workplace. This study was designed with the aim of "seroepidemiological investigation of Covid-19 in the medical staff of Dezful Ganjavian Hospital. Materials and Methods: This descriptive cross-sectional research includes 276 samples (178 Females and 98 Males) collected from the medical staff in different departments of the hospital from January to march 2021. 5 ml of venous blood was drawn from each participant and its serum was separated quickly. In order to measure IgG and IgM against SARS-COV-2, we examined the samples using ELISA method. Antibody levels were measured, and each sample was designated as positive or negative based on the cut off determined by the manufacturer. Participants completed a self-report questionnaire, comprising demographics, occupational, the work area, and personal protection data. Results: Of the 276 medical staff who participated in this study, 9.1% (n=25) and 2.1% (n=6) were seropositive for anti-SARS-CoV-2 IgG and IgM respectively. 1.1% (n=3) of the cases IgG were also reported as suspicious in terms of IgG level. On the other hand, 31.3% (n=86) of all participants in the study had a history of previous infection with covid-19. 22.1% (n=19) Of the IgG positive case and 83.3% (n=5) of IgM positive cases had a history of previous infection with covid-19. Statistically, there was no significant relationship between age and history of covid-19 infection (P-value \geq 0.05). In addition, A slight positive correlation was observed between the history of infection and the level of IgM. Conclusion: The results indicate that the treatment staff, regardless of age and gender, despite the use of protective equipment in all departments of the hospital, are exposed to the infection and re-infection of Covid-19. In addition, previous infection with this disease, considering that it does not cause a stable increase in IgM level, cannot have a protective effect against SARS-COV 2. Also, a significant proportion of infected individuals, despite the positive IgG test are completely asymptomatic and can cause the transmission of this disease in the society. Keywords: COVID-19, Medical staff, Seroprevalence, ELISA, SARS-COV-2



چهاردهمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Review on HRM (high-resolution melting) method for SARS-CoV-2 detection

¹ آسیه یلمه © (P), ¹ بهمن آقچه لی

دانشگاه علوم پزشکی گلستان ¹

G-46530 نوع پذیرش: پوستر | کد مقاله:

Abstract: Background Coronavirus disease 2019 (COVID-19), a devastating disease which was caused by Severe Acute Respiratory Syndrome (SARS-CoV-2). A simple, accurate, and fast technique is essential in managing of the SARS-CoV-2 infection. This review article aims to introduce this technique as one of the appropriate methods for SARS-CoV-2 detection. Methods We performed a comprehensive search on databases such as PubMed, ISI, Scopus, Iran Medex, and Scientific Information Database (SID), on articles published for describing HRM (high-resolution melting) technique. Result Some studies showed that the HRM technique could accurately identify SARS-CoV-2 and differentiate mutations in each marker site within approximately 2 h. These results demonstrate that this HRM-based assay is a simple screening method for monitoring SARS-CoV-2 sub-variants. Conclusion Flexible, expandable, and efficient diagnostic tools are in high demand. HRM method could be playing a pivotal role in patient management and decelerating disease spread. It will guide clinicians, epidemiologists, and researchers in identifying a more reliable, sensitive, and rapid method of diagnosing SARS-CoV-2 including the most recent variants. Keywords: COVID-19, SARS-CoV-2, HRM method, detection

Parents anxiety, stress and depression during the outbreak of COVID-19 and their relation with parents view about their children health-related quality of life

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G-40285 نوع پذیرش: پوستر | کد مقاله:

Abstract: Abstract Introduction The disease of COVID-19 can affect the mental health of parents and their children. Children are one of the most vulnerable people in the society who should be taken care of during crises like the COVID-19 epidemic. The aim of this study was to determine the parents anxiety, stress and depression and their relation with parents view about their children health-related quality of life during the outbreak of COVID-19. Methods This cross-sectional study included 396 parents having children aged 6-18 years old in Rafsanjan, Iran. We used online questionnaire includ demographic information questionnaire, Depression, Anxiety, Stress Scale (DASS-21), questions related to the coronavirus disease and Children Health-Related Quality of Life (CHQol) to collect data, as well as SPSS25 and descriptive and inferential statistics to analyze data. Results The present study showed that 28.3% participants had intense/very intense anxiety, 18.4% had intense/very intense stress and 17.1% had intense/very intense depression. A negative significant correlation was found between anxiety ($r = 0.395$), stress ($r = 0.421$), depression ($r = 0.465$) parents with CHQol ($p 0.001$). Multiple regression models shown, depression and anxiety parents predict 22% of the variance of CHQol, with depression being the best predictor ($p 0.001$). Conclusion The present study showed that parents have high levels of anxiety, stress and depression due to COVID-19 disease. Paying attention to factors affecting parents' anxiety, stress and depression can play an important role in promoting children's health and preventing the aggravation of psychological problems caused by the COVID-19, so it is suggested that health managers take effective additional measures to reduce parents' anxiety. Keywords: Anxiety, Stress, Depression, Covid-19, Children, Health, Quality of Life

Investigating the relationship between the parents anxiety, stress and depression with their children's externalized behavioral disorder during the outbreak of COVID-19

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G-09561 نوع پذیرش: پوستر | کد مقاله:

Abstract: Abstract Introduction Evaluation and recognition of the relationship between the mental health status of parents and its effects on their children in crises can help to implement effective interventions to improve children's mental health. Meanwhile, the disease of COVID-19 has had different effects on the mental health of parents and their children. The aim of this study was to investigating the relationship between the parents anxiety, stress and depression with their children's externalized behavioral disorder during the outbreak of COVID-19. Methods The present study was a cross-sectional study on 396 parents having children were selected by convenience sampling. Sampling was done by designing an online questionnaire that was distributed on social media from March to July 2021. Demographic questionnaire, Depression, Anxiety, Stress Scale (DASS-21), questions related to the coronavirus disease and Achenbach System of Empirically Based Assessment (ASEBA) were used to collect data. Data were analyzed using SPSS 22 software using independent t-test and Pearson correlation coefficient. Results 28.3% participants had intense/very intense anxiety, 18.4% had intense/very intense stress and 17.1% had intense/very intense depression. A positive significant correlation was found between anxiety ($r = 0.334$), stress ($r = 0.354$), depression ($r = 0.324$) parents with externalized behavioral disorder ($p < 0.001$). Multiple regression models shown age, stress, use masks and gloves to prevent infection and anxiety predict 19% of the variance of externalized behavioral disorder, with age being the best predictor ($p < 0.001$). Conclusion During the outbreak of Covid-19, parents have experienced high anxiety, stress and depression, and these problems can affect their children and cause behavioral disorders. Therefore, it is necessary to pay more attention to the mental state of parents and its effects on their children. Key words Anxiety, Stress, Depression, Covid-19, Children, Behavior, Disorder



چهاردهمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Study of the therapeutic effects of Sofosbuvir in patients with HCV (Hepatitis C) in previous published studies

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G-31859 نوع پذیرش: پوستر | کد مقاله:

Abstract: Background: Hepatitis C virus is a frequent cause of hepatocellular carcinoma. Sofosbuvir is an HCV NS5B nucleotide polymerase inhibitor with similar in vitro activity against HCV genotypes that have been evaluated extensively in phase II and III interferon-free clinical trials. Hepatitis C (HCV) infects more than 185 million individuals worldwide. Twenty percent of patients chronically infected with HCV progress to cirrhosis. The aims of this study were to compare the safety and efficacy of Sofosbuvir for the initial treatment of chronic hepatitis C. Materials and Methods: A literature search of PubMed, Wiley online library, Scopus, Google Scholar, and Web of Science was conducted from 2015 to 2022 using the keywords, Sofosbuvir and Hepatitis C. The Titles of articles were reviewed, and those who were more patients out of 12 were selected. Results: A total of 89 articles published from 2015-2022 were studied. In 23 of the reviewed articles, the number of patients and results were studied. In total, Sofosbuvir was found to be used in the treatment process of 4650 patients for a total duration of 15 to 30 weeks. The efficiency of the drug was estimated to be 82.1 % on average; it varied for different genotypes of the disease. Conclusion: The study shows that Sofosbuvir can be used as an effective drug for the treatment of Hepatitis C. New, short-duration, simpler therapies result in high SVR rates for HCV-infected patients. This drug is taken in combination with a Ribavirin between 10 to 24 weeks (on average). Keywords:

Clinical and epidemiological characteristics of covid-19 in Iranian children

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G-81035 نوع پذیرش: پوستر | کد مقاله:

Abstract: Background. Despite the worldwide spread of Severe Acute Respiratory Syndrome Corona Virus 2 (SARS-CoV-2), information about the epidemiological and clinical patterns of this infection is still largely unknown in children. In addition, the prevalence of this disease is still very high in some parts of the world, including Iran. +us, this study aims to evaluate the epidemiological features, laboratory and imaging findings, and the type of treatments in children with novel coronavirus 2019 (COVID-19). Method. This study is conducted from March 2020–March 2021 by using the medical records of hospitalized confirmed COVID-19 children younger than 18 years in five cities of Iran: Tehran, Ahwaz, Isfahan, Bandar-Abbas, and Khorramabad. In addition to demographic and epidemiological data, we also studied clinical signs and treatments. Results. In total 278 confirmed COVID-19 children, the average age was 5.3 years, and 59.4% were boys. A total of 37.8% had an underlying disease, in which the most common was a malignancy. +e most common symptoms were fever and cough. In this group of pediatrics, some abnormal laboratory findings have been seen. GGO (Ground-Glass Opacity) had been diagnosed in 58.6% of children. 3.6% needed oxygen therapy with ventilators, and 83.09% had received antibiotic treatments with the majority of ceftriaxone. Also, 10% had got steroids. In this study, the mortality rate was 4.3%. Conclusion. In this study, most of the children who died had an underlying disease, so timely care and action is important in them. Most children admitted to our study received antibiotics and were prescribed antivirals and steroids for a smaller number. Also, a small number of children received oxygen therapy, most of whom were in the age group of 1 to 5 years. Keywords: Covid-19, Epidemiologic, Pediatric



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Prediction the severity of covid-19 in children hospitalized to Mofid Children's Hospital, Tehran, Iran

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نوع پذیرش: پوستر | کد مقاله: G-60795

Abstract: Objective. In this study, by using clinical and paraclinical characteristics, we have aimed to predict the severity of the disease in hospitalized COVID-19 children. Method. is cross-sectional study was conducted on medical records about epidemiologic data, underlying diseases, symptoms, and laboratory tests from March to October, 2020, on 238 hospitalized confirmed COVID-19 paediatric cases in several children's hospitals of Tehran, Ahwaz, Isfahan, and Bandar Abbas. Results. From 238 patients, 140 (59%) were male and most of them were in the age group of 1 to 5 years (34.6%). Among all hospitalized patients, 38% had an underlying disease and in total, 5% of cases were expired. Conclusion. Determining patient severity is essential for appropriate clinical decision making; our results showed that in hospitalized pediatric patients, by using several variables such as SGOT, CRP, ALC, LDH, WBC, O2sat, and ferritin, we can use clinical and paraclinical characteristics for predicting the severity of COVID-19. Keywords: Covid-19, Severity, Children

آدرس دبیرخانه:

تهران، خیابان کارگر شمالی، رویروی مرکز قلب تهران،
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Isolation and Characterization of bacteriophage against antibiotic resistant *Helicobacter pylori*

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G-85214 نوع پذیرش: پوستر | کد مقاله:

Abstract: *Helicobacter pylori* is a Gram-negative, pathogenic, spiral, microaerophilic bacterium in the human stomach. *H. pylori* is the most common chronic bacterial infection in the world. Due to the increase in the rate of its antibiotic-resistant around the world the development of a new strategy against this bacterium is necessary. One of the alternative treatments for antibiotic-resistant infections is phage therapy. This research aimed to isolate and identify effective bacteriophage against antibiotic-resistant *H. pylori* strains. Materials and Methods: in this study, bacteriophages were isolated from the effluents of Imam Hossein, Taleghani, and Mofid hospitals in Tehran. Then first effluent samples were centrifuged at 6000rpm and filtered by a needle filter (0/45 μ) then, the resulting supernatant is mixed with overnight culture of bacteria and Brucella broth culture medium. and finally, 10% of the desired volume of FBS (Fetal Bovine Serum) is added and incubated for 24 hours at a temperature of 37°C with an gas-pack. then the presence of bacteriophage was confirmed using double-layer agar technique. Investigating the stability of the isolated phage against various environmental factors such as temperature, pH, and NaCl different concentrations. Results: According to the investigations and results obtained, we succeeded in isolating bacteriophage, which had the ability to create suitable plaques and lyse bacteria. the results related to the thermal range according to the initial number of 10⁹PFU/ml showed that the desired phage has a suitable lytic activity in the temperature range -20° to 70° and the best temperature is 37° also, the desired phage has a suitable lytic activity in the PH range 4 to 11. the best phage activity is related to pH 4. With the increase in salt concentration, the phage had suitable lytic activity so that by increasing the salt concentration the rate of phage activity increased. Conclusion: the isolated bacteriophage had a suitable therapeutic potential against antibiotic-resistant *H. pylori* strains. Keywords: Bacteriophage, *Helicobacter pylori*, phage therapy



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Preclinical and laboratory characterization of COVID-19 patients in Rasht, Iran

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نوع پذیرش: پوستر | کد مقاله: G-89754

Abstract: Abstract Background: In December 2019, an epidemic of an unknown respiratory virus emerged in Wuhan, China, and put the whole world in crisis; a newly emerged coronavirus, called severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). COVID-19 patients have some clinical manifestations such as fever and cough as primary clinical presentations, and shortness of breath and myalgia as the following manifestation. Since the scientific community is still evaluating the clinical and laboratory characteristics of the infection in the body; therefore, considering the large amounts of scattered information in knowledge regarding laboratory factors in COVID-19 is necessary for future decision-making of clinicians. Methods: We extracted demographics and baseline clinical characteristics from 126 Patients with polymerase chain reaction (PCR) confirmed COVID-19 in Razi Hospital, Rasht, Iran. All statistical analysis was performed with IBM SPSS Statistic, version 24.0. Results: The mean age of patients was 62 years, ranging from 28 to 92 years old. Overall, 57.1% of cases were male and 42.9% were female. 17.5% of patients had direct contact with a SARS-CoV-2 infected patient. The most common underlying diseases were diabetes (11.9%) and cardiovascular disease (CVD) (7.1%). The mean±SD of lactate dehydrogenase (LDH), creatine phosphokinase (CPK), creatine kinase MB (CK-MB), serum glutamic oxaloacetic transaminase (SGOT), and erythrocyte sedimentation rate (ESR) were remarkably higher than the normal range, (1231±866.4 U/L, 766.8±2288.6 U/L, 59.28±55.1 U/L, 112.28±213 U/L and 67.61±31 mm/hr), respectively. Also, the average O₂ Saturation (O₂Sat) was 61.4±26.3 %. Conclusion: According to our investigation, advanced age, male gender and history of underlying disease, and some out-of-normal-range of laboratory index, were the most significant risk factors, which result in being more susceptible to severe conditions of SARS-CoV-2 infection. Keywords: SARS-CoV-2, COVID-19, Laboratory findings



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The expression levels of c-MYC, BIRC5, and STMN1 cellular genes increased following the presence of EBV-EBNA1 protein in HeLa cell line

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G-92107 نوع پذیرش: پوستر | کد مقاله:

Abstract: Background: One of the most crucial Epstein-Barr virus (EBV) proteins, EBV nuclear antigen-1 (EBNA1), can alter the expression of various viral and cellular genes. So, if the expression of important cellular oncogenes are affected by EBNA1, it could play an important role in carcinogenesis. In this study, we examined the EBNA1 protein's impacts on the expression pattern of the c-MYC, BIRC5, and STMN1 cellular genes in a cervical adenocarcinoma cell line to assess the function of this viral protein in the advancement of cervical cancer. Materials and Methods: We used a DNAfectamine to transfect EBNA1 and control plasmids into HeLa cells. Hygromycin B treatment was used to select cells that were effectively transfected with plasmids. c-MYC, BIRC5, and STMN1 were three genes whose expression was assessed by real-time PCR. Morphological alterations in HeLa cells were investigated using pathological staining. Microsoft Excel 2016 and GraphPad Prism version 5.00 were used to compute the data, and compare means. Results: The presence of EBNA1, raised the expression of the cellular genes c-MYC and BIRC5 threefold ($P=0.02$) and tenfold ($P=0.028$), respectively. The expression of the cellular gene STMN1 increased two-fold in HeLa cells that had been transfected with the EBNA1 plasmid, although this change in expression was not statistically significant ($P=0.11$). Additionally, EBNA1 was shown to alter the cell shape in such a way that it led to the development of enormous HeLa cells with copious amounts of cytoplasm and nuclei. Conclusion: According to the findings, the EBV-EBNA1 protein could boost the expression of c-MYC and BIRC5 cellular genes in the HeLa cell line. As a result, simultaneous infection of cervical cells with HPV-18 and EBV may cause cervical cancer to advance more quickly. Keywords: Cervical carcinoma, Human Papillomavirus, Epstein-Barr Virus, EBNA1

Seroprevalence of COVID-19 among clients of private laboratory and relationship with demographic data and clinical signs in Sanandaj, Iran

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G-50384 نوع پذیرش: پوستر | کد مقاله:

Abstract: Background: Survey of antibodies against SARS-CoV-2 has a key role for elucidating the history of exposure to SARS-CoV-2. The study objective was to determine the seroprevalence of SARS-CoV-2 antibodies among clients of a private laboratory and its relationship with demographic and clinical data. Methods: This descriptive and analytical study was conducted on people referring to a private clinical laboratory, from April 2020 through June 2021, Sanandaj, Iran. The participants' information was collected, including, age, gender, place of residence and clinical data (fever, cough, sore throat, headaches, diarrhea, nausea and body aches). SARS-CoV-2 antibodies (IgM and IgG) were tested using commercial ELISA kits. Results: The mean age of the people was 40.24 ± 13.19 (SD) years. Out of 7703 participants 4549 (59%) were women. The major place of residence of the participants was urban 7481 (97%). The prevalence of SARS-CoV-2 IgM and IgG was 19.8% (1526/7703) and 34% (2664/7703), respectively. There was a statistically significant difference between the age groups and IgM and IgG results ($P = 0.001$), gender and IgG ($P = 0.008$), place of residence and IgM ($P = 0.001$). But, there was no statistically significant difference between gender and IgM ($P = 0.184$), place of residence and IgG ($P = 0.375$), clinical symptoms and IgM and IgG results ($p = 0.234$ and $p = 0.327$). Conclusion: the majority of the study population has no detectable antibodies to SARS-CoV-2. Therefore, Sanandaj was considered a SARS-CoV-2 susceptible area. Keywords:



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Mutations analysis of SARS-CoV-2 variants from tehran, iran COVID-19 patient

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نوع پذیرش: پوسنر | کد مقاله: G-84137

Abstract: Background: Since the emergence of the COVID-19 disease in 2019, many mutations appear in the SARS-CoV-2 genome. SARS-CoV-2 has structural and non-structural genes. Structural genes contain glycoprotein spike(S), envelope protein (E), membrane protein(M), and nucleocapsid protein(N). S protein has an important role in the transmission and virulence of SARS-CoV-2. Spike protein is a trimer protein that has receptor binding sites (RBD). The receptor binding domain (RBD) of the S1 subunit of these viruses binds to the outer surface of the claw-like structure of ACE27. Due to this searching for mutation in this part will be important. In the last two years, the following viral variants have been identified: B.1.1.7 (Alpha), B.1.351 (Beta), P.1 (Gamma), B.1.617.2 (Delta), and B.1.1.529 (Omicron). in this study, samples of COVID-19 positive patient amplified by RT-PCR and analyzed the sequences for SARS-CoV-2 variants and unknown mutation. Materials and Methods: Nasopharyngeal swabs were collected from Tehran COVID-19 patients in 2021 and positive samples were selected. RBD site of 12 samples amplified by nested and semi-nested RT-PCR and Sanger method used for sequencing. The result of Sanger sequencing was assembled with Bioedit and then analyzed by GISAID and Nextclade servers. Results: 7 sequences were 20I (Alpha, V1 - B.1.1.7), 1 sequence was 21I (Delta - AY.63) and 4 sequences were recombinant. As a result, 71 mutations, 2 deletions, 10 insertions, and 7 frameshifts were observed. Another analysis showed 42 total amino acid substitutions, 2 total amino acid Deletions, and 1 amino acid Insertion. Conclusion: as analyses declare, many mutations happen in a few samples of COVID-19 positive. These mutations may escape the immunity system due to changing the binding affinity to ACE2 and the transmissibility of SARS-CoV-2 recombinant variants. Keywords: SARS-CoV-2, COVID-19, RBD, mutation, sequencing

The frequency of HCoV-NL63 and HCoV-HKU1 coronaviruses infections in Tehran, Iran, during March 2021 to September 2022

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G-84503 نوع پذیرش: پوستر | کد مقاله:

Abstract: Background: A series of unexplained pneumonia-like illnesses were reported in Wuhan, Hubei State, China, in the last months of 2019. Following the rapid spread of this emerging infection around the world, WHO announced a new pandemic had begun, and the illness caused by this new pathogen was termed coronavirus disease 2019 (COVID-19). According to some research, those who have been infected with the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) are more susceptible to getting other respiratory infections caused by other respiratory pathogens. This study aimed to determine the frequency of HCoV-NL63 and HCoV-HKU1 infections in SARS-CoV-2 positive and negative patients with respiratory disease symptoms. Materials and methods: In this research, a total of 358 nasopharyngeal samples from COVID-19 patients were obtained over the course of a year from various medical centers. Using the multiplex RT-PCR technique, we assessed the prevalence of the HCoV-NL63 and HCoV-HKU1 viruses in Covid-19 confirmed respiratory samples as probable co-infecting agents and also in patients with clinical respiratory symptoms without SARS-CoV-2 infection. Results: Following an analytical investigation, two positive samples one HCoV-NL63 and one HCoV-HKU1 were discovered. In total, two specimens tested positive for the HCoV-NL63 and HCoV-HKU1 viruses among the 213 SARS-CoV-2 negative samples and 145 (40.5%) COVID-19 confirmed positive individuals. The majority of the participants in this study were female, and fever, tiredness, and cough were the most prevalent symptoms. Conclusion: The significance of screening for various respiratory infections should be emphasized by general practitioners. It is a requirement to check SARS-CoV-2-negative patients (but symptomatic) for other important respiratory viruses, including NL63 and HKU1 coronaviruses. Keyword: COVID-19, Co-infection, HCoV-NL63, HCoV-HKU1, Respiratory infections

Development of a SYBR-green based real-time PCR for IP10 gene expression relative quantification

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G-31067 نوع پذیرش: پوستر | کد مقاله:

Abstract: Background: Interferon-gamma (IFN- γ) induced protein 10 (IP-10), also called as chemokine (CXC motif) ligand (CXCL10), is a secreted polypeptide with a molecular weight of 10 KDa. Monocytes, T lymphocytes, natural killer (NK) cells, and stromal cells are only a few of the many cell types that produce IP10. However, monocytes are responsible for the greatest proportion of IP-10 expression. IP-10 is closely related to disease progression and increased earlier than other cytokines in inflammatory diseases including infectious diseases, immune dysfunction, and tumor development. Overall, IP-10 evaluation has been proposed as a maker of disease progression and important factor in the management of patients' inflammation and in therapeutic decision-making. Materials and Methods: Following the isolation of PBMC from whole blood samples, total RNA was extracted from the PBMC samples. cDNAs subsequently were synthesized from the extracted RNAs. Then, the appropriate nucleotide sequence of the primer was designed using the exon-exon junction method. Finally, the IP10 gene expression level was assessed by quantitative real-time polymerase chain reaction (qPCR) based on SYBR green chemistry. Results: IP10 was found in all 5 samples that were collected, by qPCR. Appropriate melting temperature for designed primer ranged from 54 to 60°C and the best annealing temperature for the test is 57°C. Evaluating the melt curve of the assays, revealed a single peak on 81.5°C and CT values ranged from 23.9 to 29.2. In total, the desired gene can be quantified using the designed primers with high efficiency and specificity. Conclusion: Considering the role and importance of the IP-10 in immune responses to viral infections, it can be concluded that the evaluation of IP-10 gene expression by a proper qPCR test is a necessity for research laboratories. In addition, relative quantification of this gene, can be employed as a potential biomarker for evaluation of different inflammatory diseases. Keywords: IP-10, CXCL10, Inflammatory disease, Immune responses, Viral infections

Seroprevalence of COVID-19 among clients of private laboratory and relationship with demographic data and clinical signs in Sanandaj, Iran

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G-01376 نوع پذیرش: پوستر | کد مقاله:

Abstract: Background: Survey of antibodies against SARS-CoV-2 has a key role for elucidating the history of exposure to SARS-CoV-2. The study objective was to determine the seroprevalence of SARS-CoV-2 antibodies among clients of a private laboratory and its relationship with demographic and clinical data. Methods: This descriptive and analytical study was conducted on people referring to a private clinical laboratory, from April 2020 through June 2021, Sanandaj, Iran. The participants' information was collected, including, age, gender, place of residence and clinical data (fever, cough, sore throat, headaches, diarrhea, nausea and body aches). SARS-CoV-2 antibodies (IgM and IgG) were tested using commercial ELISA kits. Results: The mean age of the people was 40.24 ± 13.19 (SD) years. Out of 7703 participants 4549 (59%) were women. The major place of residence of the participants was urban 7481 (97%). The prevalence of SARS-CoV-2 IgM and IgG was 19.8% (1526/7703) and 34% (2664/7703), respectively. There was a statistically significant difference between the age groups and IgM and IgG results ($P = 0.001$), gender and IgG ($P = 0.008$), place of residence and IgM ($P = 0.001$). But there was no statistically significant difference between gender and IgM ($P = 0.184$), place of residence and IgG ($P = 0.375$), clinical symptoms and IgM and IgG results ($p = 0.234$ and $p = 0.327$). Conclusion: the majority of the study population has no detectable antibodies to SARS-CoV-2. Therefore, Sanandaj was considered a SARS-CoV-2 susceptible area. Keywords:

Immunogenicity potential of propolis hydroalcoholic extract as an adjuvant vaccine candidate in a laboratory mouse model against SARS-CoV-2

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G-28910 نوع پذیرش: پوستر | کد مقاله:

Abstract: Background: Vaccination is considered as the most cost-effective preventive tool against infectious diseases. The development of vaccines against SARS-CoV-2 is an important goal for global health. Adjuvants play an important role in the vaccine strategy by strengthening immune responses and enhancing their effectiveness. Propolis is a resin-like product from honeybees having a great ability to stimulate the immune system. The aim of this study is to investigate the adjuvant effect of aqueous and alcoholic extracts of propolis on inactivated SARS-CoV-2 vaccine. Materials and Methods: In this study, the aqueous and alcoholic extracts of propolis were prepared and lyophilized. The experimental groups of Balb/C mice were vaccinated subcutaneously using inactivated SARS-CoV-2 vaccine in the presence of five milligrams of aqueous and alcoholic extracts of propolis as an adjuvant. The mice were randomly divided into six groups of six animals each. They received two shots of vaccine spaced 3 weeks apart. Proliferative responses of lymphocytes were investigated using BrdU incorporation method; IL-4, IFN- γ , the total antibody responses, IgG1, IgG2a, IgG2b, and IgM isotypes were assayed by ELISA. Results: Our findings showed that aqueous and alcoholic extracts of propolis are able to strengthen the proliferation responses of lymphocytes in comparison with the vaccine group alone (P-value=0.017). Injection of SARS-CoV-2 vaccine along with the alcoholic extract adjuvant were compared to aqueous propolis extract and did not show any significant difference (P-value=0.897). The results of the cytokines revealed that the aqueous extract and especially the alcoholic extract of propolis induced Th1 modification. The results of the total antibody response showed that the level of the responses was in line with Freund and Alum adjuvants. However, the propolis adjuvant vaccine candidate significantly strengthened the antibody response compared to the vaccine group only, and IgG1 was the predominant isotype pattern in our vaccine model of SARS-CoV-2. Conclusions: The findings of our study revealed that propolis can be used as a suitable adjuvant in the SARS-CoV-2 vaccine component. Hence, it can be considered an appropriate candidate for SARS-CoV-2 vaccine development. Keywords: SARS-CoV-2 vaccine; propolis; aqueous extract; alcoholic extract; adjuvant.



چهاردهمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



The prevalence of asymptomatic infection in variants of beta, delta, and omicron surges

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G-04861 نوع پذیرش: پوستر | کد مقاله:

Abstract: Abstract Background: The coronavirus causing COVID-19 had infected about 650 million people and killed more than 6.6 million worldwide. Asymptomatic individuals play a substantial role in the SARS-CoV-2 Transition. Therefore, the aim of this study is to compare the frequency of asymptomatic people during three waves caused by beta, delta, and omicron strains. Methods: This retrospective study was performed from December 2020 to March 2022. The subjects studied were passengers on foreign flights that referring to Gerash clinical and Molecular Diagnosis Laboratory. Real-time PCR used for SARS-CoV-2 diagnosis. Results: Out of 8592 international passengers referred to our lab, 139 (1.16%) were positive for SARS-CoV-2 infection. In beta surge, 35(1.49%) out of 2335 passengers, in delta surge, 31(0.6%) out of 5127 passengers, and in the omicron Surge, 73(6.46%) out of 1130 passengers had a positive for SARS-CoV-2 test. The frequency of asymptomatic infection was significantly higher in the omicron surge when compared to two other surges. Conclusion: Considering the asymptomatic transmission's role in the spread of covid-19 disease, it seems necessary to reform health policies in dealing with Omicron substrains in the future surge of COVID-19. We also suggest to focusing on the second generation of vaccines to prevent infection, not only disease, should be a priority of the World Health Organization. Keywords:

Application of Artificial Intelligence (AI) and Machine Learning (ML) to distinguish between influenza and COVID-19 based on laboratory findings and clinical evidence.

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G-84179 نوع پذیرش: پوستر | کد مقاله:

Abstract: Background: The corona disease pandemic emerged as a health problem in the world in 2019 and spread rapidly. Studies show that people with corona disease usually show mild symptoms of respiratory tract infection in the early stages. Influenza is an acute respiratory disease whose symptoms appear with variable severity. Influenza like SARS-CoV-2 has the characteristics of high infectivity, high incidence and easy mutation. Both of these diseases cause significant mortality worldwide. Although corona disease and influenza have significant similarities in symptoms and transmission routes, they differ in many ways, including treatment regimens and prognosis. In addition, cases of infection with COVID-19 often show a more severe range of clinical symptoms. Therefore, accurate diagnosis of these two respiratory tract infections in the early stages is very important for physicians, however, until now, there is no tool available that can distinguish between these two diseases in the absence of evidence and results of molecular diagnostic tests. Machine learning is the biggest branch of artificial intelligence, which has faced many successes in recent years. Machine learning models can manage large data sets whose processing capabilities are beyond human capacity. It can also be useful by revealing hidden relationships between data in diagnosing diseases that have similar symptoms and are difficult to distinguish from each other. Materials and Methods: In this research, reliable external databases such as PubMed, Scopus and Google Scholar, which were published until November 2022, were used for data search. Results: Our investigations show that age, sex, C-reactive protein levels, functional impairment in the senses of smell and taste, eye problems including: conjunctivitis and tear shedding, as well as in relation to hematological findings, the number of circulating monocytes, the number of platelets and mean hemoglobin concentration (MCHC) can be meaningful indicators in differentiating influenza and COVID-19. Conclusion: This study demonstrates that a machine learning-based approach provides a tool that enables rapid and accurate triage of patients to differentiate COVID-19 from influenza. This approach can be used in areas where high numbers of cases of Covid-19 and influenza occur, as well as in areas where health facilities and health professionals are not readily available. Also, machine learning can be useful in reducing treatment costs, improving patient health, improving the quality of healthcare, and making decisions to save patients' lives at the right time. Keywords: COVID-19, Influenza, Machine Learning

Machine learning-based prediction and COVID-19

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G-64105 نوع پذیرش: پوستر | کد مقاله:

Abstract: Background: On December 31, 2019, a severe lung disease of unknown origin was reported in Wuhan, China. It was later discovered that the cause was a new strain of coronavirus, now known as severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2). The virus can cause mild to severe respiratory infections in humans. Common symptoms of coronavirus disease include fever, dry cough, difficulty breathing, and weakness. Machine learning (ML) is a branch of artificial intelligence that can be used to classify datasets and predict new data by using statistics, probabilities, and mathematical relationships in data. Machine Learning includes two general categories, supervised and unsupervised, each of them includes several sub-categories that are used for classification or new predictions. Since the emergence of the corona disease, researchers have investigated of this new virus. Among the most important of them, artificial intelligence and machine learning can be mentioned. Methods: We searched PubMed, Scopus, and Google Scholar for Application of machine learning for corona disease, published up to December 15, 2022. Results: A large number of patients with corona may have mild symptoms at all but they can increase the risk of transmission to others, so it is important for health care providers to have tools for early detection of patients. The spread of the disease may be controlled through early detection of the patients. Many methods are used to diagnose the corona disease, among which we can mention things like RT-PCR test, which has limited in sensitivity and specificity and is time-consuming. In addition, there is a need for accurate collection of samples and the presence of experts, which is considered a weakness for developing countries. Other cases is the use of CT-Scan images of patients' chests. One of the problems of which can point to the high dose of radiation, which is restricted for children and pregnant women. Although viral tests are still the only way to definitively diagnose the corona disease, common and available data such as clinical symptoms, routine blood tests and chest x-ray imaging of patients, in which patients are exposed to a low dose of radiation, can be used for rapid diagnosis patients. One of the important points and advantages of this method is that these data can be collected quickly. Research shows that things like serum ferritin, WBC count, lymphocyte count, body temperature, CRP, LDH, Di-dimer, need for oxygen, respiration rate and blood oxygen level are the most important features that can help diagnose corona disease by machine learning. Conclusion: In order to effectively diagnose corona patients, researchers have used machine learning but the remarkable thing is machine learning can diagnose patients with high accuracy rapidly with the help of data that can be obtained at low cost and quickly. It should also be noted that machine learning is not only used to diagnose patients with corona, but by using other available data, it can be used for important purposes such as classifying patients in terms of risk level, probability of admission to ICU and or used to get the disease pattern in the coming days and months. Keywords: COVID-19, Machine Learning, Artificial intelligence

Effectiveness of convalescent plasma on the treatment of Ebolavirus disease: Systematic Review

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G-31094 نوع پذیرش: پوستر | کد مقاله:

Abstract: Background: During the 2014-2016 Ebola outbreak in West Africa, many treatments were tested. A prominent option for the treatment of emerging infectious diseases, including Ebola, is the use of convalescent plasma (CP). The World Health Organization encouraged using convalescent plasma from healed sufferers for empirical cure throughout the Ebola prevalence. In this study, we conducted a systematic review of the effect of convalescent plasma for the treatment of Ebola. Methods: A comprehensive search was conducted based on PRISMA guidelines on some online databases including PubMed, Scopus, Web of Science, and ClinicalTrial.gov (until 10 December 2022) to look for clinical trials and observational studies. Furthermore in this study, the researchers used the keywords such as Ebolavirus, Ebola Hemorrhagic Fever, Passive Immunization, and Convalescent plasma combined with Boolean operators “AND” and “OR”. A total of 100 studies were identified through initial searching. The reviewers excluded 15 duplicate records, 55 non-relevant articles, and 25 review articles from the studies found. Finally, they used 5 studies for their analysis. Results: The researchers identified 100 studies in their initial search in mentioned databases, and after screening articles’ titles and abstracts, finding duplicates, and reading full texts, 5 studies (containing 2 clinical trial studies and 3 case-report studies) were found eligible for inclusion in this study. Clinical trial studies (cases:128, controls:443) showed that symptoms of disease lasted less time in the convalescent plasma group than did the control group, and also the risk of death was decreased in the convalescent plasma group compared to the control group. According to the 2 case-report studies, 3 patients received convalescent plasma and certain medications, and while the patients recovered from Ebolavirus disease, the researchers were unsure if this was because of the convalescent plasma or the medications. Except for one case-report study from Madrid, which showed that a patient experienced acute respiratory distress syndrome after receiving convalescent plasma, these studies found no significant negative effects related to the usage of convalescent plasma. Conclusion: According to the articles reviewed in this study, we found that convalescent plasma therapy is an effective treatment method for Ebolavirus. Although researches in the field of evaluating the effect of convalescent plasma therapy were not enough and may lead to bias so more studies are needed in this field. Keywords: Ebolavirus, Convalescent plasma, therapy, Systematic review

Prevalence evaluation of respiratory viral infections other than SARS-CoV-2 in patients with respiratory infection symptoms from 2021 to 2022

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G-90463 نوع پذیرش: پوستر | کد مقاله:

Abstract: Background Due to the fact that even during COVID-19 pandemic, other viral respiratory infections are still important and they can be misdiagnosed as COVID-19, the prevalence of these viruses is required to be evaluated, especially during the COVID-19 peaks. Thereby, not only the prevalence of viral infections that cause the same respiratory symptoms to COVID-19 is measured, but also the diagnostic errors rate made by depending on the patients' symptoms are being determined. Methods A cross-sectional study is carried out on the referred patients to the Mehr hospital, under observation of Iran University, that had the respiratory infection symptoms but were negative for SARS-CoV-2 PCR result. The negative samples for SARS-CoV2, from Mar 2021 to Jul 2022 that were tested by Real-time PCR as primary screening, were collected. A second Real Time PCR was being done by HiTeq 17 Viro Respiratory pathogen One Step RT-PCR Kit to determine the presence and genotype of other respiratory viruses. To evaluate, the demographic data of the patients with positive samples were analyzed by SPSS v16 and the P-value less than 0.05 considered to be statistically significant. Other parametric variables such as mean age of the patients were analyzed by t-test and Mann-Whitney-Wilcoxon analysis. Results From a total of 549 specimens in primary screening, 311 underwent second PCR in which their mean age \pm SD was 48.2 ± 21.7 y (range: 1-97 y). 161 of them (51.7%) were female. Totally, 15 (4.82%) cases were positive while evaluating the prevalence and genotyping of respiratory viruses including Adenovirus, Parainfluenza, Bocavirus RSV and Human Metapneumovirus. Their mean age \pm SD was 48.5 ± 15.0 y. The prevalence of each virus included 40% (6/15) for hMPV, 26.6% (4/15) for hPiV 1,2,3, 20% (3/15) for hRSV and 13.3% (2/15) for hAdV. None of the samples were positive for Bocavirus. Fever was statistically significant symptom in studied cases. The specificity and sensitivity of the primary screening assay were 100% and 89%. Statistical analysis showed that there was no significant values by gender (P value=0.08), age (P value=0.3), the month of which the sampling was carried out (P value=0.07) and also clinical symptoms (P value=0.05). Conclusion The results of our study showed that other viral respiratory infections, other than SARS-CoV-2, still exist during the COVID-19 pandemic and are able to cause respiratory symptoms. However, as the study showed no significant values between the mean age of the patients, time of infection and their symptoms, they can't be considered as determinant factors for differential diagnosis, accordingly accurate molecular diagnostic methods are required. It is recommended that not only rely on the symptoms to diagnose COVID-19 and other respiratory viruses, and also to observe the efficiency of molecular diagnostic methods in hospitals and other health centers. Keywords: SARS-CoV-2, COVID-19, respiratory symptoms



چهاردهمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Characterization of SARS-CoV-2 mutations and variants during summer 2021 from Tehran, Iran COVID-19 patient.

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G-47203 نوع پذیرش: پوستر | کد مقاله:

Abstract: Introduction: The first case of a new coronavirus that causes severe acute respiratory syndrome was observed in December 2019 in Wuhan, China. From December 2019 until 24 September 2021, there have been more than 230 million confirmed cases of COVID-19, including approximately 4,700,000 deaths. The first submitted sequence of SARS-CoV-2 was collected from a Wuhan market worker on 26 December 2019. In the first days of 2020, the sequence's accession number in GenBank has been published (NC 045512). Due to the Covid-19 pandemic, several studies about sars-cov-2 mutations and phylogenetic analyses have been performed. WHO watch carefully variants and classifies them into a variant of interest (VOI), a variant of concern (VOC), and a Variant of High Consequence (VOHC). VOI is a variant with distinct genetic mutations that have been linked to receptor binding affinity alteration, decrease in antibody efficacy and neutralization property through past infection or immune induction by vaccination, probable diagnostic failure, or escalation in pathogenesis, disease severity, or transmissibility. It can be classified as VOC if there is evidence of a boost in disease severity, transmissibility, neutralizing antibodies inefficacy, in vaccinated or previously infected individuals, or detection inability of diagnostic assays. If there is clear clinical and research evidence for a decrease in the effectiveness of prevention measures or medical countermeasures in comparison to past variants in society, it can be considered VOHC. Previous studies revealed more than 5000 various variants comprising variants with synonymous mutations, non-coding regions mutations, frame-shift deletions, in-frame insertions, non-coding insertions, stop-gained variants, in-frame deletions, non-coding deletions, and missense mutations. D614G, L84S, G392D, L3606F, and D448 deletion are significant changes in the virus genome. Up to now, the variants of concern by WHO included: Alpha(GRY clade), Beta(GH clade), Gamma(GR clade), and Delta(G clade). Recently, the Delta variant (B.1.617.2) was found in India and after a while became the predominant variant globally. T19R, E156G, del157/158, L452R, T478K, D614G, P681R, P681R, and D950N mutations are the characteristic mutations of the delta variant. Research findings revealed that the Delta variant has significantly higher transmissibility properties and also studies showed that vaccine-induced immune response has lower efficacy than Delta. In addition, two variants of interest, Lambda (Gr clade) and Mu (GH clade) were found in Peru and Colombia, respectively that should be monitored more carefully. Keywords: SARS-CoV-2, COVID-19, mutation, Variant, genomic changes



چهارمین کنفرانس بین المللی آزمایشگاه و بائین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



The presence of EBV-EBNA1 increased the expression of the HDAC1 gene in Burkitt's lymphoma cell line

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G-90175 نوع پذیرش: پوستر | کد مقاله:

Abstract: Background: Disruption of p53 at the expression or function levels contributes to cancer progression in Epstein-Barr virus (EBV)-associated tumors retaining the wild-type p53 gene. In this study, we sought to investigate the effects of EBNA1 on the expression pattern of p53-inhibiting genes like HDAC1 and Sirt3 in a Burkitt's lymphoma cell line. Materials and Methods: BL28 cells were transfected with a plasmid containing EBNA1 gene using electroporation technique. Cells with stable EBNA1 expression were selected by Hygromycin B treatment (350 µg/mL for 16 days). The expressions of two p53-inhibiting genes, including HDAC1 and Sirt3 were evaluated with a real-time PCR assay. Results: The results showed that HDAC1 expression was considerably greater in EBNA1-containing cells (P=0.015) compared to controls, although Sirt-3 mRNA expression was only slightly elevated (P=0.342). Conclusions: The growth of EBV-related cancers appears to be facilitated by EBNA1 through upregulation of several p53-inhibiting genes like HDAC1. Furthermore, it seems that further p53-inhibiting/inducing genes should be investigated. Keywords:



چهاردهمین گنگره بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



A comprehensive review of extrapulmonary features of SARS-CoV-2

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G-60238 نوع پذیرش: پوسنر | کد مقاله:

Abstract: The coronavirus disease 2019 (COVID-19) caused a viral pneumonia outbreak in Wuhan, China, in December 2019. It is principally identified with respiratory disease and pulmonary manifestations. However, based on various reports, COVID-19 infection is not only limited to the respiratory tract system but also other organs can be affected. Cardiac manifestations, gastrointestinal complications, cutaneous manifestations, liver dysfunction, neurological abnormalities, ocular findings, musculoskeletal disorders, and hematological manifestations are among the published extrapulmonary clinical manifestations. Lack of awareness and attention to these extrapulmonary features might result in misdiagnosis, delayed diagnosis, incorrect treatment, and eventually increase the spread of the virus by unidentified individuals to others in the community. Therefore, the current study comprehensively reviews and discusses the extrapulmonary manifestations in patients with COVID-19 infection. Keywords: COVID-19, SARS-CoV-2, Extrapulmonary manifestations, Cardiac manifestations, Gastrointestinal manifestations, Cutaneous manifestations



چهارمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



A Systematic Review of the Monkeypox Outbreak in Pregnancy as a Novel Disease

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G-89061 نوع پذیرش: پوستر | کد مقاله:

Abstract: Abstract Background: Since the eradication of smallpox, monkeypox is the most prevalent Orthopox infection of the zoonosis virus in humans. The World Health Organization named this disease a global health emergency condition in 2022 due to the grave risk it raises for human public health. This study aims to investigate the outbreak of monkeypox in pregnancy as a novel disease using systematic reviews. Materials and Methods: Systematic review searches to find the published studies until 2022 in databases (PubMed, Google Scholar) and the recently published abstracts were done using the keywords monkeypox, pregnancy, vertical transmission, miscarriage, and newborn babies. Results: Previous research demonstrates that although monkeypox is a self-limiting illness, pregnant women are more at risk for its hazards and problems than men and non-pregnant women. Pregnant women typically have a variety of clinical symptoms, including fever, narcosis, headache, pharyngitis, lymphadenopathy, skin rashes, and new genital lesions (the most commonly reported place). Monkeypox in pregnancy is accompanied by a high risk of miscarriage, intrauterine fetal death, vertical transmission (transmission from the mother to the fetus during pregnancy or the first 28 days after birth), and preterm delivery. At present, most smallpox vaccines have good immunity to monkeypox. Using the non-multiplicative vaccines that limit the transmission and contagion risk of the vaccine agent is more reassuring. Conclusion: To reduce the risk of infection and transmission of monkeypox, pregnant women and new mothers need to receive careful attention and follow precautionary procedures. These precautions include designating pregnant women for closer monitoring, raising awareness among medical personnel about battling and controlling the infection, looking into cesarean delivery to prevent vertical transmission in cases of genital lesions, limiting visits to pregnant women and new babies, exercising caution when breastfeeding in cases of active lesions on the mother's breast skin, avoiding contact with animals and etc. Keywords: monkeypox, pregnancy, vertical transmission, miscarriage, and newborn babies.

Determination of cell survival in Vero cell line infected with HSV-1 by MTT in comparison with trypan blue methods

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G-27864 نوع پذیرش: پوستر | کد مقاله:

Abstract: Background: Evaluation of cell survival is an important part of cellular studies and the application of the test substance. Today, different methods are being used to evaluate cell survival, and the correlation between these methods is also considered important. In this study, we are going to evaluate cell survival of the Vero cell line infected with HSV-1 (Herpes simplex virus) using two different sensitive colorimetric methods including 3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide (MTT), trypan blue. Materials and Methods: Vero cell line cells in DMEM media with 2% Fetal Bovine Serum (FBS) were treated with logarithmic dilutions of HSV-1 virus from 10¹ to 10⁴, then the viability of cells was evaluated by MTT and Trypan methods after 0, 4, 8, and 24 hours. Survival curve were plotted using the survival results. TCID₅₀ assay was performed to determine the infectious dose of the virus using inverted microscopes, then the results of cytopathic effect (CPE) were compared to the results of MTT and trypan blue methods. Results: TCID₅₀ showed that the virus infectious dose was 2.37×10⁶/ml. There was no significant difference between the methods (P 0.05). Regression analysis for cell survival showed a linear, positive and significant correlation between methods and there was a correlation between MTT and trypan blue methods (P 0.01, r = 0.85). Conclusion: Results showed both trypan blue and MTT methods can be used to determine cell survival, and results of the trypan blue method can be confirmed by the MTT method. Keywords:

The correlation of platelet-monocyte aggregate formation and IFITM3 gene with COVID-19 severity

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G-29785 نوع پذیرش: پوستر | کد مقاله:

Abstract: Background: The COVID-19 pandemic has posed a severe health and economic burden, claiming more than 0.8 million lives throughout the world. There is growing evidence of the role of platelet-leukocyte aggregates in inflammation. An increase in platelet-leukocyte complexes levels in acute ischemic stroke, renal disease, liver, and pulmonary infection is associated with the prognosis of various inflammatory diseases. On the other hand, the IFITM3 protein has a role in elimination of various viral infections. However, the role of platelet-leukocyte aggregates and IFITM3 in the severity of COVID-19 is still far from being completely understood. Therefore, this study aimed to determine the correlation of IFITM3 mRNA expression and platelet-monocyte complex level with the severity of COVID-19 and various inflammatory and coagulation markers. Materials and Methods: This cross-sectional study was conducted on 54 COVID-19 patients. The patients were classified into two subgroups: severe and mild/moderate COVID-19. The general demographics and the general laboratory findings of the patients were extracted from their medical records. Determination of IFITM3 mRNA expression level was carried out using q-RT-PCR. Moreover, to measure the level of platelet-monocyte complex formation, the flowcytometry assay was carried out for the detection of CD61 and CD14 cell surface markers. Results: We were not found a significant difference in the level of IFITM3 mRNA and platelet-monocyte complexes between severe and mild/moderate groups (p.value 0.05). However, MNCs were significantly higher in mild/moderate COVID-19 patients compared to severe patients. Moreover, lymphocyte count was significantly higher in the mild/moderate study group. While in severe patients, the neutrophil count was significantly higher. Furthermore, the level of CRP and LDH were significantly higher in severe COVID-19 patients. As we expect, there was a relatively strong positive correlation between the hospitalization period and CRP, CRP with neutrophil and LDH as well as O₂ saturation with lymphocyte. In contrast, there was a strong reverse correlation between hospitalization period and O₂ saturation, O₂ saturation with neutrophil and CRP and LDH, lymphocyte with CRP and LDH. Conclusion: Monitoring COVID-19 patients for inflammation biomarkers is indispensable for better management and outcome for the patients. A more precise investigation with a larger sample size is needed to shed light on the involved mechanisms. Keywords:



چهاردهمین گنگره بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



To investigate HIV reverse transcriptase drug resistance among Lorestan province patients

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نوع پذیرش: پوستر | کد مقاله: G-87243

Abstract: Background: HIV Drug resistance has been considered as one of the main challenges in the treatment of patients infected with HIV all around the world. The aim of this study is to determine drug-resistance mutations of the HIV reverse transcriptase (RT) gene in patients of Lorestan who are treated with antiretroviral drugs. Materials and Methods: During a descriptive-cross-sectional study, the blood samples of 59 patients undergoing antiretroviral drugs (HAART) were collected from September 2020 to September 2021. Post-screening tests, the low CD4+ lymphocyte count under 500 cells/ml was an indicator for determining drug resistance. Subsequently, to determine the drug resistance mutations, nested RT-PCR technique was performed and PCR-product was sequenced by Seis micro synth company. Results: Out of 28 patients with the low CD4+ lymphocyte count, 57.14% (12) were male and 42.85% (16) were female. In this study, the frequency of risk factors including intra-venus drug users, prison, and unprotected sexual contact were (44.1%), (28.8%), and (23.7%), respectively Also, we observed, the most common mutations against nucleoside reverse transcriptase inhibitors (NRTIs) are M41L and T215Y mutations in 16.66% of subjects, and the most common mutations against non-nucleoside reverse transcriptase inhibitors (NNRTI) are A98G and P225H mutations in 14.28% of patients. Conclusion: In this study, our data suggested that the major mutations related to NRTI drugs are M41L and T215Y polymorphism, and mutations related to NNRTI including A98G and P225H. Keywords: HIV, HAART, Mutation, NNRTI, NRTI

Electrochemical biosensor for the detection of HBV and HCV A narrative review

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G-29845 نوع پذیرش: پوستر | کد مقاله:

Abstract: Background: In the last few decades, viruses have been a constant threat to human lives. Numerous viral outbreaks have occurred all over the world and many of them are still ongoing epidemics, such as the hepatitis caused by HBV and HCV. Therefore, rapid identification could play a crucial role in controlling the outbreaks. Current approaches for the identification of viruses are polymerase chain reaction (PCR), enzyme-linked immunosorbent assay (ELISA), viral culture, and western blotting-based tests. Despite the fact that such techniques are considered the gold standards for the identification of viruses, they are time-consuming, expensive, not suitable for a rapid point-of-care diagnosis, and require the presence of an expert. As a result, all these obstacles reduce the quality of patient care, which encourages researchers to develop a method based on biosensors, specifically given the latest developments in this field in the past few years. Considering their high sensitivity, cost-effectiveness, and the possibility of their miniaturization, biosensors have the potential to be used as a rapid and point-of-care (POC) diagnosis method. Method: This narrative review assessed studies on biosensors designed for the detection of blood-borne viruses available in the Science Direct and Pubmed databases, from 2012 to 2022. Result: Biosensors are analytical devices that can convert different biological products into measurable signals. Different parts of the virus can be applied for this purpose, thus there are several types of biosensors based on their samples including Aptamer-based biosensors, which are single-stranded oligonucleotides (RNA or DNA), with a length of 10 to 100 nucleotides that can attach to numerous biological and non-biological molecules such as organic dyes, amino acids, and whole cells. The aptamer is a recognition element for the biosensor, binding to the target with high specificity and affinity to avoid interference with other biological products. Then the transducer converts signals between the target and aptamer into a digital monitor reader. It is worth mentioning that Aptamers can bind to different parts of HBV and HCV, such as HBsAg, HBeAg, and HBcAg in HBV and core antigen, NS3 helicase, and NS5 RNA polymerase in HCV. The development of biosensors has its challenges. The sensor's performance has not yet provided enough stability and affinity in order to go through clinical trials, because all aptamers are monovalent, and parameters like sample condition, temperature, PH, and ionic strength will affect the selectivity of the test. Conclusion: Despite the challenges encountered in the development of biosensors, it still seems to be a promising approach for viral detection. Therefore, through their rapid response, high selectivity, cost-effectiveness, and small sample size, biosensors could be a useful means for healthcare centers to control and screen different diseases in the event of the occurrence of new epidemics and pandemics of viral diseases. For future studies, it is recommended to evaluate the lifetime of the biosensors, making them more suitable for POC tests. Keywords:



چهاردهمین گنگره بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Epidemiological characteristics of Delta variant of COVID-19 infection among children in Afghanistan

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G-62548 نوع پذیرش: پوستر | کد مقاله:

Abstract: Background: The delta variant (lineage B.1.617.2) was identified in late 2020, the prevalence of the delta variant greatly increased in India, and spread rapidly worldwide. About 60% of infected cases in Kabul are reported to be delta-type. In this study, we investigate the epidemiologic characteristics of cases of delta-type covid-19 pneumonia in children in Afghanistan Materials and Methods: We collect and review the information required for the study, which is approved by the Ministry of Public Health of Afghanistan, which includes age, gender, PCR test, history of contact with an infected person. Results: 169 children were infected with covid-19 delta type, of which 102 were boys and 67 were girls. The average age was 8.68 years and the age range was 8 to 18 years. 122 cases (72.18%) had a history of close contact. 47 cases (27.81%) had a history of close contact in schools, hospitals, etc. All patients with delta type were confirmed by PCR test. Variant delta infection mainly affects children through close family contact and rapid community spread. The regional distribution of infection was highest in Kabul (93 cases), followed by Herat (41 cases) and Ghazni (35 cases). 159 cases (94.08%) of mild clinical manifestations and 10 cases (5.91%) of common type were treated with clinical treatment. Conclusion: After the emergence of Delta type of Covid-19 in India, its prevalence also increased in Afghanistan. The transmission ways of non-compliance with the health protocol, close contact with the infected person, the number of children with the delta variant has also increased. Due to the weak facilities and health infrastructure in Afghanistan, a large number of patients have not been diagnosed. Early detection and control measures are essential. Keywords: COVID-19, Delta variant, Afghanistan, Epidemiology



چهاردهمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Investigating the process of infection caused by intestinal parasites in Iranian HIV positive patients: a review article

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G-28617 نوع پذیرش: پوستر | کد مقاله:

Abstract: Background: AIDS is now recognized as a worldwide crisis. Gastrointestinal parasites are the main cause of infection in HIV positive patients. Protozoa and helminth parasites are the most common opportunistic parasitic infections associated with the gastrointestinal tract in immunocompromised patients. This study was conducted with the aim of investigating the prevalence of intestinal parasites in Iranian HIV positive patients. Materials and methods: We searched MEDLINE via PubMed, Scopus, Science Direct, Web of Science (ISI), Google Scholar (as English databases); Magiran, Iran Medex, Iran Doc, and SID (as Persian databases) during 1996 to September 2021 using the terms: parasitic intestinal infections, Giardia lamblia, Cryptosporidium, Enterobius vermicularis (oxyure), Isospora belli, Ascaris lumbricoides, Entamoeba histolytica, Human immunodeficiency virus (HIV), Acquired immunodeficiency syndrome (AIDS), Iran. Results: In general, intestinal parasites have a high prevalence in the HIV+ population. In particular, most of the parasites identified in the HIV+ population during studies conducted in Iran include: Giardia lamblia, Blastocystis hominis, Chilomastix mesnili, Entamoeba coli and Cryptosporidium parvum, Endolimax nana, E. histolytica cyst, Dientamoeba fragilis, are enteromonas. IPI has been reported in different regions of Iran, and the most common parasites causing parasitic infections in the HIV+ population in Iran include G. lamblia, B. hominis and C. mesnili species. Conclusion: The present study shows the importance of infection caused by intestinal parasites in HIV positive patients and emphasizes the need to increase the awareness of doctors regarding the occurrence of parasitic infections in these patients. Routine examination of stool samples for parasitic infections can significantly benefit HIV-infected individuals by helping to reduce morbidity, mortality, and improve quality of life. Keywords: HIV+ Patients, Intestinal parasites, Iran

Increasing FOXP3 gene expression in asymptomatic HBV infected patients compared to the control group

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G-40592 نوع پذیرش: پوستر | کد مقاله:

Abstract: Introduction: Forkhead box P3 (FOXP3) is a protein that plays a role in regulating the response of the immune system through regulatory T-cells (Treg). Treg is a CD4+T cell subset which is characterized by expression of CD25 and Foxp3 and by immunological suppression. Treg cells play an important role in modulating responses and immune tolerance to self-antigens. Treg cells modulate the immune response to infectious pathogens in diseases. Effective specific T cell responses are necessary to eliminate the virus. However, viruses can escape from the T cell response. Treg cells play a role in suppressing T antiviral responses and help the virus persist in the host's body. The aim of this study was to determine the expression of FOXP3 gene in asymptomatic HBV positive donors compared to the control group. Methods: To investigate the expression of the FOXP3 gene, patients with history of HBsAg Positive test were selected as HBV positive groups and healthy individuals as control groups. There were 60 samples in both groups. RNA extraction of samples was performed by using the Total RNA extraction kit of pars tous Company. In order to ensure the quality of the extracted RNA concentration, its optical absorption was measured by nanodrop. Total RNA with Oligo dT and Randomhexamer primers were converted to cDNA. Then, Real-time PCR reactions were performed using FOXP3 and GAPDH specific primers in both groups. Data was analyzed using REST software. Results: FOPX3 gene expression in HBV positive patients were significantly increased compared to the control group. The expression of FOPX3 in HBV positive patients was 5 times that of the control sample (P = 0.01). Conclusion: The results showed that the increase of the expression of FOXP3 gene in asymptomatic hepatitis B patients can be considered as a predictive factor of disease chronicity. Keywords: FOXP3, HBV, Real-time PCR



چهاردهمین گنگره بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



The association between underlying diseases and mortality rate in patients with COVID-19 hospitalized in Shohadaie Ashayer Hospital

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G-05124 نوع پذیرش: پوستر | کد مقاله:

Abstract: Background: The outbreak of a new coronavirus (COVID-19) in Wuhan, China in late December 2019 posed a major health threat to global public health. Because patients with underlying diseases are a major risk group for Covid-19, this study was performed to investigate the effect of underlying diseases on mortality in patients with COVID-19. Materials and Methods: This study was performed on 200 patients admitted with Covid-19 in Shohadaie Ashayer in Khorramabad hospital. Required data such as disease severity, clinical manifestations, and mortality rate in patients with underlying disorders were collected with other patients and analyzed using SPSS 22 software. The reliability coefficient for all tests was 95% and the significance level was $p \leq 0.05$. Results: 96 men (48%) and 104 women (52%) participated in this study. The age range of patients ranged from 18 to 80 years. 16.8% of patients had hypertension and 10% of patients had diabetes, 1.9% of patients had cancer and 1% had asthma, 1.6% had chronic respiratory diseases. 1.2% of patients with chronic kidney disease and 8.4% of patients with heart disease. Conclusion: According to the results obtained, the presence of underlying diseases such as high blood pressure, diabetes, cancer, chronic respiratory diseases, chronic kidney diseases, cardiovascular disorders, age over 50 years, male gender, oxygen saturation level on arrival below 93% and length The duration of symptoms for more than 5 days can increase the probability of death due to Covid-19. The severity of the disease, clinical manifestations, and the mortality rate of COVID-19 in patients with underlying disease especially hypertension and diabetes were significantly different from other COVID-19-infected patients. Keywords: underlying diseases, mortality rate, COVID-19

Ligand-based 3D pharmacophore modeling, virtual screening, and molecular dynamic simulation of potential Smoothened inhibitors

مآنده مقدم @¹ علیرضا محبی ©²

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نوع پذیرش: پوستر | کد مقاله: G-72169

Abstract: Hedgehog (Hh) signaling is essential to regulating pathway. Aberrant Hh signaling mediates Smoothened (SMO)-associated cancer development. Inhibition of Hh pathways is encountered by emerging drug-resistant SMO mutants. The aim of the study was to discover novel Smoothened inhibitors with stable binding affinity to SMO and its mutants. 25 SMO inhibitors were clustered structurally to develop a ligand-based pharmacophore model with LigandScout v3.12 software. A library of 500,000 chemicals were virtually screened for hit identification. Molecular docking was performed to identify potential leads based on SMO affinities. Molecular dynamic simulation (MDS) was performed with Gromacs v5.1.4 to analyze the structural changes of SMO oncoprotein upon binding lead compound(s) and Cyclopamine as the control for 100 ns. The affinity of lead compound(s) was evaluated on clinical and laboratory SMO mutants. A model with 12 pharmacophore features were developed and validated for virtual screening (VS). VS has resulted in the identification of 145 hits. One chemical compound, LCT10312, with the highest affinity to SMO, was used for MDS. A significant conformational change was observed in the SMO structure upon binding LCT10312. PCA showed stable interaction of the lead compound with SMO and large atom motions, indicating SMO structural fluctuation. The lead compound showed high affinities to several clinically Basal cell carcinoma (BCC)-associated SMO mutants. LCT10312 is highlighted as a candidate for inhibition of the wild-type or mutant SMO oncoprotein. The stable binding of the lead chemical into SMO's extracellular domain causes structural instability of the oncoprotein and may halt the Hh signaling cascade. Keywords:



چهاردهمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Evaluation of the severity of COVID-19 in people living with HIV; a review study

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نوع پذیرش: پوستر | کد مقاله: G-73845

Abstract: Background: Patients with HIV infection may be at an increased risk for morbidity and mortality from the COVID-19. This study aimed to investigate the severity of COVID-19 disease in people living with HIV (PLHIV). Materials and Methods: We conducted a systematic review of all articles and reports conducted in the Scholar, PubMed, and Magiran databases regarding the effects of COVID-19 on PLHIV from the beginning of 2020 until today. Results: A total of 1893 articles were found. After deleting unrelated articles according to keywords, a total of 507 articles were selected, after deleting duplicate articles, 400 subjects were selected and finally, after reading the abstracts 59 studies were included in our analysis. Finally, 15 papers were selected depending on the type of review. Conclusion: The results of the present, prevalence, severity of COVID-19 in PLWH was similar general population and this finding suggests that HIV infection not a risk factor for COVID-19, and generally, PLWH should receive the same treatment approach applied to the general population. Keywords: COVID 19, SARS-CoV-2 infection, HIV, Review

Validation of Real Time PCR method to evaluate proviral load of HTLV virus with TaqMan probe

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نوع پذیرش: پوستر | کد مقاله: G-09723

Abstract: Background: Human T lymphotropic virus type 1 (HTLV-1) is one of the most important viruses that is transmitted through blood products infected with the virus. The diagnosis of this infection in blood donors is very important. HTLV-1 screening tests are performed for blood donors in seven provinces of Iran, such as Khorasan Razavi, Northern Khorasan, Southern Khorasan, Alborz, etc. Determining the HTLV proviral load is one of the reliable markers in the prognosis and progress of the disease and understanding the process of virus pathogenesis. Therefore, accurate measurement of HTLV-1 proviral load is very important. Quantitative molecular tests such as TaqMan Real Time PCR can be used to measure the proviral load of the virus. The aim of this study is to validate the TaqMan Real Time PCR test to measure the proviral load of HTLV in blood donor infected with this virus. Materials and Methods: The plasmid containing Tax gene of HTLV-1 virus was used as a standard sample. After the process of linearizing circular DNA and determining its concentration to copy number per μL , a 10-fold serial dilution of it (3.2×10^1 - 3.2×10^8 Copy/ μL) was prepared. In order to determine the accuracy and sensitivity, specificity and precision of the test, the prepared dilutions (3.2×10^1 - 3.2×10^8 Copy/ μL) were evaluated in triplicates in each run for three consecutive days. Results: The limit of detection (LOD) that can be measured in this method was 3.2×10^2 Copy/ μL . The average Ct variation coefficient of standard samples was less than 1% and 3.8% for inter and intra assay. In order to determine the linearity of the standard curve of each of the prepared dilutions were evaluated in triplicates in one run, in the range of 3.2×10^2 - 3.2×10^7 Copy/ μL and the slope of the graph was equal to -3.2, with $R^2=0.99$. In order to determine the specificity of the test, the primers used were compared with the sequences published in the gene bank. Also, the results of testing primers on genome of other viruses (HHV8, HBV, HIV, HCV and HSV) and genomic DNA were negative. Conclusion: The results of this study showed that the TaqMan Real Time PCR test used has appropriate specificity and sensitivity and can be used to determine the virus load. Keywords: Quantitative Real Time PCR, HTLV-1, TaqMan prob, Proviral load

Investigating different sources of MSCs in clinical trials for the treatment of COVID-19: a systematic review

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G-86095 نوع پذیرش: پوستر | کد مقاله:

Abstract: Background: The disease of COVID-19 is declared as a pandemic by the World Health Organization (WHO). This disease, which is a multi-system disease, requires different strategies to treat it and a single treatment is not effective for such a complex disease. The high rate of death and complications of this disease has increased its importance for researchers. Organ or tissue damage, inflammatory processes, and respiratory distress syndrome (ARDS) are some of the effects of COVID-19. Mesenchymal stem cells are a good candidate for the treatment of such diseases because they have the ability to regenerate and modulate the immune system and even protect and repair lung alveolar cells and help regenerate damaged tissue. Therefore, it can be used as a promising strategy to treat immune system disorders and tissue damage caused by COVID-19. Materials and Methods: The sources used in this study were searched in PubMed, Science Direct and Cochrane Library databases. Only studies that were included in clinical trials and as original articles were studied and selected in 2022. Among these data, it was categorized with the aim of investigating the sources of MSCs and the efficiency of this strategy. Results: Most of the studies conducted on umbilical cord-derived mesenchymal stem cells (UC-MSCs) and after that exosome derived from mesenchymal stem cells, secretions derived from menstrual blood stromal cells (MenSCs), placenta-derived (PL-MSCs) and adipose-derived exosomes (haMSC-Exos) were performed for COVID-19. No complications were observed in these treatment methods and was able to reduce lung inflammation. In a study conducted on UC-MSCs, Significant improvement in SPO2/FIO2 ratio and CRP serum level was reported. In another study using the same source of MSCs, a reduction in the spread of lung damage was observed in the fourth month. Secretions derived from menstrual blood stromal cells (MenSCs) were also able to improve oxygen levels and in hospitalized patients with severe COVID-19, to reduce the cytokine storm. Conclusion: Treatment using mesenchymal stem cells can be useful for adjuvant treatment in improving symptoms. In fact, it is a safe, beneficial and useful method. However, no significant change was found in CT-Scan and no evidence of long-term consequences was reported in the use of MSCs. The use of this treatment method requires more clinical trials with a larger sample size. Keywords: COVID-19, Mesenchymal stem cells, MSCs



چهاردهمین کنفرانس بین المللی آزمایشگاه و بائین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Prevalence of Epstein - Barr virus (EBV) Subclinical Infection in Patients with Acute Immune Thrombocytopenic Purpura (ITP)

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G-53907 نوع پذیرش: پوستر | کد مقاله:

Abstract: Background: Immune thrombocytopenic purpura (ITP) is defined as a bleeding disorder in which the number and production of platelets are reduced by the immune system; however, the destruction of peripheral blood platelets also occurs. Although its exact etiology and pathogenesis have not already known, several studies have shown that Epstein-Barr virus (EBV) is known as possible causative agent of ITP. This investigation aims to evaluate the presence of EBV in two groups of case and control by polymerase chain reaction (PCR). Materials and Methods: we considered the presence of EBV in 48 acute ITP patients and 48 healthy people. Study participants were recruited from Ahvaz Shafa Hospital between 2017 and 2018 and the presence of EBV was investigated by (PCR). Results: Out of 48 acute ITP patients, the EBV DNA was detected from the blood of 2 (4.2%) patients. Also, none of the control group was infected with EBV. Conclusion: Due to the presence of EBV in the acute ITP patients in Ahvaz, it can be considered as factor in the progression of this disease. Therefore, consideration of the methods of elimination and treatment of this virus in these patients may be used as a treatment strategy in ITP patients in the future. Keywords: Immune thrombocytopenic purpura (ITP); Epstein-Barr virus (EBV); Ahvaz



چهاردهمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Investigating the prevalence of depression in patients with Covid-19

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G-02967 نوع پذیرش: پوستر | کد مقاله:

Abstract: Background: The covid-19 disease caused by the virus (SARS-CoV-2) has been classified as a global pandemic by the World Health Organization. The symptoms of this disease may be mild or severe in the form of cough, fever and shortness of breath, and up to 20% of patients show the disease as severe pneumonia with septic shock. Materials and Methods: This study was conducted using a questionnaire on the number of 100 patients with Covid-19 whose molecular test was positive and who were admitted to the hospital. The patients included both men and women and were in the age range of 30 to 60 years. The control includes 100 healthy people from the community who have not tested positive for Corona so far. Results: This study showed that more than 70% of patients with Covid-19 experience some degree of depression. Conclusion: People who recover from the disease after being infected with Covid-19, have mental complications caused by it, such as depression, which needs treatment. Keywords: covid 19, depression, mental disorder.

Urinary Changes During the Affliction to the Renal Corona Virus Disease; A Review on Biochemical and Cell Molecular papers

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نوع پذیرش: پوستر | کد مقاله: G-84062

Abstract: Background: Coronavirus is an emerging virus in 2019 that attracted the world's attention by becoming a pandemic. This virus can transmit through breathing contaminated air and locate in different systems in the host's body. One of these targets is the urinary tract and especially the kidney due to the presence of angiotensin-converting enzyme 2 (ACE2) receptors. The incidence of renal coronavirus disease (R-COVID) is less common in patients without a background of chronic kidney disease (CKD). The spread of this virus in hospital conditions for kidney distress patients is one of the problems created in recent years. Materials and Methods: A systematic review was conducted with keywords (e.g., "COVID-19", "acute kidney injury", "urinary composition", "ACE2") applied in online databases, including PubMed, Web of Science, Scopus, Science Direct, and Google Scholar in recent years. Most relevant papers were retrieved and screened in three phases against inclusion criteria, based on their title, abstract, and their full texts, and eligible records were included in the review. Results: R-COVID is a dangerous disease and can cause kidney failure. After affliction to this disease, the urinary compounds will have some changes. By applying biochemical methods in some experiments by researchers, it was determined that these changes include increase levels of protein, red blood cells, white blood cells, squamous epithelial cells, nitrates, blood urea nitrogen (BUN), uric acid, creatinine, and decrease levels of water, glucose, and ceramides. Conclusion: After circulating in the blood and reaching the urinary system in the glomerulus and renal tubular cells, the coronavirus enters the cells through the ACE2 receptors on the surface of the kidney cells and begins its intracellular life. ACE2 receptors are more abundant in kidney cells than in other tissues. By binding and over-activating ACE2, angiotensin II is produced more and creates a pro-inflammatory state that affects the renal vessels and causes the release of protein and red and white blood cells into the urine, which is a predisposing factor for glomerulonephritis. Furthermore, the response of the immune system to deal with inflammation in the kidney is accompanied by the secretion of various cytokines (including interleukin(IL) (e.g., IL2, IL6, IL7, IL10)). Excessive release of cytokines is called cytokine release syndrome (CRS) and causes cell death and tissue failure. Keywords:



چهارمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Evaluation of the coinfection of viral respiratory influenza type A and Adeno among Covid-19 patients by Real-time PCR method, Golestan province, 2019-2020

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G-68932 نوع پذیرش: پوستر | کد مقاله:

Abstract: Background: In the coronavirus disease 2019 (COVID-19) pandemic era and the outbreak of respiratory viruses such as seasonal Influenza and Adenovirus, the simultaneous detection of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), and these viruses are important in the rapid differential diagnosis in patients with similar respiratory symptoms. Although patients infected with SARSCoV-2, Adenovirus, and influenza A show very similar manifestations, the therapeutic approaches of these respiratory viral infections are different. Since the laboratory diagnosis of simultaneous viral infections in clinical samples can be very important to evaluate the clinical consequences of the presence of several pathogens in the respiratory system of patients. We aimed to study the co-infection of Influenza and Adenovirus in COVID-19 patients. Methods: We evaluated clinical samples from 427 samples from hospitalized patients suffering from Covid19 in Golestan province. These samples were collected during a period of one year from 2019 to 2020. RNA extracts from naso- and oropharyngeal swabs were amplified by one-step Real-Time RT-PCR and Real-Time PCR for the detection of Influenza A and Adenovirus, respectively. Finally, the demographic and clinical information of the patients were collected from the existing systems and the results of the molecular test and the information related to the patients were analyzed with Chi-square statistical tests and Fisher's exact test. Results: Four hundred twentyseven samples were collected from 214 (50.1%) males and 213 (49.9%) females. All the patients were aged 1 to 91 years with an average of 58.08. 83.8% of people were more than 40 years old and 16.2% of people were less than 40 years old. According to Real-Time PCR analysis, a total of 87 (20.4%) samples were positive for 2 viruses. Twenty-three (5.4%) specimens contained SARSCoV-2 and Influenza A and 64 (15%) were mixed adenovirus infections. 7 (1.6%) samples were simultaneously infected with 3 viruses. None of the demographic characteristics of the patients were significant with the results of co-infection with other viruses. The prevalence of Influenza A and Adenovirus were higher in the cold seasons and a significant relationship was also found between adenovirus infection and seasonal distribution (P 0.05). There is a significant relationship between the underlying diseases, asthma and kidney diseases, and the consequences of the disease, such as admission to the ICU and death, with the simultaneous presence of Influenza A. Discussion: It is logical to screen clinical samples during the pandemic or epidemic of viral respiratory viruses to reduce the overall cost and management of patients, especially will be useful in influenza seasons when influenza expected co-circulate with SARS-CoV-2. Keywords:



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COVID-19 and the potential of Janus Family kinase (JAK) Pathway Inhibition: as a novel treatment strategy

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G-46782 نوع پذیرش: پوستر | کد مقاله:

Abstract: Recent evidence proposed that the severity of coronavirus disease 2019 (COVID-19) patients is a consequence of cytokine storm, characterized by increased IL-1 β , IL-6, IL-18, TNF- α , and IFN- γ . Hence, managing the cytokine storm by drugs has been suggested for the treatment of severe COVID-19 patients. Several of the proinflammatory cytokines involved in the pathogenesis of COVID-19 infection recruit a distinct intracellular signaling pathway mediated by JAKs. Therefore, inhibition of the JAK/STAT pathway may induce the inhibition of various cellular responses in COVID-19 infection. In conclusion, JAK inhibitors including baricitinib, pacritinib, ruxolitinib, and tofacitinib have beneficial potential in the recovery and reduction of novel coronavirus disease; due to anti-inflammatory and anti-viral effects. Keywords:



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Epitope mapping of Mpox using bioinformatics approaches

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G-56294 نوع پذیرش: پوستر | کد مقاله:

Abstract: Background: Monkey pox (Mpox) is a zoonotic viral disease caused by the monkey pox virus (MPXV), an orthopoxvirus in the Poxviridae family. Studying Mpox antigens could be helpful in designing rapid tests, ELISA kits, in developing vaccines and developing a basic starting material for future studies. Therefore, this study aimed to investigate the physicochemical and structural properties as well as the immunological features of Mpox antigens by using several bioinformatics tools. Materials and Methods: Eight MPXV genes including E8L, I1L, N2R, N3R, B21R, B22R, B18R and D2L were selected based on literature review. Sequences were retrieved from Uniprot. Signal peptide sequences were evaluated by Signal IP software and removed. Transmembrane domains were assessed by TMHMM server. The B cell epitopes of these eight antigens were evaluated by IEDB, BepiPred and SVMTriP software. MHC class I epitopes were checked by NetMHC and IEDB. MHCIIpan, TepiTool and RANKPEP were used to determine MHC class II epitopes. CTL epitopes and TCR epitopes were predicted by CTLPred and PAComplex software respectively. Prediction of protective antigens and subunit vaccines, antigenicity and allergenicity of selected epitopes were evaluated using Vaxijen, AllergenFP, and ANTIGENpro software. The proper linkers were used to attach selected epitopes to design the final structure. Results: Following all evaluations and screening, four antigens (E8L, B21R, D2L and N3R) were selected and predictions showed that the final structure will be able to trigger humoral and cellular immune systems significantly. Conclusion: Our analysis could determine some epitope regions in Mpox genome. The designed construct is expected to be used to detect Mpox infections or as a novel vaccine to control the infections related to Mpox. Keywords: Monkey pox, Antigens, Immune-informatics



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Molecular Detection of West Nile Virus in pediatric patients with Meningitis and Encephalitis by Real-time PCR in Karaj

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G-70562 نوع پذیرش: پوسنر | کد مقاله:

Abstract: West Nile virus is belong to Flavivirus genus in Flaviviridae family which was isolated from febrile patient in Oganda in 1973. In order to evaluate the prevalence of West Nile virus among pediatric patients with meningitis and encephalitis, RT-qPCR test was performed to diagnose and quantify West Nile virus in cerebrospinal samples. In the present study, a total of 120 CSF samples collected during a year period from pediatric patients with meningitis and encephalitis referred to Karaj Hospital were evaluated. After extraction of viral RNA genome from CSF samples, Real-time PCR test was performed to amplify the capsid region sequence of West Nile virus genome and viral titer was evaluated. Of the 120 samples examined, West Nile virus genomic RNA was detected in 2 samples (1.6%). These positive samples of West Nile virus were related to the month of July and September. The viral titer for positive samples were 3.4×10^3 to 1.2×10^5 copies per ml of CSF. Co-infection of West Nile virus with herpes simplex virus type 1 and 2 was also investigated, but no mixed infection was reported. This is the second diagnosis of West Nile virus in CSF samples of pediatric patients that proves that West Nile virus has been causing meningitis and encephalitis in Iranian pediatric patients with a low presence.

Keywords:

Investigating new techniques of hybridoma to diagnose the disease of COVID-19

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G-17925 نوع پذیرش: پوستر | کد مقاله:

Abstract: Introduction: The present study examines the technological innovations of hybridoma in the development of monoclonal antibodies (mAbs). Advanced research techniques, and various tools are guiding us in understanding the pathways of infection of Covid-19 as well as the key enzymes, and proteins required for virus replication. Viral pathogenesis are designed, and manufactured. Methods: Research strategy, and reference selection criteria for this review, which was searched in the websites, and databases of SID, Pubmed, Iranmed, Scopus, Google scholar, and Cochrane with the key words of "monoclonal antibodies", "COVID-19" compounds, "Hybridoma Techniques", "Diagnosis", and their English equivalents have been done without a time limit, and all found articles that were diagnosed according to the purpose of the study were used. Results: mAbs should be considered for people who are at high risk of developing a serious disease despite the Corona virus vaccination, such as patients with primary or secondary immunodeficiency. In addition, mAbs can be useful for people who cannot be vaccinated due to medical contraindications or allergies or for other reasons, and those who are at high risk of disease. COVID-19 is constantly changing, and mutations in its surface proteins may render it unrecognizable to the host's immune system. Therefore, it is very important that the scientific research community insist on closely monitoring these changes, and developing new practical techniques for diagnosing the Corona virus. Discussion: Considering the current situation of the mutated Corona virus disease, which has been placed in very regular intervals, and more aggressive approaches, new applied techniques such as the hybridoma technique to produce mAbs to prevent the spread of COVID-19, and defeat its epidemic, it seems necessary. Keywords: Emerging techniques, hybridoma, diagnosis, COVID-19, mAbs



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Association between Human Papillomavirus and Oral Cancer in Iran: A Review

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G-85620 نوع پذیرش: پوستر | کد مقاله:

Abstract: Background: Oral cancer, including head and neck squamous cell carcinoma (HNSCC), is a significant public health problem worldwide. Human papillomavirus (HPV) has been identified as a major risk factor for oral cancer, particularly in developed countries. However, the role of HPV in oral cancer in Iran has not been well-established. Studies have shown that the prevalence of oral cancer in Iran is high, and it is the second most common cancer among men and the fifth most common among women. Therefore, understanding the relationship between HPV and oral cancer in Iran is crucial in developing effective prevention and treatment strategies. The aim of this study is to conduct a comprehensive literature review to investigate the relationship between HPV and oral cancer in Iran and to provide a better understanding of the association between HPV and oral cancer in Iran. Methods: A comprehensive literature review was conducted to investigate the relationship between HPV and oral cancer in Iran. A search of the PubMed database and Google Scholar was carried out using the terms "oral cancer," "human papillomavirus," and "Iran" in English-published papers in journals up to December 2022. Discussion and Conclusion: HPV is a significant risk factor for oral cancer in Iran including head and neck squamous cell carcinoma (HNSCC). The studies have found that HPV is present in a significant percentage of oral cancer patients in Iran, and the most common genotype is HPV 16. These findings are consistent with studies from other countries that have shown a high prevalence of HPV 16 in oral cancer patients. Additionally, these findings highlight the need for further research on the prevalence and genotyping of HPV in oral cancer patients in Iran, as well as the implementation of HPV vaccination and screening programs to reduce the burden of oral cancer in the country. Clinicians should also be aware of the possible association between HPV and oral cancer when treating patients with oral tumors or HNSCC. Keywords: Human papillomavirus; Oral cancer; head and neck squamous cell carcinoma; Iran.

Molecular and rapid detection Iranian kit of SARS-CoV-2 based on the RT-LAMP method

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G-87603 نوع پذیرش: پوستر | کد مقاله:

Abstract: Background: Considering the possibility of the emergence of new and unpredictable strains of SARS-CoV-2 and as a result of the occurrence of different peaks of COVID-19, the use of fast, low-cost and accurate diagnostic methods can help in curbing the progress and spread of covid-19. Despite the numerous advantages of the RT-LAMP technique, reports of low sensitivity of RT-LAMP kits have been published in England, South Korea, etc. In this study, to design RT-LAMP reaction primers, we identified a region of the SARS-CoV-2 genome that has the lowest amount of secondary structure formation at the temperature of the RT-LAMP reaction and, in addition, can identify different strains of SARS-CoV-2. Materials and Methods: In this study, the RT-LAMP kit was designed and optimized, which has the ability to detect of SARS-CoV-2 by using a direct sample of the nasopharyngeal swab, and the results can be read visually. The analytical sensitivity and specificity of the RT-LAMP were measured. In addition, to determine the accuracy of the results, 50 clinical samples with indeterminate results in terms of RT-qPCR were received by the Food and Drug Organization of Golestan province to evaluate this kit, and the RT-LAMP test was repeated three times on these samples. After sending the results report, it was found that these samples include 4 samples with Ct Value less than 20, 10 samples with Ct Value between 20 and 25, 12 samples with Ct Value between 25 and 30, 14 samples with Ct Value between 30 and 35 and 10 samples was negative. Diagnostic sensitivity and specificity were calculated according to RT-qPCR results. Results: The RT-LAMP designed in this study had bioinformatics specific primers that can detect the concentration of 5.12×10^{-7} ng of SARS-CoV-2 RNA and also had no cross-reactivity with other respiratory pathogens. Out of 4 samples with Ct Value less than 20, 10 samples with Ct Value between 20 and 25 and 12 samples with Ct Value between 25 and 30, RT-LAMP results were found to be positive, and only one sample was found to be negative out of 14 samples with Ct Value between 30 and 35. Also, all 10 RT-qPCR negative samples were reported as negative by RT-LAMP. Therefore, according to the obtained results, the RT-LAMP designed in this study performance was compared with the gold standard RT-qPCR, yielding 97.5% sensitivity and 100% specificity. **Conclusion:** Iranian SARS-CoV-2 detection kit based on RT-LAMP method due to lower cost compared to similar foreign samples, high sensitivity and specificity, no need for extraction stage and appropriate speed, it can help control and prevent SARS-CoV-2 in case of different peaks of Covid-19. **Keywords:** RT-LAMP, SARS-CoV-2, Detection, COVID-19



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Clinical Performance of RT-PCR and Medical Images for COVID-19 Diagnosis: A Narrative Review

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Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) also called coronavirus disease 2019 (COVID-19) is a pathogen that has not just devastated the lives of millions but has put the entire patients and healthcare system globally under tremendous pressure. The major mean of transmission is inhalation with a predilection for respiratory system involvement, especially in the distal airways.

The current methods used for the diagnosis of SARS-CoV-2 have included reverse transcription-polymerase chain reaction (RT-PCR) that relies on nasopharyngeal swabs and the other technique is the development of computer-based strategies to detect COVID-19 from thoracic medical imaging, such as computerized tomography scan (CT scan) and chest X-ray (CXR). Therefore, the primary diagnosis of COVID-19 plays a significant role in isolating positive cases and preventing the major spread of the disease.

This study reviews the different imaging modalities used in the diagnosis and treatment process of COVID-19 and also mentioned the advantages and disadvantages of this method and compares it to RT-PCR which is considered the gold standard for COVID-19 testing.

In conclusion, our research can suggest virologists and radiologists to select and make better and faster diagnosis methods in the conflict against COVID-19.

Keywords: SARS-CoV-2, Diagnosis, RT-PCR, Medical images, Chest X-ray, CT scan

The trend and magnitude of prolactin level changes in polycystic ovary syndrome status

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G-24613 نوع پذیرش: پوستر | کد مقاله:

Abstract: Background: Among reproductive women, polycystic ovary syndrome (PCOS) and hyperprolactinemia are considered to be the most prevalent endocrine abnormalities. Since hyperprolactinemia occurs due to a range of etiologies, such as certain drugs, pituitary adenomas, hypothyroidism, and renal and liver abnormalities, finding the precise cause requires a process of complete clinical examinations. There are frequent reports of rising prolactin levels in PCOS women. The issue of whether prolactin levels increase with PCOS status or not and determining the degree of prolactin elevation are topics of debate and considered daily challenges for physicians in the practice. These open question were evaluated elegantly in this study. Materials and Methods: The design of the study was cross-sectional, and its data was gathered from two population-based studies. After implementing exclusion criteria, the PCOS group, which was diagnosed based on the Rotterdam criteria, and healthy controls were separated. The trend and magnitude of prolactin level changes in PCOS patients were evaluated using the flexible and reliable method of quantile regression. Results: As a population-based study, it might be claimed that the results are more likely to be robust due to enrolling unselected PCOS women as well as healthy controls from the community. Based on the quantile regression results, in the subgroup of PCOS women younger than 35 years old, an upward trend in the upper reference limit of prolactin levels up to 10 ng/ml was detected. Conclusion: The clinical relevance of the results of this study facilitates the interpretation of prolactin changes in PCOS status and gives the physician assurance that a mild elevation in prolactin levels in young PCOS women may not require a thorough etiological investigation and may instead be explained by changes in hypothalamic/dopaminergic control of prolactin due to PCOS status.



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Simulation and Modeling of Prediction of PARP Inhibitory Anti-Cancer Activity in BRCA Cancer Using QSAR Software

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G-17364 نوع پذیرش: پوستر | کد مقاله:

Abstract: Background: Breast and ovarian cancer is one of the most famous common diseases among women, which has been associated with a significant growth in recent years, so that the statistical results are about 5 to 15 percent of random samples. The Poly (ADP-ribose) polymerase (PARP) enzyme (in the treatment of BRCA1 disorders) is an important protein in the stabilization of various proteins in anti-cancer cells. Several drug combinations have been synthesized to inhibit the Poly (ADP-ribose) polymerase enzyme, one of the kinases, which have significant potent inhibition with IC₅₀ (Half-maximal concentration). Methods and Materials: QSAR modeling for predicting anticancer activity as a semi-inhibitory concentration (IC₅₀) for 51 compounds of the benzo di imidazole-4-carboxamide (HBDI4CA) derivative as PARP enzyme inhibitors was performed against BRCA1 disease using GA-MLR (Genetic Algorithm- Multiple Linear Regression) and LS-SVM (Least Square – Support Vector Machine). Results: The statistical results showed the relative superiority of the SVM model to the MLR method in such a way that its statistical parameters which include $R_{CV}^2 = 0.97$, $R_{LOO}^2 = 0.966$, $F = 130/730$ and $RMSE = 0.132$. Conclusion: It is a confirmation point on the acceptability of the chosen model for predicting the inhibitory activity with a high percentage of confidence. Also, molecular docking was performed in order to obtain the binding free energy and find the best binding mode of the ligand and PARP enzyme, and the results were complementary to the QSAR method. Key words: Polyadip-Ribose Polymerase Enzyme, QSAR Modeling, BRCA1 Disease, Enzyme Inhibitor.

Evaluation of anti-cancer effect of Lupeol against estrogen-receptor positive (MCF-7) and androgen-receptor positive (LNCaP) cancer cell lines

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نوع پذیرش: پوستر | کد مقاله: G-70354

Abstract: Background: Breast and Prostate cancers are among the most frequent cancer diagnosis made in men and women worldwide. The incidence and mortality of these cancers are strongly related to risk factors such as gender, age, genetic and diet. A better prognosis and better therapeutic efficiency is of particular importance for general health perspectives of the different societies. Triterpenes are structural components of plant membranes and bioactive substance in human diets with different beneficial effects. The aim of the current study was to characterize the anti-proliferative and antioxidant effects of “Lupeol” as a dietary triterpene, in line with the its effect on expression of estrogen and androgen receptors on estrogen receptor-positive breast (MCF-7) and androgen receptor-positive prostatic (LNCaP) cancer cell models. **Materials and Methods:** MCF-7 and LNCaP cells were seeded in DMEM (Dulbecco's Modified Eagle Medium) and RPMI 1640 (Roswell Park Memorial Institute Medium) respectively, then, the cells were incubated for 24h with increasing concentrations of the Lupeol (1, 10 and 100 μ M) and the cytotoxic effects of the compounds were determined by MTT and Neutral Red assays. Moreover, total antioxidant capacity (TAC), androgen and estrogen receptor mRNA expression were evaluated. 17 β -estradiol (E2) (9nM) and Dehydroepiandrosterone (DHEA) (5 μ M) selected as the associated controls for the receptors. **Results:** The highest concentration of the Lupeol induced cytotoxic effects on MCF-7 and LNCaP cell lines. Total antioxidant capacity positively correlated with increasing concentrations of the Lupeol. Quantitative PCR (qPCR) analysis showed downregulation of mRNA expression of estrogen receptors (α and β) and androgen receptors by Lupeol. E2 and DHEA treatment resulted in enhanced total antioxidant levels and alterations on mRNA expressions of estrogen and androgen receptors. **Conclusion:** Finally, based on findings from this study, it can be concluded that Lupeol has significant effects on the reducing cell viability of ER-positive breast (MCF-7) and AR-positive prostate (LNCaP) cancer cells. Furthermore, it exerted an inhibitory effect on the expression levels of androgen and estrogen receptors, which are contributing factors in the development of cancer cells. In addition to these effects, evaluating the total antioxidant capacity (TAC) induced by lupeol can account as complementary beneficial effects of lupeol in cancer cases. **Keywords:** Lupeol, Breast cancer, Prostate cancer, Estrogen receptor, Androgen receptor, Antioxidant capacity

Effect of Broccoli Methanolic Extract on Diclofenac Sodium-Induced Oxidative Damage in Wistar Rat Kidney

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نوع پذیرش: پوستر | کد مقاله: G-16240

Abstract: Background: Regarding the nephrotoxicity of non-steroidal anti-inflammatory (NSAIDs) drugs and the actual use of medicinal plants, the aim of this study was to investigate the effect of methanolic extract of broccoli on oxidative stress induced by diclofenac in rats. Materials and Methods: Thirty-two Wistar male rats were randomly divided into four equal groups (eight rat in each group). The control(C) group received physiological saline, the BC group administered methanolic broccoli extract at the dosage of 500 mg/kg (orally), the DC group received diclofenac sodium at dosage of 100 mg/kg, (Intramuscular injection), and the BC+DC group received diclofenac sodium and broccoli for 5 days. After blood collection, serum was isolated and urea, creatinine, interleukin-1, and TNF- α were measured in blood serum. In kidney tissue, malondialdehyde (MDA), superoxide dismutase (SOD), catalase (CAT), and glutathione peroxidase (GPx) were measured. Kidney tissue was stained for histopathological investigation. Results: The results of the present study indicated that diclofenac sodium causes severe kidney damage. The levels of creatinine and urea showed a significant increase in the DC group compared with the control and other treatment groups. The pro-inflammatory biomarkers in blood serum increased in the DC group and significantly decreased in the BC+DC group compare with control and other treatment groups. These changes were in line with the significant decrease of GPx and CAT enzyme levels in the DC group and its increase in the BC group. Malondialdehyde increased in the DC group and reached its lowest level in the BC group. Hyperemic changes, accumulation of inflammatory cells, and bleeding were indicators of diclofenac tissue poisoning reported in the kidney. Conclusion: This study indicated that broccoli extract with strong antioxidant properties could protect kidneys from diclofenac sodium damage. Keywords: Diclofenac sodium, Broccoli, Stress oxidative, Histopathological indicator, Kidney

Evaluation of the pharmacokinetics of molnupiravir in the treatment of covid 19 antiviral drug

فرشته فولادی © ¹

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G-31475 نوع پذیرش: پوستر | کد مقاله:

Abstract: Background: Molnupiravi, sold under the brand name Lagevrio, is an antiviral drug that inhibits the replication of some RNA viruses and is used to treat COVID-19 in people infected with SARS-CoV-2. Molnupiravir inhibits viral replication by promoting extensive mutations in viral RNA replication by RNA-directed RNA polymerase. A ribonucleoside analog is metabolized similar to cytidine, β -D-N4-hydroxycytidine 5'-triphosphate (also called EIDD-1931 5'-triphosphate or NHC-TP). Methods and Materials: QSAR modeling for predicting the COVID-19 as a semi-inhibitory concentration (IC50) for 51 compounds of the [(2R,3S,4R,5R)-3,4-dihydroxy-5-[4-(hydroxyamino)-2-oxopyrimidin-1-yl]oxolan-2-yl]methyl 2-methylpropanoate as virus enzyme incorporates NHC-TP into newly made RNA instead of using actual cytidine disease using GA-MLR (Genetic Algorithm- Multiple Linear Regression) and LS-SVM (Least Square – Support Vector Machine). Results: The statistical results showed the relative superiority of the SVM model to the MLR method in such a way that its statistical parameters which include $R_{CV}^2 = 0.99$, $R_{LOO}^2 = 0.976$, $F = 190/960$ and $RMSE = 0.160$. Results: It is a confirmation point on the acceptability of the chosen model for predicting the inhibitory activity with a high percentage of confidence. Also, molecular docking was performed in order to obtain the binding free energy and find the best binding mode of the ligand and RNA-directed RNA polymerase enzyme, and the results were complementary to the QSAR method. Key words: COVID-19, QSAR Modeling, Enzyme Inhibitor, RNA-directed RNA polymerase

The effect of IL-6 on MRP2 expression and tamoxifen resistance in MCF-7 breast cancer cells

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G-46907 نوع پذیرش: پوستر | کد مقاله:

Abstract: Background: Tamoxifen (TAM) has been widely used to treat patients with estrogen receptor-positive (ER+) breast cancer. Acquired resistance to TAM is a main obstacle to successful endocrine chemotherapy. To elucidate mechanisms underlying TAM-resistance, we aimed to investigate the molecular mechanistic effects of interleukin-6 (IL-6) as a pro-inflammatory cytokine and 17 β -estradiol (E2) on multidrug resistance associated protein 2 (MRP2) expression and tamoxifen toxicity in (ER+) MCF-7 breast cancer cells. Materials and Methods: The effects of IL-6 on tamoxifen toxicity following 20-day treatment of MCF-7 cells with IL-6 and/or E2 were measured by MTT assay. Furthermore, the effects of IL-6 and/or E2 on the mRNA expression and protein levels of MRP2 and NF- κ B (p65) in breast cancer cells were evaluated by QRT-PCR and Western blot analysis, respectively. Results: The respective IC50 values for 4-OH tamoxifen in MCF-7 cells following 20-day concomitant treatment with IL-6+ E2, E2 and untreated cells were 4.07 ± 1.7 , 3.59 ± 0.03 and 3.08 ± 0.5 μ M, respectively. Treatment of breast cancer cells with IL-6+ E2 had no significant effects on mRNA expression levels of MRP2 and NF- κ B (p65) compared to both E2-treated and untreated cells. However, the protein expression of MRP2 was slightly increased. The lack of correlation between gene expression level and protein expression can be due to post-translational events. Conclusion: It seems that IL-6 does not have much significant effect in increasing resistance to tamoxifen, and as we have shown in previous studies, TNF- α and IL-1 β are more important factors in the occurrence of drug resistance to tamoxifen. Also more researches are necessary to elucidate the molecular mechanisms of inflammation on drug-resistance in the tumor environment. Keywords: IL-6, MRP2, NF- κ B/p65, Tamoxifen, breast cancer

The effect of fucoxanthin on migration and EMT –related markers in cisplatin- resistant ovarian cancer cells

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Abstract: Background: Resistance to chemotherapy drugs induces epithelial-mesenchymal transition (EMT) and develops metastatic properties for epithelial ovarian cancer cells and targeting EMT pathway could help as a novel strategy to limit both metastasis and the related drug resistance. Fucoxanthin is a natural compound found in marine algae that has various pharmacologic properties. The aim of this study was to investigate the inhibitory effects of fucoxanthin on cell proliferation, migration and expression of the main markers of the EMT-pathway (E-cadherin, Vimentin and α -SMA) in cisplatin- resistant ovarian cancer cells. Materials and Methods: The inhibitory effect of fucoxanthin on the proliferation of human ovarian cancer cell line A2780 and its cisplatin-resistant derivative, A2780RCIS were measured by MTT assay. The cell migration ability of ovarian cancer cells were evaluated in the presence or absence of fucoxanthin using wound healing migration assay. Furthermore, the effects of fucoxanthin on the mRNA expression of E-cadherin, vimentin and α -smooth muscle actin genes were investigated by qRT-PCR. Results: Our results indicated that fucoxanthin reduced the proliferation of cancer cell lines in a dose- dependent manner. However, treatment of cells with non-toxic concentrations of fucoxanthin (1 and 2.5 μ M) showed no significant changes in cell migration after 48 and 72 hours compared with control group. The results of EMT-related markers expression analysis showed the higher expression level for α -SMA as a mesenchymal marker in A2780RCIS compared to A2780 cells. However, the expression of E-cadherin and Vimentin genes did not show any difference in these cells. No significant changes were observed in the expression of mentioned genes after treatment of resistant cells with non-toxic concentrations of fucoxanthin. Conclusion: This study showed that fucoxanthin was highly effective in inducing death in both cisplatin sensitive and resistant ovarian cancer cells. However, non-toxic concentrations of fucoxanthin are not effective in inhibiting migration in these cells. Keywords: Focuxanthin, Ovarian cancer, EMT pathway, Cell migration

Association between extract of *Euphorbia szovitsii* and expression level of microRNAs in MDA-MB-231 cell line

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Abstract: Background: The miRNAs have been shown to be involved in breast cancer. The aim of the present research was to evaluate the impacts of extract from *Euphorbia szovitsii* Fisch & C.A. May on the expression level of microRNAs in triple-negative breast cancer (MDA-MB-231) cell line. Materials and Methods: The alterations in the expression level of miRNAs in MDA-MB-231 cell line exposed to the extract of *E. szovitsii* were determined exploiting qRT-PCR technique. Results: The expression of MDA-MB-231 cell microRNAs including miR-15, miR-16, miR-21, miR-29, miR-34a, miR-146b, miR-151, miR-155, miR-181b, miR-221, miR-222, and Let-7 was evaluated at 24 and 48 h after treatment with the *E. szovitsii* extract. The treatment of MDA-MB-231 cells with *E. szovitsii* caused a significant elevation in the expression of miR-155, miR-146b (P 0.05), miR-16, miR-21, miR-151 (P 0.01), and miR-34a (P 0.001) after 24 h, and also miR-155, Let-7 (P 0.05), miR-15, miR-29, miR-151 (P 0.01), miR-146b and miR-34a (P0.001) after 48 h. Conclusion: The qRT-PCR findings at 24 and 48 h after treatment revealed that the MDA-MB-231 cell line in the presence of *E. szovitsii* extract showed an alteration in the expression profile of miRNAs implicated in the induction of cell proliferation, apoptosis and migration. These results may be helpful in determining the anticancer activity of *E. szovitsii* in MDA-MB-231 cell line.

Carvacrol induces apoptosis and inhibits colon cancer proliferation

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نوع پذیرش: پوستر | کد مقاله: G-62370

Abstract: Background: Carvacrol is a phenolic compound whose antioxidant, antimicrobial and anti-inflammatory effects have been proven. In the present study, the antitumor effects of carvacrol on SW480 cancer cell line as a model for colon cancer were investigated. Materials and Methods: MTT test was used to evaluate the cytotoxicity of carvacrol on SW480 colon cancer cells. The anticancer effect of carvacrol was calculated as the percentage of treated cells/control cells. To confirm cell death and morphological changes, cells were analyzed by acridine orange/ethidium bromide double staining method. Finally, Ki-67, caspase 3, and Annexin V flow cytometry were used to show the effects of carvacrol on cell growth, proliferation, and apoptosis. Results: Carvacrol inhibits cell growth and proliferation in a concentration-dependent manner. After 48 hours, cell survival decreased to 87.43, 81.67, 59.47, 27.68, and 10.44 percent with 100, 200, 300, 400, and 500 μ M carvacrol treatment, respectively. The IC50 value for carvacrol in the SW480 cancer cell line was approximately 350 μ M after 48 hours. Also, after 48 hours, apoptotic structures were observed in the plasma membrane in the form of bubbles. In contrast to the morphological changes, after 48 hours, the level of Ki-67 decreased to 11.5% in treated cells, while it was 84.1% in untreated cells. In addition, the level of caspase 3 increased to 89.3% in treated cells, while it was 81.9% in untreated cells. Annexin V binding was also increased in carvacrol-treated cells compared to untreated cells. Conclusion: Currently, one of the methods of cancer treatment is the use of natural products due to their non-toxicity and less side effects. We report that carvacrol inhibits the growth of SW480 cells in a concentration-dependent manner, possibly through increased caspase-3 expression. Keywords: cancer, carvacrol, MTT assay, apoptosis

Is there a common laboratory biomarker between two clinically metabolic syndromes of NAFLD & PCOS?

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نوع پذیرش: پوستر | کد مقاله: G-09156

Abstract: Background: Nonalcoholic fatty liver disease (NAFLD) is characterized with the accumulation of lipids, inflammation and ultimately with fibrosis in non-alcohol consumers. On the other hand, polycystic ovarian syndrome (PCOS), is the most prevalent endocrine-related disease in women at the reproductive age. There are increasing number of evidence indicating a tight association between these two metabolic disorders in terms of pathophysiology and also clinical feature. To highlight some overlapping laboratory biomarkers between these two metabolic syndromes the current study has been performed. Materials and Methods: to perform this study, 4 groups of female adult mice (30-35 g) were grouped as: control, NAFLD, PCOS and NAFLD/PCOS (n=6). NAFLD was induced by using high fat /high fructose diet (HFHF_r) for 8 weeks. PCOS was induced in female mice (22-days old) with DHEA (60 mg/kg/day, IP). The control group received 0.1 ml/mouse/day sesame oil for twenty eight consecutive days. The serum levels of hepatic enzymes, TNF- α , blood glucose concentrations and free testosterone and Insulin hormones were determined. Histopathological analyses and oxidative stress-related biomarkers determination on the hepatic and ovarian tissues were also conducted. Any changes in the expression of few inflammation encoding genes were studied by qPCR method. Results: our results indicate that both NAFLD and PCOS induced hepatic enzymes significantly. The serum level of inflammatory cytokine (TNF- α), glucose level, Testosterone concentration also were remarkably (p0.05) elevated in the animals with both metabolic syndromes. Histopathological findings revealed some extra injuries in the target tissues when animal were suffered from both disorders. The measured biomarkers of oxidative stress showed a significant elevation of lipid peroxidation and a significant (p0.05) depletion of total thiol molecules in both target tissues. Both experimentally-induced disorders upregulated the expression of inflammation encoding genes of TLR-2 and TLR-4. Conclusion: our results suggest that there are many similar laboratory findings between these two disorders indicating most likely a common pathophysiologic pathway of insulin resistance with low grade inflammatory reactions and remarkable oxidative stress. Keywords:



چهارمین کنفرانس بین المللی آزمایشگاه و بالین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Examining the performance of pharmaceutical nanotechnology in improving cancer treatment (A systematic review study)

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G-73940 نوع پذیرش: پوستر | کد مقاله:

Abstract: Background: Cancer is characterized by abnormal cell growth and despite major advances in treatment, it is still the main cause of death. For cancer treatment, despite the advances achieved in medicine, chemotherapies still have harmful side effects that cause many deaths. Pharmaceutical nanotechnology has been widely studied to optimize cancer treatment. Oral chemotherapeutic anticancer Nano drugs are an important topic in 21st-century medicine and may drastically change the current chemotherapy regimen and subsequently greatly improve patients' quality of life. The purpose of this study is to investigate the performance of pharmaceutical nanotechnology in improving the treatment of cancer. Methods: This study is a systematic review study that was conducted in 1401. By using the keywords of pharmaceutical nanotechnology, cancer, nanotechnology, cancer treatment, and Nano medicines in reliable databases including PubMed, Scopus, Cochrane, Web Of Science, Embase, and Google scholar search engine without a time limit. To ensure the completeness of the search results, the sources of the articles were checked and after removing the duplicate titles from the endnote software and checking the titles and abstracts, the related articles were checked using JBi tools, after checking the quality of the articles, the findings in the checklist The target was entered. Results: 56 articles were reviewed and 20 of those related to the purpose of the study were selected. According to the investigations, the results of some studies showed that the application of nanotechnology in pharmaceutical science has given us the possibility to build nano systems based on at least two carrier stages (drug/nanomaterial), which often show better pharmacokinetics and bio distribution. Currently, a large number of drug delivery systems are made of nanoparticles, and various materials have been used as drug stimulants or enhancers to improve the effectiveness of treatment and the durability and stability as well as the safety of anticancer drugs. Nano medicines based on nanoparticles, polymer micelles, liposomes, dendrimers, and Nano emulsions were studied along with cancer treatments such as photodynamic therapy, infrared phototherapy, radiotherapy, and gene therapy. Great progress has been made with nanotechnology used in cancer treatment, mainly for nanoparticles and liposomes. As a result of these advantages, Nano materials passively accumulate in the tumor, thereby reducing the side effects of the free drug. Conclusion: The results obtained from the review of articles in this field show that the combination of drugs in Nano systems helps to increase efficiency and reduce toxicity and pharmaceutical nanotechnology, which is the application and further development of nanotechnology to solve drug delivery problems, can provide a better solution and as a result, it changes the method of making medicine and the way of taking medicine, and according to the findings, nanoparticles and liposomes are the most common Nano carriers used for encapsulating medicine and can be effective in improving cancer treatment. Keywords: pharmaceutical nanotechnology, cancer, nanotechnology, cancer treatment, Nano medicines

Protective effects of sertoli cells conditioned-medium against methotrexate-induced testicular damage in rats

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نوع پذیرش: پوستر | کد مقاله: G-43160

Abstract: Background: Methotrexate (MET) is one of the most important chemotherapy agents used against various tumors and inflammatory diseases. Methotrexate cause defective cohenesis, spermatogenesis, fertility impairment and different pathological changes on testis laboratory animals. The current study aimed to investigate Sertoli cells culture conditioned-medium (SCM) recovery effects on MET-induced condition in rats. Materials and Methods: In this experimental study, 21 male mature Wistar rats were randomly divided into 3 groups. In the first group, rats received normal saline intraperitoneally (i.p). In the second group, animals received MET (1mg/kg; i.p) once a week for two weeks. The third group (MET+SCM) rats received MET and a single injection of SCM, 56 days post-MET administration. Fifty-six days later, serum, epididymis, and testicular tissue samples were collected, and the animals were euthanized. Sperm parameters, serum level of luteinizing and follicular stimulating hormones (LH & FSH), and testosterone were examined. The testicular tissues were stained using hematoxylin and eosin staining (H&E), and histopathological changes were analyzed. Results: The MET-induced condition resulted in significant pathological changes in the testis, decreased hormones level, and down regulated sperm parameters. Conclusion: This can be concluded, SCM injection improved hormonal levels, testicular changes, and sperm parameters. Thus, it can be concluded that a single intra-testicular SCM injection accelerates male reproductive system recovery post-MET treatment. Key words: Methotrexate, Testis, Sertoli cells, Rats

Protective Effects of Coenzyme Q10 On Embryos Developing Process in in vitro Fertilization Induced Vincristine Toxicity in Mice

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نوع پذیرش: پوستر | کد مقاله: G-59432

Abstract: Background: Vincristine(VIN) has been broadly used in the clinic for the treatment of various cancers. This drug has toxic effects on the tissues, specially the genital organs. One of the most important side effects is the induced-changes in the female's reproductive system which may lead to infertility. The purpose of this study was to investigate the antioxidant effects of CoA Q10 on the induced -toxicity of vincristine on embryos developing process in Vitro fertilized mice. Materials and Methods: In this experimental study for 21 days, 32 female mice with 20- 25gr weight were divided into 4 groups(n=8). The control group received normal saline (0.1 ml/kg,ip/day), and Sham control group received VIN alone (3mg/kg,ip/week) and experimental group received CoA Q10 (22mg/kg,ip/day) along with VIN(3mg/kg,ip/week).The positive control group received CoA Q10 (22mg/kg,ip/day). After the end of treatment, ovulation stimulated by PMSG and HCG.The sperms were obtained from 10 mature male mice. Animals were anesthetized to killing easily, oocyte and normal sperm were obtained and fertilized in culture medium, then incubated for 120 hours in presence of HTF+4 mg BSA, and embryonic development was examined. Finally, obtained data was analyzed using the SPSS16 software. Results: Vincristine caused a significant decrease in oocyte quality, fertilization rate, embryo developmental stage before implantation and embryo quality. CoA Q10 significantly reduced toxic effects of vincristine. Conclusion: The present study showed that CoA Q10 can protect the reproductive ability of females against vincristine damage. Key words: Vincristine, Ovary, CoA Q10, Mice, In vitro fertilization

Hepatoprotective effects of *Achillea tenuifolia* Lam. extract against nonalcoholic fatty liver induced by high-fat diet

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نوع پذیرش: پوستر | کد مقاله: G-58327

Abstract: Background: *Achillea tenuifolia* is a member of the Asteraceae family that has been used in traditional medicine for treatment of inflammations, gastrointestinal and menstrual disorders. Materials and Methods: In the current study, we assessed the efficacy of a hydroalcoholic extract from the *A. tenuifolia* for hepatoprotective properties and lipid-lowering effects on nonalcoholic fatty liver disease. 35 rats were divided randomly into control, high-fat diet (HFD) rats, and rats received high-fat diet plus a different dose of the *A. tenuifolia* extract for 6 weeks. Results: Oral administration of *A. tenuifolia* extract (100, 200 and 300 mg/kg) lowered body weights dramatically lesser than HFD group and promoted hepatic histology and enzymes and significantly reduced serum lipids and fasting glucose level in rats induced by HFD. *A. tenuifolia* supplementation increased antioxidant properties and decreased lipid peroxidation. Also, *A. tenuifolia* (200 mg/kg) significantly suppressed lipid accumulation in the liver, reduced serum lipid profile in HFD-fed rats. Conclusion: The present study showed that antioxidant properties of *A. tenuifolia* extract may represent a promising approach for the prevention and treatment of obesity-related nonalcoholic fatty liver disease. Keywords: *Achillea tenuifolia* Lam, High-Fat Diet, Nonalcoholic fatty liver disease (NAFLD), Rat



چهاردهمین کنفرانس بین المللی آزمایشگاه و بائین

دانشگاه علوم پزشکی شهید بهشتی - ۱۳ الی ۱۵ بهمن ماه ۱۴۰۱



Comparison of Neurturin protein production in three expression strains of E. coli and different culture conditions

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نوع پذیرش: پوستر | کد مقاله: G-43628

Abstract: Background: Neurturin (NRTN) protein can be used as a therapeutic agent for the treatment of neurodegenerative diseases such as Huntington's disease (HD) and Parkinson's disease (PD). Because of its broad therapeutic potential, its recombinant production is advantageous especially in an economic bacteria like E. coli. So, in this study NRTN was produced in three strains of E. coli and then the components of the culture medium were screened in order to find the most important factors that have positive effects on Neurturin expression level. Materials and Methods: Three strains of E. coli (Rosetta gami, Rosetta gami plys (S), Shuffle (T7)) were used for NRTN production. To confirm the expression, Dot blot technique was used and the results were quantified by Image J. In the next stage, a statistical method based on Fractional factorial design was employed for screening the most significant SOB medium components that significantly influenced the NRTN expression. The results were evaluated by Design Expert software (11.0.3.0). SDS-PAGE was also used to compare the expression level of NRTN in each experiment. Results: Analysis of dot blot results showed that among the three strains used, Rosetta gami had the highest NRTN production level. A fractional factorial design was applied to screen the influence of six variables including tryptone, yeast extract, MgCl₂, MgSO₄, NaCl, and KCl as carbon, nitrogen, and ion sources in 16 experiments. The accuracy of the model was confirmed with the determination coefficient (R²) = 0.9723 and F-value of 30.76. According to the model and analysis protein electrophoretic bands, tryptone, yeast extract and MgCl₂ were recognized as the most critical factors among SOB medium elements. Conclusion: The results revealed that Rosetta gami is the most appropriate strain for NRTN production. Also, tryptone, yeast extract and MgCl₂ had the most positive impact on NRTN production between the other medium composition factors. Keywords: Escherichia coli, Recombinant Neurturin, Culture medium