Pbi-1

Protective effects of curcumin against kidney injury in rat with type 1 diabetes: based on kidney injury molecule 1 (KIM-1) and neutrophil gelatinase-associated lipocalin (NGAL) expression and oxidative stress markers

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Objectives: One of the serious complications of Type1 diabetes (T1D) is diabetic nephropathy which is accompanied with overexpression of kidney injury molecule 1 (KIM-1) and neutrophil gelatinase-associated lipocalin (NGAL) and enhanced oxidative stress. The present study was conducted to examine the
protective effect of curcumin on the expression of KIM-1, NGAL genes and oxidative damage in the kidney of T1D rats. **Materials and Methods:** Thirty six adult male rats divided into 6 groups (n=6). The control and T1D group received treatment with curcumin or without it (80 and 130mg/kg). After 60 days of treatment, using spectrophotometric methods, biochemical factors and oxidative stress markers were measured. Gene expression of KIM-1 and NGAL was evaluated using quantitative PCR. Also, plasma and urine levels of these two proteins were assayed by elisa kit. **Results:** Diabetes caused a significant increase in the levels of creatinine, FBS, uric acid, urea and creatinine in serum, which were attenuated after the administration of curcumin. There was a significant reduction in the values of creatinine, uric acid, and urea in urine in the diabetic group whereas in the rats treated with curcumin, these values were normalized to the normal level (especially in 130 mg/kg). Curcumin administration had a significant role in modulation of serum lipid profile, and it was shown to decrease the expression of KIM-1 and NGAL genes in the kidney and urinary levels, and improve oxidative toxic stress in the kidney tissues. **Conclusion:** Curcumin can play a protective role in reducing the unpleasant consequences of diabetic nephropathy.
Vitamin E supplementation with Atorvastatin improve insulin sensitivity in diabetic patients with hyperlipidemia

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Background: Improvement of insulin resistance may play an important role in preventing cardiovascular diseases in patient with hyperlipidemia complicated by diabetes mellitus. Clinical studies have reported that statins affect glucose metabolism and insulin resistance and several researches revealed that vitamin E supplementation could improve glycemic control.

Methods: At the present randomized double-blinded clinical trial (IRCT code: 20170918036256N1), 30 type 2 diabetic women with hyperlipidemia were allocated into two groups and treated with 20 mg Atorvastatin plus 400 IU vitamin E supplements (n = 15) or Atorvastatin plus placebo (n = 15) per day for 12 weeks. At the baseline and after 12 weeks of treatment, serum lipid profile, fasting plasma glucose, HbA1c and insulin levels were measured for the both groups. FPG, HbA1c and lipid profile were measured by an enzymatic method
using Hitachi autoanalyzer while insulin was measured by IRMA method, HOMA-IR \[\text{fasting insulin (mU/L)} \times \text{FPG (mg/dL)} / 405\] was used.

**Results:** At the Atorvastatin + placebo group, serum LDL.C level was significantly decreased after 12 week of intervention (p=0.006). At the Atorvastatin + vitamin E group, serum insulin level (p=0.001), HbA1c (p=0.04), LDL.C (P=0.03), TG (P=0.02), TC (P=0.01), and HOMA-IR (P=0.001) were significantly decreased at the end compared to the baseline. After adjusting for the baseline measures, vitamin E supplementation led to significant improvements in insulin sensitivity in terms of HOMA-IR (-1.01 \pm 0.52 vs. -2.56 \pm 0.54, P = 0.04) and serum insulin (-0.55 \pm 0.35 vs. -6.5 \pm 1.3, P < 0.001), compared with the Atorvastatin plus placebo.

**Conclusion:** Vitamin E supplementation with Atorvastatin has a synergistic effect on insulin sensitivity which may has beneficial effects on hyperlipidemia to reduce risk of cardiovascular disease in diabetes.

**Key word:** Atorvastatin, Vitamin E, Lipid profile, Insulin sensitivity.
Effects of biochanin A, an isoflavone, on levels of CTGF and TGF-β in kidneys of STZ induced type 1 diabetic rat

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Background: Diabetic nephropathy (DN) is a common complication of diabetes. The development and progression of DN might involve multiple factors. Connective tissue growth factor (CTGF) and Transforming growth factor-β (TGF-β) are upregulated diabetes nephropathy by promote extracellular matrix accumulation. This effort was undertaken to study effects of biochanin-A (BCA: as an anti-diabetic) on CTGF and TGF-β levels in kidney tissues of STZ induced type 1 diabetic rat.

Methods: We randomly selected 2 groups from 30 male Wistar rats. We used 6 rats in each group selected 1 control group, Group 1 (which received 0.5% dimethyl sulfoxide), and a second group, Group 2, which received 10 mg/kg body weight (bw) of BCA. Type 1 diabetes was induced in other rats by a single injection of streptozotocin (55 mg/kg bw). Rats with diabetes were randomly divided into 3 groups as follows: Group 3, the control group with diabetes, which received 0.5% dimethyl sulfoxide; and Groups 4 and 5, which received 10 and 15 mg/kg bw of BCA, respectively. At the end of the study fasting blood glucose, CTGF and TGF-β levels in kidney tissues were assessed.

Results: Administration of biochanin A significantly decreased FBG (P<0.05). Furthermore, CTGF levels in kidney tissues of both groups of treated rats were significantly decreased, when compared to diabetic control group (P<0.05). TGF-β levels in kidney tissues of treated rats were decreased, compared to diabetic control group but not significant.

Conclusion: This study demonstrated that biochanin A possesses hypoglycemic activity and play important role in reducing CTGF and TGF-β in kidney tissues and it can delay progression of diabetic nephropathy. No renal toxicity was observed.
Key words: Biochanin A, Diabetic Rats, kindney, CTGF, TGF-β
Pbi-5
The effect of time, temperature and P-chloro-mercuriphenylsulfonic acid during serum storage on HDL₁-C and HDL₃-C concentration
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Background: Accurate measurement of clinical laboratory parameters plays an essential role in the correct interpretation of clinical biochemistry abnormalities. The purpose of this study was evaluation of time and temperature effect on HDL₁-C, HDL₂-C and HDL₃-C stability during storage.

Methods: 50 adult healthy persons were participated. For the isolation of HDL₁-C, we used precipitation method and HDL₁-C data was analyzed by the Abell-Kendal cholesterol reference method. The remaining serum were dispensed into 12 sample tubes and divided into two groups. One of each group was stored upright at room temperature (approximately 25 °C) while another at 4 °C and the half of each group tubes were received p-chloro-mercuriphenylsulfonic acid (PCMPS). The stored serum aliquots from all temperature and time points were analyzed on 1, 2, 3 days post collection.

Results: HDL₁-C concentration at the temperature of room in 24 hours is not changed significantly but over the time decreased (7.2% in 3 days). In addition of PCMPS inhibitor, the concentration began to increase (17.3% in 3 days). But in 4°C, with or without PCMPS, there isn’t significant change in the HDL₁-C concentration. HDL₃-C was found to be the most stable lipoprotein studied because of non-significant effect of storage time and temperature on it.

Conclusion: The results suggest 4°C as the ideal storage condition for the preservation of human serum samples for HDL₁-C assay. Also it is suggested that HDL concentration estimation should be performed in the first 24 hours of samples collection. PCMPS addition didn’t effect HDL subtypes concentration in 4°C.
Keywords: Cardiovascular disease, HDL, Storage Time, Storage Temperature, \textit{p}-chloro-mercuriphenylsulfonic acid
Vitamin D, Clinical Effects And The Measurement Methods: A systematic Review

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Background: Vitamin D is a fat-soluble metabolite which can be mainly obtained from the skin exposure to the sunlight. Foodstuffs containing vitamin D such as oily fish and mushroom are another source of this vitamin. It was long held that vitamin D act only at the skeleton, intestine and kidney. However, after the discovery of vitamin D receptor on almost every tissue in the body, scientists began to investigate nonskeletal effects of vitamin D. The aim of this study is to evaluate diseases related to vitamin D deficiency and the measurement methods.

Methods: In this study, 41 articles with the keywords Vitamin D, Gold standard methods, Deficiency, Intoxication and Disease were searched in PubMed and Google Scholar databases from the year 2012 to 2017.

Results: Although vitamin D intoxication is a very rare condition, vitamin D deficiency is common among the people all around the world. The low serum vitamin D level may increase the risk of epilepsy, hypertension, multiple sclerosis, cancer, type 1 and 2 diabetes, rheumatoid arthritis and many other disorders.

Conclusion: Scheduling a screening program in order to detect vitamin D deficient patients must be a priority for clinical laboratories. Also medicating the detected people with vitamin D supplement should be put into action in order to decrease the risk of many life-threatening diseases. The reference method used for vitamin D concentration assessment is liquid chromatography tandem mass spectrometry. However, many other measurement techniques have also been developed in order to quantify vitamin D serum levels such as competitive protein binding methods, immunoassays and chemiluminescence assays.

Keywords: Vitamin D, Gold standard methods, Deficiency, Intoxication, Disease
**Pbi-7**

**High Intensify Interval Training (HIIT) via reduction of adipose tissue iNOS expression improved diabetes feature in High Fat diet induced diabetic rat**

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**Introduction:** Due to the growing trend of diabetes and its complications as well as considering the role of exercise in diabetes management and low molecular evidence of its effectiveness of exercise on diabetes, the current study aimed to compare the effect of high intensity interval training and continuous endurance training on serum glucose level and iNOS gene modulation (mRNA and protein level) in visceral adipose tissue.

**Methods:** 45 healthy male Wistar rats, average weight of 200±10 gr after induction of diabetes by high fat diet were divided randomly to 4 groups: normal healthy control (NC), diabetic control (DC), continuous endurance training (CET) and high-intensity interval training (HIIT). Training programs were done 5 days/week for 10 weeks. CET group protocol included 30 minutes running at 50 to 60 percent of VO2max.

HIIT protocol consisted of 5 repeated interval of 2 minute rat’s sprint on the treadmill at each rat’s 80-90% VO2 max workload with 1 minute 30-35% VO2 max interval. We assessed the seromic glucose level using glucose oxidase method. In addition, iNOS mRNA expression was assessed by real time q-PCR and confirmed at protein level by western blooting.
Results: The results showed that both exercise training program reduced glucose level but HIIT more potently reduced glucose than CET group (p<0.001). The comparison of iNOS gene expression in visceral adipose tissue between groups showed that iNOS expression were significantly more in DC group than NDC group (p<0.001) but after 10 weeks of exercise, iNOS gene expression decreased significantly in both HIIT (p<0.001) and CET (p<0.05) groups than DC group. Also western blot analysis confirmed mRNA results.

Conclusion: Our findings suggest that, despite of devoting less time, HIIT workout is more effective intervention than CET for iNOS reduction in adipose tissue of high fat high fructose induced diabetic rats. Because of iNOS importance in macrophage polarization, it's resemble that sport intervention, especially HIIT intervention more potently inhibits M1/M2 polarization which would be responsible of beneficial anti diabetic effects of sport intervention.

Keywords: Diabetes, iNOS, High Intensity Interval Training, Continuous Endurance Training
Pbi-8

The gene expression levels of NPC2 and LAL in atherosclerotic patient and control group

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Background:
Atherosclerosis is the most common cause of cardiovascular disease (CVD). Disturbing of total cholesterol (TC) homeostasis is important in the foam cell formation and the hydrolysis of cholesterol ester (CE) to FC in lysosome by lysosomal acid lipase (LAL) is the rate-limiting step in the cholesterol efflux and cholesterol homeostasis. Recent studies showed that atherosclerosis is a lysosomal storage disease (LSD) that lysosomal proteins such as NPC2 which involved in removal of cholesterol from lysosome are important in the cholesterol homeostasis and atherosclerosis process. Therefor in this study, we investigate the gene expression of LAL and NPC2 levels and correlation between of them in PBMCs of atherosclerotic patients and control group.

Methods:
The expression level of LAL and NPC2 in PBMCs were examined in male atherosclerotic patients (n=40) and control group (n=40) aged>50 years using real-time PCR.

Results:
There were no significant difference in NPC2 gene expression levels (p=0.615). Expression level of LAL was significantly lower (p=0.035) in control group compared to patient group. NPC2 gene expression was directly correlated with LAL gene expression (p= 0.003, r= 0.338).

Keywords: LAL , NPC2 , CVD
Evaluate of COX-2 expression on septic rats

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Background: Sepsis is a complex illness resulted from a systemic inflammatory response to infection and the leading cause of death in ICU. Cyclooxygenase-2 (Cox-2) is an inducible enzyme responsible for the formation of inflammatory prostanoids. Its role in the pathophysiology of inflammatory states like sepsis is increasingly recognized. So, the aim of this study was evaluated the effect of sepsis through considering COX-2 gene expression in liver and lung tissues in expermental cecal ligation and puncture (CLP) rat model.

Methods: Male Wistar rats (250 ± 20 g) were used for all experiments. They were divided into three groups (control, laparatomy (LAP) and CLP). Sepsis was induced in rats by CLP. The total RNA from these tissues was extracted with the RNA total kit (BioBasic Inc, Canada). cDNA was synthesized with PrimeScript™ RT reagent kit (Takara bio Inc, Japan) and oligo dt primers (Takara bio Inc, Japan) according to the manufacturer’s protocol. The primers for PCR were designed with the Gene Runner software Version 3.05 and primer 3 servers. The real-time PCR was carried out for gene expression analysis. All expression data were normalized using GAPDH expression as the internal standard and the fold change on the COX-2 gene was calculated by the formula2^-ΔΔCt.

Results: In comparison to the control group, the COX-2 expression level was increased in LAP groups. Also, the results analysis showed that COX-2 level was significantly increased in two targeted tissues in the CLP group (P<0.05). COX-2 expression leads to elevated protein production which in turn causes inflammation. In other words, COX-2 expression is the key principle to
immunologic disharmony in septic rats, so ceasing the COX-2 expression could diminish the effect of oxidative stress and tissue injury.

Conclusion: We investigated that the cox-2 level in these two tissues can be a biomarker to diagnosis sepsis.

Keywords: COX-2, Gene expression, Sepsis, CLP.
Pbi-10

Beneficial effect of High-intensity interval training (HIIT) on miR-122 gene expression in liver of high-fat high-fructose diet induced diabetic rats

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Background: Exercise intervention is strongly recommended to manage metabolic diseases. In this study, we investigate, whether HIIT and CET can induce hepatic miR-122 expression that is related to NAFLD pathogenesis in NAFLD rats with diabetes.

Methods: 40 Wistar rats divided into 2 groups, non-diabetic (NDC) and diabetic .Type 2 diabetes was induced by high-fat high-fructose diet (HFHFD). Then diabetic rats were subdivided into three groups: diabetic control (HFHFD+DC), CET (HFHFD + CET), and HIIT (HFHFD + HIIT). After eight weeks of exercise on a rodent treadmill, we measured miR-122 gene expression in the liver of rats.

Results: HIIT could partially increase miR-122 expression as compared with HFHFD+ DC (26.8%, p =0.68). We observed negative correlations of miR-122 with biochemical parameters(p<0.05).

Conclusions: Exercise training could be a non-pharmacological intervention for improvement of NAFLD of diabetic rats by induction of miR-122. HIIT had a greater effect on NAFLD amelioration than CET.
**Keywords:** Nonalcoholic fatty liver disease; type 2 diabetes; mir-122; high intensity interval training; continuous endurance training
The Effect of Urtica dioica Hydro-Alcoholic extract on Magnesium level in diabetic Patients: A Randomized Single-Blind Clinical Trial

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Abstract

Background: some study have showed that Magnesium deficiency increases in diabetes and cause several disorder e.g. cardiovascular and atherosclerosis. Urtica dioica (UD) may have antioxidant property in T2DM patients by increasing of Mg level. The aim of this study was to assess the effect of UD extract on serum Mg level in diabetic Patients.

Methods: This randomized clinical trial was done in the endocrinology clinic of Rohani hospital (Babol. Iran). Sixty diabetic patients (Fasting Blood Glucose
>126 and HbA1c > 6.5%) were randomly divided into the two drug and control
groups. The drug group received 20 mg/kg/d of hydro-alcoholic UD extract three
times for 8 weeks and control group received placebo. The plasma Mg level was
measured by spectrophotometric method. This study was confirmed by the Iranian
registry of clinical trials (IRCT2014100119364N1) and ethics committee of Babol
University of Medical Sciences (304930). Result: the result of current study
showed that the level of Mg was significantly increased in drug group compared
with the placebo group (P < 0.5).

Conclusions: the finding showed that UD is able to improve antioxidant status by
increasing of Mg level.

Keywords: Urtica dioica, Magnesium and diabetes.
Expression changes of CD177 on septic rats

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Background: Sepsis is a major cause of morbidity and mortality worldwide. As a serious medical condition, sepsis is characterized by a whole-body inflammatory state and the presence of a known or suspected infection. CD177 is an important neutrophil gene that encodes the glycoprotein of the membrane and the expression of this gene is increased during bacterial infections, burns, and pregnancy. The measurement of CD177 mRNA levels has become a useful diagnostic tool for distinguishing some infectious diseases.

In this study, the gene expression of CD177 in major organ in septic rats were compared by real-time PCR.

Methods: The animals (Female Wistar rats; 120-150 g) were divided into 3 groups; control: wild type rats, LAP: with laparotomy surgery, CLP: induction of sepsis with Cecal Ligation and Puncture method.

The total RNA was extracted with the RNA total kit (BioBasic Inc, Canada). cDNA was synthesized with PrimeScript™ RT reagent kit (Takara bio Inc, Japan) and oligo dt primers (Takara bio Inc, Japan), according to the manufacturer’s protocol.

Then, the primers for PCR were designed with the Gene Runner and primer 3 servers. Each mRNA expression value was normalized against the threshold cycle (C_T) of a housekeeping gene expression (GAPDH) and the fold change on the CD177 gene was calculated by the formula $2^{-\Delta\Delta C_T}$.

Results: CD177 expression increased significantly in the LAP group as compared to the control group in whole blood, liver, and lung. Furthermore, there wasn’t any significant difference in the group of laparotomy with CLP in the liver. While
there were differences between LAP and CLP in whole blood and lung. In contrast, when the level of infection increased, we observed that CD177 gene is only expressed more in lung tissue (P<0.05).

**Conclusion:** Increased expression of CD177 suggests that CD177 may have a potential as a novel sepsis biomarker in lung.

**Keywords:** Sepsis, CD177, CLP rats, Gene expression
Pbi-13

Evaluation of the relationship between serum deficiency of vitamin E and selenium in the patients with coronary atherosclerosis

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Abstract

Background: Atherosclerosis is the leading cause of death worldwide. It's caused by high blood pressure, smoking, or high cholesterol, leading to the formation of plaque. Oxidative stress causes changes in vascular structure, LDL-C oxidation, macrophage function, and vascular permeability. It has been proven that antioxidant agents can effectively prevent plaque formation in atherosclerosis. The aim of this study was to evaluate the relationship between serum deficiency of vitamin E and selenium in patients with coronary atherosclerosis.

Methods: In this case-control study, 90 people who referred to Bushehr Heart Center for routine medical examination were checked using electrocardiography, echocardiography and angiography techniques. Those who found to be completely healthy entered the control group (N= 45) and those with coronary atherosclerosis plaque (> 30%) were placed in the case group (N= 45). Serum vitamin E and SE concentrations were measured by using calorimetric and atomic absorption method respectively. The statistical analysis was done using the SPSS version 18.

Results: The results showed that the level of vitamin E in the case group was significantly lower than in the control group. Moreover, those with a higher
arterial stenosis (>70%) had lower serum vitamin E level. Further, the level of serum selenium in the case group was significantly lower than in the control group. Also, in the present study, a significant inverse relationship was found between the serum levels of Se and vitamin E in both groups.

**Conclusion:** The results of the present study showed that in patients with higher arterial stenosis, serum vitamin E levels were significantly lower, and, the serum levels of selenium were higher. However, no relationship was found between the severity of arterial stenosis and serum concentrations of vitamin E and Se in the case and control groups.

**Keyword:** Atherosclerosis, Vitamin E, Selenium
Study of BUN / Creatinine levels in the population with (A, B, O) blood group referred to Golestan hospital, Ahvaz

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Background: The ABO system remains the most important of all blood groups in transfusion practice. In 1900 Karl Landsteiner described human blood group ABO. In addition to red cells, ABO antigens can be found on other tissue cells and in the secretions. The substances are glycoprotein and glycolipid. The aim of this study was to evaluate, BUN / Creatinine levels in the population with (A, B, O) blood group referred to Golestan hospital, Ahvaz.

Method: In the present study, the sera of all population with blood group (A, B, AB, and O) who referred to Golestan hospital Lab, were collected. The sera were tested for detection of BUN and Creatinine levels. The statistical tests were used.

Results: The BUN range of patients were in O blood group (74-119), A blood group (37-139) B blood group (49-149), and the Creatinine range of patients were showed in O blood group (2.8-7.2), A blood group (2-9.3), B blood group (2-9.9) The mean BUN in blood group O (86.2), A (79.7), B (89.6), mean Creatinine in blood group O (4.9), A (5.6), B (5.7), mean age of 59.1 and aged 31-86 years.

Conclusion: The results of present study showed the mean BUN and Creatinine levels in people with blood group B, was higher than other groups.

Key words: Blood Group, BUN, mean, Creatinine.
Evaluating the levels salivary biomarker stress enzymes under psychological stress and its relationship with rumination and personality traits.

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Running Title: Evaluating the Levels Salivary enzymes under Psychological Stress and its Relationship with Rumination and the Five Personality Traits.

Abstract

Objectives: Salivary enzymes are used as a noninvasive biomarker to assess the activity of the sympathetic-adrenal-medullary system. The aim of this study evaluates levels of the salivary acid phosphatase, β-glucuronidase and cathepsin
under psychological tension and its connection with rumination and personality traits.

**Materials and Methods:** In a cross-sectional study a total of 60 medical students, who wanted to participate in the ultimate exam, were chosen by simple random sampling. Two months before exam, the Inventory Emotional Control Questionnaire and the Neo-short form were completed. Saliva samples were taken from students in both the basal conditions and under exam stress. Salivary enzymes levels were measured by spectrophotometry and data was analyzed using paired samples t-test, Pearson correlation analysis and Step wise regression.

**Results:** A significant difference was found between the mean of salivary enzymes levels in the rest and under exam stress. Also, we found a positive and significant correlation between Salivary enzymes levels with Neuroticism, Agreeableness, Rumination, Extraversion at (P<0.01), (P<0.05) level. Neuroticism, Agreeableness and Rumination predicted 45% of the variance of salivary acid phosphatase, Neuroticism and Rumination predicted 49% of the variance of salivary beta-glucuronidase and Neuroticism, Extraversion and
Rumination predicted 38% of the variance of salivary cathepsin under stress exam.

**Conclusion:** According to this study, levels of salivary enzymes may increase in individuals with traits of neuroticism, Extraversion, agreeableness and rumination thought in response to psychological stressors (exam). Also, measuring salivary enzymes could be used in assessing physiological responses to stress, as a noninvasive method.

**Keywords:** Salivary enzymes, rumination, personality traits, stress, Acid phosphatase, B-glucuronidase, cathepsin.
The correlation between thyroid disorders and *H. pylori* gastritis

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**Background:** Hyperthyroidism and hypothyroidism are common thyroid disorders. Thyroid hormones have a great role in mucosal cells regulation and growth of the gastrointestinal tract. In this study, we investigated the presence of helicobacter pylori (*H. pylori*) infections in various types of thyroid disorders.

**Methods:** Our study included 798 subjects that thyroid status identified by evaluation of thyroid hormones (T₃, T₄, and TSH) by Roche-electrochemiluminescence (ECL). *H. pylori* antibodies and antigen evaluated by ELISA kit in all subjects.

**Results:** Hypothyroidism patients have a significant correlation with *H. pylori* infection (P value = <0.001). Hyperthyroidism patients have no significant correlation with *H. pylori* infection (P value = 0.171). Also, in hypothyroidism patients, females more than males have a significant correlation with *H. pylori* infection (P value = 0.004).

**Conclusion:** Decreasing thyroid hormones in hypothyroidism patients can result in dysregulation of gastric mucosal cells. Therefore, they have more chance for the acquisition of gastric inflammation such as *H. pylori* gastritis.

**Keywords:** Hyperthyroidism, Hypothyroidism, *H. pylori*, Gastritis, Inflammation
Evaluation association between PON1 Q 192 R gene Polymorphisms with Arylesterase activity and plasma level Malondialdehyde in infertile man

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Running Title: Evaluation association between PON1 Q 192 R gene Polymorphisms with Arylesterase activity and plasma level Malondialdehyde in infertile man

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Abstract

Objectives: Infertility as a disorder reproductive system and incapacity to achieve a fulfill pregnancy with no contraceptive measures taken after reasonable time of sexual intercourse. PON gene family with paraoxonase, arylesterase, and lactonase activities consists of PON1, PON2 and PON3, are relationship with
oxidative stress and lipid metabolism. According the important role of PON1 in oxidative stress and effect active oxygen species on infertility males, aim of this study was evaluation association between PON1 Q 192 R gene Polymorphisms with arylesterase activity and plasma level malondialdehyde in infertile man.

Materials and Methods: In this study blood samples collected from 100 control subjects and 100 infertile men. Q192R variants of PON1 were determined polymerase chain reaction–restriction fragment length polymorphism (PCR-RFLP) technique. and to estimate the association between genotype and allele frequency in cases and controls, P-values were assessed by chi-square ($\chi^2$) analysis. In this study, was measurement malondialdehyde by Yagi method as oxidant and arylesterase enzyme as antioxidants in both groups.

Results: The founds of this study indicate that the Q allele of PON1 Q192R gene polymorphism is significantly associated with infertility males and infertile individual either homozygote ($p < 0.029$) and heterozygote ($p < 0.014$), have shown a lower Q192R polymorphism, lower Paraoxonase activity and higher level of Malondialdehyde and Arylesterase activity.
Conclusion: In the end, we founds show the Q192 R polymorphism in the PON1 gene is strongly relationship with infertility males and the QQ genotype significant increase risk of idiopathic infertility males unlike RR genotype.

Keywords: Infertility, Paraoxonase, Arylesterase, Polymorphism Q192 R, Malondialdehyde
Pbi-18

Study of correlation between changes in lipid oxidation status and glutathione peroxidase activity with levels of body iron in patients with iron deficiency anemia

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Abstract

Background: Iron deficiency anemia is (IDA) a prevalent disorder among women in reproductive ages and can relate to oxidation situation in these women. The aim of this study was to investigate whether the malondialdehyde levels and activities of glutathione peroxidase (GPx) can be affected during iron deficiency anemia in reproductive aged women.

Method: In this clinical trial study, 30 women with IDA, 30 women with Iron deficiency (ID) and 30 healthy controls were studied. The concentration of plasma malondialdehyde was measured as a lipid oxidation byproduct. We also evaluated
the activities of glutathione peroxidase in all groups. Statistical analysis for continuous variables was performed by the calculation of one-way analysis of variance (ANOVA).

**Results:** The number of people who completed the study in each group was thirty. Mean plasma concentration of MDA was significantly higher in IDA group than ID group and healthy group women (5.18±0.46µmol/L, 3.4±0.34 µmol/L and 2.75±0.33 µmol/L respectively (p-value<0.05)). The mean glutathione peroxidase activity in IDA groups was significantly lower than healthy group women (1.4±0.2 (U/gHb), 2.91±0.12 (U/gHb) and 2.99±0.24 (U/gHb) (p-value < 0.05)). The concentration of MDA in IDA and ID group was negatively correlated with levels of hemoglobin (Hb), MCV and plasma ferritin (p-value <0.01 and p-value <0.05).in healthy control subjects also there was a revers correlation between MDA concentration and these factors amounts (p-value <0.01). Also activity of glutathione peroxidase and those factors levels showed significant positive correlation in every group (p-value<0.01 and p-value <0.05).

**Conclusion:** Our findings showed that lipid peroxidation increases in women with iron deficiency and iron deficiency anemia. And that activity of glutathione peroxidase decreases in iron deficiency anemia but not in iron deficiency and it
was also revealed not significant correlation between plasma free iron levels with MDA concentration and Gpx activity.

**Keywords:** Anemia, iron deficiency, malondialdehyde, glutathione peroxidase, lipid peroxidation
Pbi-19
Protective efficacy Cortisone and Hydrocortisone drugs on lysosomal damages induced of bacterial endotoxin in wistar rats
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Running Title: Protective effect of Cortisone and Hydrocortisone on lysosomal damages induced of endotoxin in wistar rats

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Abstract
Objectives: Endotoxin shock with multiple organ failures, resulting from inducing lysosomal enzyme leakage. Lysosome as basic cytoplasmic organelle in animal tissues, contains hydrolytic enzymes capable of degrading various cellular constituents. In the study investigated protective effect of Cortisone acetate and hydrocortisone 21-sodium hemisuccinate on lysosomal damage and the association it’s with ghange levele serum and hepatic acid phosphatase activity.
**Methods:** In this study, 30 rats equally divided to Control, Tolerance and Endotoxin groups. The tolerance group (12.5 mg/kg body weight intramuscularly injection Cortisone acetate for 3 days and on the 4th day, the intravenous injection 12.5 mg/kg of hydrocortisone 21-sodium hemisuccinate). The induce endotoxin shock in rats with 2.5 mg/kg body weight intravenous injection of Salmonella endotoxin. Partially purification and beta-glucuronidase activity were determined by sephadexG75chromatography, Polyacrylamide Gel Electrophoresis.

**Results:** The results of this study show a significant different in level serum and homogenate acid phosphatase activity in Tolerance group compared with the other groups (P<0.05). Also enzyme especial activity in all steps of purification, in Endotoxin group was more than the other groups (P<0.05).

**Conclusion:** Endotoxin shock as biological stressor by induction of lysosomal enzymes into the cell plays an important role in deterioration of cells. Also, suggest that protection of these particles by injection of cortisone acetate and hydrocortisone 21-sodium hemisuccinate can a significant resistance to induced stress by endotoxin shock.

**Keywords:** Endotoxin, shock, Lysosomes, acid phosphatase, Cortisone
Alpha-1 Antitrypsin-expressing adipose tissue-derived mesenchymal stem cells effectively improve Hepatic Cirrhosis

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Background: Chronic liver disease, its advanced form, cirrhosis, and its complications include varicose hemorrhage and hepatocellular carcinoma are among the leading causes of mortality and illness in the world. The most effective treatment for end stage cirrhosis is liver transplantation but due to lack of donation and rejection of the transplant, this method has some limitations. Cell therapy as a non-invasive treatment is an alternative approach. Mesenchymal stem cells (MSCs) improve cirrhosis due to their self-renewal ability, differentiate into other cells such as hepatocyte-liked cells and secretion of various cytokines. In addition, they are targeted cells for the transport and expression of external genes. Moreover, Gene therapy with genetic manipulation of MSCs is a new therapeutic treatment for disease. A1AT is an acute phase protein that, due to its anti-inflammatory and anti-protease effects, is a good choice for gene therapy with stem cells in the treatment of cirrhosis.

Methods: Shortly, liver cirrhosis was induced by intraperitoneal injection of carbon tetrachloride. Mesenchymal stem cells were isolated from adipose tissue and, after confirmation of their stemness, they were transduced by lentiviruses containing the A1AT gene and then injected into tail vein of mice model of liver cirrhosis. 14 days after the transplantation of the cells, the mice were sacrificed and blood samples were collected. The measurement of liver important enzymes,
ALT, AST, ALP, albumin and total bilirubin were done. Statistical analysis of the data with using SPSS software with Anova analysis and tukey post hoc test was carried out.

**Results:** MSCs expressing the A1AT gene in contrast to MSCs showed a greater improvement in terms of biochemical parameters.

**Conclusion:** MSCs expressing the A1AT gene can be a proper candidate for gene therapy for liver cirrhosis due to the anti-inflammatory and anti-proteolytic effects of A1AT.

**Keywords:** Liver cirrhosis, Adipose derived mesenchymal stem cells, Alpha 1 antitrypsin, Lentiviral Vector
The effects of glutathione on myeloperoxidase activity and nitric oxide level in the animal model of renal ischemia-reperfusion injury

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Abstract

Background: Renal ischemia reperfusion (RIR) injury is one of the causes of acute kidney failure (AKF). It may also be induced by some conditions such as trauma, sepsis, and kidney transplantation. Glutathione (GSH), as an antioxidant and a free radical scavenger, protects the cell from oxidative injury. In the current study, The effects of glutathione on myeloperoxidase activity and nitric oxide level in the animal model of renal ischemia-reperfusion injury.

Methods: 24 adult male wistar rats were randomly divided into 3 equal groups (n=8): group I as the control group, group II as the RIR group that received saline (0.25 ml/day. i.p), group III as the RIR group that received GSH (100mg/kg. i.p. daily). The treatment with saline or GSH began daily two weeks before RIR
induction. RIR was induced by clamping renal pedicles for 45 minutes and 24 hours of reperfusion. At the end of reperfusion, blood sampling was performed for biochemical evaluations.

**Results:** RIR significantly increased the serum activity of myeloperoxidase (MPO) and the serum level of nitric oxide (NO) compared to the control group. GSH treatment could significantly reduce the serum activity of MPO and the serum level of NO.

**Conclusions:** Our study indicated that GSH exerts protective effects the level of NO and MPO activity in the animal model of renal ischemia-reperfusion injury.

**Key words:** Glutathione, nitric oxide, myeloperoxidase, renal ischemia reperfusion, rat
Pretreatment with quercetin ameliorates liver oxidative stress biomarkers in renal ischemia-reperfusion in rats

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Abstract

Introduction: Renal ischemia-reperfusion causes oxidative stress and marked damages in the liver as a remote organ. Quercetin is known as a famous compound in the family of polyphenolic flavonoids with antioxidant, anti-inflammatory, anti-bacterial, and anti-cancer properties. This study was carried out to investigate the possible protective effects of quercetin pretreatment on liver oxidative stress biomarkers in renal ischemia-reperfusion in rats.

Methods: Thirty male Sprague-Dawley rats were divided into 3 groups (n=10): Group 1 as the control group, group 2 as the ischemia-reperfusion (IR) (IR + Physiological normal saline (0.25 ml/day)), and group 3 as the pretreated group (IR + Quercetin (50mg/kg/day)). The rats were pretreated intraperitoneally with physiological normal saline or quercetin for 15 days before renal IR induction. To cause renal IR, renal pedicles were occluded by safe clamps for 45 minutes. After
that, the clamps were removed and 24 hours was considered as the reperfusion phase. 24 hours after IR induction, the animals were anesthetized and the liver was removed for tissue enzymatic studies.

Results: The levels of malondialdehyde in liver in the IR group significantly increased compared with the control group; however, the levels of glutathione and the activity of catalase significantly decreased in the liver. Pretreatment with quercetin could reverse all of these findings.

Conclusions: This study implies that quercetin pretreatment has protective impacts on liver oxidative stress biomarkers in rats with renal IR.

Keywords: Quercetin, Renal ischemia-reperfusion, Liver oxidative stress biomarkers
The protective effects of D-Limonene on renal lipid peroxidation and glutathione in gentamicin-induced nephrotoxicity in rats

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Abstract

Introduction: It is well known that gentamicin sulphate (GS) induces reactive oxygen species (ROS) production in the kidney and causes nephrotoxicity. Antioxidant compounds have protective roles in the amelioration of renal damages induced by GS. D-Limonene is a natural cyclic monoterpenes and has the smell of lemon. It has antioxidant, anti-diabetic, and lipid peroxidation inhibitory effects. The aim of this study was to investigate possible protective effects of D-Limonene on renal lipid peroxidation and GSH levels in gentamicin-induced nephrotoxicity in rats.
**Methods:** Thirty male Sprague-Dawley rats were randomly divided into 3 equal groups: Group I (as control) received daily saline (0.25 ml/kg i.p) for 12 days. Group II (untreatment nephrotoxic) received daily gentamicin (100 mg/kg i.p) for 12 days. Group III (treatment nephrotoxic) received daily gentamicin (100 mg/kg i.p) and D-Limonene (100 mg/kg, by gavage tube) for 12 days. After 12 days, the animals were euthanized and kidneys were removed for the measurement of the kidney glutathione (GSH) and lipid peroxidation.

**Results:** In the untreated nephrotoxic group, the level of renal malondialdehyde (MDA) significantly increased compared to the control group, while the renal level of GSH significantly reduced. D-Limonene significantly inhibited the elevation of kidney MDA level in the treated group compared with the untreated nephrotoxic group. The kidney contents of glutathione (GSH) in the treated group were significantly higher than that of the untreated nephrotoxic group.

**Conclusion:** Our results indicated that D-Limonene has beneficial effects on the lipid peroxidation and GSH in gentamicin-induced nephrotoxicity in rats.

**Keywords:** Gentamicin, Nephrotoxicity, D-Limonene, Rat.
The role of trace elements in the cancer risk

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**Background:** Trace elements are important components in biological structures that play multiple functions in a large number of cellular processes. Trace elements can affect the activity of enzymatic antioxidants, which are involved in the reduction of intracellular reactive oxygen species (ROS). However, some trace elements may be toxic in excessive amounts beyond body requirements. The levels of some trace elements change in many types of cancer such as breast, prostate and gastrointestinal system cancers. Recently, studies have shown that some trace elements have main roles in the process of malignant tumor incidence and progression. Therefore, the aim of this article was to review the role of some critical trace elements including selenium (Se), zinc (Zn), cadmium (Cd), chromium (Cr) (VI), and arsenic (As) in the risk of cancer.

**Methods:** By literature review from 2002 to 2017 including Medline, PubMed, Scopus, and Google Scholar, 94 articles were reviewed.
**Results:** Zn and Se deficiencies have been reported in a large percentage of cancers including head and neck, breast, and gastrointestinal cancers. In addition to, most studies have indicated the carcinogenic effects of Cd, Cr (VI), and As in different cancers.

**Conclusion:** Insufficient levels of Zn and Se may be associated with cancer risk. Given the potential role of Zn and Se in cancer, they can be helpful in designing therapeutic strategies for cancer patients. In addition, because of the association of Cd, Cr (VI), and As with the increased risk of cancer, chronic exposure to them, especially occupational exposure, may be as risk factors for the development of certain cancer.

**Keywords:** Trace elements, Trace minerals, Cancer, Malignancy
Urinary Interleukin 18 predicts reduced renal function at 6 months after transplantation

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Background and aim: Accumulating evidences indicate that urinary IL-18 (uIL-18) is a predictor of delayed graft function in kidney recipients (KRis) with long ischemia time. However, information regarding the interrelationship between uIL-18 and long term kidney function is scarce. The purpose of the current study was to evaluate the diagnostic value of uIL-18 as a predictor of reduced estimated filtration rate (eGFR Cockcroft-Gault formula) in a cohort of KRIs with short ischemia time.

Material and methods: In a prospective cohort study, first-time recipients of kidney transplant with short cold ischemia (<2 hrs.) (age: 14-68 years, n=39) were recruited. Based on eGFR at 6 months post kidney transplantation (PKT), the KRis were classified into two groups: I) adequate renal function (eGFR >60 mL/min/1.73 m²), and II) reduced renal function (eGFR<60 mL/min/1.73 m²). Urinary IL-18 and creatinine at 2, 16, 24, 36 and 46 hrs PKT were measured using ELISA and Jaffe methods, respectively. Urinary IL-18 was adjusted for urinary creatinine and expressed as pg/mg.

Results: Adjusted urinary IL-18 declined with the time in both studied groups. With the exception of 16 hrs PKT, uIL-18 at the other time-points were significantly higher in the groups with reduced renal function than that with adequate renal function. The
AUCs of adjusted uIL-18 at 2, 24, 36 and 46 hrs PKT were 0.70, 0.54, 0.76 and 0.70 respectively. Optimum cut-off value, sensitivity and specificity for adjusted urinary IL-18 at 36 hrs PKT were 56.3 pg/mg, %84 and %80, respectively.

**Conclusion:** Adjusted uIL-18 at 36 hrs PKT predicts allograft recovery at 6 months with high sensitivity and specificity. Future studies with large sample size are deemed necessary to confirm our findings.

**Key words:** Interluekin-18, Kidney transplantation, Novel biomarker
Pbi-27

The protective effects of quercetin on damages caused by renal ischemia reperfusion

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Running title: The beneficial effects of quercetin on renal ischemia reperfusion injuries

Abstract

Background: Quercetin has antioxidant, anti-inflammatory, antibacterial and anti-cancer effects.

Objectives: This study was carried out to investigate the possible protective effects of quercetin on damages caused by renal ischemia reperfusion (IR).

Materials and Methods: Thirty male Sprague-Dawley rats were divided into 3 groups (n=10): Group 1 as the control group, group 2 as the IR group (IR + Physiological normal saline (0.25 ml/day, i.p)) and group 3 as the treatment group (IR + Quercetin (50mg/kg/day, i.p)). The rats were treated intraperitoneally for 12 days before the induction of renal IR. To cause renal IR, renal pedicles were clamped by safe clamps for 45 minutes. After that, the clamps were removed and 24 hours was considered as reperfusion.

Results: In the IR group, the serum level of triglyceride, cholesterol, low density lipoprotein, very low density lipoprotein, urea, creatinine, the activity of gamma-
glutamyltransferase, alkaline phosphatase, aspartate aminotransferase and alanine aminotransferase significantly increased against the control group, while serum High density lipoprotein level significantly reduced. The level of malondialdehyde in serum, kidney and liver in the IR group significantly increased compared with the control group. However, the level of glutathione and the activities of catalase and glutathione peroxidase in serum, kidney and liver in the IR group significantly decreased compared with the control group. Treatment with quercetin could reverse all of these findings.

**Conclusion:** This study indicates that quercetin has protective effects on lipid profile, renal and liver functional markers, and oxidative stress biomarkers in serum, kidney and liver of rats with renal IR.

**Keywords:** Quercetin, renal reperfusion ischemia, renal function markers, oxidative stress biomarkers, rat
Pbi-28

Serum glutathione peroxidase as a complementary biomarker of poor early graft function in renal transplant patients

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Background and aim: Poor early graft function (PEGF) inflicts harmful influences on long-term outcome in kidney recipients (KRs). Lack of reliable, non-invasive and inexpensive markers for the timely diagnosis of PEGF remains as an unsolved challenge. In the current study, serum glutathione peroxidase (sGPx) activity was explored as a complementary predictor of PEGF.

Material and methods: Kidney recipients (age: 14-68 years, n=39) were enrolled. Blood samples were collected at 2, 16, 24, 36 and 48 hrs after transplantation. PEGF was defined as the need for dialysis and/or serum creatinine ≥1.7 mg/dL on day 5 post-surgery. KRs with serum creatinine < 1.70 mg/dL on day 5 post-surgery were classified as good early graft function (GEGF). Measurement of sGPx activity and serum creatinine were carried out on BT-1500 auto-analyzer (Biotecnica, Italy).

Results: sGpx activity differed between PEGF and GEGF groups at 24, 36 and 48 hrs post-surgery (P<0.01) but not at 2 and 16 hrs. Area under curves (AUCs) for sGpx at 24, 36 and 48 hrs were 0.75, 0.75, 0.84 and 0.70, respectively. Optimum cut-off value, sensitivity, specificity, negative and positive predictive value for sGPx activity at 48 hrs PKT were 421.5 U/L, 75%, 81.5%, 80% and 64%, respectively.
Conclusion: This study has revealed that sGpx should be used as a complementary biomarker for the prediction of PEGF along with routine biomarkers such as serum creatinine and urine out-put. Due to our small sample size, a multi-center study with large sample size is merited.

Key words: Glutathione peroxidase, Kidney transplantation, Biomarker, Poor early graft function
Pbi-29

Using Amino Acid Index Technique in Early Diagnosis of Cancer

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Background: Different metabolic combinations increase or decrease in the plasma at different pathologic conditions, because amino acids are at the center of the body’s metabolism, and play significant biological roles in the body and they can be effective as the biomarkers for evaluating the disease risk and its progress and treatment selection. Amino acid index technique is recently used for screening the cancers, which includes analysis of changes in plasma amino acid profiles. This technique can diagnose the cancer at the primary stages. Cross-sectional studies indicate that profile of amino acids can be used for screening lung, gastric, breast, colorectal and prostate cancers. Given contradictory results regarding changes in amino acid profiles in cancers and high cancer prevalence in Iran as well as lack of epidemiology investigation regarding plasma level of amino acids in patients with cancer, current research can provide ground for the next studies for providing solutions to the physicians for preservative treatments.

Methods: Current research was conducted as a review search in library resources as well as databases such as Pubmed, google scholar, Elsevier and Magiran.

Results: Studies indicated that changes in amino acid profiles has different patterns in different cancers and determining amino acids profile using HPLC non-invasive method has high ability for screening, diagnosis, and pathogenicity.

Conclusion: Metabolomics is recently developing rapidly as a branch of biology systems. Metabolomics is the study and evaluation of small endocrine biochemical molecules (metabolites) in a biological system, including cells,
tissues, and organisms. These metabolites are directly or indirectly interacting with target molecules and therefore affect the risk of disease and complications associated with various diseases, including cancer. Metabolomics-based methods are widely used in diagnosis, screening, gene variations, drug effects, and toxicity.

**Keywords:** amino acid profile, HPLC, Amino Acid Index
Pbi-30

Study of serum MDA and sdLDL levels in patients with type 2 diabetes and atherosclerosis compared to healthy people
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Background: One of the main causes of death in diabetic patients is coronary artery disease (CAD), especially atherosclerosis. In this study, serum levels of sdLDL and MDA, the lipid peroxidation index, were evaluated in people with type 2 diabetes and atherosclerosis compared with healthy subjects.

Material and methods: This was a cross-sectional descriptive-analytic study. The study population consisted of 55 patients with type 2 diabetes mellitus and 55 healthy individuals as control group, referred to the Department of Cardiology and Angiography of Shahid Madani Hospital in Khorramabad in year 2017, whose was confirmed by the Gold standard diagnostic angiography in patients with atherosclerosis. For sdLDL evaluation, first using sodium heparin and magnesium chloride, lipoproteins less than 1.04 ml/g was precipitated and then we use a LDL cholesterol kit for measuring sdLDL level. The MDA level was measured using Uchiyama method.

Results The mean age of the patients was 64.5±12.73 years and the mean age of controls was 51.86±11.87 years. In the present study, the mean and standard deviation of sdLDL (patient:31.47 ±11.71, control:13.51 ±5.58 mg/dl) and MDA
(patient: 41.79 ± 24.75, control: 28.62 ± 14.68 µmol/mg protein) were significantly higher in the patient group than in the control group.

**Conclusion:** According to the results of this study, we can conclude that mean and standard deviation of sdLDL and MDA were significantly higher in the patient group than in the control group. The chance of developing atherosclerosis increases with MDA and increases in sdLDL, although this relationship was not significant for MDA and was significant only for sdLDL. By controlling the variables such as age, gender, history of hypertension, smoking and BMI, only sdLDL was significantly different in the two groups.

**Keywords:** Atherosclerosis, MDA, sdLDL.

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Pbi-31
Study of serum AOPP and TCA levels in patients with type 2 diabetes and atherosclerosis compared to healthy people
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Background: In diabetic patients, oxidative stress cause the production of atherogenic molecules. These products are associated with atherosclerosis(1). The aim of this study was to determine the relationship between serum AOPP and TCA in patients with type 2 diabetes mellitus with atherosclerosis compared with healthy subjects.

Material and methods: 55 diabetic patients with atherosclerosis was case group (58.3% male and 41.7% female) and 55 healthy individuals was control group (46% male and 54% female). This populations consisted of patients with type 2 diabetes mellitus who referred to the Shahid Madani Hospital's Khorramabad in year 2017, That confirmed by angiography in patients with atherosclerosis. The information was collected through questionnaire and biochemical tests. AOPP was evaluated by spectrophotometry and T chloramin method(2). TCA was measured by spectrophotometry method(3). The data analyzed statistically by SPSS 18 software.
**Results:** In this study; The mean age of the patients was 64.5±12.73 years and the mean age of controls was 51.86±11.87 years. The mean and SD of TCA in the patient group was lower than the control group (P<0.001), and in the AOPP in the patient group was higher than the control group (P<0.001).

**Conclusion:** Based on results of this study, The odds of atherosclerosis increase with a decrease in TCA and an increase in AOPP, although this relationship was not statistically significant. By controlling the variables such as age, gender, history of hypertension, smoking, and BMI observed, that none of the TCA and AOPP were significant in the two groups. It's suggested that in future studies, should be done with a larger and different sample population.

Keywords: Atherosclerosis, Oxidative stress, AOPP and TCA.

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Pbi-32
Association between serum levels of calcium, phosphorous, vitamin D, alkaline phosphatase, and parathyroid hormone with Parkinson’s disease

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Abstract

Objective: Parkinson’s disease (PD) is one of the most common neurodegenerative diseases (ND). Studies have demonstrated that biochemical markers have an association with PD. We aimed to investigate an association of biochemical markers including calcium, vitamin D, alkaline phosphatase (ALP), parathormone (PTH), and phosphorous with PD.

Methods: This study was conducted on 139 PD patients and 100 healthy individuals. Serum levels of calcium, phosphorous, ALP, PTH and vitamin D were evaluated. Furthermore, student’s t-test and logistic regression models were used by SPSS.

Results: The mean levels of calcium and vitamin D were higher in PD patients as compared with healthy controls, with only status of calcium being significantly different in the two groups (P<0.001). Levels of ALP and phosphorous were significantly different comparing PD patients with healthy subjects (P<0.01,
P<0.001, respectively). ALP and phosphorous were significantly different in the two groups (OR= 0.996, [CI 95%, 0.994-0.999], P <0.001, OR= 0.475, [CI 95%, 0.325-0.694], P<0.001, respectively). Furthermore, increased levels of calcium resulted in an elevated risk of PD (OR= 2.175, [CI 95% 1.377-3.435], P <0.001).

**Conclusion:** Results show that mean levels of calcium are higher in PD patients relative to healthy controls. Thereby, higher levels of calcium may be associated with PD.

**Key words:** Parkinson’s disease, Calcium, Biochemical markers
Pbi-33

Evaluation serum level of vitamin D in diabetic patients

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Background

Vitamin D is associated with insulin secretion and glucose intolerance and it is a risk factor for many chronic diseases. Regarding the role of vitamin D in the incidence and prevalence of diabetes, the aim of this study was to evaluate the serum level of vitamin D in diabetics.

Methods

In this cross-sectional study 293 individuals (212 female), who referring to the Dezyani clinic in Gorgan, were evaluated. Diabetic patients were classified into two groups controlled (normal serum level of HbA1c) and uncontrolled (serum level of HbA1c higher than normal).

Results

Individuals included 185 healthy individuals (124 female) and 108 diabetics (88 female). The average age was 42.53(SD=14.6) in healthy individuals and 54.14(10.1) in diabetics. The mean serum levels of FBS, HbA1c and vitamin D in
healthy individuals were 98.52(10.46) mg/dl, 5.42(.69) mg/dl and 27.63(18.03) ng/ml, respectively, also in diabetics were 204.72(75.49) mg/dl, 8.2(1.75) mg/dl and 29.55(18.94) ng/ml respectively. 66.2% of individuals had vitamin D deficiency (VDD). Gender distribution had a significant difference between diabetics and healthy individuals (P=0.008). 68.1% of healthy individuals and 63% of diabetics had VDD. Serum vitamin D level was not significantly different between diabetics and healthy individuals (P=0.369). 66.2% of individuals (94.1% of healthy and 18.5% of diabetics) were controlled. HbA1C level was significantly different between healthy individuals and diabetics (P<0.001). In 67.2% of controlled healthy and 81.8% of uncontrolled healthy, VDD has been observed. In addition, 70% of controlled diabetics and 61.4% of uncontrolled diabetics had VDD. The level of vitamin D was not significantly different between controlled and uncontrolled diabetics (P= 0.470).

Conclusion

These finding indicated that vitamin D levels had no significant effect on glycemic indices, however, further studies needs to evaluate clinical usefulness of our findings.

Keywords: vitamin D, HbA1c, Diabetes
Pbi-34

Evaluation of apoptotic micro RNA-326 in platelet concentrate storage treated with L-carnitine

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**Background:** Platelet transfusion is very important in the treatment of various conditions such as thrombocytopenia and platelet qualitative disorders. Platelet concentrate during the collection, processing and storage undergo changes that can affect the useful life time and quality of platelets. MiRNAs are known as the main regulator of mRNA translation in platelets and play an important role in apoptosis during platelet storage. L-carnitine (LC) has the antioxidant role in protection of oxidative stress during platelet storage. The aim of this study was to examine the effect of LC on the expression of miRNA-326 during platelet storage at 1 to 7 days.

**Methods:** In this experimental study, 5 bags of platelets were randomly selected with platelet-rich plasma method in the blood transfusion center. Each bag was divided equally into two ones with same volumes under sterile conditions. One bag was treated to 15mM of LC in physiological serum (PS) as the case bag and the other one just added by the same volume of the PS for the control bag. In this study, miR-326 was determined quantitatively by qPCR during one to 7 days of storage of Platelet concentrate.

**Results:** Data of this study showed that expression of miR-326 increased in both groups during storage, but the expression level miR-326 significantly attenuated in first and third days of storage.

**Conclusion:** It seems that LC could reduce the expression level of apoptotic miR-326. This study recommend that LC can be used as an additive to protect the
platelet storage legion and maintain the quality and survival of the platelets over the time of storage.

**Key words:** platelet concentrate, L-carnitine, miRNA, platelet storage
Pbi-35

The effect of hydroalcoholic extract of Sargassum Oligocystum on expression of SIRT1 and FGF21 genes in streptozotocin-induced diabetic rats

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Background: Diabetes mellitus causes disturbance in glycemic condition, defect in tissue function, loss of quality of life and life span. SIRT1 and FGF21 are two important factors involved in body metabolism, which by regulating insulin secretion and reducing insulin resistance, regulate glucose and lipid metabolism and play an important role in metabolic syndrome and related diseases. Sargassum oligocystum is a brown algae belonging to Sargassaceae family, which has high distribution in coast of the Persian Gulf, that due to its various pharmacological
effects including antidiabetic, antioxidant, antiinflammatory, antibacterial, antifungal and anticancer, it is used in traditional and native medicine. The aim of this study was to evaluate effect of Sargassum Oligocystum extract on expression of SIRT1 and FGF21 genes in diabetic rats.

Methods: In this study, 48 male Wistar rats were randomly divided into six groups of eight including becker control, diabetic control, positive control (receiving 100mg/kg metformin) and three diabetic groups under treatment. After induction of diabetes, treatment groups 1, 2 and 3 were tested to gavage with algae extract at dose of 150, 300 and 450 mg/kg, respectively for 30 days. Then liver tissue samples were collected to examine expression of the Cyclophilin gene as control gene and SIRT1 and FGF21 genes.

Results: Sargassum algae extract at 450 mg/kg dose increased SIRT1 gene expression, however there was no significant difference in comparison with diabetic control group. Regarding the expression of FGF21, the algae extract in three doses and also dose of 100 mg/kg of metformin increased expression of this gene, but this increase was meaningless statistically.

Conclusion: Because of short duration of treatment, algae extract and metformin could not make significantly changes in expression of SIRT1 and FGF21 genes as liver factors involved in insulin signaling pathways.

Keywords: Diabetes, brown algae, Sargassum oligocystum, SIRT1, FGF21
Evaluate the effect of essential oil of Satureja khuzestanica (SKEO) and Carvacrol on the Antioxidant enzyme defense system

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Background: The purpose of this study was to evaluate the effect of essential oil of Satureja khuzestanica (SKEO) and Carvacrol on the Antioxidant enzyme defense system, including catalase (CAT), superoxide dismutase (SOD), glutathione peroxidase (GPX) and glutathione reductase (GR) in alloxan diabetic rats.

Methods: The induction of diabetes mellitus was induced in male Wistar rats by injecting 70 mg / kg of alloxan intraperitoneally. Rats were randomly assigned to diabetic and diabetic control groups treated with carvacrol and SKEO at doses of 500 and 1000 (mg / kg) per day to the independent groups of diabetic rats for 20 days. After treatment, antioxidant defense enzymes CAT, SOD, GPX and GR, were measured in all treated groups.

Results: The activity of superoxide dismutase, catalase, glutathione peroxidase and glutathione reductase enzymes in diabetic rats significantly decreased compared with other groups treated with SKEO and carvacrol (P <0.05). Statistical differences between diabetic groups under treatment with concentration of SKEO and carvacrol were not significant (P <0.05).

Conclusion: Considering the fact that GC-Mass analysis of the oily substance of Satureja khuzestanica Plant showed that carvacrol has antioxidant properties and the main component of SKEO, therefore, it can be concluded that the effect of
SKEO on improving oxidative stress indices and antioxidant enzymes defense against reactive oxygen species in diabetic rats treated with carvacrol due to its main composition.
IRCT:41765

Keywords: Diabetes mellitus, Oxidative stress, Carvacrolol, Essential oil of Satureja khuzestanica
Neurofilament light in CSF and serum as biomarker of multiple sclerosis
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Background: Multiple sclerosis (MS) is a chronic autoimmune-mediated demyelinating disease of the central nervous system (CNS) that is usually associated with varying degrees of progressive disability.

Improved biomarkers are needed to facilitate clinical decision-making and as surrogate endpoints in clinical trials in MS. We assessed whether neurodegenerative and neuroinflammatory markers in cerebrospinal fluid (CSF) and serum at initial sampling could predict disease activity. To evaluate whether levels of CSF and serum neurofilament light (NF-L) correlate with clinical variants and treatment response in MS.

Methods: We argue that the Nf-L subunit can reflect acute axonal damage mediated by inflammatory mechanisms and can imply prognostic value for conversion from clinically isolated syndrome (CIS) to definite MS.

In this study was to investigate the association between Nf-L levels in CSF and serum in early MS and disease severity at long-term follow-up.

Results: Neurofilaments light reflect the underlying neurodegeneration and intrathecal inflammation driving progressive disease and neurodegenerative axonal damage. These biomarkers are especially relevant as new therapies aimed at neuroprotection and neural repair are developed, including stem cell-based regenerative therapies.

Conclusion: We conclude that elevated levels of neurofilament light in cerebrospinal fluid and serum were associated with unfavourable prognosis. These data suggest that the neurofilament light level could be used as a prognostic marker in early relapsing-remitting multiple sclerosis.
Keywords: Neurofilament light chain, neuroinflammation, multiple sclerosis
Pbi-38

Evaluation of the frequency of depression, anxiety and thyroid hormones level in patients suffering from Graves

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Background: Graves’ disease is an autoimmune thyroid disease caused by thyroid stimulating hormone receptor antibodies which stimulate the thyroid to synthesize and secrete the excess thyroid hormone. Since thyroid hormones play an important role in maturation and regulation of central nervous system activity, increased levels of thyroid hormones in Graves' disease may have psychological and depressive effects directly on the central nervous system or indirectly on adrenergic activity. The aim of the study was to examine the association between depression, anxiety and thyroid hormones level in patients with Graves.

Method: We investigated the association between Graves disease and anxiety, depression and thyroid hormones level in 90 patients with Graves disease in three groups (30 hyperthyroid, 30 euthyroid and 30 new case). We used the Beck anxiety and depression scale to assess anxiety and depression in groups. Thyroid hormones level was determined using ELISA method.

Results: The rate of depression and anxiety in the hyperthyroid group was
significantly higher than euthyroid group. Also, the level of the TSH hormone had a significant negative correlation with depression. Although, there was no significant relationship with anxiety. Levels of T3 and T4 hormones were not significantly correlated with depression and anxiety in three groups. Conclusions: Graves’ disease and reduction in level of TSH hormone, can cause anxiety and depression in patients. Keywords: Graves, thyroid hormone, depression, anxiety
The increased level of OPN was associated with inflammation in patients with Functional GH secreting Pituitary Adenoma

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Abstract

Background and aim: Osteopontin (OPN) is an O-glycosylated phosphoprotein that is synthesized in a variety of tissues and cells and secreted into body fluids. OPN is a putative cytokines with positive roles in development, bone formation and immune regulation also is associated with pathological situations likewise cancer. Meanwhile, tumors initiated in pituitary gland imposes morbidity and difficulties among patients. The aim of the present study was to investigate the expression level of local OPN in tumor tissue of patients with Functional Growth hormone secreting pituitary adenomas which is one of the most common pituitary-related tumors with high morbidity. The relevance of the OPN expression level with patient's clinic pathophysiology and inflammation was also determined.
Materials and Methods: In this case-control study, 30 patients with Functional Growth hormone secreting pituitary adenomas who were referred to the Firouzgar Hospital in Tehran were participated. Tumor tissue samples were used to extract mRNA and cDNA, and to determine the gene expression of OPN, the Real-Time PCR-based Cyber Green method was used. The correlation of OPN with patient's clinic pathophysiology features were evaluated. Finally, statistical analysis was performed using version 6 of GraphPad Prism software and independent t-test.

Results: Measurement of OPN expression level in tumor tissues of patients with Functional Growth hormone secreting pituitary adenomas revealed that the level of this gene was significantly increased in patients comparing to healthy subjects and normal tissues. Also, the increased level of this gene was associated with elevated level of tumor grade and stage. Based on our results, in tumors with more than 10 mm in size also tumors with invasive grade, the level of OPN was more elevated. Also, the level of OPN was associated with inflammatory responses in patients.

Conclusion: The results of the current study have shown that the OPN gene can account as a local cancer marker in patients with Functional Growth hormone secreting pituitary adenomas and can be noticed as a possible biomarker for controlling disease.

Key Words: functional pituitary adenoma, GH secreting adenoma, OPN, cancer.
S100A8 and S100A4 protein as new tumors markers in serum and saliva can be used to diagnosing prostate cancer

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Background: S100 protein family has been implicated in multiple stages of tumorigenesis and progression. In recent years, the use of saliva as a specimens, due to its non-invasive and easy access increased. However, so far there are few studies about its diagnostic value for cancer. Therefore, we conducted a study to investigate the relationship between serum S100A8 and S100A4.

Methods: A case-control study was conducted with 60 men: 30 Prostate cancer patients (PCa) and 30 benign prostatic hyperplasia (BPH) from the Hospital Ayatollah Khansari in Arak, Iran. The S100A 8 and S100A4 concentrations in saliva and serum samples were assessed using an enzyme immune assay (ELISA). We used Mann-Whitney test to assess and compare S100A8 and S100A4 concentrations between two groups.

Results: We observed that there was a significant difference between PCa and the BPH in terms of S100A8 concentration in serum and saliva (P<0.05). As well as, the serum S100A8 concentration in PCa and BPH groups was positive and statistically significant correlated with salivary S100A8 concentration (r= 0.789, P<0.05), (r=0.866, P<0.05) respectively. The S100A4 level in serum was statistically significant between PCa and the BPH groups (P<0.05). The S100A4 level in saliva was statistically significant between two groups. The correlation between salivary and serum S100A4 concentration in PCa
group and BPH group was positive and significant ($r= 0.850, P<0.05$), ($r=0.773, P<0.05$) respectively.

**Conclusion:** According to the results of the present study, serum and saliva S100A8 and S100A4 level can be used as a tumor marker for prostate cancer. Although, more studies must be done.

**Keywords:** S100A8; S100A4; Prostate cancer (PCa); Benign prostatic hyperplasia (BPH).
Amelioration of high-glucose induced inflammation by Quercetin through macrophage polarization in RAW624.7 cell line

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Background:
Macrophages are divided into two phenotypes (M1 and M2) based on their surface markers. M1 markers include CD11, iNOS, etc. and M2 markers include CD206, CD163, etc. These markers' activations are affected by several mechanisms such as ER stress, hypoxia, lipotoxicity, ROS production and NF-kB activation. High glucose concentration give rise to lipotoxicity and ROS products that result in M2 to M1 shift and lead to inflammation. Pro-inflammation cytokines are released by M1 macrophages and M2 macrophages release anti-inflammation cytokines. Furthermore, the balance between M1/M2 has an important role in inflammation mechanisms. Many studies have been shown polyphenols have anti-inflammation potential and safety effects. Quercetin is a flavonol, one of the six subclasses of flavonoid compounds. This polyphenol possesses strong anti-inflammatory capacities; through an increase of antioxidative activities, reduction of lipogenesis and macrophage polarization regulation.

Methods:
This study has surveyed the glucose (53mM) modulation of RAW 264.7 macrophages activation and effects of Quercetin (25µM) on high glucose-induced lipotoxicity and macrophage polarization. We have measured high glucose-induced lipogenesis by oil red O staining. For investigating macrophage polarization, we assessment M2 marker, CD206, as an anti-inflammatory factor and M1 marker, CD11c, as an inflammatory factor via flow cytometry.

Results:
Our results suggest that high glucose induce RAW264.7 lipogenesis and modify RAW264.7 morphology. Flow cytometry analyses showed that high glucose increase M1 marker, CD11c, significantly (about 80%) in vitro. RAW264.7 were treated with Quercetin strongly reduce lipid droplet in oil red O staining and decrease M1 marker, CD11c to approximately 20%. Our data have shown quercetin Caused a very slight increase in M2 marker, CD206 (4%) that isn’t signed.

**CONCLUSION:**
These results show that Quercetin produces a potential anti-inflammatory effect by modulating macrophage polarization and attenuate high glucose-induced lipogenesis in vitro. Decreasing M1 phenotype involved in the anti-inflammatory property of Quercetin.

**Keywords:** LAL, NPC2, CVD
The effect of blood sample storage conditions on HbA1c concentration

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Abstract

**Background:** HbA1c concentration is an indicator of the development of long-term complications in diabetic patients. Different sample storage conditions can affect HbA1c results and consequently, clinician’s diagnosis. In this study, we investigated the effect of different temperatures of storage through the time on HbA1c results.

**Methods:** A total of 40 fresh whole blood samples with different levels of HbA1c were selected for separate HbA1c measurements at three different temperatures (-20°C, 4°C and 25°C) on subsequent days (0, 7, 14 and 21 days after sample collection) with Cobas Integra 400 assays (Roche Diagnostics, Mannheim Germany).

**Results:** The value of HbA1c at initial measurement (7.05±1.45) was insignificantly higher than results of temperature of -20°C and 4° but compared to results at the temperature of 25°C, (6.08% ± 0.86% after day 7, 5.52% ± 0.80 after day 14, 4.81 % ± 0.66 after day 21) values of initial measurements was significantly higher.
Conclusion: It can be concluded that refrigerator or freezer storage temperature is applicable for the measurement of HbA1c by Cobas Integra 400 without negative effects on the stability of samples on subsequent days.

Keywords: HbA1c, Diabetes mellitus, stability of sample, Cobas Integra 400
Pbi-44

Differences between glomerular filtration rate values using Jaffé and enzymatic assays for creatinine measurement

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Abstract

Background: Diabetic kidney disease develops an end-stage renal failure and is a major cause of death in diabetic patients. Therefore, the development of an accurate test for diagnosis and monitoring the mentioned disease would be necessary. Here, we examine the effects of two different methods using Jaffé and enzymatic assays on the creatinine values.

Methods:

Blood samples were collected from 80 participants referring to the clinical laboratory. The levels of serum creatinine were assessed by using two IDMS-traceable methods MAN and Roche from different manufactures using Jaffé and enzymatic assays, respectively. Then to assess the eGFR levels, MDRD equation was used. Descriptive parameters such as mean, standard deviation, maximum and minimum of methods were also calculated. SPSS statistical software version 25 was used for analysis and the p-values of less than 0.05 were presumed as statistically significant.

Results:
Here, descriptive analysis of the data demonstrates a slight increase in the serum creatinine measured by Jaffé assay which leads to a significant decrease in the levels of eGFR compared to the eGFR by the enzymatic assay. Moreover, 27.5% of participants showed eGFR over 60 in enzymatic assay whereas eGFR of the same individuals was below 60 when measured by with Jaffé method. Therefore, 27.5% positive discordant cases were reported by Jaffé assay followed by misclassifying them as DKD patients compared with the enzymatic assay.

**Conclusion:** A low level of eGFR is observed when using Jaffé assay which causes more misclassification into the DKD group and demands to an inclusive consideration by physicians in order to diagnose and monitor the DKD patients.

**Keywords:** Diabetic kidney disease; Creatinine, Glomerular filtration rate; Jaffé assay; enzymatic assay
The relationship between vitamin D and thyroid hormones level

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Introduction:

Vitamin D have an important role in various aspect of body function (1). There is supporting evidence indicating vitamin D deficiency is associated with various disease such as Thyroid disorders (2). In contrast some studies showed no significant correlation between vit D and thyroid hormones (3, 4). To clarify this controversy, we aimed to evaluate association between vitamin D serum and thyroid hormone profile.

Methods:

The number of 115 individuals included in this study. The serum levels of TSH and T4 were evaluated by chemiluminescence method. The serum level of vitamin D was evaluated using enzyme linked immune sorbent assay (ELISA)kit. The data was analyzed using SPSS software.

Results:

The results showed that the mean concentrations of vitamin D, TSH and T4 were 27.7ng/mL, 3.1 IU/ml and 6.6 pg/ml respectively. As expected serum levels of T4 and TSH were inversely correlated (R=-0.44, p value<0.001). Vitamin D level was directly correlated with T4 (R=0.45) but inversely with TSH (R=-0.64), however the correlation was non-significant.

Conclusion:

The present study showed that no significant correlation between vitamin D, TSH and T4 hormone. These findings were consistent with the results of Zhou P et al that indicated thyroid related measures and 25OHD serum levels are not related.
(3). In contrast, Richards and et al reported that a lack of vitamin D contributed to the possibility of low thyroid hormones (4). In conclusion this study showed no significant correlation between Vitamin D and thyroid hormone profile.

Keyword: vitamin D, thyroid hormones level, TSH, T4
Investigation of the lipid profile in patients with subclinical hypothyroidism

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Abstract

Background: Hypothyroidism is a thyroid gland-related disorder which causes lipid metabolism disturbance. Subclinical Hypothyroidism (SCH) is a compensatory stage in the course of this disease, in which TSH production increases while the levels of thyroid hormones are in normal or low-normal range. There are no studies about the lipid profile abnormalities in SCH. Therefore, the aim of this study was to evaluate the lipid profile in SCH patients and compare it with normal individuals.
Methods: In this case-control study, subjects were randomly chosen among 800 individuals referred to Neka city hospital in Mazandaran province, Iran in order to routine biochemical and thyroid hormone checkup. Participants were divided into two groups; cases (n=400) and controls (n=400). Thyroid hormones were measured by ELISA, and lipid profile parameters were evaluated colorimetrically by AutoAnalyzer.

Results: There were no significant differences in age and sex distribution between the two groups. Among the measured thyroid hormones, TSH was significantly different between the two groups (p≤ 0.05). In case of lipid profile, high-density lipoprotein cholesterol (HDL-C) was significantly different between the two groups (p≤ 0.05). However, no significant differences were observed in the amount of low-density lipoprotein cholesterol (LDL-C), triglyceride (TG) and cholesterol (p>0.05).

Conclusion: SCH patients, showed a decrease in HDL-C. It can be concluded that subclinical hypothyroidism similar to hypothyroidism can cause lipid metabolism disturbance.

Keywords: hypothyroidism, thyroid hormones, lipid profile, thyroid
Relationship between thyroid hormones, ferritin and vitamin D

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Background: There is evidence that thyroid hormone levels may be regulated by vitamin D and ferritin. Vitamin D have an significant role in several aspect of body function. Low vitamin D and slightly elevated TSH levels have been described together in obese population. Vitamin D may affect thyroid functioning in patients with autoimmune thyroiditis. However, population based studies supporting this relationship are lacking. Ferritin is an iron storage protein found in almost all of the body tissues. Serum ferritin levels also have been reported to be altered in patients with thyroid disorder. Thus, changes in the serum concentrations of ferritin reflect thyroid function. The purpose of this study is to examine measure the relationship between serum 25-hydroxyvitamin D (25(OH)D), ferritin and thyroid hormones in Iranian population of Isfahan city, Iran during 2018.

Methods: The number of 202 individuals included in this cross sectional study. The serum levels of TSH, T₃ and T₄ were evaluated by RIA gamma counter method. The serum level of vitamin D was evaluated using (ELISA) kit monobind. The serum ferritin level was elevated using kit monobind. The data was analyzed using SPSS.

Results: In the original data set (N=202) showed that the mean concentrations of vitamin D, TSH, free T₃, free T₄ and ferritin were 26.07ng/ml, 3.19 mIU/l, 1.49ng/ml, 0.82 pg/ml and 44.55 ng/ml respectively. Although, the results of our findings showed 25(OH)levels show a strong correlation with BMI, Weight, height and ferritin. 25(OH) D levels were not significantly correlated with any of the thyroid hormones.
Conclusion: No relationship was found between thyroid function and vitamin D levels. Although, Significant correlation between was found between thyroid hormone and serum ferritin (p value=0.009, R=0.199).

Keywords: Thyroid hormones, TSH, ferritin, vitamin D
Correlation between mir-103 and mir-133a expression with the circulating ANGPTL8 in type 2 diabetic patients and healthy control subjects.

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Abstract

Aims: Angiopoietin-like protein 8 (ANGPTL8) is a circulatory hormone that plays an important role in the proliferation of the pancreatic beta cells and lipid metabolism. MicroRNAs are small non-coding RNAs that play an important role in the pathogenesis of diabetes mellitus. Therefore, we investigated the correlation of mir-103 and mir-133a expression with the ANGPTL8 and other type 2 diabetes mellitus (T2DM) - related factors.

Methods: Seventy subjects (controls; n=35 and type 2 diabetic patients; n=35) participated in this study. The ANGPTL8 concentration and mir-103/133a expression were measured using ELISA and real-time PCR respectively. Results:
The Circulatory ANGPTL8 concentration and mir-103/133a expression was significantly higher in T2D patients than the healthy controls (P<0.05). There was a positive and significant correlation between mir-103/133a with triglyceride (TG), total cholesterol, fasting blood sugar (FBS) and glycated hemoglobin (P<0.05) in T2D group. The results also showed a negative and significant correlation between mir-103/133a expression with ANGPTL8 levels in T2D group (P<0.05).

**Conclusion:** Our results suggest that mir-103/133a expression is correlated with the ANGPTL8 and T2D-related factors.

**Key words:** ANGPTL8, type 2 diabetes mellitus, mir-103, mir-133a.
Pbi-49

Effect of olive leaf extract on glucose homeostasis, cytokine and nitric oxide in patients with essential hypertension, a double-blind randomized controlled clinical trial

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Background: Hypertension is considered as the primary risk factor for cardiovascular diseases. Millions of people still suffer from this disease that indicating the need for further research to control it better. In this project, effects of olive leaf extract (OLE) as an important traditional herbal medicine was evaluated on glucose homeostasis, cytokines and nitric oxide as a vasodilator.

Methods: This research was a parallel double-blind randomized controlled that was recorded in the Iranian registry of clinical trials (IRCT20170430033730N5). At first, subjects were matched one-by-one according to age, body mass index, gender, dosage and type of medications. Then these subjects were randomly allocated into two groups to receive either 500 mg/day OLE supplements (n = 30) or placebo (n = 30) for 12 weeks. OLE supplement (Olivin brand) and placebo were produced by Barij Essence Pharmaceutical Company, Kashan, Iran.
milliliter of blood sample was taken from participants after overnight fasting at study baseline and after 12 weeks intervention at the BU-Ali hospital laboratory affiliated to QUMS for measurement of the related markers. Fasting plasma sugar and Nitric oxide were measured based on colorimetric and Grease method, respectively. Serum insulin, IL6 levels were evaluated using ELISA technique.

**Results:** The results showed that fasting plasma glucose (P-value: 0.650) and insulin (P-value: 0.412) levels did not have significant changes between two studied groups. OLE treatment resulted in significant reduction in IL-6 (-5.9±13.4 VS. 0.93±11.5) and increase in nitric oxide (4.1±9.6 VS. -1.6±13.3) levels compared to placebo received group.

**Conclusion:** It should be concluded that Olive leaf extract should have useful effect in decreasing inflammation and increasing vasodilation in essential hypertension patients.

**Key Words:** Olive leaf extract, Oxidative stress, Hypertension
**Pbi-50**
**Investigation the oxidative stress markers and antioxidant enzymes activity in newly diagnosed type 2 diabetes patients and healthy subjects, association with IL6 expression**

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**Abstract**

**Objective:** Oxidative stress plays an important role in the pathogenesis of diabetes and its complication. In this study, we aimed to evaluate and compare oxidative stress markers and antioxidant enzymes activity in newly diagnosed type 2 diabetes mellitus (T2DM) patients and healthy subjects.

**Material and methods:** 20 newly diagnosed type 2 diabetes patients and 20 healthy subjects (age and sex matched) were recruited in this study. After anthropometric parameters measurement, blood sample were collected from all participant. Serum, plasma and Peripheral blood mononuclear cells (PBMCs)
were isolated. Biochemical parameters were evaluated in serum. Plasma was used to measure malondialdehyde (MDA), total oxidant status (TOS), total antioxidant capacity (TAC), superoxide dismutase (SOD) and glutathione peroxidase (GPx) activity. Interleukin 6 (IL6) gene expression in PBMCs was investigated using real-time PCR.

**Results:** MDA and TOS levels were significantly higher in T2DM patients than the control group. However, TAC and SOD were significantly lower in T2DM as compared with healthy subjects. There was a significant positive correlation between IL6 with MDA and TOS. In addition, a negative correlation was observed between IL6 and SOD activity.

**Conclusion:** Hyperglycemia leads to increase oxidative stress and inflammation in diabetic patients. So, hyperglycemic control may improve oxidative stress and inflammation, which further relieve diabetes complication.

**Keywords:** Type 2 diabetes mellitus (T2DM), malondialdehyde (MDA), total oxidant status (TOS), total antioxidant capacity (TAC), superoxide dismutase (SOD) and glutathione peroxidase (GPx)
Pbi-51

Relationship between serum Ferritin Status and thyroid hormone profile

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Background: Iron is one of the key factors necessary for the normal thyroid function. In most of the human tissues, iron is mainly stored in form of Ferritin. It has been reported that Serum ferritin level is dys-regulated in thyroid disease and ferritin level in circulation is associated with thyroid hormone function. Indeed, many studies have indicated the relationship between serum ferritin levels and Thyroid stimulating hormones (TSH and T4). The purpose of this study was to measure serum ferritin levels in relation to serum concentration of TSH, T4 and in Iranian population of Gogan city, Iran during 2017-2018.

Methods: The number of 110 female individuals were requited in this cross sectional study. The serum ferritin level, TSH and T4 were evaluated using chemiluminescence method. The data was analyzed using SPSS v.16 and the p-value≤0.05 was considered as significant.

Results: The results of our findings showed that most of the included individuals were in normal range for serum ferritin (53.11), TSH level (2.50) and T4 level (8.68). The pearson’s correlation test revealed that the ferritin level is not significantly correlated with the measured TSH (R=0.316) and T4 (R=0.086).
Conclusion: Altogether our findings indicated there is no significant correlation between the ferritin, iron storing protein and serum thyroid hormone.

Keywords: Ferritin, thyroid hormone profile, TSH, T4
Pbi-53

NADPH oxidase mediates TGF-β induced ChSy-1 and C4ST-1 mRNA expression in vascular smooth muscle cells

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Background:
Vascular proteoglycans play an important role in the initiation and progression of atherosclerosis. Proteoglycans modifications specifically hyperelongation of their glycosaminoglycan (GAG) chains by the atrogenic factors lead to an increase in their binding to LDLs in the blood vessel walls and subsequently the development of atherogenesis. Therefore, targeting the signaling pathways of atherogenic factors involved in GAG elongation can be considered as a therapeutic approach to prevent atherosclerosis. In vascular smooth muscle cells (VSMCs), transforming growth factor (TGF)-β regulates hyperelongation of GAG chains via stimulation of GAG synthesizing enzymes. NADPH oxidases (Noxs) are main ROS producer in vasculature which are implicated in the pathogenesis of atherosclerosis. It has been shown that Nox enzymes mediate many TGF-β induced effects. However, the role of Nox in atrogenic signaling involving GAG elongation on biglycan is not known. Hence, we investigated the involvement of Noxs, as possible signaling molecules in TGF-β induced C4ST-1 and ChSy-1 (rate-limiting enzymes in GAG chain elongation) mRNA expression in VSMCs.
Methods:
This study was performed on cultured human VSMCs. The mRNA levels of C4ST-1 and ChSy-1 enzymes were determined by quantitative polymerase chain reaction (q-RT-PCR). GAPDH was used as a housekeeping gene.

Results:
VSMCs were treated with TGF-β (2ng/ml, 6h) resulting in an up-regulation of the C4ST-1 and ChSy-1 mRNA expression (p<0.01) compared to untreated cells. TGF-β stimulated C4ST-1 and ChSy-1 mRNA expression was significantly blocked by using Nox inhibitors [(DPI, 20µM) and (Apocynin, 20 µM)]. A similar result for two genes was obtained. TGF-β receptor antagonist (SB431542, 10µM) was used as positive control.

Conclusion:
Our results indicate that Nox is a key signaling mediator in TGF-β induced of C4ST-1 and ChSy-1 expression and TGF-β mediated GAG chain hyperelongation occurs via Nox-dependent pathways.

Keywords: Transforming growth factor-β, glycosaminoglycan enzymes, NADPH oxidase, vascular smooth muscle cells
Pb1-54

**Vitamin D and thyroid hormones, T4 and TSH, in patients with beta thalassemia major**

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**Background.** Beta thalassemia major due to mutation in hemoglobin beta chain genes. Accumulation of alpha globin in Red blood cell cause to severe hemolysis and ineffective erythropoiesis. Frequent infusion of blood for compensation of anemia in patients can increase the iron load of the body, which can cause various complications with deposition in the glands and general problem such as vitamin deficiency, so this study was performed for evaluating fluctuations of vitamin D, T4 and TSH hormones in these patients.

**Methods.** This descriptive cross-sectional study was done on all patients with beta thalassemia major in Bushehr city. Vitamin D, T4 and TSH were measured in each patient. SPSS software v.16 was utilized for data analysis

**Result.** The statistical population included 106 patients (female: 54.5%, male: 45.5%) with an average age of 23 years old. The mean values of T4, TSH and vitamin D were 7.4±1.8 ng/dl, 3.59±0.9 ng/ml and 29.1±23.6 ng/ml respectively. Prevalence of primary hypothyroidism was 5.55%. Vitamin D in 41% of patients
was less than 20 ng/ml. There were significant correlations between age/TSH and age/vitamin D. There was inverse and significant correlations between age/T4.

**Conclusion.** This study showed that the average of T4, TSH and vitamin D in the population were into the normal range but somebody had hypothyroidism disorder and vitamin D deficiency. Aging could reduce T4, vitamin D and increased TSH values.

**Keywords**

Thyroid Hormones, T4, TSH, Hypothyroidism
Potential protective effects of *Rosa damascena* Mill. essential oil against liver inflammation induced by sepsis in rats

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**Background:** Sepsis is a serious clinical condition that represents a patient's response to a severe infection. The incidence of sepsis is increasing with a consequent rise in hospitalizations and resource utilization in providing care to septic patients. The essential oil from *Rosa damascena* Mill. (RD) has bioactive compounds with various pharmaceutical activities. The objective of the study was to evaluate the anti-inflammatory potency of RD in CLP model.

**Methods:** The rats were randomly divided into 5 five groups: LAP, CLP, two treatment groups treated with RD essential oils at both doses (50 and 100 mg/kg.bw) and indomethacin. After CLP surgery, the blood and liver tissues were
removed for the measurement of antioxidant/oxidative stress parameters such as MPO, MDA, GSH, GST and FRAP.

**Results:** Anti-inflammatory properties of the administration of RD essential oils at both doses (50 and 100 mg/kg.bw) showed a significant reduction of MPO and MDA levels as well as a remarkable increase of GSH, FRAP and GST levels when compared with the control and the standard drug (Indomethacin).

**Conclusion:** RD essential oils showed anti-inflammatory effects which might be attributed to the antioxidant components of the studied oil.

**Keywords:** *Rosa damascena* Mill., Essential oil, anti-inflammatory, CLP model, Oxidative stress parameters
Pbi-56

Biochemical and Hematological profile of Beta thalassemia major patients in Bushehr

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Introduction

Frequent infusion of blood in Beta thalassemia major can increase the iron load of the body which cause various complications with deposition in the liver, glands and other organs. The present study is the analysis of liver and kidney function, Hematological status, lipid patterns, FBS and serum ions in beta-thalassemia major patients.

Method

This descriptive cross-sectional study which was done on all patients with beta thalassemia major in Bushehr city. The amounts of ALT, AST, ALP, Alb, Bili total, BUN, Cr, uric acid, TG, Cholestrol, LDL, HDL, FBS, Na, K, P, Ca, Hb, HCT, MCV, MCH, MCHC and ferritin were assessed. SPSS software v.16 were utilized for data analysis.

Result
The statistical population included 106 patients (female: 59.5%, male: 40.5%) with an average age of 24.5±11.5 years old. Serum ALT (39.52 U/L) and AST (42.24 U/L), ALP (371±176 U/L), Bili total (2.49±1/76 mg/dl), Bili Direct (0/58±0/20 mg/dl), FBS (123.77±71.79 mg/dl), P (5.35±0.87 mg/dl), Ca (9.9±0.63 mg/dl), TG (137±75 mg/dl) were significantly higher in patients group in comparison to the control group. Lower serum Na (135.3±1.8 mmol/l), cholesterol (112.5±30.5 mg/dl), HDL (27±9.5 mg/dl), LDL (55±20.5 mg/dl), K (4.2±0.3 mmol/l) and Alb (4.6±0.3 g/dl) have been found in patients in comparison to the healthy group. The averages of Serum BUN, Cr and Uric acid were (14.85±6.26 mg/dl), (0.78±0.22 mg/dl) and (4.93±1.56 mg/dl) respectively. Hematological parameters as Hb (8.6±0.97 g/dl), HCT (27.1±2.6%), MCV (80±4.14 fl) and MCH (25.9±2.0 pg) have been significantly reduced in patients except MCHC (31.8±1.14 g/dl) and ferritin (3516±3087 ng/ml).

**Conclusion**

This study demonstrates that beta-thalassemia patients and healthy group have difference in serum contents of ions, liver function and biogenesis of lipids and lipoproteins is impaired.

**Keywords**

Thalassemia major, Liver Enzymes, Ions, lipid patterns, Bushehr
Does Biochanin A Have Antidiabetic Effects In Diabetic Rats?

**Background:** Biochanin A (BCA) is a bioflavonoid with antioxidant properties that acts as insulin mimetic agent. In addition, it has been shown that flavonoids, as natural antioxidant, could improve insulin sensitivity in patients with diabetes. The aim of this study was to examine the BCA effects on FBS, oxidative stress and serum adiponectin, resistin and insulin in type 1 diabetes induced rats.

**Material and method:** Forty Wistar rats were divided into five groups (n=6). BCA was administered orally (10 and 15 mg/kg body weight). Diabetes was induced using STZ. Biochemical parameters including FBG, insulin, resistin, adiponectin, γ –Glutamyl transferase (GGT), alanine transaminase (ALT), aspartate transaminase (AST), and Glutathione (GSH) were measured in all groups.

**Results:** BCA treatment significantly reduced the FBS in diabetic rats (p<0.05). Serum insulin, GGT activity and GSH were significantly increased in BCA treated rats (p<0.05). The obtained data revealed that the administration of BCA significantly increased the serum adiponectin (p<0.05). Additionally, serum resistin were remarkably decreased in treated rats (p<0.05).

**Conclusion:** Taken together, BCA represents a natural phytoestrogen that has an important role in improvement of glucose metabolism by regulating adipokines secretion; moreover, it shows the beneficial effects against oxidative stress in diabetes.
Keywords: Adiponectin, Biochanin A, Oxidative stress, Resistin, Type 1 diabetes
Pbi-59

Abstract
Evaluation of biochemical parameters and serum enzyme in bodybuilders thirty days after creatine monohydrate and (oxymetholone) anabolic steroid supplementation in Tehran city

Introduction
There has been the taking of performance-enhancing nutrients at the beginning of body building exercise to increase the efficiency of organs. Emerging supplements such as creatine and anabolic steroids that are synthetically prepared have harmful effects on internal organs. The aim of this study is that evaluate the effects of these supplements on bodybuilders in one-month.

Method
In this study, thirty bodybuilders had chosen who had no history of any additional material and divided into three groups (control, creatine and steroid). A blood sample was taken before the start of the study and then one group was given a placebo and the second group creatine monohydrate and another group taken the oxymetholone. Then all individuals follow the resistance and stretching exercises for a month. Then the second blood was taken after 30 days, next the serum was separated of each of them.

Result and discussion
After thirty days it was found that taking creatine and steroids supplements in bodybuilders, had no significant effect on body mass index, serum electrolytes
and biochemical factors with the exception of creatinine. Changes in more serum enzymes was not significant but the changes of AST between the control group and steroids (P value: 0.0001), ALT between control and steroid groups (P value: 0.002) and also creatine and steroid groups (P value: 0.005), and the changes of GGT enzyme between the control group and steroids groups (P value: 0.007) were significant differences. The results obtained in this study were very similar to the results of other researchers, but with some of the results contradicted especially, those studies that reported that the using supplements have any harm to organs.

**Conclusion**

From the results, we conclude that taking supplements in bodybuilding has damaging effects on organs, and should be used wisely and in consultation with the doctor.

Key words: bodybuilding, creatine monohydrate, (oxymetholone) anabolic steroid
Correlation of Thyroid Hormones with FSH, LH and Prolactin in menstrual irregularities woman in the Reproductive Age

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Background: Thyroid dysfunction is an important causative etiology of menstrual abnormalities. Thyroid hormones play an important role in achieving and maintaining reproductive functions. Present study was done to evaluate correlate thyroid hormones level with FSH, LH and prolactin in patient with menstrual irregularities of reproductive age group from 18 to 50 years of age.

Methods: This study includes 271 menstrual irregularities women. Patients were divided into two groups: Age group less than 33 years and over 33 years. In third day of menstrual cycle, sample blood was taken for determination of LH, FSH, PRL, TSH, T3 and T4. Laboratory tests were performed by ELISA method. The thyroid function status is determined by measuring TSH, T3, and T4.

Results: The result showed LH and age were positively correlated with each other in woman Age group less than 33 years and over 33 years. There was a positive correlation between FSH and T4.

Conclusion: In both hypo and hyperthyroidism menstrual irregularities observed, indicating that the thyroid hormones play an important role in reproductive physiology

Keywords: Thyroid hormones, FSH, LH, Prolactin, menstrual irregularities
Study of neonates hypothyroid screen during the 1st of 6 month year 1397 in province Qazvin

Neonatal congenital hypothyroid is a clinical syndrome due to decay in thyroid hormone. Some defects that result in this disease are anatomical deficiency of thyroid gland, iodine deficiency of thyroid gland, iodine deficiency and congenital metabolic deficiencies of thyroid.

Regarding side effects as mental retardation and cretinism, screening program began in Qazvin since in last 6 month we tested 9598 newborns samples taken from Qazvin, Takestan, Booeen-zahra and Abyek.

In this cross-sectional prospective Study neonatal TSH (thyroid Stimulation Hormone) test using ELISA method, with two antibodies, simple antibody and antibody with peroxidase as a Marker. Blood Sampling Was taken from newborns foot heel, 72 hours after birth on gutery 303 Paper. Kits were prepared from reliable corporation by reference laboratory approval. Results analysed by SPSS software from 9598 cases 9200(95.85%) were normal, 358(3.73%) were doubt. Doubted results rechecked by vein blood. Finally 22(0.23%) definitely positive. In the other word 2.3 from 1000 newborns are involved in congenital hypothyroid.

According to findings, prevalence of hypothyroid in Qazvin is higher than the country's mean this (about 2 folds). This recognize in test importance, personal expertness and correct sampling, more than previous screening, hypothyroid Qazvin, neonatal
Evaluation of Tow Methods of Direct measurement and Friedewald equation to estimate the LDL-Cholesterol in Medical Laboratories

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Abstract

Background
Blood levels of LDL cholesterol (LDL-C) are often assessed when evaluating the risk of future cardiovascular diseases. The amount of cholesterol carried by different lipoproteins can provide valuable information about the risk of developing cardiovascular disease (CVD). LDL-C reflects the amount of cholesterol carried by LDL. Available evidence suggests that lowering blood levels of LDL-C reduces the risk of CVD. LDL can be measured directly, such as enzymatic method or can be calculated with Friedewald equation. Despite the development of enzymatic methods still in most laboratories is calculated using Friedewald's formula. This study was done to evaluate of direct measurement and Friedewald equation to determine the LDL-C from serum.

Methods:
This descriptive study was conducted on the 912 patients, 53.6% men and 46.4% women whom referred to paymbar-rahmat hospital Sanandaj in Kurdistan province of Iran during 2016-2018 years. Blood samples (4ml) were drown from patient. Parameters such as, LDL (mg/dl), HDL (mg/dl), Total cholesterol (TC) (mg/dl), triglyceride (TG) (mg/dl) of serum are measured with Pars azmon company kits. Friedewald equation used to estimate of LDL concentration for samples with triglyceride concentration of less than 400 mg/dl. Data were analyzed using SPSS software.
Results: Of the 912 serum samples in this study, 53.6 % men and 46.4 % women and average patient age was 41.8±10.4 years. This study showed mean serum LDL, HDL, cholesterol, triglycerides were 77.5±16.4, 45.8±14.9, 183.1±52.2 and 148.3±55.6 mg/dl, respectively. Average calculated concentration was 99.7±41.1 by Friedewald's equation.

Conclusion: Our research revealed that direct method is less in compared to Friedewald method. In conclusion, direct method can be used in laboratories.

Keywords: Direct, LDL, Friedewald, patient
Pbi-63

Therapeutic effects of resveratrol and quercetin in management of polycystic ovary syndrome
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Introduction
Polycystic ovary syndrome (PCOS) is recognized as the most common heterogeneous endocrine disorder characterized by adverse reproductive and metabolic implications in reproductive-aged women around the world. Multiple disturbances including oxidative metabolism, insulin signaling and inflammatory responses have been suggested as inducing factors in the pathogenesis of PCOS. A lot of investigations have demonstrated that higher level of oxidative stress in PCOS patients correlated with insulin resistance, hyperandrogenemia, obesity and chronic inflammation which finally could increase the risk of developing gynecological cancers. Several flavonoids including resveratrol and quercetin as
plant-derived antioxidants are being widely used to treat metabolic and reproductive disorders in PCOS.

**Methods**

The current review has been achieved by using an organized search of the scientific data published on the effects of resveratrol and quercetin in PCOS treatment in various databases, including PubMed, Science Direct and Google Scholar.

**Results**

Based on the literature discussed, resveratrol and quercetin through improvement of insulin resistance, anti-androgenic properties, reduction of oxidative stress and inflammatory factors have a considerable function in PCOS amelioration.

**Conclusion**

This study provides evidence for potential therapeutic effects of dietary flavonoids such as resveratrol and quercetin against metabolic and reproductive disturbances in PCOS.

**Keywords:** Polycystic ovary syndrome, resveratrol, quercetin
Curcumin suppresses high glucose-induced lipotoxicity and lipid droplet accumulation in RAW264.7, involvement of suppression of skew RAW264.7 toward M1

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Background: Macrophages are flexible cells and able play multiple functions in inflammatory states. These major components of innate immunity cells secrete various cytokines and a vast number of mediators molecules and CD markers. These process tightly regulated and these molecules have both beneficial and detrimental outcome in health. Macrophages can acquire specialized phenotypes; M1 (pro-inflammatory phenotype) and M2 (anti-inflammatory phenotype). M1 subset secreted inflammatory mediators such as iNOS, TNF, MCP1, IL-6, and have CD11c surface marker. In contrast, M2 markers are CD206, CD163, TGFβ, Arginase. M1/M2 balance has a critical role in inflammation. Diabetes Mellitus is an inflammatory condition and polarization pattern of macrophage is going toward to M1.

Curcumin is an active plant compound that is extracted from turmeric, which has strong anti-inflammatory properties. This study was conducted to evaluate the anti-inflammatory effect of curcumin.

Methods: RAW 264.7 macrophages were stimulated by high glucose concentration, then we have studied effects of curcumin (10 µM) on high glucose-induced lipotoxicity and macrophage polarization. We have measured high glucose-induced lipogenesis by oil-red O staining. For investigating macrophage polarization, we assessment M1 marker, CD11c, as an inflammatory factor via flow cytometry. Also, inflammatory genes expression include: iNOS, IL-6, TNF and MCP1 were assayed by Real-time PCR.

Results: This study suggests that high glucose induce RAW264.7 lipogenesis. Flow cytometry analyses showed that high glucose skew RAW 264.7 toward M1.
subset, whereas Berberine attenuated M1 marker up to about 70%. RT-PCR confirmed the anti-inflammatory effect of curcumin through attenuation of inflammatory genes expression (P < 0.05).

**Conclusion:** Reduction of lipogenesis, M1 surface marker and above inflammatory genes approve that curcumin can be used as a therapeutic drug in inflammatory diseases.

**Keywords:** Curcumin, Inflammation, Macrophage polarization
Clinical Diagnosis of diabetes and prediabetes in the Sirjan Imam-Reza hospital in 2017

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Introduction:

Diabetes is a disease that occurs when blood glucose rising up. Blood glucose is the main source of energy and comes from the food you eat. Insulin, a hormone made by the pancreas, helps glucose from food get into cells to be used for energy. Sometimes the body doesn’t make enough—or any—inulin or doesn’t use insulin well. Glucose then stays in the blood and doesn’t reach cells. Over
time, having too much glucose in the blood can cause health problems such as heart disease, stroke, kidney disease, eye problems, dental disease, nerve damage foot problems. As of 2015, 30.3 million people in the United States, or 9.4 percent of the population, had diabetes. More than 1 in 4 of them didn’t know they had the disease. Diabetes affects 1 in 4 people over the age of 65.

**Material and methods:**

This studied surveyed 71 samples. we evaluated FBS and HbA1C for all the patient. Now we will use the spectrophotometer to measure the concentration of glucose (sugar) and HbA1C. amount of colored substance is directly proportional to the amount of glucose and HbA1C. present. we will create a standard curve that translates the absorbance of the colored substance into the concentration of glucose and will use it to determine the amount of glucose in Reagent.

**Result and discussions:**

After clinical examination and Lab test, our result showed 49.3% of patients had high FBS and 35.2% has Abnormal HbA1C. the prevalence of Diabetes is high among people with undiagnosed diabetes and prediabetes. These individuals might benefit from interventions aimed at preventing the development and/or progression of both prediabetes and diabetes.

**Key words:** FBS, HbA1C, Diabetes, Pre Diabetes
Evaluation of biochemical – hematological parameters and thyroid hormones (TSH, T4, T3) in Thalassemia minor patients

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Background: β-thalassemia is one of the most common disorders and blood diseases that are genetically transmitted from generation to generation. One of the common types of diseases with anemia is β-thalassemia minor. This research was based on the alteration to measure these indicators in differentiating patients with thalassemia minor of others, especially iron deficiency anemia as a screening test.

Methods In this case-control study, samples of thalassemia minor (40) and healthy subjects (30) referring to Ali Asghar hospital (Tehran) in 1396 were evaluated for biochemical status (Fe, TIBC, Ca, Na, K, ALT, AST), hematological (Hemoglobin, Hematocrit, Ferritin, MCV, MCH, MCHC) and Thyroid hormones (T3, T4, TSH). Then, using SPSS software, statistical tests were performed using independent t-test and logistic regression and comparison of means.

Results: The results of TIBC(1486.546±96.158 of patients and 274.243±7.146 of control), Fe(249.491±11.667 of patients and 91.950±7.335 of control) Ferritin(228.250±15.962 of patients and 22.900±1.516 of control) showed that there was a significant difference in patients’ group in comparison with control. Also, results showed that thyroid dysfunction was not significantly different in patients and also was not significantly different in other tests compared to healthy subjects.
Conclusion: The following of determination of biochemical - hematological parameters and thyroid factors in thalassemic patients every year and the importance of regular follow up of β-thalassemia patients for early detection and proper treatment of complications and disease control in the community.

Keywords: β-thalassemia minor, biochemical tests, hematological parameters, thyroid hormones
The Status of Liver Markers in Coronary Heart Disease

Abstract

Background: An association exists between the alterations of liver markers and the risk of coronary heart disease (CHD).

Objectives: This study was designed to investigate the status of liver markers in patients with CHD.

Materials and Methods: In this study, 100 subjects, including 50 patients with CHD and 50 healthy voluntaries, were studied. Serum activities of alkaline phosphatase (ALP), alanine aminotransferase (ALT), aspartate aminotransferase (AST), and gamma-glutamyltransferase (GGT) and fasting blood sugar (FBS) were evaluated. Unpaired Student’s t-test was used to analyze the data.

Results: FBS and activities of ALT, ALP, and GGT in CHD patients were significantly greater than that of healthy people. In CHD patients, the activity of serum AST was higher than that of controls, but it was not statistically significant.

Conclusions: This study indicated that CHD is related to elevation of liver enzymes activity. CHD is a deadly disease that requires appropriate medical care.
The use of antioxidant agents might be useful for the inhibition of disease progression.

**Keywords:** Liver markers, Coronary heart disease.
Pbi-68

Effects of Coenzyme Q10 and L-carnitine on Biochemical and Hormonal parameters of chickens

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Background: CoQ10 is endogenous antioxidant that play a role as a coenzyme for oxidative phosphorylation. L-carnitine is an essential factor for β-oxidation through transportation of long-chain fatty acids into the mitochondria. The aim of this study was to evaluate the effects of L-carnitine and Coenzyme Q10 individually and in combination on some biochemical parameters and concentration of thyroid hormones (T3 and T4) of broiler chickens.

Method: Total of 80 one-day old male chickens were separated randomly to 4 treatment groups. In each group, there was 4 replicates with 5 birds. Two levels of L-carnitine (0 and 200mg/kg) and Coenzyme Q10(0 and 40 mg/kg) were used as an additive feed. A completely randomized design with a 2×2 Factorial arrangement was applied. Blood samples were collected from the wing vein (two birds from each replicate) in test tubes containing sodium citrate at the end of finisher (day 42) period. The biochemical parameters including: Glucose and Uric Acid (calorimetric method), Albumin (Bromocresol Green method), Globulin, Total protein (Biuret method) and Thyroid hormones (Radioimmunoassay) were measured. The statistical analysis was performed with SPSS 20 for windows. Anova GLM (general linear procedure) and Duncan’s Multiple Range test were used.

Results: Level of Albumin, Globulin, total protein, Uric Acid and Glucose were not affected significantly by using these additives(p>0.05). However, there was a
significant increase of T3 level by using Coenzyme Q10 individually and in combination with L-carnitine (p<0.05).

**Conclusion:** Coenzyme Q10 and L-carnitine additives did not affect biochemical parameters significantly (except T3 level). Different levels of L-carnitine and Coenzyme Q10 may result in more obvious effects.

**Keywords:** Coenzyme Q10, L-carnitine, Thyroid Hormones
Association of paraoxonase1 (PON1) genotypes with the activity of PON1 in patients with Parkinson's disease

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Background: Parkinson’s disease is thought to be secondary neurodegenerative disease after Alzheimer’s disease. Various numbers of factors such as oxidative stress, neurotoxins, and pesticides have been implicated in its pathophysiology as possible causative agents. Paraoxonas1 (PON1) metabolizes xenobiotics, including pesticides. Therefore, we investigated the relationship between PON1 polymorphisms with its activities in the pathogenesis of Parkinson’s disease.

Methods: We selected 70 subjects with Parkinson's disease for patients group and 75 healthy ones for the control group. We investigated polymorphisms of the PON1 (L55M and Q192R) by PCR-RFLP assays; we also measure the levels of paraoxonase1, TAC (total antioxidant capacity) and TOS (total oxidant status) with ELISA (Enzyme-linked immunosorbent assay) and spectrophotometric method for their activities.

Results: Paraoxonase and arylesterase activity of PON1 as well as their concentrations were lower in patients with PD compared with control group, but from the view of the specific activity, it was not significant between two groups. In the compare of TAC, TOS, and OSI in our groups, TOS and OSI were higher in the patients than controls, while patients had lower levels of TAC compared with controls. We obtained statistically significant differences in PON1 55 genotype frequencies among our studied groups but PON1192 was not significant. Serum paraoxonase concentrations and activities were higher in LL (comparison
with LM and MM) and RR (comparison with QR and QQ) genotypes while we did not observe any significant differences in arylesterase levels among mentioned polymorphisms.

**Conclusion:** we reported associations between PON1 polymorphisms (55, 192) and enzyme activities in Parkinson's disease as there was a significant reduction in paraoxonase levels in patients with Parkinson compared with healthy cases. Taken together, paraoxonase enzyme in subjects with different genotypes could be a potential biomarker for determining the severity and prognosis of Parkinson.

**Keywords:** Parkinson's disease; paraoxonase1; Polymorphism.
Pbi-70

MCU- knockdown attenuates high glucose-induced inflammation through regulating MAPKs/NF-κB pathways and ROS production in HepG2 cells.

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Abstract:

Mitochondrial Ca²⁺ is a key regulator of organelle physiology and the excessive increase in mitochondrial calcium is associated with the oxidative stress. In the present study, we investigated the molecular mechanisms linking mitochondrial calcium to inflammatory and coagulative responses in hepatocytes exposed to high glucose (HG) (33mM glucose). Treatment of HepG2 cells with HG for 24 h induced insulin resistance, as demonstrated by impairment of insulin-stimulated Akt phosphorylation. HepG2 treatment with HG led to an increase in mitochondrial Ca²⁺ uptake, while cytosolic calcium remained unchanged. Inhibition of MCU by lentiviral-mediated shRNA prevented mitochondrial calcium uptake and the inflammatory (TNF-α, IL-6) and coagulative (PAI-1 and FGA) responses in HepG2 cells exposed to HG. The protection from HG-induced inflammation by MCU inhibition was accompanied by a decrease in the generation of reactive oxygen species (ROS). Importantly, MCU inhibition in HepG2 cells abrogated the phosphorylation of p38, JNK and IKKα/IKKβ in HG treated cells. Taken together, these data suggest that MCU inhibition may represent a promising therapy for prevention of deleterious effects of obesity and metabolic diseases.
Keywords: Mitochondrial calcium, Mitochondrial Calcium Uniporter (MCU), inflammation, Coagulation factor, liver, HepG2
PB-2

High prevalence of carbapenem-resistant Klebsiella pneumonia in Tehran hospital

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Abstract

Background: The extended-spectrum β-lactamase (ESBL) carbapenems-resistant Klebsiella isolates are considered one of the most significant challenging in the
treatment of patients in hospitals. The aim of this study was to determine the prevalence of important carbapenem resistance genes ESBL subtypes and between *K. pneumoniae* from patients at hospital in Tehran, Iran.

**Methods:** Fifty-four isolates of *K. pneumoniae* were isolated from Shariatee Hospital in Tehran from February 2013 to July 2016. Antibiotic testing was done by using the standard disk diffusion method and E-test MIC. The confirmation of carbapenemase activity was performed using an MHT and a new method called the carbapenem inactivation method test (CIM). Finally, a polymerase chain reaction (PCR) and sequencing of related genes was performed.

**Results:** Our PCR data demonstrate that blaCTX-M group’s 40 (81.4%) genes were the most prevalent in our hospital followed by group genes bla_CTX-M-3 (18.51%) and bla_CTX-M-2 (20.38%). The distribution of the CTX-M group revealed that bla_CTX-M-15 23 (42.6%) was the dominant subtype. The coexistence of multiple genes included blaTEM, CTX-M 14 (25.9%) and blaSHV, and CTX-M 20 (37.0%). The presence of blaNDM1, blaOXA-48, and blaKPC were identified in the carbapenem-resistant isolates, 2 (40.7%), 10 (18.5%), and 7 (12.9%) respectively.
Conclusion: Our research showed that a CIM test for the first time in Iran is possible and has a high facility for the fast identification of carbapenem-resistant Klebsiella (CRK). We are encountered with the emergence of CTX-M, OXA-48, KPC, and NDM1 harboring CRK strains in our hospitals. Therefore, the treatment of patients infected with these isolates will be an important future concern in our clinical settings.

Keywords: New Delhi metallo-beta-lactamase-1, Klebsiella pneumoniae, Carbapenem, Extended-spectrum β-lactamase
PB-3

Genotyping of Vancomycin Resistant Enterococci faecium

in Tehran Hospital

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Abstract:

Background: Owing to restricted treatment options, Vancomycin-resistant Enterococci (VRE) is a common cause of nosocomial infections. This present
study was undertaken to evaluate the presence of Van-type and virulence determinants in the clinical isolates of E. faecium (fm) in Tehran hospital.

**Materials and Methods:** A total of 150 Enterococcal isolates were performed. Antimicrobial susceptibility testing was done by disc diffusion and E-test as well as the genotypic test. The presence of virulence factors, including gelatinase (gelE), hyaluronidase (hyl), Enterococci surface protein (ESP), and aggregation substance (asa1) were detected by Polymerase chain reaction (PCR).

**Results:** Overall, 66.67 percent (80/120) of VRE fm strains were confirmed by the PCR method. The maximum number of isolates was from urine specimens (p < 0.05) and blood samples. Among the 80 VRE fm isolates, 76 isolates showed high-level resistance and carried a VanA phenotype (p < 0.05). In all the isolates, asa1, gelE, and ESP genes were detected in 14% (17/5), 26/3% (21/80), and 45% (36/80), respectively. E. fm carried ESP at a significantly higher frequency presented in VRE strains (p < 0.001). The prevalence of hly determinants in the E. faecium was 20% (16) (P < 0.001).

**Conclusion:** We, in our hospital, are faced with a high rate of VRE E.fm isolates with a VanA-positive phenotype. With increasingly resistant strains of VRE
strains to linezolid, we will encounter a serious worldwide public health challenge in treating VRE patients in future years.

**Keywords:** *Enterococcus faecium*, antibiotic resistance, Vancomycin-resistant enterococci, virulence factors
The Investigation of Relationship between Phenol and Anti-quorum Sensing Efficacy of Six Plant Extracts

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Abstract

Background and objectives: Nowadays, there is a tendency to utilize natural herbs in the pharmaceutical industry as an alternative approach for synthetic chemical drugs; therefore, the active compounds existing in the plants has increasingly taken scientists consideration. The fundamental purpose of the study was to investigate the total phenolic compounds, antioxidant, anti-QS and antimicrobial properties of the plant extracts of Althaea officinalis, Salvia officinalis, Rubus ulmifolius Blossom, Haplophyllum canaliculatum Boiss., Amygdalus scoparia Blossom and Juglans regia leaves against Staphylococcus aureus.

Materials and methods: Ten strains of Staphylococcus aureus were isolated from patients with dental implant infection. Plant species were collected from Fars Province and extracted using 96% ethanol. Determination of phenol was performed through the Folin–Ciocalteu method with synthetic antioxidant BHT (concentrations 2000, 670, 220, 75, 25, 8 μmol/L). The anti-QS and antimicrobial susceptibility methods were then done to evaluate their bactericidal and QS properties using Agrobacterium tumefaciens NTL/PZLR4, as a biosensor.
**Results:** There was a significant relationship between the total phenol content (Haplophyllum canaliculatum Boiss (1.130), Rubus ulmifolius (1.014), Althaea officinalis (0.557) and Juglans regia (0.324)), and the inhibitory effect of QS (Haplophyllum canaliculatum (>37 mm), Rubus ulmifolius (>30 mm), Althaea officinalis (>14 mm) and Juglans regia (>10 mm)). As a result, with increasing phenol content, the more inhibitory effect was observed; however, the relationship was insignificant in Amygdalus scoparia and Salvia officinalis. Moreover, the plants showed antimicrobial activity, with the highest antimicrobial in Haplophyllum canaliculatum (<19 mm) and the least in Juglans regia (<11.27 mm).

**Conclusion:** According to the results obtained, the total phenolic compounds in the extracts of Althaea officinalis, Salvia officinalis, Rubus ulmifolius, Haplophyllum canaliculatum, Amygdalus scoparia, and Juglans regia could be considered as a rich source of antioxidant and antimicrobial compounds in the pharmaceutical industry for treatment of bacterial diseases.

**Keywords:** Extract, QS, Plant, Anti-QS, Agrobacterium tumefaciens, Phenol.
Seroepidemiological Study of *Helicobacter pylori* Infection in Fardis of Alborz Province
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**Background:** *Helicobacter pylori* is a spiral gram-negative bacterium with which more than half of the world’s population are infected. This bacterium is one of the most prominent causes of gastric cancer which leads to 6500 deaths around the world annually. The epidemiologic pattern of *Helicobacter pylori* infection is differed between developed countries and developing countries. At the present study, the seroprevalence of *Helicobacter pylori* infection among residents of Fardis region of Alborz province was evaluated.

**Methods:** In this cross-sectional study of the blood of 80 volunteers who referred to clinical lab were collected. Using anti-*Helicobacter pylori* kit (IgG), the serum samples were tested for *H. pylori* infection. In other words, the titer of total IgG against *Helicobacter pylori* was evaluated by ELISA method. Data and different factors were analyzed by SPSS statistical software.

**Results:** The existence of total IgG against of H. pylori was detected in 41 (51.3%) of 80 volunteers and was negative in 33 people (41.3%). The result was equivocal in 6 people (7.5%). There was statistical meaningful correlation between positive result of serology test of IgG to some risk factors such as age and sex. Most infected volunteers were in the age range of 25-30 years old. In addition, statistics analysis showed in total infected individuals 45.8% was male and 67.0% were female.

**Conclusion:** Prevalence of *H. pylori* infection is high in Karaj Fardis. Also the infection rate is more in women compared to men, which is needed to be noticed in clinical care.
Keywords: *Helicobacter pylori*, IgG, ELISA, prevalence,
Detection of SlpA, Fbp68 genes in the toxigenic and resistant isolates of Clostridium difficile

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Background: Clostridium difficile is currently the leading hospital-acquired infection in the world. Clostridium difficile is a gram-positive, spore-forming, obligate anaerobic bacillus responsible for antibiotic-associated diarrhea. The pathogenesis of C. difficile infections has been attributed to two toxins, TcdA and TcdB. C. difficile, SLPA and Fbp68 have been shown to play a role in adherence to gastrointestinal tract cells and extracellular matrix components. The main purpose of this study was to characterize MDR C. difficile isolate adhesion.

Methods: In total 20 C. difficile clinical isolates were tested. Toxigenic MDR C. difficile isolates from patients with colitis were selected. All the isolates were confirmed by PCR for ccd-3 gene. Subsequently, PCR was performed for detection genes encoding, SlpA and Fbp68 adhesions.

Results: we detected SlpA and Fbp68 adhesins is 100% C. difficile isolates.

Conclusion: The present study report the highest prevalence of SLPA and Fbp68 in toxigenic and resistant C. difficile clinical isolates. This present research revealing a possible role of these adhesins in the colonization and pathogenesis of C. difficile.
Keywords: *Clostridium difficile*, adhesin, SlpA, Fbp68, Toxigenic, Antibiotic resistance
Mycobacteriosis and Tuberculosis: Laboratory Diagnosis

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Background: Tuberculosis is one of the most important infectious diseases that has claimed its victims throughout much of known human history. With Koch's discovery of the tubercle bacillus as the etiologic agent of the disease, his sanitary and hygienic measures, which were based on his discovery and the development of a vaccine against tuberculosis by Albert Calmette and Camille Guérin in 1921, an attenuated Mycobacterium bovis strain, bacilli Calmette-Guérin (BCG), and the discovery of the first antibiotic against tuberculosis, streptomycin by Selman Waksman in 1943, soon led to the opinion that appropriate control measures had become available for tuberculosis and it had been assumed that the disease could ultimately be eradicated. The emergence of resistant strains of this bacteria and widespread distribution of the disease in the world, and the emergence of the AIDS epidemic destroyed any possibility of global control of tuberculosis in the foreseeable future. The purpose of this review is to highlight the current scientific literature on mycobacterial infections and provide an overview on the laboratory diagnosis of tuberculosis and non-tuberculosis infections based on conventional phenotypic and modern molecular assays.

Methods: In this study, a number of 65 papers comprising 20 reviews, 9 case reports, and 36 original research in association with mycobacteriosis and the laboratory diagnosis of mycobacterial infections, were reviewed.

Results: Based on our analysis on the published documents methods applied for the laboratory diagnosis of tuberculosis are continually assessed and developed in
order to achieve more rapid, less expensive, and accurate results. Acid-fast staining and culture for mycobacteria remain at the core of any diagnostic algorithm with the sensitivity of 20-70% and specificity of 95-98% for AFB microscopy and the sensitivity of 95% and the specificity of 98% for culture based diagnosis. Following growth in culture, molecular tests such as nucleic acid hybridization probes and DNA sequencing may be used for definitive species identification. Nucleic acid amplification methods provide the means for direct detection of *Mycobacterium tuberculosis* in respiratory specimens without the prerequisite to isolate or culture the organism, leading to more rapid diagnosis and better patient care.

**Conclusion:** As the researchers in a developing country, we strongly believe that despite significant advances in laboratory capacity, in many countries reliable confirmation of suspected mycobacterial diseases is hindered by a lack of knowledge on proper standardized methods, sufficient funds, suitably trained staff and laboratory supplies.

**Keywords:** Mycobacteriosis, Mycobacterial disease, Acid-fast staining, Laboratory diagnosis, Mycobacterium bovis.

*Please note that Presenting Author is underlined and Corresponding Author is indicated by *. 
PB-14
Determine the prevalence of *Brucella* spp. and *Leptospira* spp. in blood samples by multiplex polymerase chain reaction collected from cattle, sheep and goats in herds located in provinces of Iran

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**Background:** Leptospirosis and brucellosis are common zoonosis that affect many species of mammals mostly causing economical losses. Further, very important fact is huge danger for human and animal health around the world. The purpose of the study is to determine the prevalence of *Brucella* spp. and *Leptospira* spp. using multiplex polymerase chain reaction (mPCR) method, in blood samples collected from cattle, sheep and goats.

**Methods:** In this study, a total number of 250 blood samples (5 cc of blood with ethilen diamin tetra asetic acid) were collected randomly from 100 cattle, 80 sheep and 70 goats located on 6 herds in Chaharmahal Va Bakhtiari and Esfahan provinces, Iran. After DNA extraction and setting of mPCR for *Brucella* spp. and *Leptospira* spp. mPCR products were screened.

**Results:** The DNA of these microorganisms was detected by multiplex PCR from 31 and 21 out of 100 cattle, respectively. Four of 70 goat’s blood samples from goat breeding farms were positive for *Leptospira* spp. and 11 were positive for *Brucella* spp. Out of 80 sheep blood samples 23 were positive for *Brucella* spp. and 14 for *Leptospira* spp.

**Conclusion:** The results of the present study show ruminant as an important reservoir for transmission of these zoonotic diseases to humans in Iran. mPCR has the ability to concurrently detect both *Brucella* and *Leptospira* species from blood samples of ruminants. The convenience and the possibility of detection of both bacteria at a time, strongly support the use of this mPCR for routine diagnostics.
Keywords: *Brucella* spp., *Leptospira* spp., Iran, multiplex polymerase chain reaction, ruminant, blood
PB-15

Molecular Study of the Prevalence of *Leptospira* spp. Serovar *Hardjo* in Blood Samples of Iranian Cattle and Sheep

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**Background:** *Leptospira* is an emerging global public health problem which involves both animals and human. The aim of this study was to appraise the presence of *Leptospira* DNA in blood samples from cattle and sheep via Polymerase Chain Reaction (PCR) method in Chaharmahal VaBakhtiari and Isfahan provinces of Iran.

**Methods:** One hundred and ninety-five samples (92 blood samples of cattle and 103 blood samples of sheep) were collected randomly from clinical healthy animals. DNA was extracted from the blood samples and stored at -20°C before examination. PCR reaction was performed for detection of *Leptospira* DNA using specific primers for 16s rRNA gene and PCR products were visualized in a 1% agarose gel electrophoresis.

**Results:** Results showed that 18.63% of the blood samples were positive. *Leptospiral* DNA was found in 20 of 92 (21.73%) and 16 of 103 (15.53%) of cattle and sheep blood samples, respectively. Nine (9.78%) out of the 92 cattle sampled and 5 (4.85%) out of the 103 sheep sampled were positive for *Leptospira* spp. serovar *Hardjo*.

**Conclusion:** This indicated that these cows and sheep are reservoirs and dangerous for human health. Moreover, the PCR method is sensitive and specific for diagnosis of *Leptospira* in suspected cases.

**Keywords:** blood, cattle, Leptospirosis, PCR, prevalence, sheep
Design and Application of a Loop Mediated Isothermal Amplification (LAMP) Assay to detect *Yersinia pestis*

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Introduction:
From military point of view, a number of pathogenic bacteria can be considered as possible biological warfare agents (BWAs). *Yersinia pestis* (the causative agent of plague) is further a bacterial agent enlisted by CDC into the category A of potential biological weapons. A quick and accurate diagnosis of the organism is essential to manage infection cases. The LAMP method amplifies DNA with a high degree of specificity, efficiency, and rapidity under isothermal conditions. A LAMP method was developed for the detection of *Y.pestis*.

Materials and methods:
The LAMP was developed using specific primers designed based on the sequence of the *Caf1* gene of *Y.pestis*. Analytical specificity and sensitivity of the *Caf1*-LAMP were evaluated.

Results:
The LAMP reaction was performed at 60°C for 30 min. The amplification obtained with the *Caf1*-LAMP was detected by visual inspection of turbidity and fluorescent color change and confirmed by gel electrophoresis. The LAMP assay was highly specific and no amplification products were observed from the non-*Yersinia* organisms.

Conclusion:
The Caf1-LAMP is a simple, rapid, specific and sensitive technique for detection of *Y. pestis* that may improve diagnostic potential in field and battlefield.

**Key Words:**
*Yersinia pestis*, plague, LAMP, Detection.
PB-17

Comparison of PCR and Nested-PCR to detect of Tick-Borne Relapsing Fever *Borreliae* in Patient DNA samples

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Introduction:

Tick-borne relapsing fever (TBRF) is characterized by fever followed by *Borreliae* spp. is transmitted via bites of the soft tick *Ornithodoros* spp. TBRF is an endemic disease in Iran, with more 100 annual cases. In this study, the IGS-Nested PCR and IGS-PCR assays were used to detect of TBRF *Borreliae* in DNA of serum patients collected from the endemic area from Iran.

Material and Methods:

39 patient serological samples were obtained from endemic areas of Iran and DNA extraction was performed. Serological test of these 39 patients were obtained positive. The extracted DNA samples were examined by IGS-Nested PCR and IGS-PCR along positive and negative controls. Agarose gel electrophoresis were used to detect amplification products in IGS-Nested PCR and IGS-PCR methods.
Results:

The results of *IGS*-Nested PCR showed to *IGS* gene amplification of 540 bp fragment in 3 patient DNA samples. Whereas agarose gel electrophoresis analysis in *IGS*-PCR method no showed any amplification of 540 bp fragment in extracted DNA.

Conclusion:

The comparison of the *IGS*-Nested PCR and *IGS*-PCR assays were showed more sensitivity in *IGS*-Nested PCR to detect of TBRF *Borreliae*.

Key Words:

*Borreliae* - TBRF – Nested PCR – PCR- *IGS*.
PB-20

New applied of bacteria for Inhibition of breast cancer growth and metastasis by Helicobacter pylori

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Abstract

Introduction: Treatment of breast cancer by bacteria is a promising new strategy. So, Helicobacter pylori is the good candidate for this purpose. The aims study is Evaluation of Metastatic inhibition effect of helicobacter pylori lysate on cancer cell line.

Material and methods: The cell cytotoxicity of 4T1 cell exposed to OipA protein of H. pylori was determined by a MTT colorimetric assay and trypan blue exclusion. Furthermore, migration assay was determined by scratch test.

Results: We found that treatment of 4T1 cell with OipA protein of H. pylori significantly reduced cell proliferation and induced cell death in a dose-dependent manner with that in the untreated control.

Discussion: OipA protein of H. pylori induced migration inhibition of breast cancer cells. These observations suggest an anti-cancer activity of recombinant protein. OipA protein of H. pylori can reduce cancer cell viability so this strategy can be used to develop a drug component in for cancer therapy.

Key words: helicobacter, scratch assay, cancer
PB-21

Frequency and pattern survey of Antibiotic resistance of clinical isolates of ESBL strains and determination of enzymatic relationship with clinical specimen type

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Abstract

Background: Differences in clinical isolates may affect the frequency of β-lactamase enzymes (ESBLs) in some gram-negative bacteria. The aim of this study was to investigate the relationship between clinical specimen type and β-lactam resistance.

Methods: Escherichia coli, Pseudomonas aeruginosa, Acinetobacter baumannii, Klebsiella pneumoniae and Enterobacter cloacae were identified by biochemical tests. Combination disk test was used to determine ESBL strains. Chi-square test with significant range of P≤0.05 was used to examine the relationship between variables.

Results: Out of 270 isolated gram-negative isolates, 95 isolates produced the ESBL enzyme. Of the 95 isolates, 28 isolates (29.47%) were E. coli, 22 isolates (23.15%), P. anro gensosa, 19 isolates (20%), A. baumani, 17 isolates (17.89%) of K. pneumonia and and 9 isolates (33.3%) were E. cloacae. There was a significant relationship between the presence of ESBL and the type of clinical specimen. The isolates with this enzyme were the most frequent in wound, urine and burn wounds. The values obtained for E. coli, P. aeruginosa, A. baumani, K. pneumoniae and E. cloacae were p = 0.03, p = 0.09, p = 0.015, p = 0.026 and p = 0.02 , respectively.
Conclusion: Some environmental factors and underlying variables such as the type of clinical specimen can increase the induction of ESBL enzymes.

Keywords: Nosocomial Infection; Enterobacteriaceae; Extended-Spectrum Beta-Lactamase (ESBL); Clinical specimen; Drug Resistance
PB-22

Preparation of chitosan nano - particles carriers of FlgE2 recombinant protein candidate to Helicobacter pylori vaccine

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Abstract

Background: Helicobacter pylori is a stomach-specific human pathogens, at least in the stomach more than half of the world people colonized .the organisms most recently is classified by the WHO as Class 1 Carcinogenic Factor. Due to the complications of the infection as well as the incidence of infection Increasing antibiotic resistance of bacteria. Studies on the availability of an alternative method for antibiotic treatment of the infection as well as the possibility of preventing it in is expanding. The purpose of this study was to Design and manufacturing of the nano- particles carriers of FlgE2 recombinant protein to prevent Helicobacter pylori infection.
Methods: Chitosan nano-particles were produce. The size and morphology of the nano-particles were investigated. FlgE2 recombinant protein carrying of Chitosan nano-particles were produced by ionic gelation method.

Results: SDS-PAGE analysis showed the expression of an approximately 66,000 Dalton protein. DLS confirm size and zeta potential of the nanoparticle.

Conclusion: Today, the technology of using nano-particles containing recombinant protein of antigens is underway to further enhance immunization. Which has made immune responses stronger, protects the recombinant peptide and eases the work and increases the complex protection.

Keywords: Helicobacter pylori, gastric cancer, vaccination, FlgE2 protein, Chitosan
The frequency of beta-lactamase enzymes and susceptibility patterns of bacteria isolated from Tabriz Children’s Hospital personnel

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Background: Hospital potential sources of pathogenic bacterial in hospital Antshabactry hand hospital personnel is the most important factor. The aim of this study was to evaluate the prevalence of beta lactamase Enzyme and susceptibility patterns of bacteria isolated from staff hand children’s Hospital of Tabriz.

Method: From 100 employee’s children’s hospital were collected and were identified by staining and biochemical tests, then lactamase production was assessed by Acidometric and then their antibiotic resistance pattern was performed by disk diffusion method.

Result: 74 cases (74%) negative Staphylococcus, 13 (13%), Staphylococcus aureus, 3(3%) Bacillus, 1 cases of Staphylococcus non A,B,D, 1 patient (1%), Klebsiella pneumonia, 1(1%) Diphtheroid and 7 patient with negative Staphylococcus with Bacillus (7%) were isolated. 16 pathogenic organisms identified 12 species (75%) were able to produce beta-lactamase enzymes and 4 species (25%) did not produce beta-lactamase enzymes. The susceptibility patterns of 12 species (80%) compared to erythromycin, 3 species (20%) compared to vancomycin, one species (67%) to Gentamicin, 3 species (20%) compared to Imipenem. 8 species (53,3%) compared to Cotrimoxazole, 6 Species (40%) to Tetracucline. 4 Species (26,7%) compared with Ceftriaxone and 4 Species (26,7%) were resistant to Ampicillin.

Conclusion: The results show high prevalence of bacteria resistant to antibiotics and extensive lactamase producing strains isolated from hospital staff.
Keywords: Beta-lactamase enzymes, Susceptibility, Personnel antibiotic resistance
PB-24

Detection of IMP Gene among Pseudomonas aeruginosa isolated from sari teaching hospitals, Iran

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Background: Pseudomonas aeruginosa is an opportunistic bacterium and a cause of infection in human. Metallo-β-lactamases enzymes are involved in bacterial resistance. This study investigated the prevalence of IMP gene in p. aeruginosa isolates.

Methods: In this cross-sectional study, 100 Pseudomonas aeruginosa isolates from clinical specimens were collected from sari teaching hospitals. Antibiotic susceptibility tests were performed by Kirby-Bauer disc diffusion method according the CLSI guidelines. The frequency of MBL (Metallo-Beta-Lactamase) producers was evaluated by CDDT. The β-lactamases genes were detected by PCR method.

Results: In our study, the highest and the lowest resistant patterns were related to Levofloxacin and Piperacillin tazobactum with 40% and 13%, respectively. Of 100 Pseudomonas aeruginosa isolates, 43 isolates (43%) were Resistant to Carbapenem. Based on the results of Imipenem-EDTA combined disk method, production of metallo-beta-lactamases was known in 33 (76.74%) Pseudomonas aeruginosa isolates. The prevalence of IMP gene was (9%).

Conclusion: The prevalence of MBLs-producing Pseudomonas aeruginosa strains detected in this study is a major concern identification of these organisms.
is essential in the hospitals in order to get a better therapeutic response and control of bacterial dissemination.

**Keywords:** *Pseudomonas aeruginosa*, Antibiotic resistance, *IMP*
PB-25
Evaluating the prevalence of *E.coli* uropathogenic and determination of antibiotic resistance and virulence genes in strains isolated from patients referred to hospitals in the city of Abadan

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**Background:** Antibiotic resistance due to the widespread use of antibiotics is one of the major causes of failure in antibiotic treatment. The aim of this study was to investigate the rates of antibiotic resistance and aer and traT genes among *Escherichia coli*.

**Methods:** In total, 100 isolates of *Escherichia coli* strains, obtained from outpatients, were studied. The identity of the isolated strains was confirmed by bacteriologic methods. The drug sensitivity definition test to 12 antibiotics was done via the disk diffusion antiibiogram method. The aer and traT genes were detected by PCR method.

**Results:** In this study, the resistance rates of the isolates to Nalidixic acid and Tetracycline by disk diffusion antiibiogram method were 92% and 91%. The prevalence of aer and traT genes were 66.66% and 73.33%, respectively.

**Conclusion:** The results of this study indicated that the higher resistance of *Escherichia coli* to Nalidixic acid and Tetracycline compared to the other antibiotic. Also, the prevalence of aer and traT genes detected in this study is a major concern and highlights the need for infection control measures such as antibiotic management protocols.

**Keywords:** *Escherichia coli*, antibiotic resistance, aer gene, traT gene
Identification of Hemolysin genes and their association with antimicrobial resistance pattern among clinical isolates of *Staphylococcus aureus*

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**Background:** *Staphylococcus aureus* is expressing a broad range of different hemolysins enhancing its ability to establish and maintain infection in humans. The aim of this study was to identify the types of hemolysins in different clinical isolates of *S. aureus* and their association with antibiotic resistance patterns.

**Methods:** In this cross-sectional and descriptive study, clinical isolates of *S. aureus* were collected from Hamedan's hospitals during an 11-month period from June 2016 to January 2017 and identified by using biochemical tests. To determine the antibiotic resistance pattern, Disk diffusion method and minimum inhibitory concentration (MIC) were conducted. Genomic DNA was extracted using extraction kit. The polymerase chain reaction (PCR) was done with specific primers for identification of *hla*, *hlb*, *hld* and *hlg* genes.

**Results:** Among a total of 389 clinical samples, 138 isolates (35.45%) of *S. aureus* were identified, which 87 isolates (63.04%) were cefoxitin MIC of more than 4μg/ml and resistant to methicillin. The highest frequency of antibiotic resistance was observed against erythromycin in 108 isolates (78.26%) and penicillin in 133 isolates (96.37%) and the lowest resistance was against gatifloxacin in 50 isolates (36.23%) and Cefazolin in 11 isolates (97.7%). Furthermore, the *hla*, *hlb*, *hld* and *hlg* genes were detected among 11(7.97%), 7(5.07%), 16(11.59%) and 4(2.89%) isolates, respectively. There was a significant relationship between the presence of alpha and delta hemolysin-encoding genes and the antibiotic resistance pattern of isolates (p<0.05).

**Conclusion:** The results exhibited that the association between the presence of the hemolysin genes and the antibiotic resistance pattern can be considered as a serious issue.

**Keywords:** *Staphylococcus aureus*, antibiotic resistance, virulence factors, alpha-hemolysin, beta-hemolysin, Delta-hemolysin
Synergistic effect of Carum copticum and Mentha piperita essential oils with ciprofloxacin, vancomycin, and gentamicin on Gram negative and Gram positive bacteria

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Background: Infectious diseases have always been an important health issue in human communities. In the recent years, much research has been conducted on antimicrobial effects of nature-based compounds because of increased prevalence of antibiotic resistance. The present study was conducted to investigate synergistic effect of Carum copticum and Mentha piperita essential oils with ciprofloxacin, vancomycin, and gentamicin on Gram-negative and Gram-positive bacteria.

Materials and Methods: In this experimental study, the synergistic effects of C. copticum and M. piperita essential oils with antibiotics on Staphylococcus aureus (ATCC 25923), Enterococcus faecalis (ATCC 29212), Escherichia coli (ATCC 8739), Pseudomonas aeruginosa (ATCC 9027), Staphylococcus epidermidis
(ATCC 14990), and Listeria monocytogenes (ATCC 7644) were studied according to broth microdilution and the MIC and fractional inhibitory concentration (FIC) of these two essential oils determined.

**Results:** C. copticum essential oil at 30 µg/ml could inhibit S. aureus, and in combination with vancomycin, decreased MIC from 0.5 to 0.12 µg/ml. Moreover, the FIC was derived 0.24 µg/ml which represents a potent synergistic effect with vancomycin against S. aureus growth. C. copticum essential oil alone or combined with other antibiotics is effective in treating bacterial infections.

**Conclusions:** In addition, C. copticum essential oil can strengthen the activities of certain antibiotics, which makes it possible to use this essential oil, especially in drug resistance or to lower dosage or toxicity of the drugs.

**Keywords:** Antimicrobial effect, essential oil, Antibiotics, synergism
Prevalence and antibiotic resistant patterns on isolated *Klebsiella pneumoniae* from different words Bouali Sina Hospital Sari

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**Background:** *Klebsiella pneumonia* an opportunistic pathogen associated with nosocomial infections. Antibiotic resistance in *Klebsiella pneumoniae* has become a worldwide problem, and is leading to multi-drug resistance (MDR: Multiple drug resistance). The aim of this study was to determine the antibiotic resistance patterns and to detect *Klebsiella pneumonia* in clinical isolates.

**Methods:** The clinical specimens were collected from patients during 9 months. Using routine microbiological methods, we identified the bacteria. The antibiotic resistance pattern of the isolates was detected by the disk agar diffraction method. The gathered data were analyzed using SPSS-20 software.

**Results:** The more *Klebsiella pneumonia* strains were from urine specimens 63 (56.3%). In antimicrobial susceptibility testing, Amikacin exhibited the greatest anti-*Klebsiella pneumonia* activity (10.7%). Isolates Out of the 112 clinical *Klebsiella pneumonia* isolates collected, 73 (65/2%) were multi drug resistant (MDR). 

**Conclusion:** High antimicrobial resistance in *Klebsiella pneumonia* species was observed in the present study; therefore, it is necessary to implement some approaches for the prevention of bacterial spread.

**Keywords:** Antibiotic resistance, *Klebsiella pneumonia*, bacterias
PB-31

Variable number of tandem repeat analysis (VNTR) a rapid and precise tool for source-tracking the origin of infection in bacterial diseases

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Background: In the last decade, advent of new Genotyping methods based on Sequencing great advances have been made in the diagnosis of clinically relevant bacteria. Variable number of tandem repeat analysis (VNTR) is a new genotyping method, based on the variation in the copy number of short tandem repeat sequences, called VNTRs, found at different loci on the genome. Several MLVA schemes for bacterial diseases have been designed and used to type this pathogen.

Methods: This paper, is a content analysis study that has been performed by searching VNTR, tandem repeat and Genotyping key words in Science Direct, PubMed, msgiran, google scholar, sid, Civilica and Scopus websites.

Results: comprehension Pathogenic bacteria epidemiology, detection, characterization and transmission is important in preventing future infections and realize the transmission chains. VNTR is a portable, rapid, and very stable method that easily and unambiguously differentiates among strains based on comparison of variation of the copy number of these tandem repeats depends on the isolate.
tested. This method will play an effective role in controlling, preventing, detecting and eradicating diseases.

**Conclusion:** VNTR is robust, Inexpensive, highly standardized method, fast compared to other typing methods and does not require any live bacteria or complex equipments.

**Keywords:** tandem repeat, VNTR, pathogen
PB-32

Frequency and of Antibiotic resistance pattern of *Staphylococcus aureus* strain isolated from Burn ward of Zaareh sari hospital

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**Background:** *Staphylococcus aureus* is an important opportunistic pathogen causes clinical infections among burn patients. Increasing antibiotic-resistance cause a lot of problems for patients. The aim of this study was to determine the antibiotic resistance patterns and to detect *Staphylococcus aureus* in clinical isolates.

**Methods:** In this study, 126 *Staphylococcus aureus* strains isolated from different clinical specimens were used. And evaluated by phenotypic and biochemical methods. Antibiotic sensitivity was tested for all bacteria using disk diffusion method based on CLSI standard table.

**Results:** *Staphylococcus aureus* strains were isolated from different specimens consisting wound 76 (60/3%), blood 23 (18/3%), urine 22(17/5%) and Sputum 5(4%). In antimicrobial susceptibility testing, vancomycin exhibited the greatest activity 107(84/9%) against isolated strains. 81 (64/3%) isolates demonstrated resistance to Oxacillin.

**Conclusion:** Results showed that resistance to antibiotics is increasing in the studied population. Therefore proper and rapid diagnosis of pathogenic agents and treatment of patients according to antibiogram pattern can reduce mortality rate, period of hospitalization and treatment costs.
Keywords: Antibiotic resistance *Staphylococcus aureus*, bacterias
Patterns of antibiotic resistance of Helicobacter pylori isolated from patients with dyspepsia in East of Iran

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Background: Helicobacter pylori is an important pathogen for gastroduodenal diseases. Based on serological studies the prevalence of H. pylori infection is up to 80 % in Iranian adults. Gastritis, peptic ulcer and gastric adenocarcinoma are common clinical outcomes of this infection in Iran. H. pylori Infection can be limited by regimens of multiple antimicrobial agents. Since antibiotic resistance patterns of H. pylori are different geographically, local studies are highly required.

Method: The study group consisted of 80 patients with dyspeptic symptoms undergoing endoscopy in Ghaem Hospital, Mashhad, IRAN between 2015-2016 year. Demographic features including age, gender, symptoms were recorded. The stomach biopsy samples were transferred to laboratory for culture. The base culture medium consist of blood agar supplemented with 5% horse blood,
vancomycin, trimethoprim and amphotericin B. Cultures medium were incubated in an anaerobic jar with gas pack C at 37°C for 5 to 7 days. After incubation time, urease, catalase, oxidase and gram staining tests were performed to confirm *H. pylori*. Then sensitivity to five common antibiotics used for the treatment of *H. pylori* infection was determined. Agar dilution method was used for antibiotic susceptibility testing. Data analysis was done through SPSS 16 and using Pearson chi-square test.

**Results:** In this cross-sectional study out of 80 patients with *H. pylori* infection 42 patients were female (52.5%) with mean age of 48.96 years and 38 male (47.5%) with an average age of 44.6% years. The patterns of antibiotics resistance are recorded as below:

- Metronidazole 41.3%
- Clarithromycin 13.8%
- Amoxicillin 8.8%
- Furazolidone 6.3%
- Tetracycllin 6.3%

**Conclusion:** Different amounts of antibiotic resistance in various studies can be due to the method of taking the drug and the length of the course of the therapy and the methods for testing the antibiotic susceptibility. According to the obtained antibiotic resistance rates in this study, performing antibiogram tests before starting the treatment is necessary.

**Keywords:** *Helicobacter pylori*, Agar dilution, Antibiotics resistance
PB-34

Antibiotic resistance pattern of isolated Klebsiella isolates from patients and determination of frequency of ESBLs producing cluster strains in three selected centers in Isfahan

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Background: Klebsiella is one of the most important pathogens in the development of a wide range of infections, especially urinary tract infections. The purpose of this article is to investigate the prevalence of broad spectrum beta-lactamase-producing Klebsiella strains and determine the antibiotic susceptibility pattern collected from patient samples in three selected centers of Isfahan.

Materials and Methods: A total of 142 samples isolated from 350 patients (185 inpatients and 165 outpatients) with urinary tract infections, wound, blood, and sputum was isolated according to standard methods. Then, the disk diffusion method (Kirby-Bauer) was used to determine antibiotic susceptibility of isolates. The results were matched to CLSI standards.

Results: Among 142 isolates, there are 113 isolates (80%) for urine and 29 isolates (20%) for wound, sputum and blood. According to antibiotic
susceptibility, the highest level of antibiotic resistance of Klebsiella isolates is due to Ceftizoxime (29.6%), Cefetaxime (20.8%), and Ciprofloxacin (20.7%) antibiotics. Also, 88% of Klebsiella strains producing beta-lactamases were resistant to at least 6 antibiotics used in this study.

**Conclusion:** According to the result, Amikacin (With the least resistance percentage) compared to other antibiotics studied in the study was the most effective antibiotic against Klebsiella species. On the other hand, the prevalence of ESBL producing Klebsiella strains has led to the inactivation of antibiotics in the treatment of hospital infections caused by this bacterium.

**Key words:** Klebsiella, Urinary tract infections, Antibiotic resistance, ESBLs
Detection of *Helicobacter pylori* in the patients with gastric cancer base on various virulence genes using Multiplex PCR

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Prevalence of cagA, cagT, cagE, vacA and hrgA in *Helicobacter pylori* isolated from patients with gastric cancer using Multiplex PCR

Abstract

**Background:** It is estimated that *Helicobacter pylori* colonizes the stomachs of half the world’s population and cagA-positive strains are present in 60–70% of infections in Western countries. Our aim was to determine the prevalence of the
cagA/E/T, vacA and hrgA in H. pylori isolates among patients with gastric cancer (GC) in Karaj, Iran.

**Materials and Methods:** A total of 50 non-repeated gastric biopsies obtained from patients undergoing endoscopy in Shahid Fayazbakhsh endoscopy center. The presence of cagA/E/T, vacA and hrgA genes were determined by multiplex-PCR method.

**Results:** Of 50 gastric biopsies, 44 (88%) samples were positive for various H. pylori virulence genes. Molecular analysis of these virulence factors showed that the frequency of cagA, cagT, cagE, vacA and hrgA were 16 (32%), 8(16%), 13 (26%), 7 (14%) and 17 (34%), respectively.

**Conclusion:** The presence of different pathogenic genes has considerable effects in causing gastric ulcer, peptic ulcer, and gastric cancer. The effects of other genes, such as hrgA, in tissue damage and inflammation response are markedly important.

**Keywords:** H. pylori, cagA/E/T, vacA and hrgA
Molecular identification of papillomavirus type 16 and 18 isolated from women with cervical cancer

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Abstract

Women with human papillomavirus (HPV)-associated with cervical and breast cancer have a higher mortality than the general female population. The purpose of this study was to identification HPV-16 and HPV-18 genotypes in patients with cervical cancer or breast cancers by multiplex-PCR. In this experimental study, after collecting of samples from malignant cervical cancer, the viral DNA was
extracted by SinaClon kit and PCR was done by specific primers for HPV-16 and HPV-18 gene of human papillomavirus in all samples. After the analysis of PCR products by 2% agarose gel electrophoresis. Among 60 patient samples, 19 cases were confirmed to be positive for HPV infection and 41 cases were negative, showing high frequency of HPV in this patient population (about 31.6%). The frequency of HPV-16 and HPV-18 were 8 (1/42%) and 11 (2/57%) cases, respectively. This study showed that PCR by specific primers for HPV-16 and HPV-18 gene of human papilloma virus is a proper and accurate method for detection of this virus and the results confirm the previous reports of correlation between HPV and cancer samples.

Keywords: Cervix cancer, Human Papilloma Virus, M-PCR.

Running title: Molecular identification of papillomavirus type 16 and 18.
PB-37

Antibiotic Resistance Among Staphylococcus aureus and Escherichia coli Isolated From Traditional and Industrial Food Samples

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Abstract
Background Foodborne diseases are one of the serious problems in the world. Every year, more than 100 million people are affected by foodborne and waterborne diseases particularly immunocompromised diseases.
Objectives: aim of the present study was to evaluate bacterial load and antibiotic resistance pattern in bacterial isolates from food samples of meat, dairy, and pastry products from west of Tehran.
Materials and Methods: A total of 1625 different food samples including dairy products, meat and pastries were collected randomly from different parts of Tehran. The samples were first cultured according to the standard bacteriological methods and then Staphylococcus aureus and Escherichia coli isolates were
identified using standard bacteriological tests. Antimicrobial susceptibility test was performed by disk diffusion method according to (CLSI) guidelines.

**Results:** During 2007 and 2008, 2.8% and 3% of the food samples were contaminated with *S. aureus*. Similarly, 3.5% and 6.4% of the food samples were contaminated with *E. coli*. *E. coli* isolates were highly resistant to amikacin and cephotaxime and this resistance was increased in 2008. Similarly *S. aureus* isolates were resistant to ciprofloxacin, cephotaxime, gentamicin, and tetracyclin. There was no significant difference during 2007-2008.

**Conclusion:** Rate of contamination during 2007 was 2.8% and during 2008 was 3% for *S. aureus*. This strain was isolated from the food samples. Further studies should be done to determine the changes of bacterial resistance pattern for various food samples. Thus, the baseline for comparison with future prospective studies should be established, enabling the determination of trends over time.

**Keywords:** Antibiotic Resistance, *Staphylococcus aureus*, *Escherichia coli*, Food
PB-38

Role of *Fusobacterium nucleatum* on oral cancers

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**Introduction:** *Fusobacterium nucleatum* is fusiform rods or spindle-shaped, gram-negative and obligate anaerobic bacteria, which is commonly found in the dental plaque of humans. *F. nucleatum* is frequently associated with gum disease and recent research has shown that it plays a role in the development of oral cancer.

**Methods:** This review aimed to evaluate carcinogenesis mechanisms of *F. nucleatum* in the oral cavity in 20 years back and up to end of October 2018.

**Result:** *F. nucleatum* LPS activated inflammatory cytokines such as TNF-a, IL-1β, and IL-6. The continuation of this process leads to periodontal attachment,
tissue damage and carcinoma. The Fap2 protein of *F. nucleatum* interacts with the TIGIT receptor of immune cells, resulting in the inhibition of NK and T cell activities and generate a proinflammatory microenvironment. FadA binding to E-cadherin activates β-catenin signaling, leads to increase of proinflammatory cytokines, Wnt signaling, oncogenes, such as Myc and cyclin D1, and stimulation of cell proliferation. In addition, by activation of p38 leads to secrete matrix metalloproteinase-9 (MMP-9) and MMP13, which cause a crucial role in transformed squamous epithelial cells and cell invasion.

**Conclusion:** The implications of oral bacterium involvement in cancer are many. *F. nucleatum* can contribute to the development of oral squamous cell carcinoma. Improved oral hygiene and treatment of periodontal disease could also be helpful in limiting the development or spread of cancer.

**Key words:** *Fusobacterium nucleatum*, Squamous cell carcinoma, Oral cancer, Oral microbiota
Role of *Prevotella gingivalis* on oral cancers

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**Introduction:** *Prevotella gingivalis* is a gram-negative and obligate anaerobic bacteria, which often causes oral diseases, such as periodontitis and recent research has shown that it plays a role in the development of oral cancer.

**Methods:** We were reviewed roles of F. nucleatum in oral cancer and were evaluated its tumorigenesis mechanisms in 20 years back and up to end of October 2018

**Results:** *P. gingivalis* could cause cell-cycle changes and apoptosis by different ways. *P. gingivalis* can cause to release gingipain in extracellular, which engage the PAR2 receptor, and activates PAR2 signaling pathway which together Erk1/2 and p38 signaling pathway activated by Intracellular *P. gingivalis* could cleave the
matrix metalloproteinase-9 (MMP-9). MMP-9 and extracellular matrix degrades basement membrane, which promotes carcinoma cell invasion and migration. They allowing carcinoma cells to enter the lymphatic system and blood vessels for dissemination and metastatic growth at remote sites. In other pathway, *P. gingivalis* activates jak 1 and miR-203 signaling pathway, which could cause inhibited Bad leading to apoptosis. *P. gingivalis* secretes NDK in extracellular. NDK by hydrolyzing extracellular ATP prevents apoptosis through P2X7 receptor in EP and activates caspase 1 through this receptor in DC which leading to produce Tumor antigen specific CD8+.

**Conclusion:** *P. gingivalis* can contribute to the development of oral squamous cell carcinoma. Improved oral hygiene and treatment of periodontal disease could also be helpful in limiting the development or spread of cancer.

**Key words:** *Prevotella gingivalis*, Squamous cell carcinoma, Oral cancer, Oral microbiota
Detection of Virulence Factors Genes in Avian Escherichia Coli, Isolated from Suspected Broiler to Colibacillosis by Multiplex PCR

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**Background:** Avian colibacillosis is general term that refers to wide variety of complex syndrome such as pericarditis, peritonitis, airsacculitis, salpingitis and other exteraintestinal disease caused by Avian Pathogenic Escherichia coli (APEC). The pathogenisity of APEC associated with serogroups and virulence factors coded by virulence associated genes (VAG). APEC virulence factors are involved in colonization, adhesion, invasion and survival of E.coli against host defenses. Among these factors, the fimC gene has important role in the biosynthesis of type 1 fimbriae, an important bacterial adhesion molecule. Most of the APEC strains have Col plasmids that are involved in the establishment of avian infection and encoded by cvaA/B. Another virulence gene is iutA an aerobactinsiderophore receptor gene that, contribute to iron uptake. The aim of this study was to detection of virulence factors genes in Avian E. coli, isolated from suspected broiler to colibacillosis in broiler farms in the Hamedan, West of Iran by multiplex PCR.

**Method:** Avian Escherichia coli strains (n= 100) isolated from suspected broiler to colibacillosis from different poultry flocks in the Hamaden, West of Iran were
investigated for the presence of the *fimC*, *cvaA/B* and *iutA* virulence associated genes using multiplex PCR.

**Results:** The multiplex PCR results showed that the *iutA*, *fimC*, and *cvaA/B* virulence associated genes had detection rates of 97%, 85%, and 52% respectively. Half of 100 isolates (50) harbored two VAG and 44 isolates contains all three all three VAG and 7 Isolates had only one VAG.

**Conclusion:** Our results suggest that *fimC*, *cvaA/B* and *iutA* VAG are candidates for predicting the pathogenicity of avian *E.coli* strains and these genes could be used for future vaccine production against colibacillosis and requires further study.

**Keywords:** *Escherichia coli*, colibacillosis, virulence genes, Multiplex PCR
Prevalence of *Chlamydia trachomatis* in patients attending to women’s hospitals in Tehran, Iran

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Background: *Chlamydia trachomatis* is a pathogen that is frequently sexually transmitted worldwide. The global prevalence of *C. trachomatis* is 4.2% between women. Two-thirds of infected women develop asymptomatic infections and in the rest of population the cervicitis is the most frequent sign of infection. Evidence has shown that untreated *C. trachomatis* infections can lead to irrevocable damage in the fallopian tubes leading to infertility. The aim of this study was to detect *C. trachomatis* in endocervical samples by PCR method and evaluate the correlation between the infection, risk behaviors and clinical manifestations.

Methods: During November 2017 to June 2018, endocervical specimens were collected from 350 women using sterile Dacron swabs and were transferred to laboratory in PBS, demographic information was recorded. DNA extraction was performed by FAVORGEN DNA extraction mini kit. PCR for detection of *C. trachomatis* was done using primers for cryptic plasmid of the bacterium.

Result: Out of 350 samples, 36 (10.3%) were positive for *C. trachomatis*. The mean age of all participants was 36±9.2. Of all the patients infected with *C. trachomatis*, 26 (72.2%) patients were not educated. Eighty nine infertile women was included in this study and 13 (14.6%) of them were positive for *C. trachomatis* and of 24 patients which had the history of in vitro fertilization (IVF) 5 (17.2%) cases were CT positive. Only 3 patients had the history of protected sex.
Conclusion: Our study shows that prevalence of *C. trachomatis* is high among Iranian women and factors like education and safe sex have roles to play in preventing this infection. Our results also underscore the fact that *C. trachomatis* infections can lead to infertility.

**Keywords:** Cervicitis, Chlamydia trachomatis, Infertility, PCR
The most common bacteria collected from out patients with urinary tract infections in reference laboratory in Ilam, Iran

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Abstract

Background: the Urinary tract infections (UTI) considered as the second important site of infections after Respiratory tract infections. Unfortunately there is some complain from patients and physicians about the results obtained in the laboratory. So, in an attempt we got all bacteria from laboratory and evaluate the pathogenic bacteria and compare with the results of Reference laboratory.

Methods: we collected 61 bacteria from UTI during 6 month period from April 2014 to October 2014. The bacteria were diagnostic with standard protocols and were tested against antibiotics as CLSI.

Results: our findings demonstrated that among 61 isolates, E.coli was dominant (85.2%) and following Klebsiella pneumonia (6.6%), Proteus mirabilis (3.3%), Pseudomonas aeruginosa (1.6%), Staphylococcus epidermidis (1.6%) and one isolates could not growth. The results of laboratory was a little different about E.coli  (86.9%) and there is no detection of S. epidermidis. They detected one isolates as Enterobacter while it was identified as Klebsiella. The antibiotic pattern mostly was different as their selected antibiotics in many cases was different from CLSI and the disc diffusion methods was applied by non-reputable antibiotioc Synthesis Company. We used the hi-Media disks that the most
resistance observed for ceftazidime (52%) in *E.coli* and the lowest resistance observed in *S.epidermidis* that was sensitive to all chosen antibiotics. The imipenem fortunately showed the best chosen sensitive antibiotic in gram negative bacteria.

**Conclusion:** we concluded that reported bacteria by reference laboratory was acceptable but they are not following the CLSI protocol in antimicrobial therapy methods. So, it seems to be necessary that they should be evaluated annually.

**Key words:** antibiotic resistance, bacteria, CLSI
PB-43

Antibacterial and Antioxidant Activities of *Oliveria decumbens* Collected from the East of Iran

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Abstract

**Objective:** The aim of this study was to evaluate the antibacterial and antioxidant activities of *Oliveria decumbens* collected from the east of Iran. **Methods:** Firstly, ethanolic extract of *O. decumbence* was prepared. Secondly, the extract was evaluated for toxicity by MTT assay; then subjected for antibacterial activity via MIC and antioxidant activity via ABTS, DPPH and FRAP assays. **Results:** Our findings demonstrated that *O. decumbence* extract has high rate of phenolic content, 116 mg catechol/µl extract. This extract showed a highest antioxidant activity. The inhibitory percentage of free radical DPPH in *O. decumbence* extract was 75.7%. Our results showed that antioxidant activity via ABTS and FRAP tests were 6.4mMol Fe2+/µl extract and 2.6 mmol Terolox/µl, respectively. MIC
and MBC value of extract against indexed bacteria was equal (30μg/ml). We found considerable effects of *O. decumbens* extract such as antioxidant activity and antibacterial activity against *P. aeruginosa, E. coli* and *K. pneumoniae* with low cell toxicity. **Conclusion:** Finally, despite very good antibacterial and antioxidant activity of *O. decumbens* as medicinal plant, we need more studies about side effects and other unwanted activities to recommand using *O. decumbens* as a medical plant in clinics.

**Keywords:** *Oliveria decumbens;* Ethanolic extract; Antibacterial; Antioxidant; MIC
PB-44
Toxin antitoxin System in Clinical isolates of Acinetobacter baumannii

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Background: Acinetobacter baumannii is a gram-negative bacterium that is commonly associated with multi drug resistance of opportunistic infections. This bacterium can cause a wide range of infections including bacteremia, pneumonia, meningitis, urinary tract infections and wound infection in susceptible patients. Toxin-antitoxin (TA) system is a regulated system that could be used for new antimicrobial targets. Therefore, in this study, the TA system was evaluated as an antimicrobial target in clinical isolates of A.baumannii

Methods: Eighty clinical isolates were collected from ICU and burn wards of Ilam hospitals during the year 2016 and were confirmed by biochemical and molecular methods as A. baumannii. Antibiotic resistance was performed by disfiguring disk on all isolates. The presence of MazE, MazF and HighA TA loci was performed by PCR method and expression of these systems by RT-PCR method.

Results: Resistance to antibiotics were detected for kanamycin (81.3%), tetracycline (48.8%), amikacin (51.3%), gentamycin (48.8%), tobramycin (28.8%), doxycycline (8.28%), and minocycline (7.5%). The frequency of toxin and antitoxin genes on chromosome of MazE, MazF,HighA, and HighB among isolates were 62.5%, 46.3%, 38.8%, and 37.2% respectively. The frequency of plasmid TA systemes of MazE, MazF, HighA, and HighB in all isolates was 43.8%, 33.8%, 23.8%, and 21.0% respectively. The expression of the MazEF loci was confirmed in all isolates by RT-PCR
Conclusion: Our findings indicated that there is a high antibiotic resistance in the *A. baumannii* isolates. In this study, the high prevalence of the MazEF toxin-antitoxin system and the expression of this system in isolates has been proven. Therefore, the deactivation of the MazEF loci could be used as a new antimicrobial strategy in the treatment of resistant infections caused by this bacterium.

Keyword: A.baumannii, Antibiotic resistance, Toxin-antitoxin, MazEF, PCR, RT-P
Uropathogenic Bacteria and Antibiotic Resistance Pattern among patients refereeing to Imam Khomaini Hospital, Ilam, Iran

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Abstract

Background:

Urinary tract infections (UTIs) are known as a second important infection in humans. The bacteria responsible for UTI commonly are resistant to antibiotics like cephalosporin and carbapenems. The current study was aimed to evaluate uropathogenic Bacterial and and their antibiotic resistance pattern among patients Refereeing to Imam Khomaini Hospital, Ilam, Iran via phenotypic and genotypic methods.

Methods:
In this cross-sectional study, the patients with urinary tract infection in Imam Khomeini Hospital in Ilam were evaluated over a period of 9 months. All isolates were identified by routine biochemical methods and antimicrobial susceptibility testing carried out by Kirby-Bauer method. Phenotypic confirmation test was performed to detect ESBL, MBL, MRSA, VRSA and VRE. The results were interpreted according to the CLSI guideline. Identification of SHV, CTX-M, TEM, VanA, meca, bla VIM and bla IMP genes was performed using the PCR method.

**Results:**

114 isolates were examined that 61.4% of *Escherichia coli*, 7% of *Citrobacter freundii*, 7% of *Pseudomonas aeruginosa*, 8% of *Enterobacter cloacae*, 8% of *Klebsiella poneumoniue*, 4.1% of *Proteus mirabilis*, 0.9% of *Acinobacter baumannii*, 0.9% of *Staphylococcus aureus*, 0.9% of *Enterococcus faecalis* and 1.8% of *Corynebacterium urealyticum* were obtained. The majority of isolates were resistant to cotrimoxazole (55%), cefotaxime (49%), ceftriaxone (41%). 46 isolates (49.5%) were considered as Extended-spectrum Beta-lactamase (ESBL) and 6.3% of isolates showed MBL production. In between isolates of Gram-positive, none genotyped of MRSA, VRSA and VRE obtained.
Conclusion:

The results of this study especially showed gram-negative bacteria were the main bacteria causing urinary tract infections. Since, according to the study in Ilam high prevalence of ESBL-producing bacteria in the urinary tract infections and the prevalence is rising MBL. It is recommended that standard programs to be seriously considered in antibiotic use.

Keywords

UTI, ESBL, MRSA, VRE
Frequency Survey of Bacterial Contamination of Mobile Cell Phones in General Population in Tehran, Iran

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Background: Mobile smart phones have become increasingly integrated into the daily lives of individuals in society. Recent studies indicated the considerable role of these devices as reservoirs for various micro-organisms. The objective of this study was to assess the prevalence of microbiological contamination of mobile phones in general population.

Methods: This cross-sectional study included a large sample of mobile phones of general population Tehran in 2015. Samples for culture were collected from mobile phones and transported for microbiological identification based on standard laboratory methods.
**Results:** Bacteriological analysis revealed that in total of 5220 sample retrieved, 5180 (98.9%) mobile phone devices were contaminated with bacteria. The most common microorganisms that were isolated include: *Staphylococcus epidermidis* (63.9), *Escherichia coli* (12.3%) and *Staphylococcus aureus* (11.4%).

**Conclusion:** The prevalence of mobile phone contamination is high in general population in Tehran. Although most of the isolated organisms seemed to be non-pathogenic, their colonization may endanger certain populations particularly in health care settings.

**Keywords:** Mobile Phones; Hygiene; Contamination
PB-47
The pattern of antibiotics resistance to levofloxacin and ciprofloxacin in patients with leukemia in Shariati Hospital in Tehran

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Background

Bacterial infections are the most common cause of morbidity and mortality in patients with leukemia after undergoing intensive chemotherapy. fluoroquinolone prophylaxis recommend for high-risk patients (who patients are neutropenic for >7 days). For many years, had discussed the use of fluoroquinolone prophylactic after chemotherapy in patients with leukemia. The fluoroquinolones,first presented in the 1980s, as the prophylactic antibacterial agents in neutropenic patients because of their broad antimicrobial spectrum.

Methods

In the present study, on 80 clinical samples during one year. After the identification of isolates in species, Ecoli and K. pneumonia strains isolated from patients with leukemia that suffering from infection bacterial.Clinical specimens including urine, blood, stool, The Kirby-Bauer disk diffusion method on Mueller Hinton agar (Merck, Germany), based on Clinical Laboratory Standards Institute (CLSI) guidelines 2013 ,2 was used to perform
antimicrobial susceptibility tests on ciprofloxacin (CIP: 30μg), and Levofloxacin (GEN: 30μg), all purchased from Mast Group.

Results:

Rates of antibiotic resistance to levofloxacin, ciprofloxacin were %, 51.2%, 47.5 %, respectively.

Conclusions:

This survey says the cause of high resistant Escherichia coli and Klebsiella pneumoniae strains to Ciprofloxacin and Cefotaxime are use too take this antibiotics. Then, preventing from use of un necessary antibiotics and take care of production new and drastic antibiotics will be recommend.

Keywords: levofloxacin, ciprofloxacin, leukemia
Antibiotic resistance of Gram-positive bacteria isolated from patients with blood infections referring to Besat Hospitals of Sanandaj city during 1396-1397 years.

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Background: Antibiotic resistance is one of the biggest threats to health. The aim of this study was to evaluate the antibiotic resistance of Gram-positive bacteria isolated from blood infections. These infections and antibiotic resistance can increase the length of hospitalization and cost of treatment.

Methods: This cross-sectional study was conducted on 132 patients in the Besat Hospital, Sanandaj, Kurdistan Province, Iran, from 21 March 2017 to 20 March 2018. Patients' information was collected from the Hospital Information System.
Culture and biochemical tests used for detection of bacteria in blood samples. Disk diffusion was used for antibiotic pattern survey. Statistical analysis was done in the Stata/SE 12 by chi-square test.

**Results:** Prevalence of blood infection in women (65/13%) was higher than that of men (34/87%). The most common cause of infection was *staphylococcus epidermidis* (59/32%), and *staphylococcus saprophyticus* (16/11%) and *staphylococcus aureus* (11/71%). There was no significant association between bacterial type and gender (P>0.05). The highest antibiotic resistances were erythromycin (76.14%), Aztreonam (63/17%), ciprofloxacin (43/21%) and ofloxacin (33/78%), respectively. A statistically significant association between the antibiotic resistance with gender was no observed (p>0.05).

**Conclusion:** Survey of the pattern of antibiotic resistance in the isolated bacteria in hospitals can be prominent and necessary in the choice of treatment and appropriate antibiotics by physicians.
PB-49

Evaluation of fluoroquinolone resistance mechanisms in clinical *Escherichia coli* isolates in kerman

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**Background:** Resistance to fluoroquinolones such as ciprofloxacin are due to mutational in gyrA and parC, plasmid-mediated resistance determinants (qnrB, qnrS, and aac(6)-Ib-cr) or overexpression efflux pumps. The main objective of this study was to investigate the importance of qnr genes, aac(6')-Ib-cr and efflux pumps in resistance to ciprofloxacin among *E. coli* isolates.

**Methods:** A total of 104 clinical isolates of *E. coli* were collected from afzalipour hospital in Kerman. Antibiotic susceptibility test was done by disc diffusion method. Minimum inhibitory concentrations (MICs) of ciprofloxacin was determined for all isolates. The effect of efflux pumps was determined by repeating the susceptibility in the presence of the efflux pump inhibitor carbonyl cyanide m-chlorophenyl hydrazone (CCCP). PCR was used for detecting *qnrA*, *qnrB*, *qnrS* and *aac (6 ’)-Ib* genes.

**Results:** The highest rate of resistance was against trimethoprim/sulfamethoxazole(%76.9), followed by nalidixic acid(69.2%), ceftriaxone(66.3%), cefotaxime(55.8%), ciprofloxacin(36.5%), gentamicin(24%)
meropenem (15.4%). The MIC of most isolates which were resistant to ciprofloxacin was above 32 μg/ml. The MIC of ciprofloxacin was not significantly changed in the presence of CCCP. qnrS and qnrB were detected in both ciprofloxacin-resistant and -susceptible isolates, but aac(6)-Ib-cr was only detected in 26% of ciprofloxacin-resistant isolates.

**Conclusion:** In our E. coli isolates, qnr genes and efflux pumps played a limited role on the fluoroquinolones resistance. Although aac(6)-Ib-cr plays a significant role in conferring resistance to fluoroquinolones, it seems that other mechanisms such as mutations in gyrA and parC are the main causes of clinical resistance to fluoroquinolones.

**Key words:** Escherichia coli, qnr, aac(6′)-Ib-cr, PCR, ciprofloxacin
PB-50

Phenotypic and genotypic evaluation of extended spectrum β-lactamase producing Escherichia coli isolated from patient with UTI in Bushehr province

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Background: urinary tract infections (UTI) have been one of the most common bacterial infections in children, women, elderly and patients in hospitals. Meantime Beta- Lactam Antibiotics which are used to treat infections originated from E. coli, have been a factor causing some types of resistance. The aim of this research is to study E.colis producing Extended Spectrum Beta-Lactamase both phenotypically and genotypically which are isolated from patients suffered from UTI in Boushehr city.

Methods: this research was conducted by sectional-descriptive method on 140 samples of E-coli strains isolated from UTI patients in Boushehr. At first E.coli isolations were detected using common biochemical Tests and Disc Distribution method was used in order to asses Antibiotic resistance, and Combined Test (according to the instructions of CLSI) was used to detect strains producing ESBL (Extended Spectrum Beta-Lactamase). Finally bla-tem, bla-ctx and bla-shv gens break out were checked by using Single PCR.

Results: The most antibiotic resistance refers to Amoxicillin (82/1%) and Ampicillin (80%) and the less resistance belongs to Meropenem (0.7%) and Nitrofurantoin (1.4%). Bla-tem and bla-ctx gens are simultaneously existing respectively in 57 strains (43.2%) and 5 strains (3.8%) individually and in 70 strains (53%). Bla-shv was not observed in none of strains.

Conclusion: Regarding to the high percent resistance of Cephalosporins out of third generation, it is strictly recommended to conduct Antibiogram carefully...
before prescribing antibiotics in infections originated from organisms producing Ebl.

**Keywords:** esbl, E-coli, Single- PCR, Genotype

*Please note that Presenting Author is underlined and Corresponding Author is indicated by *. 
PB-51

Evaluation of Antibiotic Resistance of *Escherichia coli* Strains Isolated from Urinary Tract Infections in Patients of Payambar-rahmat Hospital in Sanandaj

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Abstract

**Background:** Urinary tract (UT) infections typically occur when bacteria enter the urinary tract through the urethra and begin to multiply in bladder. UT infections are the second most common human infection by family of the Enterobacteriaceae, particularly *Escherichia coli* (E. coli). According to the increasing antibiotic resistance among strains of E. coli, the purpose of this study was to determine the current pattern and also to investigate changes in the antibiotic resistance patterns of E.coli strains isolated from urinary tract infections in outpatients referring to Payambar-rahmat Hospital in Sanandaj city during the two years (2016 to 2017).

**Methods:** This descriptive study was conducted on 51 cases of E. coli isolated from patients with urinary tract infections in a hospital in the city of Sanandaj. The drug sensitivity test for antibiotics: imipenem (IPM), gentamicin (GM), ceftazidime (CAZ), nalidixic acid (NA), amikacin (AN), nitrofurantoin (FM) and cotrimoxazole (SXT) for isolates of E. coli was performed.

**Results:** Of a total of 51 samples, 65.3% of isolates were women and 34.7% of isolates were isolated from men. Patients' age range was of 10-52 years. The popular resistance to antibiotics: cotrimoxazole (73.9%), nalidixic acid (70.7%),
ceftazidime (37.3%), nitrofurantoin (31.9%), gentamicin (20.7%), amikacin (18.6%), and imipenem (3.9%) were evaluated.

Conclusion: Our research showed that antibiotics imipenem and cotrimoxazole had the highest resistance and susceptibility, respectively. Therefore, it is recommended to stop the administration of cotrimoxazole antibiotics to treat urinary tract infections and use Imipenem. These advantages can result in increased speed of reporting, which may reduce hospital stay and patient morbidity as well as providing needed information more rapidly in critically ill patients with bacterial infections.

Keywords: E.coli, Antibiotic resistance, UI infections, Patients
PB-52

Phylogenetic groups of pathogenic *E. coli* strains isolated from patients in Imam Reza Hospital, Kermanshah

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**Background:** The *E. coli* strains have been assigned to four main groups – A, B1, B2 and D. Group A and B1 are generally associated with commensals, Strains from phylogenetic group B2 and D are generally more virulent, but also less resistant and contain resistance encoding integrons. Recently, contradicting data about the higher resistance of *uropathogenic* *E. coli* strains belonging to phylogenetic group B2 have been published. The aim of this study is to determine the prevalence rate of each phylogenetic group of *E. coli* strains obtained from clinical samples in order to help improve the control and treatment of infection in the region.

**Methods:** 96 clinical samples (urine, stool, blood and body fluids) have collected from the patients referring to Imam Reza hospital in Kermanshah, Iran. The samples were cultured on MacConkey agar medium and subsequently various biochemical tests were performed to confirm the isolates. DNA extraction of *E. coli* isolates was done by boiling method. To classify the *E. coli* strains, specific primers for the *chuA* and *yjaA* genes and the TSPE4.C2 were applied for the PCR test.
Results: Of all samples collected from patients, a total of 96 isolates were identified as *E. coli* by conventional biochemical methods. The PCR method showed that the most common phylogroup was group B1 (33 isolate; 33.37%), followed by groups B2 (24 isolate, 25%), D (22 isolate, 22.91%) and group A (17 isolate, 17.7%).

Conclusions: Our study revealed the frequency distribution of phylogenetic groups in different strains of *E. coli* in our study has been as B1>B2>D>A. Regarding to the different prevalence of each phylogenetic group of *E. coli* in each region, different strains of *E. coli* can determine the prevalence of pathogen strains in the environment. Further studies in addition to controlling the infections caused by *E. coli* contribute to the reduction of MDR strains.

Keywords: *E. coli*, phylogenetic group, MDR
Evaluation of the Carba NP method for the rapid identification of Pseudomonas aeruginosa producing Carbapenemase enzymes

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Abstract:

Background and purpose: Pseudomonas aeruginosa is one of the most important pathogens in hospitals. Recently, increased resistance to carbapenem antibiotics among this bacteria has raised concerns. There are many methods for identifying carbapenem enzymes. The carbaNP test is one of these methods. Therefore, the purpose of this study was to use the carba NP test method to quickly identify P. aeruginosa isolates producing carbapenem enzymes.

Material and Methods: A total of 97 clinical specimens were collected from patients in educational hospitals from November 2017 to May 2018 in Hamedan,
Iran. After confirmation of isolated strains, antibiotic susceptibility tests were performed by disc diffusion method. MIC was done by E-test for imipenem. To detection of carbapenemases enzymes, combined disk (CDT), carbaNP and Modified Hodge test (MHT) were performed. Finally identification of carbapenemase genes were performed by PCR method. Statistical analysis of all data was performed using SPSS (VERSION 16) software.

**Results:** The results of antibiotic susceptibility tests showed that the highest level of resistance was to Cefoxitin 94.8% and the lowest resistance to Ceftazidime 52.6%. Among 49 (50.51%) isolates that had positive results for carbapenemase genes by PCR, 48 (48.49%) isolates had positive carbaNP assays and out of 48 (49/48%) that had negative PCR results for the carbapenem gene, 48 (49/48%) of their carbaNP test were negative. Therefore, the sensitivity and specify, of this test was 100% and 96% respectively.

**Conclusion:** The results of this study showed that a high percentage of *P. aeruginosa* was resistant to Carbapenem antibiotics and the carbaNP method was highly sensitive and specific for identification of carbapenemase enzymes.

**Keywords:** *Pseudomonas aeruginosa*, Disk diffusion antibiotic test, PCR, carba NP
PB-54
Detection of Metallo- β-lactamase genes in *Klebsiella pneumonia* in sanandaj in West of Iran

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Abstract

**Background:** *Klebsiella* spp. is prominent causing nosocomial infections among Gram-negative bacteria. The aim of this study was to evaluate the prevalence of Metallo- β-lactamase (MBL) genes in clinical *Klebsiella pneumonia* isolates in two teaching hospitals in Sanandaj west of Iran.

**Methods**

A total of 400 samples were collected from different clinical specimens (urine, wound, sputum, tracheal aspirate and blood) in patients hospitalized or referred to hospitals in Sanandaj in 2013–2014. Obtained *K. pneumonia* strains identified using microbiology standard tests. MBLs-producing *K. pneumoniae* detected by Double Disk Synergy Test (DDST). The MBL positive isolates were examined for the presence of VIM-1, VIM-2 and IMP-1 genes using PCR assay.
Results: Of 400 clinical samples, 98 isolates of *K. pneumoniae* were identified, 22 (22.4%) were resistant to imipenem in disk diffusion method. Sixteen strains (72.7%) were positive for MBL enzymes production. PCR results showed that gene frequency is 3 (18.8%) and none of the isolates tested positive for *bla* VIM-2 and *bla*, IMP-1 genes. Meropenem and imipenem were found as the most effective antibiotic against *K. pneumonia* in this study.

Conclusion

The study results showed prevalence of MBLs producing *K. pneumoniae* (72.7%) was high at two hospitals in sanandaj, Iran. This study should be repeated in other hospitals to assess the level of the problem. Therefore the infection control methods and use of antibiotic agents must be considered.

Keywords: *Klebsiella pneumoniae*, Metallo- β-lactamase, Imipenem- resistant
PB-56

Antibacterial effect of Alcoholic extract of Ruscus Hyracanus on Staphylococcus aureus

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Introduction: Staphylococcus aureus is major pathogens in humans. The most common food poisoning is caused by Staphylococcus aureus. Misuse of antibiotics, leads to the emergence of antibiotic-resistant pathogens and resulting in greater need for new drugs or more effective medications. Ruscus hyracanus has medicinal properties and has antioxidant, anti-inflammatory, antimicrobial and anticancer effects. The aim of this study was to investigate the antibacterial effect of alcoholic extract of Ruscus hyracanus on S. aureus bacteria.

Materials and Methods: The plant sample was collected from the forests of the city of Amol and was removed from direct sunlight in a shadow then the dried sample by the mill was powdered and stored. Extraction was done by maceration (soaking). To evaluate the antimicrobial effect by microdilution, concentrations of 2.5, 5, 10, 20, 40 and 80 mg/ml of extract were used. MIC (Minimum Inhibitory Concentration) and MBC (Minimum Concentration Rate) of extracts were determined.

Results: S. aureus was almost susceptible to concentrations of 10, 20, 40 and 80 mg/ml of ethanolic extract of Ruscus hyracanus. Staphylococcus aureus inhibited at MIC 5mg/ml of ethanolic extract and MBC 10 mg/ml.
Conclusion: According to the results, the Ruscus hyracanus had antibacterial activity against S. aureus. This study could be a better and more accurate understanding of medicinal plants traditionally used without limitations for many years as a safe drug and without anxiety about side-effects.

Keywords: Antimicrobial activity, Ruscus Hyracanus, Staphylococcus aureus
PB-57

A case report of brain abscess caused by Nocardia cyriacigeorgica in a diabetic patient

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Abstract

Introduction: Nocardia are Gram-positive partially acid-fast bacilli capable of inducing a wide range of infections in patients with immunodeficiency, AIDS, cancer, lupus erythematosus and diabetes. Nocardia cyriacigeorgica was first isolated in 2001 from a patient with chronic bronchitis. Since then, there have been reports on the clinical significance of this organism in patients with bronchitis, brain abscess and lung diseases. We, herein, report a case of brain abscess in an elderly diabetic patient from Iran.

Case presentation: The patient was a 73 year-old woman admitted to hospital due to severe headache and shortness of breath. The patient had lived with diabetes for 20 years and suffered from chronic foot ulcer. She was admitted to hospital with fever, weakness, drowsiness and vomiting. Clinical examination and the head CT scan of the left frontal lobe of the brain revealed a metastatic carcinoma involving
skull bone in the tumor that resulted in two surgical operations in the following two years. The brain abscess biopsy revealed an infection with Nocardia cyriacigeorgica confirmed by phenotypic and molecular tests including a PCR-based amplification of a target genetic marker, a 596 bp fragment of 16S rRNA gene, followed by almost full 16S rRNA sequencing.

Conclusion:

The rare infections, such as brain abscess with Nocardia, are easily neglected or misdiagnosed due to the fastidious nature of the organism and inadequate microbiological experience of laboratories in the hospitals of developing countries. This case shows that hospitals should consider a better laboratory protocol to deal with the clinical cases in which fastidious organisms, and in particular Nocardia, are involved.

Keywords: Brain abscess, Diabetic foot ulcer, Nocardia cyriacigeorgica, 16S rRNA.
PB-58

Antibacterial and Antifungal Effect of Ginseng Powder

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Background: The increasing rate of bacterial and fungal resistance to the traditional antibiotic has reached a warning level (1). According to control the treatment of infections caused by several resistant drugs bacteria, the search for antimicrobial agents is essential. To this purpose, we design a study to determined anti-bacterial and anti-fungal activity of Ginseng.

Materials and Methods: In this study, at first level, we determined MIC and MBC of Ginseng powder on gram positive, gram negative and fungi as Staphylococcus aureus ATCC25923, Pseudomonas aeruginosa ATCC27853, Escherichia coli ATCC25922, Enterococcus faecalis ATCC 29212, and Candida albicans ATCC10231. Then, we used the disc diffusion method to determine the inhibition zone.

Result: The result of this investigate, showed that MIC Ginseng powder is 0.16 g/ml for Pseudomonas aeruginosa ATCC27853, and Candida albicans ATCC10231, 0.083 g/ml for Staphylococcus aureus ATCC25923, Escherichia coli ATCC25922, and Enterococcus faecalis ATCC 29212, and results in disc
diffusion method showed all strains didn’t have any significant zone inhibition to Ginseng powder.

**Conclusion:** Our results showed Ginseng powder have anti-bacterial and anti-fungal activity.

**Keyword:** Ginseng powder, MIC, MBC

**Reference:**

Investigation of antibacterial effect of Yarrow alcoholic extracts on antibiotic-resistant Streptococcus pneumoniae

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**Background:** Pneumonia, respiratory tract infections, is associated with high mortality and complications in humans. Although antibiotics are used to treat this infectious disease, but lead to many problems such as unwanted side effects and resistance to antibiotics. This study investigated antibacterial activity of the hydro alcoholic extracts of the native medicinal plants Yarrow, as a natural alternative to antibiotics, on antibiotic-resistant Streptococcus pneumoniae, the main bacteria that cause pneumonia.

**Methods:** Antibacterial activity of the hydro alcoholic extracts of medicinal part of the plants was evaluated by the disk diffusion susceptibility test method and broth dilution test method on bacteria.

**Results:** The rate of MIC for Yarrow bacteria were 220µg/µl (S. pneumoniae) and the rate of MBC were 180 µg/µl (S. pneumonia as well as the maximum amount of inhibition zone diameter were in concentration 500 µg/µl, S. pneumoniae (15.8, 13.5, 2.3 mm).

**Conclusions:** This work showed that substances in the hydro-alcoholic extracts of medicinal plants prevented the growth of bacteria. So these plants with having effective ingredients can be used as an affordable and available source for medicinal purposes.
Keywords: Yarrow, Streptococcus Pneumonia, resistance antibiotics
The effect of (aqueous-alcoholic) extracts and *Silybum marianum* essence on *Staphylococcus aureus*

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Background: Plants been biological basis of drug substances in thousand years. Some of the plants have inhibitory effects on growth of intestinal infections. Black pepper is the plant that uses as classical medicine in the infections. *Staphylococcus aureus* are two important bacterial agents in the food contamination. In study, inhibitory effects of watery-alcoholic extractions and essence of *Silybum marianum* were studied against *Staphylococcus aureus*.

Material and Method: Extraction produced by soaking method then for determined antibacterial effects were used cylinder method. For preparation essence 120 gr powder of *Silybum marianum* added on the water in the Clevenger and extracted essence, then for determine MIC/ MBC were used micro dilution method.

Result: Essence of *Silybum marianum* showed good antibacterial effect on this bacteria. MIC of essence on the *Staphylococcus aureus* was 65 μg/ml, but alcohol and watery extractions didn’t have antibacterial effect on these bacteria.

Conclusions: essence of black pepper showed so good result on this bacteria and Can be used this essence as antibacterial compound for inhibit of grows intestinal infection agents especially in food industry.

Keywords: *Staphylococcus aureus*, resistance antibiotics, *Silybum marianum*
PB-62

The role of the laboratory in the diagnosis of tuberculosis

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Abstract

Tuberculosis is one of the most important infectious diseases during the history of humans’ life, various societies always have been trying to control and struggle against this disease. Tuberculosis could be controlled by Koch's discovery of the tubercle bacillus as etiologic agent and the discovery of Bacillus Calmette–Guérin (BCG) vaccine all around the world. In fact, it had been assumed Tuberculosis could ultimately be eradicated, however any possible global control of tuberculosis will be destroyed in the near future because of the existence of tolerant strains, the worldwide distribution of the disease, as well as the emergence of the AIDS epidemic. The fact that one-third of the world's population is infected with Tuberculosis which can consider as a reservoir of infection. This issue has become even more complicated now since non-tuberculous mycobacteria (NTM) is indistinguishable than tuberculous mycobacteria because they are environmental organisms which present in all places and cause lung diseases and tuberculosis. Therefore, the laboratories diagnosis of tuberculosis (TB Laboratories) play a key role in diagnosing, monitoring and control of tuberculosis by providing prompt and reliable laboratory results, which can be the guidance clinical for control of tuberculosis. The aim of this research is a review of some scientific works (achievements) in relation to the quality and performance of TB Laboratories. As the researchers in the field of tuberculosis laboratories believe that increasing the capacity of laboratories using trained staff, implementation of quality control of equipment and procedures, can enhance the quality and accuracy of laboratory results.
Generally, by creating a System National Administration for diagnostic laboratories, TB can be more effectively controlled.

**KeyWords:** Tuberculosis, Laboratory diagnosis, Non-tuberculous mycobacteria.
PB-63

Study on Urinary tract infections of women referred to health center in Shoshtar, Iran 2018

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Background:
The Urinary tract infections is one the best bacterial infection that commonly bother pregnant women that it involve them with some problem such as illness and healthcare outlay so the purpose of this study detect urinary tract infection sample of women that referred to health center laboratory in order to do pregnant tests which discover diseases to precaution and control them.

Methods:
In this study carried out on women that refer to the health center in order to do test of before pregnancy. Then urine sample of them have been carried to bacteriology labarotory and cultured. In this investigate we used Culture media such as Nutrient Agar, blood agar, MacConkey Agar and detecting media as triple suger iron agar (TSI), KIA, Selenite F broth (SF), Methylred-Vegesprokaure broth (MR-VP), SIM, Mannitol sault agar, Lysin, Simmon citrate, E.M.B, XLD, Mueller Hinton agar and Urea as bacterial culture methods.

Results:
In this study 10 species of Bactria have been detected from urine culture test of women that refer to health center of Shoushtar in the other hand 163 case positive that Escherichia coli had 40.4% (66 case) that it was most frequency, and others
cases including to  *Staph epidermidis* 14.11% (23 case), *Staphylococcus aureus* 10.4 % (17 case),  *Staphylococcus spp.* 7.3% (12 case), *Staph saprophyticus* 6.74 % (11 case), *Enterobacter* 6.74% (11 case), *Micrococcus* 6.13 % (10 case), *Klebsiella pneumoniae* 5.5 % (9 case), *Pseudomonas aeruginosa* and *Proteus mirabilis* with 1.2% (9 cases) were the least frequency between our results.

**Conclusion:** regards to obtain results specially in pregnant women sound it is important urine culture and detect bacteria for prevention and control programs health care in this group women then it is necessary points such as personal hygiene, tight clothing, reinfection and relapse and exercise post coital voiding and evading skin allergens have been educated to women also there is advises for drinking mass fluid (two to three litres per day) in daily Schedule.

**Key words: Urinary tract infection, Urine culture**
PB-73

VALUATION OF HUMORAL IMMUNE RESPONSES AGAINST ACUTE STRAIN OF BACILLUS ANTRACIS

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Background: Anthrax is one of the most important zoonotic diseases in the world that it caused by Bacillus Anthracis. Nowadays, different vaccines are available to protect from this disease which they are based on 34F2 strain (spore-forming). In order to investigation of the humoral immunity in infected or vaccinated animals, a fast and reliable serological test should be develop. In this study, the humoral immune responses of vaccinal and acute strains of Bacillus anthracis have been investigated.

Methods: Two different vaccinal and acute strains (34F2 and 17jb respectively) of Bacillus anthracis has been cultured on blood agar medium. Different amount of bacteria was injected to rabbit for three times and the levels of specific polyclonal antibody was measured by indirect ELISA method.

Results: The results indicated that antibody level was increased after first immunization and it was reached to the highest levels after 30 day (p<0.05). The levels of antibody have not significant difference between vaccinal and acute strains (p>0.05). The best responses were observed in animals who injected by 5×10⁵ bacteria. The 17jb strains have been noted as best antigen for ELISA method based on this study.
Conclusion: In this study polyclonal antibody against both acute and vaccinal starins produced and it detected by ELISA method. Furthermore, the produced antibody could be purified and used for next diagnostic studies.

Keywords: Bacillus anthracis, ELISA, 34f2, 17jb, antibody
URINARY TRACT INFECTION IN SPINAL CORD INJURIES
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ABSTRACT Objective: Spinal cord injuries are typically associated with major
trauma from motor vehicle accidents, falls, sports injuries, and violence. Urinary
Tract Infections (UTI) is one of the most frequent conditions seen in spinal cord
injuries patients. Diagnosis is not always easy due to lack of symptoms. Present
study is survey about urinary tract infection and pyuria in these patients. Methods:
All of patients with spinal cord injuries, who admitted to “Brain and Spinal Injury
Repair Research Centre” in Imam Hospital in duration one year, were included in
this study. Clean catch midstream urine samples were collected of patients and
were analyzed by biochemical and microscopically surveys. Results: In total 103
patients, 22 patients have cervical spinal cord injury, 52 patients have thoracic
spinal cord injury and 13 patients have lumbar spinal cord injury. 83 patients were
urine culture positive with urinary tract infection and pyuria were seen in 65
patients. the highest incidence of UTI and pyuria were demonstrated in patients
with cervical spinal cord damage. E.coli, Klebsiella pneumoniae and Enterobacter
cloacae were isolated in urine samples respectively. the high incidence of
resistancy to Nitrofurantoin and Imipenem in E.coli were seen. Conclusion:
Patients with spinal cord injuries have to use catheter for long time and or for all
of life, and they are high risk to recurrent urinary tract infections and other infections. These patients need to monitor for urinary tract infection although without any symptoms of infections and sometimes they need to take prophylactic antibiotics.

Keywords: spinal cord injury, urinary tract infection, pyuria
Molecular Characterization of Exotoxin Genes in *Staphylococcus aureus* Recovered From Hospitalized Patients

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Abstract

Introduction: *Staphylococcus aureus* is considered as a major cause of skin and soft tissue infections, arthritis, osteomyelitis, infective endocarditis, and
pneumoniae though community or nosocomial transmission. In this study, attempts were made to investigate the distribution of some important exotoxin genes, including \textit{hla}, \textit{hlb}, \textit{tsst-1}, \textit{eta}, \textit{etb}, and \textit{etd} among methicillin-resistant \textit{S. aureus} (MRSA) isolated from a hospital patients in Tabriz, Tehran.

**Methods:** In the present cross-sectional study, a total of 90 \textit{S. aureus} were isolated from children who admitted to a hospital during six-month in 2017. Isolates were identified using biochemical tests and then, using PCR, the isolates were tested for the presence of, \textit{hla}, \textit{hlb}, \textit{tsst-1}, \textit{eta}, \textit{etb}, and \textit{etd} genes.

**Results:** It was found that 40% of the \textit{S. aureus} were considered as MRSA strains by biochemical and molecular tests. The results of molecular detection of virulence determinants showed that \textit{eta}, \textit{hla}, \textit{etb}, \textit{tsst-1}, \textit{hlb} and \textit{etd} were detected in 86.1%, 80.5%, 30.5%, 27.7%, 22.2%, and 19.4% of isolates, respectively.

**Conclusions:** Our findings clarify characterization of toxin production status of \textit{S. aureus} isolates from patients in Iran. The current study showed that a majority of \textit{S. aureus} isolates harbored \textit{eta} and \textit{hla} virulence gene.

**Keywords:** Exotoxins, Methicillin-Resistant \textit{Staphylococcus aureus}; Toxic Shock Syndrome Toxin-1; \textit{Staphyloccocal Exfoliative Toxin}; Pediatrics.
PB-76

Frequency of bacterial agents and their antibiotic susceptibility pattern in blood culture of neonates with bacterial sepsis admitted to the NICU and Neonate wards of Imam Sajjad hospital of Yasuj, 2017-2018

Marjan Salahi 1, Seyed Sajjad Khoramrooz 2*, Abdolkarim Ghadimi moghadam, Seyed Ali Mousavizadeh, Ramin Jannesar, Seyed Jabar Taghavi, Mohamadtaher Rezanejad, Sedighe Moradi, Masoud Marashifard

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Background: Neonatal sepsis refers to the presence of systemic microorganisms in the first 28 days of life. The undesirable effects of this clinical syndrome due to the dysregulated inflammatory response against infection and are associated with significant mortality and morbidity among neonates. The aim of this study was to detect neonatal sepsis microorganisms and their antibiotic susceptibility patterns in neonatal and Neonatal Intensive Care Units (NICU) wards.

Method: In this descriptive-analytical study, 207 and 135 neonates were diagnosed with infectious diseases and pediatric pediatricians suspected of sepsis and admitted in NICU and neonatal wards, respectively. Automatic blood culture system (BACTEC) was used to identification of microorganisms. Their antibiotic susceptibility pattern was identified by Kirby Bauer disc diffusion method. Neonates with positive blood culture were categorized into two groups including early onset sepsis (EOS) and late onset sepsis (LOS) according to the time of positive blood culture.

Result: Out of 342 suspected infants, 51 infants had positive blood culture and 52.5% had early onset sepsis. Gram-positive pathogens are the most common isolated organisms, of which the most common were the coagulase negative
staphylococci (CONS). gram-negative organisms and yeasts were the other isolated organisms. Gram-positive organisms had the highest susceptibility to teicoplanin (81.5%) and vancomycin (73.6%), respectively, followed by amikacin and ciprofloxacin (68.4%). Gram negative had the highest susceptibility to tazobactam/ piperacillin (81.8%), ciprofloxacin and amikacin (63.6%).

**Conclusion:** More than half of the newborns were diagnosed with this clinical syndrome due to normal skin flora and pathogens of hospital. By increasing the antibiotic prescription, in addition to increasing the reservoir of antibiotic resistance genes in bacteria, the newborn microbial population declines and immunity decreases and thus facilitates the replacement of risky pathogens such as candida and pathogens in the hospital. In this study, the most effective antibiotics for the experimental treatment of gram positive bacteria were teicoplanin, aminoglycosides, and fluoroquinolones. The most common and effective antibiotics for the treatment of gram negative organisms were beta-lactam antibiotics such as piperacillin with beta-lactamase inhibitors, aminoglycosides, and ciprofloxacin.

**Key words:** neonatal sepsis, early onset sepsis, late onset sepsis, Microbial Sensitivity Tests, Coagulase-negative Staphylococcal Bacteremia
PB-77

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**Key words:** neonatal sepsis, early onset sepsis, late onset sepsis, Microbial Sensitivity Tests, Coagulase-negative Staphylococcal Bacteremia
β-Lactam Family Resistant Pattern of Gram Negative Bacteria Isolated from Patients with Urinary Tract Infection Referring to Besat Hospital in Sanandaj

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Introduction: Antibiotic susceptibility and resistance in gram-negative bacteria are one of the main concerns of the world due to their increasing resistance to antimicrobial agents. Therefore, this study was conducted to determine the frequency of gram negative bacteria isolated from urine specimens and their antimicrobial resistance pattern in patients referring to Besat Hospital in Sanandaj in 2017.
Materials and Methods: About 1473 patients were examined through the hospital information system of Besat Hospital. The bacteria were isolated and identified by microbiological laboratory methods. Antibiotic susceptibility pattern using disc diffusion method according to laboratory standards was used to measure their drug resistance pattern. For data analysis, SPSS software version 16 and independent t-test and chi-square test were used (p <0.05).

Results: Of the 1473 patient records, 1281 urine cultures were positive. A total of 1058 (73.70%) gram negative bacteria were isolated in this study, of which 905 (83.41%) were from urinary specimens. The highest contamination in female was 74.94%. The most isolates were *Escherichia coli* (79.11%) and the lowest were related to *Stenotrophomonas* (0.88%). *Enterobacter* (9.28%), *Citrobacter* (6.96%), *Serratia* (2.98%), *Proteus* (2.65%), *Klebsiella* (2.54%), *Pseudomonas* (1.98%) and *Acinetobacter* (1.10%) were classified in the category of other gram-negative bacteria that were isolated from urine, respectively. 943 (73.61%) cases were susceptible to most antibiotics in the β-lactam family (cephalosporin and carbapenems), 132 (10.30%) of bacteria were semi-susceptible and 827 (64.55%) were resistant. Urinary tract infection had a direct relationship with the type of bacteria and patients' genus. This type of infection was more common in female and also the most common cause was *E. coli* (p <0.05).

Concussion: Importance of performing appropriate antibiotic susceptibility tests prior to administration of the drug for patients with urinary tract infections and bacteria detection is recommended in the treatment and control of drug resistance.

Key words: β-Lactam, Gram Negative Bacteria, Patients, Urinary Tract
PB-79

Determination of *Campylobacter* frequency in patient and healthy samples by *dnaJ* amplification

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**Background:** one of the most bacterial causes of diarrhea in the developing countries is *Campylobacter*. These narrow, curved, microaerophilic gram-negative rods bacteria may cause disease in humans and domestic animals. *Campylobacter* infection was associated with abdominal pain, fever and a history of bloody diarrhea. *Campylobacter* transmission was created by oral contact with fecal material from infected animals and humans or by contaminated food, water and milk. The minimal dose of *Campylobacter* that produces human infections is 9*10⁴. Accurate detection of *campylobacter* with new molecular methods is necessary in clinic. In this study we evaluated molecular detection of *campylobacter* by *dnaJ* gene.

**Material and Methods:** Genomics samples were collected from the DNA Bank of infectious diseases research center of Arak University of Medical Sciences. Among 60 extracted DNA from the stool, 30 isolates were patient and 30 isolates were healthy samples. PCR method was designed by F and R primers amplifying *dnaJ* gene. PCR products were analyzed by electrophoresis technique.

**Results:** 50% of total used diarrhea samples were infected with *campylobacter* which have positive band of *dnaJ*. Also, according to PCR results among 30 healthy samples, 5 isolated were positive. These results were significant statistically.
Conclusion: *dnaJ* gene coded a 40 KD heat shock protein which is critical for *Campylobacter* survival. Our results showed that this infectious agent causing diarrhea, was well detected by *dnaJ* gene in stool samples of healthy and patient people. Therefore; the *dnaJ* gene can be suitable for molecular detection of *Campylobacter* probably.

**Keywords:** diarrhea, *Campylobacter, dnaJ*
PB-80

Inactivation of non-thermal plasma on bacterial spores

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ABSTRACT

Background: The inactivation of micro-organisms and the removal of biological hazardous contaminants are generally great interest that plays a substantial role in the entire field of life science.

Non-thermal plasma (NTP) has been widely considered to be an effective method for surface decontamination. Numerous studies report that NTP also has antimicrobial ability. Plasma is ionized gas that consists of a large number of different species such as electrons, positive and negative ions, free radicals, gas atoms and molecules. The reactive spices in plasma have been caused the oxidative effects on the outer surface of microbial cells. These acts on the doubled bond of unsaturated fatty acid of membrane cell, thereby disturbing the transport of biomolecules across it.

The aim of this study is to investigate the potential of NTP to inactivate spores of bacteria.
Materials & Methods: Spore disc of Geobacillus stearothermophilus in Biological Indicator (BI) were used. In NTP a vacuum pump was used to reduce pressure inside the plasma chamber. Gas was connected to the chamber, and gas flow was regulated. Compressed air was pumped into the chamber that was maintained at the vacuum pressure range of 0.1-1 Torr, the power density of 30-90 watt, flow range of 3 SCCM, and exposure time was 20-70 min.

After treatment sample was prepared to dilution series and spread on Tryptic Soy Agar (TSA). Then incubation for 3-5 days, and counted plates with colony count devices.

Results: At the power of 50 watt and 30 min exposure to plasma, 6log reduction observed and all bacterial spores were killed.

Discussion: NTP known as an effective way to surface decontamination for different kind of bacteria. Geobacillus stearothermophilus is one of the most resistant bacteria because of forming spore. In this experiments we find out that NTP is an effective way to reduce decontamination of a wide range of bacteria.

Keywords: non-thermal plasma (NTP), Geobacillus stearothermophilus, Biological Indicator (BI).
PB-81

Microscopic Detection of *Arcobacter* in human fecal samples

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**Background:** *Arcobacter* is clinically important because it mainly causes gastroenteritis in humans. This bacterium is belonged to the *Campylobacteraceae* family. *Arcobacter* is gram negative, curved, spiral organism and can move speedily through its flagellum. The phenotypic characteristics of *Arcobacter* are similar to *Campylobacter* but they can be separated by growth power of *Arcobacter* at lower temperatures and its power of tolerance to aerobic condition. In clinical laboratories, preparation of bacterial smears and microscopic observation are the first step of identification of bacterium in different samples. The aim of our study was to detect *Arcobacter* in human non-diarrheal feces by microscopic observation.

**Material and methods:** In this study, 50 non-diarrheal fecal samples from human were used. Thin bacterial smears of each fecal samples were prepared on the slides, then they were stained by modified gram staining method with 3% fuchsine, observation of stained bacterial smears were done by 100× lense of microscope.

**Results:** Among of 50 bacterial smears prepared from non-diarrheal fecal samples from human, 7 samples (14%) were identified as gram-negative, curved, spiral organisms that can be *Arcobacter* spp. probably. Their length and width were 1-3 and 0.2-0.9 microns, respectively that was accordant to standard size of *Arcobacter*. 
**Conclusion:** According to the results, we observed the organisms that were apparently similar to *Arcobacter* in non-diarrheal fecal samples from human. Nevertheless, due to similarity of phenotypic characteristic of *Arcobacter* to *Campylobacter*, we were unable to name them *Arcobacter* definitively. So they should be identified by cultural and molecular methods. However, microscopic observations can be the first step and helpful method for detecting of *Arcobacter*.

**Keywords:** *Arcobacter*, bacterial smear, microscopic observation
Assessment the presence of Non Tuberculous Mycobacteria (NTM) species in Transplant patients in northwest of Iran during 2018.

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Background: Non-Tuberculosis Mycobacterium (NTM) in people with immunodeficiency disease, such as cancer patients, transplant recipients, and those who are suffering from HIV, considered to be as an opportunistic and auxiliary agent which can worsen the patient's condition. The purpose of this study was diagnosis of non-tuberculosis mycobacterium using Petroff phenotypical method. In order to grow bacteria, bacteria were inoculated into Lowenstein-Jensen culture.

Methods: 45 sputum sample from transplant patients were collected for NTM analysis in Shahid Ghazi Tabatabaei and Imam Reza hospital Tabriz. The
Modified Petroff method was used to decontaminate the specimens while sodium hydroxide effects liquefaction. Petroff eliminates the associated flora in sputum specimens and treated specimens should not be submitted to further decontamination prior to cultivation. In this method, the volume of NaOH 4% sputum is added. Specimens treated with Petroff preferentially inoculated in egg-based culture media. Isolates were confirmed by PCR method.

**Results:** overall, 9 NTM was isolates from samples which in 2 cases (6.8%) were slow growth mycobacteria and 7 cases (93.2%) were rapid growth mycobacteria. All isolates were confirmed by 16s rRNA PCR.

**Conclusion:** Findings of the present study indicates importance and high prevalence of NTM in transplant patients. These infections mostly ignored in patients. These results indicates need for identification and introduction of NTMs in hospitals which has transplant department.

**Keywords:** Non- tuberculosis mycobacteria, Transplant, sputum sample, Petroff method
PB-85

Non-Tuberculosis Mycobacterium (NTM) in Bone marrow transplant patients.

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Background: Non-tuberculous mycobacteria (NTM) are ubiquitous environmental organisms that have generally been considered as an uncommon cause of human disease.

Methods: A systematic review of non-tuberculous mycobacterium studies published the last 5 years was conducted with respect to microbiological and clinical outcomes of current treatment regimens.

Results: We which yielded 3 studies eligible for evaluation. NTM are more common in transplant patients who are immunocompromised, in 2012 report the case of a post- bone marrow transplant adolescent male presenting with Mycobacterium abscessus. In 2010 the specific polymerase chain reaction for Mycobacterium tuberculosis was negative, and a diagnosis of intestinal non-tuberculous mycobacteria (NTM) was made, and per year 2014 a 5-year-old
female patient underwent stem cell/bone marrow transplant with disseminated NTM, the pyrosequence of the hypervariable region A definitively identified the infecting organism as *Mycobacterium avium*.

**Conclusion:** NTM infection is easily neglected. Physicians must keep a high suspicion for NTM infections in bone marrow transplant recipients. We also review recent innovations for the diagnosis of NTM immunocompromised and immunocompetent patients disease, summarize treatment recommendations, and identify future research priorities to improve the management of patients affected by NTM immunocompromised and immunocompetent patients disease.

**Keywords:** Non- *tuberculosis mycobacteria*, bone marrow, transplant
PB-86

Pulsed-field gel electrophoresis (PFGE) analysis of various serotypes of *Listeria monocytogenes* isolated from clinical sources in Iran

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INTRODUCTION

Information about asymptomatic fecal carrier rate of *L. monocytogenes* is helpful in evaluating risk of fetal infections. The carrier rate is 3% among normal population (26% in high-risks). Knowledge about the prevalence of bacteria in pregnant women is important too. PFGE has provided the most sensitive differentiation up to now and has developed as gold standard typing method in
outbreaks. To the best of our knowledge, this is the first study in which *L. monocytogenes* from the feces of healthy individuals (fecal carriage) were characterized by both PCR-serotyping and PFGE in northwest Iran.

**METHODS**

The frequency of *L. monocytogenes* in clinical samples was evaluated in a total of 600 healthy fecal and urine samples collected during 2015. Additionally, 14 *L. monocytogenes* isolated from clinical origins during 2009-2011 were included in this study. Finally, *L. monocytogenes* isolates were analyzed by sequencing, serotyping and pulsed-field gel electrophoresis (PFGE).

**RESULTS**

Eight strains of *Listeria monocytogenes* were isolated from fecal samples of healthy individuals in different professions. Twenty-two isolates *L. monocytogenes*(including 14 non-fecal isolates) were characterized in present study. The majority of isolates (19/23, 83%) belonged to serotypes 1/2c followed by 1/2a, 4c, 4e and 4b (one isolate for each). The results of PFGE showed 13 PFGE patterns with 5 common type (CT), constituting 15 (65%) isolates with ≥95% similarity, and 8 single type (ST). The most shared PFGE CT was CT5 with six isolates. CT4 covered 3 isolates. Remaining CTs (CT1, CT2, and CT3) consisted of 2 isolates each.

**CONCLUSION**

These observations show need to pay attention to the contamination with bacteria in high-risk jobs and to perform an accurate typing method. The unique serotype, such as 4c belonging to Lineage III, as well as serotypes less reported in Iran, such as 4e and 1.2c, indicated the importance of some serotypes, especially 1.2c during listeriosis outbreaks.

Keywords: *Listeria monocytogenes*; pulsed-field gel electrophoresis; PCR-serotyping
PB-87

Antibacterial effects of methanol and aquatic extracts of eight plants in traditional medicine


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Abstract:

Introduction: *Escherichia coli* bacteria often cause infections in the gastrointestinal tract and other parts, such as the urinary tract. *Staphylococcus aureus* is a common pathogen that causes infections in the skin, upper respiratory tract, and many parts of the body. In recent years resistance to these bacteria has become one of the medical problems of antibiotics. Flowering herbs from the past are used to treat genital and gastrointestinal tract infections, and traditional herbal remedies are used to treat prostatic inflammation, gastric and intestinal ulcers, lungs, kidneys and bladder. *Hypercom perforatum* is used to relieve the cough symptoms of colds and common cold, sputum, healing wounds and injuries. *Artemisia absinthium* are beneficial for the treatment of arthritis, inflammation of the spleen and hepatitis, and the lavender plant is antiseptic.

Methods: In this study, the antimicrobial effects of aqueous and ethanol extracts of the above mentioned plants on standard bacteria were studied.
Methanol and aqueous extractions were performed using standard methods. Serial dilution of the extracts was prepared. The extracts were then concentrated in water bath. Determination of hypersensitivity was done by disc diffusion method for each extract and the findings were extracted and measured. The aim of this study was to determine the antimicrobial effect of the extracts of the plants studied using standard bacteria and dilutions of alcoholic and aqueous extracts of medicinal plants, which were carried out by appropriate laboratory methods and evaluated. **Results:** The results of this study showed that the alcoholic and aqueous extracts of *Artemisia absinthium* on *Escherichia coli* and *Achilles millefolium* aqueous extract have the highest effect on *Staphylococcus aureus*. The antimicrobial effect of the aqueous extract of *Ruta graveolens* and alcoholic extract of *Artemisia absinthium* was more than the others. **Conclusion:** The widespread use of antibiotics and drug resistance has led to more attention to medicinal plants. Some plants extracts have a significant antimicrobial effect. The plants studied in this study on the growth of *Escherichia coli* and *staphylococcus aureus* strains had an inhibitory effect. It can be hoped that with further investigation of the various forms of the extracts effective and safe drugs were obtained to control the bacteria.

**Keywords:** *Escherichia coli* bacteria, *Staphylococcus aureus*, Medicinal plants extracts, Antibacterial effects.
PB-88

Evaluation of Atypical Pneumonia caused by *Mycoplasma Pneumonia* (P1 Gene) with two methods of culture and molecular PCR in Tehran, Iran

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Abstract

**Background:** Atypical pneumonia is an upper and lower respiratory tract infection. *Mycoplasma pneumonia* is one of the major causes of acquired pneumonia from the community.

**Objectives:** The aim of this study was to determine the prevalence of atypical pneumonia caused by *mycoplasma pneumonia* in Tehran with two methods of culture and molecular PCR.

**Materials and Method:** Throat samples were collected from 102 patients with respiratory problems. All samples were placed in the PPLO broth. After genome cultivation and extraction using phenol / chloroform technique, PCR technique with specific primers was performed.

**Results:** From 102 samples of patients, 27 cases (%47.26) afflicted with *Mycoplasma pneumonia* were isolated in PPLO Agar medium. Using specific
primers, it was determined that 33 samples (%32.4) were positive in view of mycoplasma genus and 14 samples (%13.7) were positive regarding the presence of mycoplasma kind.

**Conclusion:** *Mycoplasma pneumonia* is the major cause of atypical pneumonia, and its prevalence in this study is (%13.6). The prevalence of this disease is relatively low during this study, which can be due to the high age of the patients and the season for the collection of samples.

**Keywords:** Atypical Pneumonia, *Mycoplasma pneumonia P1 Gene*, Culture and molecular
Antibacterial effect of different fractions of a total aqueous extract of *Elaeagnus angustifolia* fruit against *Enterohemorrhagic Escherichia coli*

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Enterohaemorrhagic E. coli (EHEC) is an important human pathogen that causes verity diseases include diarrhea and hemorrhagic colitis. The aim of this study was to investigate the antibacterial activity of fractions from *Elaeagnus angustifolia* fruit (E.A.) extract and to determine the bioactive compounds of the most effective fraction. Aqueous and organic fractions of E.A. extracts were screened for antimicrobial activity against *enterohemorrhagic Escherichia coli* by MIC and MBC method. As the aqueous fraction proved to be most active in our study, the aqueous fraction was selected for isolation and identification of chemical compounds using gas chromatography–mass spectrometry (GC-MS). Among the four types of fractions examined, aqueous fraction was found to possess high antibacterial activity, while the three organic fractions did not show any antibacterial activity. Aqueous fraction showed a bacteriostatic effect on exponentially growing of all tested bacterial strains at 60μg/ml (MIC). Thirty one chemical constituents were isolated and characterized from the aqueous fraction of E.A. Six phytocomponents including were found to be the major components (approximately 80% of the active ingredients) of aqueous fraction. Our data showed that aqueous fraction of E.A. was composed of diversity of soluble metabolites and remedial bioactive phytocomponents to treat bacterial infections.
that might be the central context behind using this plant directly as a traditional tribal remedy.

**Key words:** *Elaeagnus angustifolia*; antibacterial activity; GC-MASS, *enterohemorrhagic Escherichia coli*
PB-91

Elaboration of an ELISA-based diagnostic system for screening of

*Vibrio Cholera*

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**Background:** Diarrhea is one of the major causes of death in children under the age of 5 years. In developed countries, the most important cause of these diseases is the virus, but bacterial infections are one of the most important causes of mortality in developing countries. Among the bacterial agents that can affect intestinal infections are *E. coli*, *Vibrio*, *Campylobacter*, *Shigella* and *Salmonella*. *Vibrio cholera* is a major contributor to the development of endemic and epidemic diarrhea through poison production around the world.

**Methods:** In this study, a chimeric protein containing the connecting element of bacterial *vibrio cholera* bacteria was used to design the ELISA kit.

**Results:** Similarly, the recombinant protein was purified after expression in host *E. coli BL21 (DE3)*, and the immunization of mice and rabbits to produce specific anticoagulants was carried out on the protein.

**Conclusion:** After confirmation of immunity and the presence of specific immunoglobulins against this protein, purified *IgG* immunoglobulins were used in ELISA design. The results show that the designed ELISA sandwich can detect a bacterial infection of *vibrio cholera*.

**Keywords:** Diarrhea, immunological diagnosis, *vibrio cholera*
Association of gut microbiota with heart failure

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Introduction: Heart failure (HF) is a health problem and a major cause of mortality and morbidity in the world. The microbiota exerts a considerable influence on the host’s physiological, immunological and nutritional status. Alteration in the gut microbiota correlate with many disease such as heart failure. Some metabolites such as Trimethylamin N-oxidase (TMAO) has been directly linked to adverse cardiovascular events and all-cause mortality. These metabolites may be used as indicator to determine cardiovascular diseases. Sources including choline, phosphatidylcholine, l-carnitine, and other methylamine-containing nutrients provide substrates for microbiota-mediated production of trimethylamine (TMA). After that, TMA is linked by host hepatic flavin-containing monooxygenase (FMO) enzymes to form TMA–N-oxide (TMAO). Finally, TMAO can promote the development of atherosclerosis, thrombosis, kidney disease, and heart failure.

Method: Our reference methodology was that we reviewed all the articles in the pubmed and Google scholar with the keywords “Heart Failure” and “microbiome”. All of the considered papers were used 16S rRNA Gene
amplification and Sequencing for analysing the microbiota profile and CE-TOFMS technique for detection of TMAO.

**Results:** According to the result, Clinical trials on patients with heart failure and cardiovascular disease indicate an increase in the level of TMAO in patients which may show the role of this substance in development of CVD. High level of TMAO level has been found in CKD patients with or without HF.

**Conclusion:** There is strong relationship between gut microbiota-produced metabolites such as TMAO and Heart failure (HF). TMAO is an importance marker to HF disease and a possible therapeutic target. Also, The results showed that there is correlations between specific bacterial genera and circulating levels of harmful metabolites such as TMAO.

**Keywords:** TMA,FMO,TMAO, CVD, Heart failure (HF), gut microbiota
Increased Resistance to Tetracycline and Erythromycin in Vibrio cholerae Clinical Isolates Isolated from Patients with Cholera Disease during 2012-2013 Outbreaks in IR Iran

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Background: Vibrio cholerae is one of the intestinal Gram-negative bacterium, causing cholera disease in developing countries, the two serogroups of O1 and O139 are the main cause of diarrhea. The bacteria resistance pattern to antibiotics varies in different countries. The aim of this study was to determine the resistance pattern of the isolates to representative antibiotics.

Materials and methods: A total of 20 V. cholerae clinical strains were isolated from patients with cholera in Sistan and Baluchestan province of Iran during 2012-2013 outbreaks. After being identified by biochemical and molecular techniques, antibiotic susceptibility testing was performed for 6 antibiotics according to CLSI standards. Then minimum inhibitory concentration (MIC) was also determined for tetracycline and erythromycin using E-Test method.

Results: All of the isolates were EL Tor biotype, O1 serogroup, and Inaba serotype. All of isolates were resistant to erythromycin and nalidixic acid, and 50% were resistant to tetracycline while no resistance was observed against ciprofloxacin, gentamicin, and ampicillin.

Conclusion: The sensitivity of all clinical isolates to antibiotics mentioned suggests that these antibiotics can likely be used in cholera disease treatment.

Keywords: Vibrio cholerae, Resistance, Outbreak

Presenting Author is underlined and Corresponding Author is indicated by *.
Prevalence of plasmid-mediated AmpC β-Lactamase genes in *Escherichia coli* and *Klebsiella pneumoniae* Isolated from Clinical samples

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**Background:** Emergence of antibiotic resistance among pathogens, particularly in health centers and hospitals, has become a major public health problem. Bacteria use different strategies to remain immune from the deleterious effects of antibiotics. One of the most important of these mechanisms is to produce β-lactamase enzymes. AmpC β-lactamases are one of these hydrolyzing enzymes. These organisms can acquire the ability to produce AmpC β-lactamase on the plasmid.

**Method:** 429 *E. coli* and *Klebsiella pneumoniae* Organisms, were isolated from urine samples, during one year. Initial screening was performed on isolates, by using an antibiotic cefoxitin disk (30 μg). Based on the CLSI Protocol. Subsequently, non-susceptible isolates of Cefoxitin (with a diameter of ≤18 mm inhibition zone) were tested for the presence of the producing plasmid-mediated AmpC β-lactamase enzyme genes by multiplex PCR.

**Results:** In the screening step, out of 429 samples, 64 (14.9%) samples was non-susceptible with cefoxitin (30 μg). 37 (57.8%) out of 64 screened samples were identified to have producing AmpC β-lactamases genes by standard multiplex PCR method. 31 of the samples (83.8%) formed 462 bp bands on the agarose gel (CITM primer). 8 of the samples (21.6%) formed 405 bp bands (DHAM primer). 11 of the samples (29.7%) formed 302 bp bands (EBCM primer). 5 of the samples (13.5%) formed 190 bp bands (FOXM primer). In PCRs conducted with MOXM and ACCM primers, there was no band.

**Conclusion:** This study indicate that number of producing AmpC β-lactamase strains in urinary tract infections is noticeable. In most studies that have been conducted on the prevalence of producing AmpC β-lactamase genes, CMY and DHA genes have been reported as the most common genes. However, in the recent study, the prevalence of the ACT gene in this Strains was more than DHA gene. Therefore, the prevalence of AmpC β-lactamase plasmid-mediated genes in
Enterobacteriaceae seems to be variable in different parts of the world, and should be considered.

**Keywords:** AmpC β-lactamase, *Escherichia coli*, *Klebsiella pneumoniae*, Genotypic method, Multiplex PCR
PB-97

Evaluation of the effect of Essential oil of *Satureja khuzestanica* on *Pseudomonas aeruginosa* clinical strains

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Background: *Pseudomonas aeruginosa* is an opportunistic bacterium and is one of the main causes of hospital infections. Treatment of *Pseudomonas aeruginosa* infection can be difficult due to the inherent resistance to antibiotics in this bacterium. The aim of this study was to evaluate the antibacterial effect of Essential oil of *Satureja khuzestanica* on *Pseudomonas aeruginosa* clinical strains.

Methods: Strains were collected from Bandar Abbas Hospital. Essential oil of *Satureja khuzestanica* was extracted by Clevenger method. Minimum inhibitory concentration (MIC) was determined on strains by micro broth dilution method.

Results: The result of the micro broth dilution results of the bacterial absorption of the control group was as follows: We worked on six clinical strains that one of the strains was resistant, but the remaining strains were dead.

Conclusion: Due to the fact that *Pseudomonas aeruginosa* is an opportunist bacteria resistant to antibiotics, and today it is confronted with the problem, it is suggested that this compound, although it is a medicinal plant and very well responses to *Pseudomonas aeruginosa*, is suggested in studies Next, this compound is used as an antibiotic substitute for treatment, or even from the derivatives of this plant can be used for antibacterial compositions of surfaces.
Keywords: *Pseudomonas aeruginosa*, *Satureja khuzestanica*, Antibacterial activity, MIC, MBC

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Identification of Adherent invasive E. coli isolated from Iranian patients with Ulcerative colitis

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Abstract

Background: Ulcerative colitis is a kind of inflammatory bowel disease that is considered as immunological response to commensal bacteria colonizing gut lumen. Adherent-invasive Escherichia coli strains are pathogens responsible for ulcerative colitis disease. These bacteria have special virulence factors, including type 1 fimbriae, which could be involved in inflammatory bowel disease.
Objectives: The present study was conducted to determine the prevalence of adherent-invasive *E. coli* with *fimH* gene isolated from Iranian patients with ulcerative colitis.

Methods: Sixty intestinal biopsy samples of 30 patients with ulcerative colitis and 30 individuals without inflammatory bowel disease were examined. Biopsies from rectum, descending, ascending, terminal ileum, and colon were taken during colonoscopy.

Results: All biopsy samples were cultured for isolation of *E. coli* strains. Using polymerase chain reaction assay, the invasive plasmid antigen H and invasion-association locus genes were detected from both isolated bacteria and tissue specimens to confirm the presence of adherent-invasive *E. coli*. The frequency of adherent-invasive *E. coli* with type 1 fimbriae was much higher in patients with ulcerative colitis than control subjects. Among isolated bacteria, type 1 fimbriae of adherent-invasive *E. coli* were detected in 53.3% and 13.3% of ulcerative colitis patients and control subjects, respectively. In addition, from 60 biopsy samples, type 1 fimbriae were detected in 56.7% of ulcerative colitis patients but in 10% of healthy subjects.
Conclusions: Subjects without inflammatory bowel disease had a high rate of *E. coli* strains than patients with ulcerative colitis via cultivation detection. We found a high rate of type 1 fimbriae of adherent-invasive *E. coli* in ulcerative colitis patients by polymerase chain reaction assay. It appears that the presence of adherent-invasive *E. coli* with type 1 fimbriae in the gastrointestinal tract of patients with ulcerative colitis is more likely than previously supposed.

*Keywords: Escherichia coli, Colitis, Ulcerative, Inflammatory Bowel Diseases, PCR*
Presence of adherent invasive *E. coli* in Iranian patients with Crohn's disease

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Abstract

**Background:** Crohn's disease and Ulcerative colitis are known as inflammatory bowel disease with high morbidity which are as a result of increasing immune responses to intestinal microbiota in genetically susceptible individuals. The association of adherent invasive *Escherichia coli* with Crohn's disease in human has been discussed for decades. The principal aim of this study was to assess the relationship between adherent invasive *Escherichia coli* in Iranian patients with Crohn's disease.

**Methods:** The presence of adherent invasive *Escherichia coli* DNA and viable adherent invasive *Escherichia coli* cells were identified through PCR and conventional culture methods, respectively. All the specimens were subsequently cultured in Hi Chrome Agar medium.
Results: Using molecular assay, the invasive plasmid antigen H and invasion-association locus genes were detected from tissue samples confirming the presence of adherent-invasive *Escherichia coli*. The invasive plasmid antigen H was detected in 46.7% of CD and 13.3% of healthy peoples. The invasion-association locus gene was found in 36.7% of patients with Crohn's disease and 10% in individuals without IBD.

Conclusion: This study demonstrated an increased frequency of adherent invasive *E. coli* with invasive plasmid antigen H and invasion-association locus genes from patients with CD in comparison to control individuals. Moreover, it was shown that adherent invasive *E. coli* with the invasive plasmid antigen H and invasion-association locus genes can act as a predisposing factor in the development of IBD.

Keywords: Crohn Disease, Inflammatory bowel disease, *Escherichia coli*, PCR
Early-onset sepsis remains a common and serious problem for neonates, especially preterm infants. Group B streptococcus (GBS) is the most common etiologic agent, while *Escherichia coli* is the most common cause of mortality. Current efforts toward maternal intrapartum antimicrobial prophylaxis have significantly reduced the rates of GBS disease but have been associated with increased rates of Gram-negative infections, especially among very-low-birth-weight infants. The diagnosis of neonatal sepsis is based on a combination of clinical presentation; the use of nonspecific markers, including C-reactive protein and procalcitonin (where available); blood cultures; and the use of molecular methods, including PCR. Cytokines, including interleukin 6 (IL-6), interleukin 8 (IL-8), gamma interferon (IFN-γ), and tumor necrosis factor alpha (TNF-α), and cell surface antigens, including soluble intercellular adhesion molecule (sICAM) and CD64, are also being increasingly examined for use as nonspecific screening measures for neonatal sepsis. Viruses, in particular enteroviruses, par echoviruses, and herpes simplex virus (HSV), should be considered in the differential diagnosis. Empirical treatment should be based on local patterns of antimicrobial resistance but typically consists of the use of ampicillin and gentamicin, or ampicillin and cefotaxime if meningitis is suspected, until the etiologic agent has
been identified. Current research is focused primarily on development of vaccines against GBS.

Key words: Sepsis, Group B streptococcus, procalcitonin
PB-104

Diversity of *Salmonella* serogroups among the isolates of diarrhea stool samples and chicken meat in distinct districts of Tehran, Iran


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Background: Food animals are assumed as main source of infection with enteric pathogens. To analyze this relationship, infection rate of Salmonella enterica in patients with community acquired diarrhea was studied and serogroups of their isolates were compared with the isolates of distributed chicken meat among allowable shopping centers in 22 municipal districts of Tehran, Iran during same time period.

Methods: Diarrhea stool and chicken meat samples were collected from 22 municipal districts of Tehran, Iran from June to December 2018. Pre-enrichment of the meat samples was done in Buffered Peptone Water (BPW) medium. The culture was enriched in Rappaport Vassiliadis Soy Broth (RVS) and Tetrathionate Broth media. The fecal samples were enriched in Selenith broth. Growth of the colonies was analyzed on Xylose Lysine Desoxicolate Agar (XLD) and Bismuth Sulphite Agar (BS) plates (for the chicken samples), and MacConkey agar plates (for the stool samples). Suspected colonies of Salmonella were confirmed by IMViC tests and PCR. The isolates were serogrouped by agglutination method using antisera against Salmonella serogroups A to D.

Results: In total, 76 and 8 Salmonella isolates were obtained from the chicken meat and stool samples, respectively. While most of the chicken meat isolates were belonged to serogroup C (89.5%, 68/76), the remaining isolates were related to serogroup B (2.6%, 2/76), serogroup D (3.9%, 3/76), and non-A to D serogroups (3.9%, 3/76). RVS Broth and XLD agar media showed greater sensitivity compared with Tetrathionate Broth and BS agar for isolation of the Salmonella isolates (92.63% vs 7.37%). The fecal isolates were belonged to serogroup C (12.5%, 1/8), serogroup B (37.5%, 3/8), serogroup D (37.5%, 3/8), and non-A to D serogroups (12.5%, 1/8).
**Conclusion:** Results of this study showed a preliminary link between serogroups of *Salmonella enteric* isolates in the stool and the chicken meat samples.

**Keywords:** *Salmonella enterica*, Foodborne diseases, Diarrhea, Chicken meat, Serogrouping.
Investigation of Burdetellapertusis & parapertusis from collecting samples hospitals Qazvin province in 9 months of 1397 sent to Tehran from central lab of Qazvin city to Tehran,

Introduction and Objectives: The etiologic agent of whooping cough or pertussis is a gram negative bacilli named of Burdetella. B. Pertusis is a human phatogen incriminated in the majority cases of whooping cough. A common childhood infection B. Parapertusis is also occasionally found in whooping cough (these organisms colonize mucous membranes of throat and nasophary, area and by producing various toxins) the characteristic clinical manifestation of the disease predominantly coughing and cyanosis starts. Chronic stages of disease lasts for several days to weeks. The aim of this study was epidemiologic survey on clinical specimens collected from hospitals Qazvin province in 9 months 1397

Materials and Methods: In a retrospective descriptive cross sectional studied by Dacrons samples taken from nose of children a mean age 3.0 years in. The swabs transferred to transport media and send to the Pasteur Ins.

Result: In the year of 1397 from 38 samples totally of the cases were not positive in P.C.R. with culture.

Conclusion: Therefore mass vaccination for pertussis (DPT) during last decades results total control in children in adults, and the youngest however the disease could be observed sporadically that may transmit to neonants and predisposed childs.

Keyword: B. Pertusis, childs, whooping cough, vaccination
Evaluation of Antimicrobial Resistance and Biofilm Formation among Clinical Isolation *Pseudomonas aeruginosa* obtained from burn patients

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**Background:** *Pseudomonas aeruginosa* is one of the most serious causes of morbidities and mortalities in burn wards. Wet burn tissues provides a good environment for colonization and infection by *P. aeruginosa*. Ability of biofilm formation and high rate of antibacterial resistant in this organism are leading to treatment of burn infections are very difficult and expensive.

The purpose of this study was to determine the antibiotic resistance pattern and biofilm formation rate of clinical isolates of *Pseudomonas aeruginosa* in patients with burn infections.

**Method:** *Pseudomonas aeruginosa* was identified by conventional biochemical tests. The antibiotic susceptibility testing of these isolates were carried out by disc diffusion method. Screening for biofilm formation was done by microtitre plate assay.
Result: Out of these 118 isolates, 109 (92.77%) was found to be MDR *P. aeruginosa*. Based on the obtained results by the Agar disk diffusion test, (92%), (91%), (90%), (90%), (87.5%), (87.5%), (76.25%), (75%) and (68.75%) of the strains were resistant to levofloxacin, meropenem, tobramycin, amikacin, ciprofloxacin, gentamicin, cefepime, piperacillin and ceftazidime respectively. The result of microliter plate was 53 (44.91%) showing biofilm formation.

Conclusion: Our result show increased prevalence of MDR strains among *Pseudomonas aeruginosa* in burn infections and their ability to form biofilms.

Key words: Antimicrobial Resistance, Biofilm, *Pseudomonas aeruginosa*
Prevalence of Fosfomycin Resistance genes and Antimicrobial Susceptibility of Urinary Extended-spectrum Beta-lactamase-producing Enterobacteriaceae

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Objectives: In order to determine the prevalence of plasmid-mediated fosfomycin resistance genes and antimicrobial susceptibility in urinary extended-spectrum beta-lactamase-producing *Escherichia coli* and *Klebsiella pneumoniae*, a total of 172 non-duplicate ESBL isolates were collected from 423 urine samples at Milad Hospital in Tehran, Iran between May and November 2016.

Methods: The ESBL genes *bla* _SHV_, _bla_ _TEM_, and _bla_ _CTX-M_ as well as plasmid-encoded fosfomycin resistance genes _fosA_ and _fosA3_ were amplified by PCR. Antimicrobial susceptibility testing was performed by disk diffusion to fosfomycin. Additionally, the minimum inhibitory concentration (MIC) of fosfomycin for ESBL isolates was determined by the agar dilution method according to CLSI guidelines.

Results: The MIC of fosfomycin for the ESBL producing *E. coli* and *Klebsiella pneumoniae* strains ranged from 0.25-256 µg/ml to 0.5-512 µg/ml, respectively. Approximately 9.4% (13/138) and 5.9% (2/34) of the ESBL-EC and ESBL-KP were resistant to fosfomycin (MIC ≥ 256 µg/ml). Of the 15 isolates resistant to
fosfomycin, 6 (5 *E. coli* and 1 *K. pneumoniae*) isolates harboured *fosA3* and all of them co-harboured *bla CTX-M*.

**Conclusions:** Fosfomycin presented a good in vitro activity against ESBL isolates.

**Keywords:** Urinary tract infection, ESBL, *Escherichia coli*, *Klebsiella pneumoniae*, fosfomycin, antimicrobial Susceptibility
Background: This study conducted to determine the prevalence of Ciprofloxacin resistant E.coli and its related genes in clinical samples in Neka.

Methods: Clinical samples collected from hospitals in Neka, such as Bouali and Imam Hossein (n=1372) and were identified to the genus and species level by cultural characteristics and biochemical tests. The susceptibility of the isolates samples to antibiotic drugs was determined by the Kirby-Bauer Disk Diffusion Susceptibility Test Protocol. PCR test and identification of qnrA, qnrB and qnrS genes in ciprofloxacin resistant isolates performed.

Results: Based on the results of microbial tests, only 208 samples of the collected urine samples were infected with bacteria that among the pathogenic bacteria, Escherichia coli and staphylococci were the most frequent with 57.7 and 26.88%, respectively. The highest frequency of isolates resistant to antibiotics related to ceftriaxone and Nalidixic acid with 76.9% and the percentage of resistance to antibiotics such as Ciprofloxacin, Cefotaxime and Norfloxacin, Ofloxacin and Ceftazidime were 50, 42.9, 40.40 and 33.3%, respectively. In the PCR assay, 60 (50%) isolates resistant to ciprofloxacin used to detect qnrA, qnrB and qnrS genes, which consisted of 10 samples (16.66%), 31 samples (51.66%), and 28 samples (46.66%), respectively. The highest frequency was observed for the qnrB gene with 51.66%. There were more than one gene or the absence of these genes in the strains, in which 3 (5%) had no qnrA, qnrB and qnrS genes, and 8 samples (13.33%) had all three genes.
Conclusion: In this study, regarding the identification of the antibiotic susceptibility pattern in the most common organisms in the studied area, its report to doctors can be considered in empirical treatments.

Keywords: ciprofloxacin, E.coli, Clinical samples, antibiotic, PCR, qnr
PB-109

Bacteremia due to Campylobacter fetus

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Background: Campylobacter fetus can cause intestinal illness and, occasionally, severe systemic infections. Infections mainly affect persons at higher risk, including elderly and immunocompromised individuals and those with occupational exposure to infected animals. Outbreaks are infrequent but have provided insight into sources. Source attribution of sporadic cases through case-control interviews has not been reported. The reservoirs for C. fetus are mainly cattle and sheep. Products from these animals are suspected as sources for human infections. 74-year-old man with stomachache and fewer presented with 6 month history of gallbladder surgery. Blood culture test(x2) has been done by BacTalert system.

Methods: Process of Blood culture test by BacTalert system showed positive result after 48 hours. We use wet mount method and also gram straining with long term duration of Carbol fuchsin. For diagnosis species of campylobacter we use cefalothin and nalidixic acid disc by disc diffusion method.

Result: Process of Blood culture test by BacTalert system showed positive result after 48 hours. In wet mount motile vibrio like bacilli were seen also in gram straining with long term duration of Carbol fuchsin, presence Gram negative rods with gull-wing shape in blood of patient suggests Campylobactor spp. The incubation temperature of 37°C, which is often routinely used to isolate these Campylobacter species. For diagnosis species of campylobacter we use cefalothin and nalidixic acid disc by disc diffusion method. The bacteria showed resistance to nalidixic acid and sensitive to cefalothin disc.
Conclusion: Most Campylobacter infections present as diarrheal illness. However, in about 0.15% of cases, intestinal campylobacteriosis leads to bacteremia, often with infection involving distant organs [1]. The symptoms of such invasive campylobacteriosis will then vary with the affected organ. Although the majority (>90%) of cases of intestinal campylobacteriosis are caused by Campylobacter jejuni or Campylobacter coli [2], a small proportion is caused by Campylobacter fetus. In one Irish study, the DNA of C. fetus was detected in only 2.4% of cases of intestinal campylobacteriosis [3]. In contrast, C. fetus is the most commonly detected pathogen causing Campylobacter bacteriemia (19%–53%, dependent on the study) [4–6]. The fatality rate of such invasive C. fetus infections is reported at 14% [7]. Given the worldwide high incidence of campylobacteriosis, these data suggest that C. fetus infections are not uncommon and may constitute a public health issue. Nevertheless, relatively little is known about the infection sources and the people at risk. Samples from extraintestinal infections, for example, blood or cerebrospinal fluid, will have fewer contaminating organisms, which may allow detection at a permissive temperature and using a microaerobic atmosphere without the use of selective media. The routine blood culture methods used in clinical microbiology should allow C. fetus growth; however, the efficacy of recovery from such approaches is unknown.
Emergence of oxacillinase-mediated resistance to carbapenem in Acinetobacter baumannii

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Introduction and Aims: Carbapenem is a selective antibiotic for the treatment of infections caused by Acinetobacter baumannii. The presence of the blaOXA genes in A. baumannii contributes to carbapenem resistance. The present study was aimed to determine the prevalence of blaOXA-type carbapenemases in clinical isolates of Acinetobacter baumannii.

Materials and Methods: This study was conducted on 65 clinical isolates of Acinetobacter baumannii. Antimicrobial susceptibility test was performed by disc diffusion agar method for ceftazidime, cefepime, piperacillin/tazobactam, ampicillin/sulbactam, imipenem, meropenem, gentamicin, tobramycin, ciprofloxacin, levofloxacin, tetracycline and minocycline. Minimum Inhibitory Concentration (MIC) of isolates were determined for the imipenem, meropenem, polymyxin B, colistin and tigecycline using standard microbroth dilution method. The frequency of the genes encoding oxacillinase, including OXA-143-like, OXA-23-like, OXA-58-like, OXA-24-like, OXA-51-like and OXA-235-like in carbapenem resistant Acinetobacter baumannii (CRAB) isolates were studied by PCR.

Results: Amplification of the ITS fragment of Acinetobacter baumannii isolates confirmed the genus and species of the bacteria. The resistance pattern of A. baumannii isolates for ceftazidime, cefepime, piperacillin-tazobactam, ampicillin-sulbactam, imipenem, meropenem, gentamicin, tobramycin, ciprofloxacin, levofloxacin, tetracycline and minocycline was 96.92%, 92.30%, 96.92%, 7.69%,
The resistance pattern to the seven different antibiotic classes in *A. baumannii* isolates showed that the prevalence rate of multidrug-resistant (MDR), extensively drug-resistant (XDR) and pandrug resistant (PDR) were 92.96%, 39.62%, and 0%, respectively. The minimum inhibitory concentration of the isolates showed that the resistance rate to the imipenem, meropenem, polymyxin B, colistin and tigecycline was 100%, 100%, 0%, 12.7% and 36.51%, respectively. The presence of genes encoding oxacillinase such as bla\textit{OXA}-51-like, bla\textit{OXA}-58-like, bla\textit{OXA}-23-like, bla\textit{OXA}-24-like, bla\textit{OXA}-143-like, and bla\textit{OXA}-235-like was 100%, 0%, 0%, 74.61%, 42/62%, 0%, and 0%, respectively.

**Conclusion:** The present study indicated that the frequency of multidrug-resistant (MDR) is high in clinical isolates of *Acinetobacter baumannii*. This is a serious warning for public health organizations and healthcare systems. These in vitro results show that the polymyxin B has a good antimicrobial activity on *Acinetobacter baumannii*.

**Key words:** carbapenem, MIC, antibiotic resistance, *Acinetobacter baumannii*, bla\textit{OXA}
Detection of Airway Mycobiome in Iranian Cystic Fibrosis Patients and to Assess Their Antibiotic Resistance

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Abstract

Lung diseases due to respiratory infections are the major cause of death in patients with cystic fibrosis (CF). CF is a systemic inherited metabolic disorder that predisposes the human body to microbial colonization of the airways.

There is little information about prevalence of pathogenic bacteria in Iranian CF patients. This study was aimed to detect airway microbiome in oropharyngeal swabs of Iranian CF patients and study of their antibiotic resistance.

Methods

oropharyngeal swabs were collected from 64 children and adults (aged ≥ 7 months to < 20 years) referred to Children's Medical Center of Tehran university. Bacterial prevalence was determined using standard microbiological culture-based techniques. The antibiotic susceptibility testing was determined using Kirby-Bauer disk diffusion method as recommended by CLSI.

Results

Out of the 79 bacterial isolates detected in oropharyngeal swabs, 38 (59.37%) were Staphylococcus aureus, followed by Pseudomonas aeruginosa 19(29.68%), Streptococcus pyogenes 5(7.81%), Streptococcus group C or G 5(7.81%), Enterococcus faecalis 4(6.25%), Citrobacter diversus 2(3.12%), Shigella sp.
1 (1.56%), Moraxella sp. 1 (1.56%), Citrobacter freundii 2 (2.53%).

Gram positive bacteria revealed resistance to oxacillin (45.51%), trimethoprim sulfamethoxazol (57.69%), vancomycin (19.22%) and novobiocin (17.94%). Gram negative bacteria showed resistance to aztreonam (75.21%), ceftazidime (70%), meropenem (20%), ciprofloxacin (52.6%) and tobramycin (40%).

Conclusions

S. aureus and P. aeruginosa are the most abundant bacteria isolated from oropharyngeal CF population. However, using the strategies to prevent the colonization of these bacteria can improve the life expectancy of CF patients.

Keywords: Cystic fibrosis (CF), Oropharyngeal swabs, antibiotic resistance
PB-112

Frequency of *aacA4* gene in clinical isolates of *Klebsiella pneumoniae* in Khorramabad

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**Background:** *Klebsiella pneumoniae* is a gram-negative intestinal bacilli and is a member of Enterobacteriaceae family and forms part of the natural microflora of the human body. *Klebsiella* causes 5 to 7.5% of all hospital infections and infections caused by it in the pediatric and intensive care sector are a major problem. Reports around the world emphasize resistance to aminoglycoside antibiotics in recent years. The aim of this study was to determine the frequency of *aacA4* gene in clinical isolates of *Klebsiella pneumoniae* in Khorramabad.

**Methods:** In this study, the patients were referred to hospitals in Khorramabad city during 7 months. Samples were subjected to molecular evaluation after biochemical and antibiotic tests. DNA extraction was performed by boiling method and detection of genes by specific primers was performed using PCR technique.

**Results:** After molecular studies, using PCR technique, 100% of the isolates studied had 40% of the *aacA4* gene.

**Conclusion:** Due to the 40% prevalence of the gene *aacA4*, one of the most effective genes in resistance to aminoglycoside antibiotics. It was determined that in the future, antibiotics resistance should be increased in clinical isolates and resistant to resistant isolates.
Keywords: Klebsiella pneumoniae, molecular diagnosis, aminoglycoside antibiotics, aacA4
Antibacterial activity of *Cinnamomum zeylanicum* methanolic extract and essential oil against *Escherichia coli* isolated from burn wound infection

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**Background:** *Escherichia coli* (*E.coli*) are an important pathogen in the burn wound infection. Increasing of antibiotic usage for *E.coli* infections, created antibiotic resistance. Medical herbs with anti-microbial activity have always been important role in traditional medicine. The purpose of this study was to determine the antibacterial activity of methanolic extract and essential oil of *Cinnamomum zeylanicum* against *E.coli* isolated from burn wound infection in vitro.

**Methods:** This research is a descriptive analytic study. First, samples of methanolic extract and essential oil of *Cinnamomum zeylanicum* were prepare by maceration method. Then its antibacterial activity against 25 isolates of *E.coli* from 250 samples of burn wound infection was evaluated by well diffusion and then agar serial dilution method. Also, the MIC (Minimum Inhibitory Concentration) and MBC (Minimum Bactericidal Concentration) of essential oil was determined.

**Results:** The diagrams, T-test were used to compare the results. The results demonstrated that the methanolic extracts of *Cinnamomum zeylanicum* show an average inhibitory zone diameter of 15mm. The methanolic extract shows best result having ZOI greater than that of the selective antibiotics. The MIC and MBC of essential oil against *Cinnamomum zeylanicum* were 600 and 1500 µg/ml respectively. There was no significant difference between the effects of the plant and antibiotics on *E.coli* (P>0.05).

**Conclusion:** This study demonstrates that a methanolic extract and essential oil of *Cinnamomum zeylanicum* have antibacterial activity against *E.coli* isolated
from burn wound infection and its effect is similar selective antibiotic. Further investigations will be necessary.

**Key words:** burn wound infection, *Escherichia coli, Cinnamomum zeylanicum, Antibacterial Activity*
PB-114
The occurrence of plasmid-mediated quinolone resistance genes in uropathogenic *Escherichia coli* isolates in Shiraz, Iran

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**Abstract**
**Background:** Urinary tract infections (UTIs) are one of the most prevalent infectious diseases and can lead to a high rate of morbidity and mortality. Fluoroquinolones are routinely used in the treatment of these infections; however, in recent years, a growing rate of resistance to these drugs has been reported globally. Our study aimed to investigate the prevalence of plasmid-mediated *qnrA*, *qnrB*, and *qnrS* genes among the quinolone-nonsusceptible uropathogenic *Escherichia coli* (UPEC) isolates obtained from hospitalized patients.
Methods: This cross-sectional study was performed during 2016 to 2017 on 121 E. coli isolates recovered from patients with clinical symptoms of UTIs, referred to Shiraz Nemazee Hospital. The isolates were identified by standard microbiologic tests and confirmed by API 20E strip. Antimicrobial susceptibility testing was determined using the disk diffusion method. The presence of qnr genes was determined using the polymerase chain reaction.

Results: In overall, 81% of isolates were non-susceptible to nalidixic acid, 58.7% to ciprofloxacin, 50.4% to levofloxacin, 49.6% to ofloxacin, and 48.8% to norfloxacin. Of the 121 isolates, qnrS, qnrB and qnrA genes were positive in 33.1%, 12.4%, and 5% of isolates, respectively.

Conclusion: Our study results were indicative of the prevalence of qnr genes among the clinical isolates of E. coli in Shiraz, which emphasizes the necessity of restricted infection control policies to prevent further dissemination of resistant strains.

Keywords: Urinary Tract Infections; Escherichia coli; Antibiotic Resistance; Fluoroquinolones; qnr genes
Prevalence of aminoglycoside phosphoryl transferases (APHs) and 16S ribosomal RNA (16SrRNA) methylase genes among *Escherichia coli* isolated from intensive care unit (ICU) centers

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**Background:**
Infection is a major cause of mortality in intensive care units (ICU) worldwide. *Escherichia coli* are one of the most common causes of infection in ICU. Aminoglycoside in combination with beta-lactam antibiotics has been the standard therapy for empirical therapy of these infections. Genes encoding aminoglycoside modifying enzymes (AME) and 16SrRNA methylases are the main causes of aminoglycoside resistance. The aim of this study is to determining the prevalence of aminoglycoside resistance and aminoglycoside phosphoryl transferases (APHs) and 16SrRNA methylase genes among *E. coli* isolates collected from ICUs.

**Methods:**
From 2013-2017, a total of 254 *E. coli* isolates were collected from ICU of 16 hospitals in Qazvin, Karaj and Tehran. The isolates were identified by the biochemical tests and 16SrDNA gene. The antibiotic susceptibility test was conducted according to the clinical and Laboratory Standards Institute (CLSI)
guideline using seven aminoglycosides antibiotics. The gentamicin MIC was determined with agar dilution methods; using a range between 0.5-256 µg/ml. The PCR amplification of APH genes; \textit{aph (3')-Ia} and \textit{aph (3')-VI} and 16SrRNA Methylase Genes; \textit{armA, rmtA, rmtB, rmtC, rmtD, rmtE, rmtF, npmA} was performed with specific primers and conditions.

**Results:**
A total of 254 \textit{E. coli} isolates, 237 (93.3%) isolates were non-susceptible against at least one of the aminoglycosides tested among those gentamicin 136 (53.5%), and streptomycin 134 (52.8%) showed the highest rates of resistance whereas amikacin and netilmicin revealed high susceptibility rates of 93.3% and 78.7%, respectively. A total of 254 isolated were positive for the presence of \textit{rmtB} (11%) and \textit{aph(3')-Ia} (0.3%).

**Conclusion:**
The results of this study showed that despite high prevalence of resistance to aminoglycosides, the prevalence of APH and 16srRNA methylase genes are not prevalent in \textit{E. coli} isolates collected from ICUs in this study.

**Keywords:** \textit{Escherichia coli}, aminoglycosides resistance, aminoglycoside phosphoryl transferases, 16SrRNA methylase
PB-117

Comparison of the frequency of Chlamydia pneumonia infection in IgG and IgM in children under 14 years old with and without pneumonia admitted in Tabriz Children's Hospital

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**Background:** Pneumonia is one of the acute and respiratory infections that occurs around 4.1 million deaths annually around the world, with 1.9 million of them being children under the age of 5 years. One of the important factors contributing to the disease is Chlamydia pneumonia. The aim of this study was to investigate and compare the frequency of Chlamydia Pneumonia IgG and IgM infection in children under 14 years old with and without pneumonia admitted in Tabriz Children's Hospital.

**Methods:** In this descriptive cross-sectional study, 186 children under the age of 14 years were included. Of these, 93 children with pneumonia and 93 healthy children were the controls. Antibody titers of Chlamydia pneumonia were determined by ELISA method. Statistical analysis was performed using SPSS 21 and t-test.

**Results:** In the control group, the mean IgG antibody was 11.7% and the mean IgM was 3.2%. In the group, the mean IgG antibody level was 30.2% and the mean IgM antibody was 6.4% positive. There is no significant correlation between IgG and IgM anti-chlamydia and pneumonia titers with age. There is a correlation between the two antibodies (P=0.025) and There is no correlation between sex and frequency of antibody G (P=0.47) But there is a correlation between the frequency of M antibodies and gender (P=0.013).
Conclusion: There is a significant correlation was found between IgM and IgA antibodies and there is a correlation between the frequency of IgM antibody and gender. But There is no significant correlation between gender and frequency of IgG Antibody and on the other hand no significant correlation between IgG and IgM anti-chlamydia and pneumonia titers with age. In the control group, a significant correlation was found between the population and the age of the population, so that there is a greater resistance against the disease in the female population in the low-age group.

Keywords: Pneumonia, Elisa test, IgG and IgM antibodies
Antibacterial activity of *Nigella sativa* ethanolic extract against two pathogenic bacteria

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**Background:** Medical herbs with anti-microbial activity have always been important in traditional medicine and might be useful in antibacterial activity against the many pathogenic bacteria cause serious infections. The aim of this study was to determine the antibacterial activity of ethanolic extract from *Nigella sativa* against 2 pathogenic bacteria in vitro.

**Methods:** At first the seed of *Nigella sativa* extracts were prepared by the ethanolic wetting extraction method in five different concentrations (400, 200, 100, 50, 25µg) and then its antibacterial activity against 2 standard strain bacteria (*Staphylococcus aureus* and *Salmonella typhimurium*) was tested for the determination of MIC (minimum inhibitory concentration) and inhibitory zone diameter (ZOI) using disk diffusion method and agar serial dilution assays. Also the antibacterial activity of 15 antibiotics such as chloramphenicol, trimethoprim, streptomycin, gentamicin, erythromycin, doxycycline, nalidixic acid, ampicillin, ciprofloxacin, kanamycin, cefixime, and methicillin was tested by the disk diffusion method.

**Results:** Statistical methods were using to analyze the data. The results demonstrated that the *Nigella sativa* ethanolic extracts been effective against the one of the 2 standard strain bacteria (*Staphylococcus aureus*) and no effective against *Salmonella typhimurium*. For *Staphylococcus aureus* the ethanolic extract of *Nigella sativa* was highly effective with 500 µg concentration and exhibited greater antibacterial activity than all of the selective antibiotics.
Conclusion: This study demonstrates that ethanolic extracts from the combination of the *Nigella sativa* constituents have excellent antibacterial activity against *the Staphylococcus aureus*. Further investigations will be necessary.

Keywords: *Staphylococcus aureus*, *Salmonella typhimurium*, Antibacterial activity, *Nigella sativa*, 
PB-119
Partial characterization of MDR Acinetobacter baumannii phage

Introduction: *Acinetobacter baumannii* is a major pathogen in the hospital, especially in ICU and the resistance to multiple drugs as a major contributor to hospital infection, makes its association with significant mortality, especially in Immunodeficient patients. Bacteriophages are viruses that attack bacteria and kill them that could be used for clinical treatment.

**Aim:** With the increased resistance of bacteria to most antibiotics, the treatment of bacterial infection become very difficult. The aim of the study is in evaluating the function of bacteriophage specificity of multi-drug resistant *Acinetobacter baumannii*, to be used as a useful method for treating of Acinetobacter Infections.

**Methods:** Cross-sectional study during the year 1395, 48 *Acinetobacter baumannii* was isolated from patients admitted to the ICU, First, *Acinetobacter baumannii* were identified by Phenotypic method and amplified with blaOXA-51 gene, Then, with a diffuse method according to the CLSI instruction antibiotic resistance pattern determined and separation of phage from water sources was done. After that, using the method presented by Huang et al, Phage optimal titer to reduce bacterial concentration, One-Step Growth Curve detected. Finally, the sensitivity of phages to different hosts, such as *P. aeruginosa, E. coli, K. pneumoniae* evaluated.

**Results:** In the bacterial resistance pattern, the highest resistance belongs to ciprofloxacin, Cefipime, Ceftazidime, Amikacin and Rifampin respectively. In optimal phage test, at dilution of $10^{-4}$ it produced the best effect on bacteria in 30 minutes. By dilution of phage and treating with bacteria, the growth curve was determined at a dilution of $10^{-3}$ and a duration of 40 minutes, as a result the bacterial titer decreased to the lowest amount. Phage sensitivity to different hosts performed by double layer agar method, the phage was treated with *P. aeruginosa, E. coli, K. pneumoniae* bacteria and after 24 hours’ incubation at 37°C, no Plaque created.

**Conclusion:** Due to the resistance of *Acinetobacter baumannii* to most antibiotics and the difficulty of treating its infections, phage therapies can be used as a therapeutic approach to deal with bacterial infections.

**Keyword:** *Acinetobacter baumannii, Bacteriophage, Phage Therapy, Antibiotic Resistance*
Antimicrobial Resistance Trends Of Klebsiella Pneumoniae, Isolated from urinary In AlZahra Hospital

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Background: Urinary tract infection (UTI) is the second prevalent infection in human. The second factor is among the gram-negative bacteria of Klebsiella pneumoniae. The drug resistance among Klebsiella Pneumoniae is increasing day by day; therefore, antibiotic senility test is necessary before prescribing antibiotics. The aim of this research was to determine the antibiotics resistance patterns of Klebsiella species isolated from urinary specimens AlZahra hospital in Tabriz of patients.

Methods: In this descriptive cross-sectional study, 172 isolates of Klebsiella pneumoniae isolated from urine specimens sent to Alzahra Hospital in Tabriz were identified by using culture methods in specific environments and biochemical tests. The antibiotic resistance pattern was determined using the Kirby-Bauer method (release of disk in Agar medium).

Results: Based on the results, the resistance of isolates is as follows: Nitrofurantoin 84.88%, Ceftriaxone 75.58%, co-trimoxazole 63.37%, Amikacin 45.93%, Chloramphenicol 37.20% ;Of the total isolates, 172 samples)98.25% (had multiple drug resistance.

Conclusion: These results indicate that multidrug-resistant (MDR) isolates of Klebsiella pneumoniae are rising, and fewer antibiotics may be useful for treating infections caused by these strains. Since, distribution of antibiotic resistance is variable in different regions and periods of time, periodic monitoring of antibiotic resistance is recommended to control the infection.
Keywords: Klebsiella Pneumoniae 1, Multidrug-resistant (MDR) 2, Antibiotic Resistance 3
PB-121

Prevalence of metallo-beta-lactamase enzyme and pattern of antibiotic resistance in Klebsiella pneumoniae isolated from AlZahra Hospital of Tabriz

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Background: Metallo Beta Lactamase enzymes have an important role in making the resistance against various antibiotic factors particularly beta-lactams and carbapenems. Today, the resistant Klebsiella pneumoniae to carbapenem is considered as one of the important hospital infections and have made many medical problems. This research aims at studying the frequency of the Metallo Beta Lactamase enzyme in the separated Klebsiella Pneumoniae species from the referring women urethral infection to AlZahra hospital of Tabriz city.

Methods: This study was conducted on 172 isolates of Klebsiella pneumoniae isolated from urine specimens in women referred to Alzahra Hospital in Tabriz. The Standard disk diffusion method (Kirby Bauer) was used to determine the antibiotic resistance model. Combined disk method (Imipenem-Imipenem + EDTA) was used to isolate the isolates of metallo-β-lactamase producer.

Results: Klebsiella Pneumoniae species have the maximum resistance against Ampicillin with 100% resistance and the minimum resistance to the Ciprofloxacin antibiotic with 33.13%. 117 (68.02%) isolates were resistant against imipenem and the obtained results from the combined disk (Imipenem-Imipenem + EDTA) showed that 34.30% of isolates produce Metallo Beta Lactamase.

Conclusion: results of this research showed that the metallobetalactamas productive enzymes in the Klebsiella Pneumoniae isolates are high in this research. The existence of such resistance can be a caution for the present medical protocol.

Keywords: Klebsiella Pneumoniae 1, Metallo Beta Lactamase 2, Antibiotic Resistance3
PB-122

Molecular Characterization of Vancomycin, Mupirocin and Antiseptic Resistant Staphylococcus Aureus Strains

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Background. *Staphylococcus aureus* is a common cause of nosocomial infections leading to a broad spectrum of diseases. Increasing antibiotic resistance among *S. aureus* strains, particularly methicillin-resistant *S. aureus* (MRSA), is a serious concern. In addition, the emergence of antiseptics resistance in MRSA helps the organism to persist and spread in healthcare environments easily. The aim of this study was to determine the molecular characteristics of vancomycin, mupirocin, and antiseptic resistant *S. aureus* strains.

Materials and Methods. This cross-sectional study was performed on a total of 120 MRSA isolates collected from two major hospitals in Shiraz, Iran. Minimum inhibitory concentrations (MICs) of vancomycin and mupirocin were determined by E-test method according to CLSI and Eucast guidelines. Presence of resistance genes was investigated by PCR method.

Results. Antibacterial susceptibility tests for MRSA isolates showed that three isolates (2.5%) were vancomycin-intermediate *S. aureus* (VISA), seven isolates (5.8%) were vancomycin-resistant *S. aureus* (VRSA), and 15 isolates (12.5%) were high-level mupirocin-resistant (MuH). None of the isolates had vancomycin resistance gene (*vanA*), but the frequency of mupirocin resistance gene was significant, and 55 (45.8%) isolates carried the *mupA* gene. Moreover, *norA*, *smr*
and *qacA/B* genes were detected in 110 (91.7%), 55 (45.8%) and 36 (30%) strains, respectively.

**Conclusion.** This study showed the existence of VISA and VRSA strains in our region, and we also found a high frequency of mupirocin and biocide resistance genes among them.

**Keywords:** MRSA, VRSA, Antiseptics, Antibiotic resistance, Mupirocin.
The role of chlamydia trachomatis in preterm delivery: A case control study

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Abstract

**Background:** Preterm delivery is an important topic in gynecology, obstetrics, and pediatric specialists. Preterm delivery is defined as regular uterus contractions every 5 to 8 minutes or less, lasting for 30 seconds, and associated with progressive changes in the cervix, which results in delivery after 22 weeks and before week 37 of gestation. The aim of this study is defining a more precise study on the role of Chlamydia Trachomatis (CT) infection in preterm delivery in women.

**Methods:** This is a case-control study. The present study was performed on 75 women that had preterm delivery as the Case group and 75 women with normal delivery as the Control group. Research tools were a questionnaire and performing PCR assay on cervical swab samples as well as an ELIZA test on the serum
sample of umbilical cord blood of placenta. The Fisher’s tests and T tests were used for comparing different qualitative variables between the two groups.

Results: In this study, the averages for the ages were 26.55±0.53 in the Control group and 26.76±0.56 in the Case group. The prevalence rate of CT in cervical swab samples of the Control group was 7 (9.33%) and it was 2 (2.67%) in the Case group. The prevalence of the IgM antibody CT in both groups was zero and the amount of IgG antibody CT in both groups was zero 1 (1.33%).

Conclusion: The results of the present work showed that there is not a significant relationship between CT infection and preterm delivery, P-Value (0.166).

Keywords: Chlamydia trachomatis, preterm delivery, Women, Iran
Emergence of oxacillinase-mediated resistance to carbapenem in Acinetobacter baumannii

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Introduction and Aims: Carbapenem is a selective antibiotic for the treatment of infections caused by Acinetobacter baumannii. The presence of the blaOXA genes in A. baumannii contributes to carbapenem resistance. The present study was aimed to determine the prevalence of blaOXA-type carbapenemases in clinical isolates of Acinetobacter baumannii.

Materials and Methods: This study was conducted on 65 clinical isolates of Acinetobacter baumannii. Antimicrobial susceptibility test was performed by disc diffusion agar method for ceftazidime, cefepime, piperacillin/tazobactam, ampicillin/sulbactam, imipenem, meropenem, gentamicin, tobramycin, ciprofloxacin, levofloxacin, tetracycline and minocycline. Minimum Inhibitory Concentration (MIC) of isolates were determined for the imipenem, meropenem, polymyxin B, colistin and tigecycline using standard microbroth dilution method. The frequency of the genes encoding oxacillinase, including OXA-143-like, OXA-23-like, OXA-58-like, OXA-24-like, OXA-51-like and OXA-235-like in carbapenem resistant Acinetobacter baumannii (CRAB) isolates were studied by PCR.

Results: Amplification of the ITS fragment of Acinetobacter baumannii isolates confirmed the genus and species of the bacteria. The resistance pattern of A. baumannii isolates for ceftazidime, cefepime, piperacillin-tazobactam, ampicillin-sulbactam, imipenem, meropenem, gentamicin, tobramycin, ciprofloxacin, levofloxacin, tetracycline and minocycline was 96.92%, 92.30%, 96.92%, 7.69%,
96.92%, 96.92%, 73.84%, 60%, 93.84%, 72.30%, 27.69%, and 0%, respectively. The resistance pattern to the seven different antibiotic classes in *A. baumannii* isolates showed that the prevalence rate of multidrug-resistant (MDR), extensively drug-resistant (XDR) and pandrug resistant (PDR) were 92.96%, 39.62%, and 0%, respectively. The minimum inhibitory concentration of the isolates showed that the resistance rate to the imipenem, meropenem, polymyxin B, colistin and tigecycline was 100%, 100%, 0%, 12.7% and 36.51%, respectively. The presence of genes encoding oxacillinase such as *bla*OXA-51-like, *bla*OXA-58-like, *bla*OXA-23-like, *bla*OXA-24-like, *bla*OXA-143-like, and *bla*OXA-235-like was 100%, 0%, 0%, 74.61%, 42/62%, 0%, and 0%, respectively.

**Conclusion:** The present study indicated that the frequency of multidrug-resistant (MDR) is high in clinical isolates of *Acinetobacter baumannii*. This is a serious warning for public health organizations and healthcare systems. These in vitro results show that the polymyxin B has a good antimicrobial activity on *Acinetobacter baumannii*.

**Key words:** carbapenem, MIC, antibiotic resistance, *Acinetobacter baumannii*, *bla*OXA
PB-125
The Role of Catecholamines in Increasing Microbial Infection

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The concept of endomicrobiology represents a combination of microbiology and neurobiology that links microbe and host interactions with the pathogenesis of infectious diseases. The term “neurohormone” is used to detect the secreted materials from neuroendocrine cells in the digestive tract. Each neurochemical plays multiple roles and can both have the role of a neurotransmitter and a neurohormone. Neurochemicals, which are associated with mammalian nervous systems, are scattered all over the nature. The family of catecholamines has been identified in insects, fish, vertebrates, plants, and microorganisms. The important issue is that microorganisms have the same neurochemicals found in vertebrates. There are wide ranges of neurochemicals and microorganisms producing them. These neurochemicals include acetylcholine, histamine, catecholamines, serotonin, and agmatine. The complete biosynthetic pathways of catecholamines in bacteria are similar to those of animals. In association with the host, the produced neurochemicals by the host affects the microorganism and those produced by the microorganism can affect the host. Also, the production of a neurochemical by a microbe may affect any neighboring microbial communities. This ability influences on the microbiota-gut-brain axis, which can have an impact on the host brain and behavior, besides increasing the pathogenicity of pathogens. Luminal epithelial chemical sensors respond to the transmitted information or transmit it in turn. The neuroactive compounds present in the luminal space can play an important role in the relation
between the intestine and the brain. Bacterial metabolites can affect mental health problems, such as depression. The intestine is a site where the association of stress and microbiota can lead to an interaction with the pathogenesis of infectious diseases. The sudden and high release of neurochemicals associated with physical and physiological stress is responsible for restructuring the microbial community in the intestine and the emergence of potential gram-negative pathogens. The rapid growth of pathogens in response to norepinephrine has been already documented. In conclusion, the release of catecholamines in the intestine may be a contributing factor to the injury-associated infections.

**Keywords:** catecholamine, microbiota, intestine, brain
PB-126

Early and Late Onset Ventilator Associated Pneumonia in intensive care unit patients.

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Introduction and objectives: Ventilator-associated pneumonia (VAP) is a common complication in patients using mechanical ventilation. If it occurs within 4 days or less, it is an early onset and within 5 days or more, referred to as late onset pneumonia. The objective of this study was to determine the prevalence and causative agents of early and late onset VAP in Intensive Care Unit (ICU).

Methods: In this descriptive study, the medical records of ICU of Khalij Fars Hospital, Bandar Abbas, from April 2013 to March 2017 were analyzed. All early and late VAP cases were evaluated according to microbial profile.

Results: Among 135 cases of VAP diagnosed, early onset was found in 62 (45.9%), while late-onset was in 73 (54.1%). VAP showed an increasing trend
in both early and late-onset groups, during the study period. The most common organisms in early-onset were *Staphylococcus aureus* 13(21%) that 2(9.5%) were MRSA and *Esherichia coli* 13(21%) that 5(38.5%) were ESBL. In late-onset *Pseudomonas aeruginosa* 17(23%) with 7(41.2%) ESBL and *Klebsiella pneumoniae* 16(22%) with 6(37.5%) ESBL were the most common isolates. Isolation of two organisms was 3(4.8%) in early-onset and 5(6.8%) in late-onset. Gram positive bacteria were more common in early-onset and gram negative in the late-onset, and this difference was statistically significant. (P=0.04).

**Conclusion:** Increasing antibiotic-resistant organisms during the study period indicated that more attention should be paid to controlling the nosocomial infections, especially in the intensive care unit.

**Key-Words:** Ventilator associated pneumonia, Early - Onset, Late -Onset, ICU
Detection of Extended Spectrum β Lactamases (ESBLs) in Urine Isolates of Klebsiella pneumoniae and Escherichia coli by phenotypic method

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Introduction and objectives: Multidrug-resistant Gram-negative bacteria, including ESBL –producing organisms in recent years have led to limitations of treatment options. The main objective of this study was phenotypic detection of beta-lactamases in Urine Isolates of E. coli and Klebsiella pneumoniae.

Material and Methods: A total of 2038 non-repetitive mid-stream urine samples of inpatients admitted to Khalij Fars Hospital (Bandar Abbas, Iran) were collected during March to August 2017. E. coli and K. pneumoniae were identified by API 20E system and Extended-spectrum beta-lactamase phenotypes were screened by
phenotypic confirmatory disc diffusion test. The data was analyzed by SPSS software.

**Results:**

Out of the 2038 urine samples processed for culture, 336 Gram-negative bacilli were isolated. The most common isolate was *E. Coli* 207 (85.5%), followed by *K. pneumoniae* 35 (14.5%). Of 242 isolates, 135 were ESBL positive (55.8%). 59% (122) of *E. coli* isolates and 36% (13) of *K. pneumoniae* were ESBL producers. ESBL producing *E. coli* showed maximum resistance to ceftazidime (92.9%) and ampicillin (77.6%), while minimum resistance was seen with imipenem (11.1%). ESBL producing *K. pneumoniae* showed maximum resistance to ampicillin (85.5%) and ceftazidime (66.7%) while minimum resistance was seen with imipenem (1%).

**Conclusion:** According to our findings, it is necessary to pay special attention to ESBL production in *E. coli* and *K. pneumoniae* and in order to monitor the development of antibiotic resistance, phenotypic confirmatory disc diffusion test which can be used in all clinical laboratories is recommended.
Key-Words: ESBL detection, E. coli, K. pneumoniae
Bi-directional Relationship between Periodontitis and Diabetes

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Background: The human mouth harbours one of the most diverse microbiomes in the human body. For many years an association between diabetes and periodontitis has been suspected and today many evidence support a higher incidence and severity of periodontitis in patients with diabetes mellitus. This relationship has been suggested to be bidirectional with each condition being able to influence the other. Recent research suggests that periodontitis may adversely affect glycaemic control, which can be improved by periodontal treatment with reduced risk of diabetic co-morbidity, thereby creating a two-way relationship. Furthermore it appears possible that periodontitis may stimulate inflammatory change in adipose tissue, creating a triangular self-generating cycle of morbidity linking diabetes and periodontal disease. Possible mechanisms of how diabetes affects periodontitis include adipokine-mediated inflammation, neutrophil dysfunction, uncoupling of bone and advanced glycation end products–receptor for advanced glycation end-products interaction. Chronic inflammation of periodontitis aggravates glycemic control in type 2 diabetic patients through aggravation of insulin resistance. Increased or decreased release of various inflammatory mediators, such as high sensitivity C reactive protein, tumor necrosis factor, interleukin 6 and adipokines, such as adiponectin, leptin, and resistin, are presumed to be responsible for developing and progressing insulin resistance. Some investigators have reported that periodontal treatment may enhance the metabolic control of diabetes.

Conclusion: Adipocyte production of proinflammatory cytokines is a pathogenic factor linking obesity to diabetes and periodontal infections. Treatment of
periodontitis is associated with HbA1c reductions of approximately. Oral and periodontal health should be promoted as integral components of diabetes management and treatment to help reduce the development of systemic disease.

**Keywords:** microbiome, diabetes, periodontal disease, insulin.
PB-129

The prevalence and antimicrobial susceptibility pattern of Shigella species isolated from hospitalized patients, Kermanshah with phenotypic and genotypic methods

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Background: Shigella species are the most important agent of diarrheal diseases that is known as shigellosis. In this study we investigated the prevalence of shigella species and their antimicrobial susceptibility pattern isolated from hospitalized patients in Kermanshah in 2017 with phenotypic and genotypic methods.

Methods: At first DNA is a diarrhea sample (Without blood) was extracted using a kit, and then strain Shigella was determined using a 16srRNA gene By the PCR method. The susceptibility of bacteria was ased using disk diffusion method. The results were analyzed with SPSS 16.

Results: Of the total 400 patients, 16 cases (4%) were diagnosed as Shigellosis By the PCR method for the 16srRNA gene. The highest rate of infections were seen in under 10 years old patients. Results of antimicrobial susceptibility testing showed that all of isolates were resistant to Cotrimoxazole and tetracycline. The lowest resistant rate of was against cefixime and ciprofloxacin.

Conclusion: The results of this study indicated a low prevalence rate of shigellosis and the other hand a high resistance rate of shigella species to some antibiotics. The physicians should pay special attention to prescribe appropriate antibiotics to treatment of this infections in order to reducing of their mortality.

Keywords: shigella, shigellosis, disk diffusion method, PCR.
PB-132

Antibiotic resistance and biofilm formation of *Pseudomonas aeruginosa* strains isolated from clinical samples in Kerman, Iran.

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**Background:** *P. aeruginosa* strains are common pathogens in hospitals as they have ubiquitous nature, ability to survive in moist environments and innate resistance to many antibiotics. The aim of this study was the survey of biofilm formation and drug resistance of *Pseudomonas aeruginosa* strains.

**Methods:** A total 15 isolates of *Pseudomonas aeruginosa* were isolated during April to June 2018 from different clinical samples obtained from hospitals in Kerman. All isolates were identified on the basis of their cultural, morphological and biochemical characters and antibiogram was evaluated by Kirby-Bauer’s disk diffusion method as well as MIC against common antibiotics by CLSI2016 guide line. Cell surface hydrophobicity (CSH) test and biofilm formation on glass and polypropylene surfaces in shaking and static states were also performed.

**Results:**

20 strains of *P.aeruginosa* were identified by characteristics as oxidase-positive, motile bacteria with production of a blue, red or brown pigment on King’s medium. They were resistant to tetracycline (95%), Chloramphenicol (80%), Imipenem (75%), ceftizoxime (65%), norfloxacin (30%), and Gentamycin (15%). MICs were observed in different values. Maximum cell surface hydrophobicity was 81% about *P.aeruginosa* IAUK8717 was reported with maximum biofilm formation in shack and static states on glass and polypropylene.

**Conclusion:** Antibacterial surveillance should be performed periodically to monitor the present resistance patterns of *P. aeruginosa* in different parts of local hospitals such as ICU. Finding accurate information about multidrug resistant
strains of \textit{P. aeruginosa} will allow us for better programming in resistance interruption in the future.

\textbf{Keywords:} \textit{Pseudomonas aeruginosa}, biofilm, Gentamycin.
Detection of introtoxin and tsst-1 genes among staphylococcus aureus isolates collected from Alzahra Hospital-Isfahan-Iran

**Background and Aim:** Methicillin resistant staphylococcus aureus (MRSA) is one of the most important etiological agents of hospital and community acquired infections and is associated with a range of diseases including: endocarditis, food poisoning, septic shock syndrome and septisemia. The entrotoxins and toxin shock syndrome toxin (TSST-1) are among the most common virulent determinants of this bacterium. They are also well known for their super-antigenic properties. The incidence of entrotoxine producing strains is also very alarming. The aim of this investigation was to survey the prevalence of entrotoxin gene in clinical isolates of S. aureus recovered from hospitalized patients in Alzahra hospital of Isfahan, Iran.

**Methods:** During one year period, 100 S. aureus specimens obtained from Alzahra and shariati patients were investigated. The isolates were identified by routine bacteriological methes including catalase, coagolase, manitol and DNase was performed. The samples were then subjected to susceptibility tests using agar screening and disk diffution method. Following genomic DNA extraction, the presence of entrotoxine gene was analyzed by mPCR.

**Results:** A total 100 S. aureus isolates were recovered. MRSA samples was 56% of isolates. Of the strains tested, 32% of the isolates contained sea, 4% seb, 28% contained sec and 60% tsst-1.

**Conclusions:** The high prevalence of entrotoxin gene in studied S. aureus strains and their circulation in the community can have a potentially alarming effect on general health of community.

**Keywords:** Methicillin Resistant Staphylococcus aureus (MRSA), mPCR, entrotoxines, TSST-1
PB-134

Antibiotic resistance and biofilm formation of *Pseudomonas aeruginosa* strains isolated from clinical samples in Kerman, Iran.

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**Background:** *P. aeruginosa* strains are common pathogens in hospitals as they have ubiquitous nature, ability to survive in moist environments and innate resistance to many antibiotics. The aim of this study was the survey of biofilm formation and drug resistance of *Pseudomonas aeruginosa* strains.

**Methods:** A total 15 isolates of *Pseudomonas aeroginosa* were isolated during April to June 2018 from different clinical samples obtained from hospitals in Kerman. All isolates were identified on the basis of their cultural, morphological and biochemical characters and antibiogram was evaluated by Kirby-Bauer’s disk diffusion method as well as MIC against common antibiotics by CLSI2016 guideline. Cell surface hydrophobicity (CSH) test and biofilm formation on glass and polypropylene surfaces in shaking and static states were also performed.

**Results:**

20 strains of *P. aeruginosa* were identified by characteristics as oxidase-positive, motile bacteria with production of a blue, red or brown pigment on King’s medium. They were resistant to tetracycline (95%), Chloramphenicol (80%), Imipenem (75%), ceftizoxime (65%), norfloxacin (30%), and Gentamycin (15%). MICs were observed in different values. Maximum cell surface hydrophobicity was 81% about *P. aeruginosa* IAUK8717 was reported with maximum biofilm formation in shack and static states on glass and polypropylene.

**Conclusion:** Antibacterial surveillance should be performed periodically to monitor the present resistance patterns of *P. aeruginosa* in different parts of local hospitals such as ICU. Finding accurate information about multidrug resistant strains of *P. aeruginosa* will allow us for better programming in resistance interruption in the future.
Keywords: *Pseudomonas aeruginosa*, biofilm, Gentamycin.
Probiotics, New treatment for Multiple sclerosis

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Background:

Multiple sclerosis (MS) is an autoimmune disease that destroys myelin. There is no effective therapy for the infection, although disease modifying therapies are being used for the management of disease. Gut microbiome plays an important role in autoimmunity, and several studies have reported alterations in the gut microbiome of MS patients. Probiotics represent an oral, nontoxic immunomodulator agent that could be used in combination with current MS therapy. Types of probiotics in treatment of MS including: Lactobacillus strains, L. paracasei DSM 13434, L. plantarum DSM 15312, L.murines CNRZ, strains of L.casei and Lactobacillus rhamnosus GG. Recent studies demonstrated the anti inflammatory effects of certain lactobacilli via NOD2 mediated signaling. Probiotic effects on the innate immune responsive pathways including toll-like receptor (TLR), nuclear factor kappa B (NF-κB), mitogen-activated protein kinase (MAPK), c-Jun NH2 terminal Kinase (JNK) has been extensively investigated.

Methods:

We considered to include all the articles retrieved from PubMed, Google scholar search with the keywords “Multiple sclerosis”, “probiotic” and “gut microbiota”. The results were filtered by limiting the search to English manuscripts published within the last 5 years that discussed studies of mammalian subjects.
Result:

Probiotics prevent the progression of inflammation in Multiple sclerosis patients with suppression pathways signaling which contribute to cytokine production and inflammation. Probiotic administration induced an anti-inflammatory peripheral immune response characterized by decreased frequency of inflammatory monocytes, decreased mean fluorescence intensity (MFI) of CD80 on classical monocytes, as well as decreased human leukocyte antigen (HLA) D related MFI on dendritic cells.

Conclusion:

In our opinion, the immunomodulatory properties of several probiotics and bacteria-associated molecules should be used to develop treatments that complement currently available therapeutic choices for MS patients.

Keywords: “Multiple sclerosis”, “probiotic”, “gut microbiota”
PB-136

The frequency and antibiotic resistance of hospital acquired pneumonia (HAP) in a clinic in Iran

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Background: The term hospital acquired pneumonia (HAP) was defined as pneumonia in hospitalized patients who administered more than 24 hours. These patients were believed to be at an increased risk for infection with multidrug-resistant (MDR) pathogens. Patients who would have met the criteria for HAP should not be empirically treated with antibiotics. The purpose of our study was to report the frequency and antibiotic resistance of hospital acquired pneumonia (HAP) in a clinic in Iran.

Methods: A total of 265 sputum samples were collected from a clinic in Iran during 2017 till 2018. Biochemical tests were done for diagnosis of the bacteria. The pattern of antibiotic resistance was defined by disk diffusion tests according to CLSI methods.

Results: The most common gram positive cocci was S.aureus which showed the high resistance to Erythromycin, co-trimoxazole were documented. The most common gram negative bacilli were Acinetobacter spp. followed by Pseudomonas aeruginosa and klebsiella pneumonia. Among the Acinetobacter spp. the resistance rate for ciprofloxacin, ceftriaxone was 83%, 73% and 65% respectively.
Conclusion: In this study the rate of antibiotic resistance among *Acinetobacter* spp, the most prevalent pathogen, showed that management of antibiotic policy is required to prevent the resistance development. Also regions surveillance studies in Iran will be helpful to deciding out the correct empirical treatment and will help to control infections.

Keywords: Hospital acquired pneumonia, Antibiotic Resistance, Iran
PB-137

The frequency and antibiotic susceptibility of pathogens associated with nosocomial UTI in a clinic in Iran

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Background: Nosocomial urinary tract infections (UTI) are a common obstacle in hospitals in the world. Resistance of urinary bacteria to common antibiotics is a topic of complication. This study was focused about the frequency and antibiotic susceptibility of pathogens associated with nosocomial UTI in a clinic in Iran.

Methods: A total of 508 specimen were collected from a teaching hospital in Iran during 2017 till 2018. The biochemical tests were done for diagnosis of the bacteria. The pattern of antibiotic resistance was defined by disk diffusion test according to CLSI methods.

Results: The most common pathogen isolated from urine culture were Escherichia coli, Klebsiella pneumonia and Proteus mirabilis which together made up 70.3% of all organism. The rate of Imipenem (95%), Amikacin (92%) and piperacillin/tazobactam (85%) susceptibility showed that these antimicrobial agents were most consistently
active in vitro against this gram negative bacilli. The high resistance was observed to Ciprofloxacin and Co-trimoxazole in *E.coli* isolates.

**Conclusion:** According to the results of the previous reports the rate of resistance in nosocomial infections is more than community acquired infections. In this study the rate of antibiotic resistance among isolated pathogen indicated that infections cause by resistance microorganisms are an emerging problem in the patients. This result showed the importance of antimicrobial testing for effective treatment of UTI.

**Keywords:** Nosocomial UTI, Antibiotic, Iran
Study the association of *Mycobacterium avium* subspecies *paratuberculosis* and autoimmune disease

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**Background:** *Mycobacterium avium* subspecies *paratuberculosis* (MAP) is an obligatory intracellular organism that can be detected using acid fast stain but it can be difficult to isolate from the human body due to changes in the bacterial cell wall. Since the bacterium is resistant to chlorination and pasteurization and environmental stress, it can transmit various routes of water, food to humans. There are some studies indicated the association of this bacterium with autoimmune diseases, such as Type I diabetes mellitus, Hashimoto Multiple Sclerosis and Rheumatoid Arthritis. The aim of this study was to review the association of *Mycobacterium avium* subspecies *paratuberculosis* and autoimmune disease.

**Method:** We reviewed thereports that determined the association of MAP with various autoimmune diseases by ELISA method from 2005 to 2017 in the world.
Result: The prevalence of MAP antibodies in type 1 diabetic patients were 30.8% to 70.37% and in control subjects were 37.5% to 37.6%. In patients with multiple sclerosis MAP antibodies detected from 23% to 26% and in the control group were 2% to 6.5%. MAP antibodies reported in 20.35% to 48% of Hashimoto's thyroiditis patients and in 5% to 7.43% of the control subjects. In the patients with inflammatory bowel disease MAP antibodies were 29% to 64% and in control subjects were 5% to 20%.

Conclusion: Autoimmune diseases are multifactorial disease which genetic and environmental factors such as microorganisms are involved in the development of these disorders. The antibodies produced against MAP antigens through the mechanism of molecular mimicry affects the body and causes inflammation in the target organ. Given the high prevalence of bacteria and the increasing trend of autoimmune diseases in the recent years suggested the importance of applying more studies about this issue.

keywords: Mycobacterium avium subspp paratuberculosis, autoimmune, ELISA
PB-140

Study and analysis of herbal ointments against wound infection

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Background:
The location of deep and surface burns is a protein-rich site and containing necrotic tissue, which is provides a special place for colonization of microbes and their reproduction, and some bacteria have the ability to form biofilms, as well as the ability to spread in burn infections. On the other hand, due to drug resistance genes, it is difficult to treat these bacteria and it threatens the death of these patients. So we decided to have a review of previous studies in this field. (1)

Material and Method:
The searching process was conducted for herbal ointment that were published by the end of 2017 using Web of Science, PubMed, Scopus, MEDLINE, Cochrane Library, Science Direct, Google Scholar, and the Scientific Information Database. The original articles published in English were included in our research. The keywords such as ointment, herbal ointment, burn and burn infection were used for searching process.

Result:
In this research we considered about 7 ointment. This ointments were prepared herbal extract such as Eucalyptus globus, Ziziphus spina, Aegle marmelos, Acalypha wilkesiana, Peperomia pellucida, Cymbopogon citrate, Azadirachta indica, Chromolaena odorata, Samadera indica, Mimosa pudica, Peperomia
pellucida and Cymbopogon citrate. These ointments can inhibited gram positive and gram negative bacteria and had different potential in wound.

**Conclusion:**
One of the ointment that was prepared with Alcoholic extract of Acalypha wilkesiana can be used as an ointment that can inhibit some gram positive and gram negative bacteria and, on the other hand, has the ability to inhibit growth and it has suitable inhibition zone of growth. (2)

**Keyword:**
Herbal ointment, resistance, wound infection
PB-141

ZOUSH Lotions Associated to Antibiotic for Treatment of Wounds

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Background

*Pseudomonas aeruginosa* is a cross opportunistic pathogen. It is also one of the priorities of treatment in military medicine due to the formation of blue pus in War Woundsoldiers. Therefore, the aim of this study is to formulate a natural ointment to control the infection of burn and war wounds.

Material and methods

Natural ZOUSH lotions was formulated with natural ingredients including *Satureja khuzestaniea, Zataria multiflora, Mentha Mozaffariani Jamzad*, Honey, and Polyurethane. Burn wounds were induced by Ian Allen Holder, and treatment
was continued twice a day for 20 days. Real Time-RT PCR was used to investigate the expression of Pseudomonas aeruginosa virulence genes.

Result
The results showed that the antibacterial effects of ZOUSH lotions can compared with Gentamycine 30 μg, and Polymyxin B 300 u. Furthermore, the In vitro results indicated that wound infection reducing the number of P. aeruginosa in the culture of the liver and ZOUSH lotions has the ability to improve wound infections in 10 days and has the ability to control infection in 20 days. ZOUSH lotions also reduces the expression of Pseudomonas aeruginosa virulence genes.

Conclusion
Thus, due to the effectiveness of ZOUSH lotions on the virulence genes of Pseudomonas aeruginosa, this lotions is recommended for the treatment of burn and war wounds.

Keywords
ZOUSH, Pseudomonas aeruginosa, Real Time-RT PCR, Infection, War Wound, Burn Wound, lotions
PB-142

Relationship between Antibiotic Resistance with Spa Gene Polymorphism Coding Protein A and its typing with PCR-RFLP Technique in S. aureus Isolated from Foodstuffs

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Background: Staphylococcus aureus is an important cause of hospital and community acquired infections. Food borne diseases are an important problem in public health. Protein A is a protein 42 KDa, which is expressed in all strains of this bacterium. Objectives: This study aimed to evaluate the relationship between antibiotic resistances with spa gene polymorphism.

Methods: A total of 1,050 food samples were collected during 8 months in Hamedan, Iran. Food samples were evaluated for the presence of spa genes of S. aureus. The antibiotic susceptibility testing was performed using disk diffusion agar. After extraction of genomic DNA, nuc and spa genes were detected. Finally, with the PCR-RFLP method, spa typing was performed. The relationship between the antibiotic resistance rate and Spa types were analyzed by the SPSS software.

Results: Results showed that the 98 cases (9.33%) of S. aureus were isolated. The most frequent resistance was observed against tetracycline (8.41%). Spa gene was reported in all isolates and 4 different patterns of spa gene was seen. Furthermore, a significant correlation between different strains isolated from diverse foodstuffs and different patterns of spa (P < 0.05) was also found. In addition, the relationship between resistance to different antibiotics with obtained types showed
that there is a significant correlation between resistance to erythromycin (P = 0.014) and clindamycin (P = 0.016) with different spa types.

**Conclusion:** In regards to the increased resistance to antibiotics in strains isolated from foodstuffs, rapid and accurate typing of S. aureus to identify transmission of the infectious organisms is very important. Molecular typing of Spa protein can prevent epidemics and reduce the infections and costs of nosocomial infections.

**Keywords:** S. aureus, Antibiotic Resistance, spa Gene
PB-143

Investigating the microflora of Iranian traditional sourdough

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Background

Sourdough is a combination of flour, water and other additives (such as NaCl), which is fermented by a heterogeneous population of microorganisms including yeast and Lactic acid bacteria (LAB). Due to the nature and essence of substrate, fermentation of traditional sourdough is done under non-sterile conditions. Flour and other additives to the dough are not microbiologically standard and are not thermally treated before consumption. Therefore, when water and flour are mixed, existing microorganisms in flour and the environment begin to grow. Sourdough has a high variety of microorganisms. Microbiological ecology of sourdough is based on exogenous and endogenous factors. Endogenous factors include chemical and microbial composition of dough and exogenous factors include temperature, water activity, and additive salt, potential for recovery, temperature and duration of fermentation.

According to the differences in the technology of sourdough production, sourdough is divided into three types:

Type 1: this type of sourdough is produced with traditional methods and its property is being consecutive and daily refreshment, which makes
microorganisms to be kept in an active metabolic mode. Production of this type of sourdough is performed in 20 to 30 degrees centigrade (maximum 30 degrees centigrade) room temperature and its final pH is 4.

Type 2: this type is essentially used as the acetifier for sourdough. Fermentation lasts 2 to 5 days and is carried out at a temperature above 30 degrees centigrade. Microorganisms of this type of sourdough have a limited metabolic activity.

Type 3: sourdough has a powder form that is fermented by certain starter culture medium. This type of sourdough is used as an acetifier and aromatic material carrier during bread fermentation. In comparison with type 1, type 2 and 3 need to add bread yeast (Saccharomyces cerevisiae) in order to ferment. It is obvious that any type of fermentation nurtures its own microflora. Many efforts have been done in order to isolation and identification of microorganisms in sourdough. More than 50 LAB types have been identified in sourdough, most of them belong to Lactobacillus genus. These species contribute essentially to acidify the dough. 23 different types of yeast have been identified, Saccharomyces cerevisiae, Saccharomyces exiguis, Candida krusei, Candida milleri, Pichia norvegensis, Pichia anomala, Torulaspora delbrueckii are dominant species existing in most of sourdoughs.

Tafton refers to bread with 3mm thickness, which is made by low fermented doughs. Its ingredients are flour, water, salt NaCl and sourdough, which is the fermentation factor. The sourdough used for this bread is type 1 dough, whose prominent feature is being consecutive and having daily refreshment. The aim of this survey is to investigate the microflora of sourdough in traditional Tafton bread and to describe the chemical properties of sourdough. Finally, we hope that by isolating proper strains, they can be used to provide proper starters for bread.

Materials and methods

Data collection:

Sourdough sample was collected from the industrial unit of NanAvaran in Tehran. In this unit, sourdough is prepared traditionally, in this way 1/3 of prepared dough for baking Tafton bread is placed at room temperature for 16 to 20 hours to be
fermented. This fermentation is used to prepare the next dough and this process is repeated continuously.

**pH** determination and **TTA**:

**pH** sample and final titratable acidity are measured by 02-52 and 02-31 methods, respectively(1). 10g of sourdough were added to 90ml of distilled water. The solution mentioned above was mixed by glass stirrer for 10 minutes, until a homogeneous solution was provided. **pH** solution was measured by **pH** meter model (Digital pH METER MTT65). This suspension was titrated with NaOH, normal 0/1 and by using 1g/100ml phenol phethalin reagent. Final titratable acidity was estimated via normal 0/1 NaOH used for the titration of this suspension.

Determination of both indexes (**pH** and **TTA**) was performed twice and their average was recorded as the final value.

**Enumeration and isolation of LAB and yeast:**

10g sourdough in 90ml dilution NaCl, 0/85g/100ml for providing suspension was diluted uniformly and 10 times serial dilutions were prepared in NaCl dilution, 0.85g/100ml.

In order to **LAB** count, for each serial dilution, 100ml of suspension was poured into sterile plate containing 20ml of melt isolation medium, (MRS agar), Rogosa and sharpe agar, De man (pour plate method) and were incubated at 30 degrees centigrade for 72 hours. The total number of colonies was counted as **Lactic acid bacteria** and the average of two plates was reported for each dilution. Pure cultivation of each selected colony with linear culture method was obtained on MRS agar medium. The isolated strains were kept in MRS broth, as stock sample, at -70 degrees centigrade.

In order to check yeasts, 100μl of each dilution in Agar medium, Dichloran Glycerin(DG) was surface cultivated and incubated in 25 degrees centigrade for 3 days. Cell morphology and appearance of colonies were observed and the number of colonies was counted and average of both plates was reported for each dilution. Pure cultivation of each colony was obtained with linear culture method on
Sabouraud Dextrose Agar (SDA) medium. For performing next steps (identifying yeasts), the isolated strains were kept in slant containing SDA and at 4 degrees centigrade.

**Results and Conclusion**

Chemical properties of traditional sourdough:

The average pH of sourdough was **3.24** and its average final titratable acidity was **23.8ml** via normal **0.1 NaOH** on **10g** sourdough.

LAB count and yeast:

The total number of LAB colonies in sourdough was **1.8×10^6 cfu/gr**, while the total number of yeasts was much lower and approximately **5.6×10^2 cfu/gr**. In general, **18 LAB** strains and **25** yeast strains were isolated from this sample.

**Discussion**

The experiments of LAB and yeast strains obtained from sourdough of traditional Tafton from the industrial unit of NanAvaran, shows that LAB number was **10^6** colonies, while the number of yeasts reaches to **100** colonies. Although this sample was too small for generalizing, further systematic studies are needed.

In a research, while checking **25** types of sourdough, LAB number was reported to be **log7.5-log9.3cfu/gr** and the yeast number was reported to be **log5.5-log8.4 colonies**(2). Moreover, in another report, the LAB number was **10^9-3×10^9cfu/gr** and the yeast number was **10^6-5×10^7cfu/gr**(4). In fact, cell density more than **10^8** colonies in each gram of sourdough are usual(3). In addition, the ratio of yeast/LAB in sourdough varies between **1:1000** to **1:10**, while this ratio is **1:10^4** in traditional sourdough in Iran. So, the density of microorganism in Iranian traditional sourdough is less than the sourdough of European breads, which is the difference of these two types of sourdoughs.

Since the traditional sourdough is prepared under non-sterile conditions, these kinds of differences are usual and different sourdoughs are various in terms of the number and variety of microorganisms.
The pH of sourdough was about **3.24**. It is reported that the pH in wheat sourdough was stated as **3.5-4.3** and this amount depends on the nature of sourdough and its preparation method (1).
Differentiation of methicillin resistant *Staphylococcus aureus* (MRSA) from methicillin resistant coagulase negative *Staphylococci* (MRCoNS) among staphylococci isolates from Shiraz teaching Hospitals

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ABSTRACT

**Background:** Globally nosocomial infection is a major problem. Prevalence and antibiotic resistance of methicillin-resistant *Staphylococcus aureus* (MRSA) strains is reported to be increasing globally. MRSA and methicillin resistant coagulase negative staphylococci (MRCoNS) are the important agents causing nosocomial infections.

**Materials and Methods:** This cross-sectional study was performed on a total of 221 staphylococcus isolates obtained from clinical specimens during 2016-2017 from two major hospitals of Shiraz, southwest of Iran. Antibiotic susceptibility profile was determined by the disk diffusion method according to CLSI guidelines. Bacterial DNA was extracted by using boiling and used as PCR templates for detection of *mecA*, *femA* and *pvl* gene.

**Results:** Phenotypical tests showed that among 221 collected isolates, 168 (73%) were *Staphylococcus aureus* and 53 (24%) were coagulase negative staphylococci (CoNS). Among *S. aureus* isolates, 70 isolates determined as MRSA and of CoNS isolates, 26 isolates (53%) were methicillin resistant (MRCoNS). Among whole isolates 96 (43.4%) were positive for *mecA* gene, 168 isolates for *femA* gene and among *S. aureus* isolates only six isolates had *pvl* gene. Antibiotic resistance pattern for MRCoNS isolates showed that resistance to erythromycin was (70%), gentamicin (69.2%) and chloramphenicol (65%) were the most and
for MRSA isolates resistance to chloramphenicol (82.8%), gentamicin (68.5%) and tobramycin (64.2%).

**Conclusion:** frequency of CoNS isolates especially MRCoNS isolates in this region is increasing significantly so it is necessary to pay more attention to these pathogenic agents.

**Keywords:** MRSA, MRCoNS, Antibiotic susceptibility
PB-145

Molecular identification of *Mycobacterium tuberculosis* complex and drug resistance ratio to Isoniazid and Rifampin in Shiraz reference laboratory of Tuberculosis 2017-2018


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Introduction and Objectives: *Mycobacterium tuberculosis* complex (MTBC) are causative agents of human tuberculosis. Rapid detection of MTBC has important public health and therapeutic implication. Resistance to Isoniazid and Rifamicin is the main problem for successful therapy and has been associated with mutations in genes katG and inhA for Isoniazid resistant and rpoB in Rifampicin resistance cases.

Material and Methods: 420 tuberculosis suspected samples from Fars and southern provinces collected for DNA extraction During years 2017 and 2018. PCR of IS6110 performed for identification of MTBC. Afterward multiplex PCR by using the primers of inhA, katG, rpoB genes performed for evaluation of Isoniazid and Rifampicin resistance.

Results: Of 420 specimens, 121 were MTBC by PCR. 89 cases were subjected to molecular drug resistance tests which 8 (9%) cases were resistant to isoniazid and Rifampicin (MDR-TB), 18 (20%) and 7 (8%) were monoresistant to Isoniazid and Rifampicin respectively. 56 (63%) cases considered as sensitive.

Conclusion: PCR is rapid and promising approach for identifying of MTBC and analyzing of drug resistance to decrease MDR-TB.
Key-words: MTBC, Drug resistant, MDR_TB, PCR, Mutation,
Evaluation of drug resistant *Tuberculosis* cases by conventional method in Reference laboratory of *Mycobacterium* Shiraz, Iran, 2017-2018

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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 drug resistant cases in Shiraz Reference TB laboratory.

Materials & Methods: During the study 126 drug resistant suspected cases from southern provinces of Iran were subjected to Drug Sensitivity Test (DST) by proportional method in Lowenstein- Jensen media. Results were checked after 28 and 42 days.

Results: Among 126 cases 76 cases were sensitive to Isoniazid, Rifampicin, Ethambutol. 34 cases recognized as Atypical mycobacterium through biochemical and molecular tests. 9 cases were MDR, 2 cases were monoresistant to Rifampicin, 4 cases were monoresistant to isoniazid, 1 case was resistant to Isoniazid and Ethambutol.

Conclusion: Ratio of laboratory proven multidrug resistance in *tuberculosis* patients was 7.1% and monoresistant to Rifampin and Isoniazid was 1.6% and 3.1% respectively. Resistance to Isoniazid and Ethambutol was 0.8%.

Keywords: Multidrug – resistant TB, Drug sensitivity test, proportional methods
Effect of the aqueous extract cichorium root on sperm parameters and testicular tissue and testosterone after exposing with diazinon in mice

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organophosphorus insecticides (OPIs), such as diazinon (DIA) have dangerous effects on living organisms. Upon entering the body, DIA converts to diazoxon which inhibits acetylcholinesterase function. In traditional medicine, plants such as the Compositae family (Asteraceae) including chicory, have been mentioned to have anti-toxic effects. Chicory can be used to treat indigestion, heartburn and toxic liver. This study aims to investigate the effects of preventive therapy with chicory root concentrate on DIA-induced toxicity in sperm parameters of mice.

Materials and methods:

Mice were randomly divided into 5 groups.

Group 1: control: distilled water by gavage.

Group 2: chicory concentrate: 100 mg/kg chicory by gavage.

Group 3: DIA: 30 mg/kg diazinon by Intra Protaneal injection.

Group 4: 30 mg/kg DIA + 100 mg/kg chicory.

Group 5: 30 mg/kg DIA + 200 mg/kg chicory.

In groups treated with both chicory and DIA, chicory was administered 20 minutes before diazinon.

Animals were sacrificed under deep anesthesia and then Vas deferens and left Epididymis tail were extracted.

Results
Diazinon caused a decrease in reproductive parameters. Chicory root concentrate caused a decrease in this toxicity (p<%05).

Conclusion

Chicory root concentrate can probably be useful in decreasing diazinon effects on the reproductive system and the chicory’s protective effect decreases as its dose increases.

Keywords: Diazinon, Chicory root concentrate, Sperm parameters.
Determination of heavy metals (Cu and Zn) concentration in the tissues of *Clupeonella cultriventris* and *Gasterosteus aculeatus* collected from Babolsar coastal waters of Mazandaran Province, Caspian Sea

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**Background:** The heavy metals are the results of industrial, urban and agricultural sewages. They are usually resistant to chemical dissociation. They can easily contaminate aquatic animals especially fishes which are one of the food chains of humans. The aim of this study was to evaluate the concentration of heavy metals in the tissues of different types of *Clupeonella cultriventris* and *Gasterosteus aculeatus* in the Caspian Sea waters of Mazandaran Province.

**Methods:** This cross-sectional-descriptive study was performed on 50 *Clupeonella cultriventris* and 50 *Gasterosteus aculeatus* fishes obtained from Mazandaran coastal by multi mesh gill nets in 2012. In this study, the (Cu and Zn) heavy metals concentration in the liver, intestine, muscle and skin tissues of fishes.
were measured and compared. The samples were digested by concentrated 65% nitric acid, and then were analyzed for zn and cu in a flame atomic absorption spectrophotometer.

**Results:** Mean concentration of Cu and Zn in *Gasterosteus aculeatus* was 0.161 and 2/036 and Mean concentration of Cu and Zn in *Clupeonella cultriventris* was 0/932 and 1/393 (μg/g dry weight), respectively. The results showed no significant correlation between these metals concentrations with sexes and different kind of fish tissues.

**Conclusion:** The results of this investigation showed that the concentration of heavy metals including Cu and Zn in both types of the fishes were less than the amounts reported by WHO and so there is any risk for health. Also we suggest that these fishes could be considered as bioindicator for assessment the sea water and rivers pollutions.

**Keywords:** *Clupeonella cultriventris* fish, *Gasterosteus aculeatus* fish, Heavy metals, Bioindicator, Caspian Sea
New approaches about control of the American cockroaches, *Periplaneta americana*, (Blattaria) in sewers: a systematic review

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Abstract

**Background:** The American cockroach, *Periplaneta americana*, is the most important invasive urban pest of sewer environments colonizing there with high significance of human public health and household allergens need to be controlled. Therefore this practical approach systematic review perform internationally to highlight and provide a detailed *P. americana* control in sewers.

**Methods:** Of the 474 papers, 129 papers were selected to become this practical approach systematic review study of cockroach control in sewers.

**Results:** To control the American cockroaches, many studies have been conducted in various fields describing from an angle. The results were classified and discussed in getting cockroaches from sewers into buildings and their elimination, insecticide susceptibility, application of dust, bait and Inesfly paint insecticide formulations, biocontrol and futuristic action categories. A recommending manner to achieve a successful *P. americana* cockroach control in
sewers is using a combination of IPM (Integrated Pest Management) strategies resulted in significant reductions of cockroach infestations and asthma health outcomes.

**Conclusion:** Use of *P. americana* breeding thelytoky, push-pull strategies and an automated sewer robot, and integrating health into the future buildings, may be new approaches of *P. americana* control strategies.

**Keywords:** New approach, *Periplaneta americana*, American cockroach, sewer cockroach control
The effects of resveratrol in cirrhotic rats with hepatopulmonary syndrome

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Background: Hepatopulmonary syndrome (HPS) is a serious complication of chronic liver disease characterized by arterial oxygen desaturation and abnormal alveolar-arterial oxygen gradient. Rats with bile duct ligation (BDL) are widely used as an animal model of cirrhosis. These rats also develop intapulmonary vasodilation and hypoxemia, and thus are recognized as a model of human HPS. Several studies have shown that resveratrol have anti-inflammatory and antioxidant effects. The objective of the study was to examine the effects of resveratrol against hepatopulmonary syndrome induced by BDL in rats.

Methods: Four groups of male Sprague-Dawley rats including Sham, a BDL group receiving vehicle, and two BDL groups receiving resveratrol (10, 20 mg/kg/day) were used. Arterial blood gas analysis was studied 4 weeks after sham or BDL operation and samples were collected from the abdominal aorta. The alveolar-arterial oxygen gradient (AaDO2) was calculated as 150-(PaCO2/0.8)-PaO2.

Results: Compared with sham-operated rats, BDL rats had lower partial pressure of oxygen (PaO2) and higher AaPO2. Treatment with resveratrol (20 mg/kg/day) significantly reduced the AaPO2 in BDL rats compared to the vehicle group. The PaO2 significantly increased after resveratrol treatment in BDL rats. There was no significant difference in PCO2 and PH levels between groups.
Conclusion: Administration of resveratrol ameliorated gas exchange abnormalities in cirrhotic rats with hepatopulmonary syndrome

Keywords: Hepatopulmonary syndrome, Bile duct ligation, Resveratrol, Rat
The effects of chronic exposure to contaminated air on blood lead level and 8-Hydroxy-2-Deoxy-Guanosine biomarker (8-OHdG) in Tehran traffic police officers and its effect on hematological factors in 2018

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Background: Concerns about the harmful effects of lead and other heavy metals and toxic substances released from cars exhaust and their effects on human health are increasing.

The aim of this study was to determine the level of lead and one biomarker of DNA damage called 8-hydroxy-2-deoxy-guanosine (8-OHdG) and its effects on hematopoietic system of Tehran traffic police officers between two groups of outdoor traffic officers as test group and indoor traffic officers as control group.

Materials and methods: This study was conducted on 41 outdoor traffic officers and 41 indoor traffic officers as control group. Blood samples were collected from individuals in test and control group and to determine the concentration of blood lead the atomic absorption device used, to investigate hematological factors cell counter device was used, and to measure the biomarker 8-OHdG, Elisa Reader was used. Data were analyzed using SPSS software version 25.

Results: Average blood lead level in outdoor traffic officers was 9.4±4.5 and in indoor traffic officers as control group was 8.6±4.8 µg/dl. Average hemoglobin level in outdoor traffic officers was 13.8±2.5 and in the control group was 13.8±2.5 g/dl. Average level of 8-OHdG in outdoor traffic officers was 18.92±13 and in the control group was 12.41±7.0 ng/ml.
Conclusion: Blood lead levels in outdoor Tehran traffic officers was higher than the indoor traffic officers. The mean of hemoglobin and hematocrit in the police officers of Raouf was significantly lower than those of police officers. Hemoglobin and hematocrit considerably decrease with increasing blood levels of lead. And the incidence of anemia due to chronic poisoning with lead in the test group is quite evident. Also, the average 8OHiDg level in the Raw police police officers is 92.18, which is significantly higher than the staff of the police police, which is 41.12 (p <0.05).

Keywords: Lead, Traffic police officers, indoor and outdoor, 8-oHdG biomarker, Hematological effects.
The evaluation of hepatoprotective effects of hesperidin in bile duct ligated rats

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Background

Hesperidin (HP) is a major bioflavonoid in citrus species, such as grapefruit, lemon and orange. This study evaluated the protective effects of hesperidin against liver injury occurring in rats with biliary obstruction as a model of cholestasis.

Methods

The rats were categorized into five groups (n = 6, 250-300 g). Control group (C), the bile duct ligation (BDL), and BDL + hesperidin groups. Bile duct ligated rats have been treated with hesperidin at doses of 50, 100, 200 mg/kg orally for 14 days. In blood samples, total bilirubin, direct bilirubin, liver enzymes level of alanine aminotransferase (ALT), aspartate aminotransferase (AST) and alkaline phosphatase (ALP) were measured via an automated chemistry analyzer. Malondialdehyde (MDA) was measured as marker of lipid peroxidation in liver tissues by thiobarbituric acid method.

Results

Plasma levels of total bilirubin, direct bilirubin, ALT, AST and ALP were significantly high in the BDL group, while ALT,AST levels significantly decreased in the BDL groups administrated with 100 and 200 mg/kg of hesperidin.
Liver tissue level of MDA increased dramatically in the BDL group while decreased significantly after hesperidin treatment (100 mg/kg and 200 mg/kg) \( p = 0.001 \).

**Conclusion**

The current study suggests that hesperidin attenuates oxidative damage in liver following BDL via its antioxidant activities.

**Keywords:** liver, BDL, hesperidin, rat.
Evaluation of antibacterial activity of hydroalcoholic extract of *Trachyspermum ammi*

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**Background:** Ajwain, ajowan, or *Trachyspermum ammi*—also known as ajowan caraway, bishop's weed, or carom—is an annual herb in the family Apiaceae (or Umbelliferae). It originated in India. Both the leaves and the seed-like fruit (often mistakenly called seeds) of the plant are consumed by humans. Ajwain's small, oval-shaped, seed-like fruits are pale brown schizocarps, which resemble the seeds of other plants in the Apiaceae family such as caraway, cumin and fennel. They have a bitter and pungent taste, with a flavor similar to anise and oregano. They smell almost exactly like thyme because they also contain thymol, but they are more aromatic and less subtle in taste, as well as being somewhat bitter and pungent. Even a small number of fruits tends to dominate the flavor of a dish. Ajwain is used in traditional Ayurveda primarily for stomach disorders such as indigestion, bloating, fatigue, abdominal pain, flatulence, diarrhea, and colic, along with respiratory distress and loss of appetite. In Siddha medicine, the crushed fruits are applied externally as a poultice and in this research we
evaluated of antibacterial activity of hydroalcoholic extract of Ajwain, ajowan or *Trachyspermum ammi* for *Staphiloccus aureus* and *Escherichia coli*.

**Methods:** Bacterial species, *Escherichia coli* and *Staphylococcus aureus* were obtained from Microbiology Department, Research Center of Azad University branch of zanjan. In this experimental study, hydroalcoholic extracts have been prepared from *Trachyspermum ammi*. A modification of the dilution method for the determination of MIC and MBC was used. Using standard wire loop (Merck), a loopful (10 µl) of *E. coli* culture, 0.5 McFarland standard (Eucaet, 2003). Similarly, this was repeated for *S. aureus*. The tubes were incubated at 37°C for 18 to 24 h and there after observed for growth or turbidity.

**Results:** The Minimum Bactericidal Concentration (MBC) is the lowest concentration of an antibacterial agent required to kill a bacterium over a fixed, somewhat extended period, such as 18 hours or 24 hours, under a specific set of conditions. It can be determined from the broth dilution of MIC tests by subculturing to agar plates that do not contain the test agent. The MBC is identified by determining the lowest concentration of antibacterial agent that reduces the viability of the initial bacterial inoculum by a pre-determined reduction such as ≥99.9%. The MBC is complementary to the MIC; whereas the MIC test demonstrates the lowest level of antimicrobial agent that greatly inhibits growth, the MBC demonstrates the lowest level of antimicrobial agent resulting in microbial death. In this research evaluated of antibacterial activity of hydroalcoholic extract of Ajwain, *Trachyspermum ammi*, finally MIC/MBC test showed antibacterial activity extract of *Trachyspermum* for *Staphiloccus aureus* and *Escherichia coli*.

**Conclusion:** Minimum Inhibitory Concentration for *Staphiloccus aureus* and *Escherichia coli*: for *Staphiloccus aureus* were respectively 6.25 and 12.5 µg/ml, for *Escherichia coli* were 11.56 and 12.5 µg/ml.

**Keywords:** *Trachyspermum ammi*; *Staphiloccus aureus*; *Escherichia coli*; Hydroalcoholic Extract; Antibacterial Activity; *in vitro* evaluation.
PPT-8

Asthma: Beyond Corticosteroid Treatment

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Abstract

Asthma is one of the most common chronic diseases in the world, affecting over 300 million people. It is an inflammatory disorder characterized by bronchoconstriction and airways hyperresponsiveness, followed by inflammatory manifestations in the respiratory system. The prevalence of asthma is rising and there is a clinical need to develop more effective treatments. While corticosteroids (glucocorticosteroids) remain the mainstay of asthma therapy, they have limitations because of their potentially severe side-effects and the presence of corticosteroid-resistance in some patients. This review discusses current strategies in the treatment of asthma and considers new therapeutic regimens of asthma in the drug development pipeline.

Keywords: Asthma, Corticosteroids, Inflammation
The beneficial effects of mountain tea hydroalcoholic extract on methotrexate-induced liver toxicity through

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Background: Methotrexate (MTX), a chemotherapy and immune suppressant drug has side effects including hepatotoxicity. In this study we investigated protective effect of mountain tea extract on MTX-induced liver toxicity.

Results: In this study, 56 male Wistar rats were divided into 5 groups. The first group was treated with normal saline. The second group (MTX) received methotrexate at 20mg/kg dose intraperitoneally at day 7. The third, fourth, and fifth groups received the mountain tea extract at 30, 50 and 70 mg/kg doses per day, respectively, daily, and on day 7 received methotrexate intraperitoneally at a dose of 20 mg/kg. After 11 days, liver was isolated to measure MDA, TAC, GSH and CAT, SOD activity in tissue homogeneity. The results showed that SOD, CAT, TAC and GSH levels decreased in methotrexate group compared to control group (P <0.05). These values increased in the third to the fifth groups compared to the methotrexate group. The MDA content in methotrexate group increased compared with the control group, which decreased in the third to fifth groups compared to the methotrexate group.

Conclusion: Our results demonstrate that mountain tea extract has a protective role against MTX-induced liver toxicity, which can be due to its antioxidant property.

Keywords: methotrexate, mountain tea, oxidative stress
PPT-11

Effect of Garlic (*Allium sativum*) on Male Fertility: A Systematic Review

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Abstract:

**Background:** Fertility in men mainly depends on the number, quality, motility, and morphology of the sperms, and disruption of each of these factors leads to infertility. A large number of couples suffer from infertility problems. Among the various therapies, medicinal herbs are used in many countries to treat male infertility. Current systematic review was conducted to study the effects of garlic on male fertility.

**Methods:** The information of this systematic review was collected by searching the key words: treatment, fertility, infertility, male, herbal medicine, garlic, *Allium sativum*, medicinal plant, sperm, sex hormones, testis and spermatogenesis in international databases such as: Web of Science (ISI), Pubmed, Scopus and Embase until March 2018. This study was conducted in accordance with the PRISMA statement for systematic reviews and meta-analysis. and the SYRCLE risk of bias tool was used for qualitative assessment.

**Results:** A total of 18 experimental studies were included in the study. Thirteen studies evaluated garlic and 5 studies compared garlic effect with adriamycin, titanium dioxide, furan, vitamin E, N-acetylcysteine and cadmium. All studies were conducted in *in vivo* condition. The results of the studies indicated the potential effect of garlic on enhancing fertility and spermatogenesis, increasing the level of testosterone and improving the testicular structure.

**Conclusion:** Garlic can increase fertility probably due to its antioxidant properties. However, more clinical trials are recommended.
Key words: Garlic, Allium sativum, Fertility, Infertility, Spermatogenesis, Medicinal plants.
A systematic review of the effects of Tramadol on male fertility

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Abstract

Background: Fertility is one of the main indicators of population growth and defines the socioeconomics of a society. Fertility problems and infertility are considered as major complications in the field of medicine, and consumption of diverse types of drugs may evoke side effects during a lifetime. This study presents a systematic review of the effects of Tramadol on male fertility.

Methods: Data was obtained from Web of Science (ISI), PubMed, Scopus, Ovid and EMBASE entries by May 2018. The main keywords include treatment, fertility, infertility, male, drug-therapy, Tramadol, sperm, sex hormones, and spermatogenesis. This study is carried out according to PRISMA (Preferred Reporting Items for Systematic Reviews and Meta-analyses) guidelines. Moreover, the SYRCLE risk of bias tool was employed for quality assessment.

Results: There were 14 studies reviewed, comprising 11 reports on the effects of Tramadol and 3 on the comparison of the effects exerted by Tramadol and other drugs, including the investigation of the effects of Tramadol and Selenium, Pumpkin seed extract and Sildenafil, separately. Results have revealed damage to seminiferous tubules, Sertoli cells, Leydig cells as well as the tissue of testis and epididymis, in addition to spermatogenesis defects, reduced levels of the sex hormones LH, FSH and testosterone and increased levels of prolactin.

Conclusions: Due to the antagonistic effects of Tramadol on the Hypothalamic-pituitary-gonadal axis, the levels of GnRH, LH, and in consequence, the level of testosterone is reduced. Reduction of these hormones leads to testicular and epididymal atrophy, and therefore, subfertility. Since there are few reports on human cases, more clinical trials are recommended.

Keywords: Tramadol, Fertility, Infertility, Male.
PPT-15

Investigation Effects of Lorazepam on Oogenesis and Ovaries in Balb/C adult female mouse (abstracts)

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Background: Lorazepam (Ativan) is one of the drugs used in the treatment of depression, especially use worldwide among young people. The use of antidepressants such as lorazepam, which is readily available, including complications such as Temporary or permanent infertility, is. In the present study, we investigated the effect of lorazepam on the reproductive system Adult female mice Balb/C.

Methods: In this study After determining the proper dose of lorazepam Intraperitoneal injections(IP) On 75 mice With doses 2mg/ kg.b.w for 3 groups (5day) (10day)and (15 day) and control (no injection) And sham (injection) Done. SPSS Data Software Duncan and Anova With a significant (P <0.001) and (P <0.05) were measured.

Results: Histological studies in the ovary parameters include the reduction of large and small Diameter the ovary, the number of primary and secendery follicles, corpus luteum, growing and graph with significant (P <0.05) (P <0.001)and Lower secondary follicles Was observed. While witness Increase the number of follicles vacuolization, destruction and zona pellucida folded with meaningful (P <0.05) (P <0.001).

Conclusion: Generally, it can be concluded that fluoxetine damaging effect On the female reproductive system and its use under medical supervision, especially in young girls should be informed.

Key words: Lorazepam, Ovary, Follicle, Mice
PPT-16

Ethanolic extract of *Hyssopus officinalis* moderates blood parametric (glucose, total cholesterol and triglycerides) in alloxan-induced diabetic rats

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**Background and aim:** Diabetes mellitus results from the autoimmune destruction of the insulin-producing beta cells in the pancreas. Subsequent lack of insulin leads to increased blood and urine glucose. *Hyssopus officinalis* is a medicinal plant which had been has various used in traditional medicine. Traditionally, this medicinal plant used for treatment of asthma, fever, epilepsy and has have antidepressant effect. In addition, recent studied revealed that this plant has antioxidant effect. In the current study, the effect of ethanolic extract of *Hyssopus officinalis* on the levels of blood glucose, total cholesterol and triglycerides in normal and alloxan-induced diabetic rats were evaluated.

**Materials and methods:** The effect of intra-peritoneal administration of ethanolic extract of *Hyssopus officinalis* (5, 10 and 20 mg/kg) for 15 days consequently on the level of serum glucose, total cholesterol and triglycerides in normal and alloxan-induced diabetic rats were evaluated.
Results: Intra-peritoneal administrations of Hyssopus officinalis extract significantly decreased blood glucose, total cholesterol and triglycerides in diabetic rats but not in normal rats. The administration of Hyssopus officinalis extract did not change the serum parameters in normal rats. A comparison was made between the action of Hyssopus officinalis extract and glibenclamide (20 mg/kg), the known antidiabetic drug. The antidiabetic effect of the extract was the same of that observed with glibenclamide.

Conclusion: These finding revealed that this plant has hypoglycemic and hypolipidemic activities. It is concluded that the plant can be considered as excellent candidate for future studies on diabetes mellitus.

Keywords: Diabetes mellitus; Hyssopus officinalis; blood glucose; cholesterol; triglycerides
Alteration of core body temperature and weight in experimental obstructive cholestasis mice

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Background: Cholestasis is a condition where bile cannot flow from the liver to the duodenum. The two basic distinctions are an obstructive type of cholestasis where there is a mechanical blockage in the duct system that can occur from a gallstone or malignancy, and metabolic types of cholestasis which are disturbances in bile formation that can occur because of genetic defects or acquired as a side effect of many medications. The effect of cholestasis on core body temperature and weight in cholestasis mice was evaluated.

Methods: There were two experimental groups: sham-operated and bile duct ligation (BDL) mice. Laparotomy was performed under general anesthesia, induced by intraperitoneal (i.p.) injection of ketamine hydrochloride (50 mg/kg) plus xylazine (5 mg/kg). Sham group consisted of laparotomy and bile duct identification and manipulation without ligation or resection (with the aim of measuring possible stress induced by surgery). In the bile duct ligation groups, the main bile duct was first ligated using two ligatures approximately 0.5 cm apart and then transected at the midpoint between the two ligatures. In the immediate postoperative period, each animal was placed in a cage by itself to prevent wound dehiscence and was moved to its original cage 4 h after the surgery.

Results: Induction of experimental obstructive cholestasis increased core body temperature [$P < 0.05$] while decreased body weight [$P < 0.05$] in mice.

Conclusion: The results indicate that induction of experimental obstructive cholestasis change metabolic processes including core body temperature and weight in mice.

Keywords: cholestasis, core body temperature, weight, mice
Melissa officinalis extract decreases hormonal signs of post-traumatic stress disorder (PTSD) induced by electric shock in rat

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**Background and Aim:** *Melissa officinalis* is a medicinal plant which has been has various used in traditional medicine. Traditionally, this medicinal plant has sedative and anti-anxiety effects and has been used to cure different diseases such as migraine, sleep disorders, and etc. The post-traumatic stress disorder (PTSD) is among the most important mental disorders of our century which causes great stress and several complications for the afflicted person. Nowadays, the definition of PTSD comprises not only those affected by the accident, but also those who have witnessed it. Therefore, in the current study, we aimed to investigate the effects of *Melissa officinalis* extract on hormonal signs of PTSD caused by electric foot shock.

**Methods:** Male Wistar rats (250-300 g weight) were used in this study. The animals randomly received electric foot shock (0.1 mA) for 100 seconds over a period of 10 days. After returned to cages to repose for 21 days, the animals were put back into the stress box but received no stress. The animals received different doses of *Melissa officinalis* extract (3, 9, 18 mg/kg) intraperitoneally 10 min
before placing into the stress box (n = 7-9 rats/group). Control group received saline (1 mg/kg). Plasma corticosterone levels were assessed in control and treated animals.

**Results:** One-way ANOVA showed that stress elevated plasma corticosterone level (138 nmol/L) concentration in the control animals. Intraperitoneal administration of the *Melissa officinalis* extract reduced plasma corticosterone level (73 nmol/L).

**Conclusion:** These findings indicate that *Melissa officinalis* extract can reduce hormonal signs of PTSD and can use as an agency for moderation of PTSD signs.

**Keywords:** *Melissa officinalis*; Post-traumatic stress disorder; corticosterone
Anti-Inflammatory MicroRNAs and Their Potential for Inflammatory Diseases Treatment

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Abstract

Inflammation is a complicated biological and pathophysiological cascade of responses to infections and injuries, and inflammatory mechanisms are closely related to many diseases. The magnitude, the complicated network of pro- and anti-inflammatory factors, and the direction of the inflammatory response can impact on the development and progression of various disorders. The currently available treatment strategies often target the symptoms and not the causes of inflammatory disease and may often be ineffective. Since the onset and termination of inflammation are crucial to prevent tissue damage, a range of mechanisms has evolved in nature to regulate the process including negative and positive feedback loops. In this regard, microRNAs (miRNAs) have emerged as key gene regulators to control inflammation, and it is speculated that they are fine-
tune signaling regulators to allow for proper resolution and prevent uncontrolled progress of inflammatory reactions. In this review, we discuss recent findings related to significant roles of miRNAs in immune regulation, especially the potential utility of these molecules as novel anti-inflammatory agents to treat inflammatory diseases. Furthermore, we discuss the possibilities of using miRNAs as drugs in the form of miRNA mimics or miRNA antagonists.

**Keywords:** anti-inflammatory microRNA; immune regulation; inflammation; inflammatory diseases; microRNA
Evaluation of renal system in varicocele rat model and NaHS administration

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Background

Varicocele is one of the most common causes of male infertility. It is characterized by abnormal dilation and tortuosity of veins of the pampiniform plexus. Oxidative stress is one of the pathophysiology of this disorder. Nutcracker syndrome is the left renal vein (LRV) squeezing between the aorta and the superior mesenteric artery (SMA). The main aim of this study was to evaluate renal system in a varicocele rat model.

Methods and materials

Thirty-six rats were randomly assigned to 3 experimental groups: 1) sham 2) varicocele 3) varicocele + sodium hydrosulfide. The sham group was underwent sham operation and experimental groups were underwent partial ligation of the renal vein to induce experimental varicocele. Animals in varicocele + sodium hydrogen sulfide group received 30 µmol/l NaHS in drinking water for 56 days. At 57th day of treatment, all rats in three groups anesthetized and blood and kidney tissue were collected for evaluation of BUN (blood urea nitrogen), plasma creatinine (Cr), urine protein, Cr clearance rate (Ccr) and measurement of renal oxidative stress (MDA level & SOD activity).

Results

Varicocele did not alter kidney function but the oxidative stress markers were changed significantly (renal MDA levels increased and SOD activity decreased). The protective effects of NaHS was observed in the current study.
Conclusion

Varicocele can affect kidney via oxidative stress. This study suggested that notice to remote organs such as kidney in patients with varicocele is as important as reproductive organs.

Key words: kidney, varicocele, nutcracker syndrome, NaHS, oxidative stress
Effect of Phytoestrogen on Depression and Anxiety in Menopausal Women: A Systematic Review

Abolfazl Fattah

Objectives
In this systematic review, the effectiveness of herbal medicines in improving depression and anxiety in menopausal women was assessed.

Methods
Three following databases were individually searched: MEDLINE (1966-March 2017), SCOPUS (1990-March 2017), and the Cochrane Library (Cochrane Central Register of Controlled Trials; 2017).

Results
A total of 9 trials were included in this systematic review. Overall, soy was found to have a beneficial effect. Also, fennel had a significant positive effect on menopausal women with depression and anxiety disorder, but not on healthy women. Red clover showed varying effects ranging from significant to non-significant on depression and anxiety. Moreover, kava was found to have a significant beneficial effect on depression and anxiety at dose of 200 mg/days.

Conclusions
Our study demonstrated that herbal medicines could improve anxiety and depression in among menopausal women. However, the beneficial effect still remains indefinite due to the poor methodology.

Keywords: Anxiety; Depression; Menopause; Phytoestrogens
Correlation between plasma and salivary oxidative stress during acute renal injury induced by ischemia - reperfusion in male rats

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Introduction: Saliva, a biological diagnostic fluid, has been widely used in the clinic due to its advantages compared to blood sampling. Ischemia - reperfusion is a major cause of acute renal injury, which occurs as a result of sudden restoration of blood flow to the renal system. This disease is associated with oxidative stress as a destructive event. The main aim of this study was to evaluate the correlation between the end product of lipid peroxidation (malondialdehyde, MDA) in the saliva and plasma in this model of acute kidney damage.

Methods and Materials: In this study, 24 male rats were randomly divided into 4 groups: 1) control 2) 3 h – reperfusion after ischemia 3) 6 h reperfusion after ischemia 4) 24 h reperfusion after ischemia. By clamping both renal arteries for 55 minutes, we induced an experimental reperfusion injury model to establish acute renal injury. In the control group, the renal arteries were not clamped. Salivary samples were collected after injection of 1 mg / kg of pilocarpine. Blood samples were collected from the inferior vena cava. The end product of lipid peroxidation, MDA was measured in blood and saliva as the reaction product with thiobarbituric acid by spectrophotometry.
Results: There was a significant increase in MDA as an indicator of oxidative stress in both blood and saliva samples in all experimental groups of 3, 6 and 24 h reperfusion injury compared to the control group.

Conclusion: The results of this study showed that there is a correlation between the extent of oxidative stress of the saliva and plasma in acute kidney damage. Therefore, saliva may be used to assess the renal status of these patients as well as measurement of other indicators of this disease.

Key words: acute renal injury, ischemia - reperfusion, saliva, oxidative stress
PPT-23

Early life stress reduced pancreatic HB9 protein expression along with plasma corticosterone and TNF-α elevation in young adult male rats

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Abstract

Background: The HB9 Transcription Factor is one of the markers of beta cells' differentiation, and their persistent expression in mature beta cells plays an important role in normal functioning of the pancreatic beta cells in later life. Given that early life stress may have long term adverse metabolic effects in later life and considering that there is a relationship between early-life stress and markers of low-grade inflammation (such as TNF-α), which in turn may affect gene expression, this study examined the effect of foot shock stress, during
weaning, on pancreatic HB9 protein expression as well as plasma TNF-α level in chronically stressed young adult male rats.

**Methods:** During weaning the rat pups were randomly divided into control and foot shock stress groups, then during young adulthood, they were further divided into non-stress, early life stress, young adulthood stress and early+young adulthood stress subgroups. The animals were exposed to foot shock stress twice daily for 5 consecutive days at 2 (weaning time) and 8 (young adulthood) weeks of age. Blood samples were taken after the stress exposure to measure plasma corticosterone and TNF-α concentrations. One day after the last stress exposure the animals were dissected, and their pancreases were removed to assess its HB9 protein amount.

**Results:** This study showed that plasma corticosterone concentration increased at 2 weeks of age in the foot shock stress group, and during young adulthood, in the young adulthood and early+young adulthood stress groups. The plasma TNF-α level decreased in the young adulthood stress group, but increased in early life stress group. The HB9 protein level decreased in the early life stress group.

**Conclusion:** Early life stress has a suppression effect on the pancreatic HB9 protein expression possibly by plasma corticosterone concentration increment in early life along with TNF-α elevation in adulthood.

**Keywords:** Early life stress, HB9, corticosterone, TNF-α
Scolicidal agents for protoscolices of *Echinococcus granulosus* hydatid cyst: Review of literature

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Hydatid cyst is the larval stage of dog tape worm *Echinococcus granulosus*. Protoscolices are parasite larvae that develop into adult worms in the final host intestine. During surgical treatment of human hydatidosis spillage of live protoscolices is the major cause of hydatidosis recurrence. To prevent this problem scolicidal agent such as hypertonic salt are used to kill the protoscolices that may disseminate into the patient’s tissues during surgery. However, they may have some unacceptable side effects. To find scolicidal agents with high efficacy, the effect of different compounds on protoscolices of hydatid cyst in vitro has been reviewed. Using PubMed, Scopus, Google Scholar, and SID databases articles about scolicidal effects of different agents on protoscolices of hydatid cyst in vitro were collected. *Foeniculum vulgare* after 5 min, metalonic extracts of *Allium sativum* and hypertonic saline after 10 min and warm water after 2 min kill all alive protoscolices. The above agents that in minimum time and minimum concentration have 100% scolicidal activity could be good candidates for further investigations.

Key words: Hydatid cyst, protoscolices, scolicidal agents, surgery, surgery
PP-2

Diagnosis of Acute Toxoplasmosis by IgG Avidity Method in Pregnant Women Referred to Health Centers in South-Eastern Iran

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Abstract

Objective: Toxoplasmosis is one of the most common parasitic infections in humans and can lead to irreparable abortions or fetal lesions in pregnant women. The purpose of this study was to determine the seroepidemiology of toxoplasmosis and diagnosis of acute form of infection in pregnant women referred to health care centers in Saravan in 2016.

Methods & Materials: In the present study, 208 pregnant mothers who referred to Saravan health center were taken under study after signing a consent form and filling a checklist. The blood samples were collected from them and the sera were stored at -20 °C. For those with high levels of IgG or IgM antibody titers, IgG Avidity test was performed to determine the acute infection. The correlations between different obtained data were determined using Chi-square test and analyzed by SPSS software (IBM SPSS Statistics 18) with 95% confidence interval.

Results: 208 pregnant women at an average age of 27.5 years, were recruited. The positive results of evaluation of the sera by IgG were 88(42.3%) of which 7 persons had borderline titer and 81 patients had high titer antibody. High level of IgM antibodies was seen in 33 cases (15.8%) and the Sera with yielding borderline and low results for IgM were 4 and 171, respectively. Then, the samples with positive and borderline antibody titers for IgM and IgG were evaluated by IgG avidity test. The most important factor in toxoplasmosis was contact with cats, which had the greatest chance among other factors.
Conclusion: According to the results of this study, approximately 60% of pregnant women in this parasite have no specific immunity against Toxoplasma, therefore this group is prone to primary infection of toxoplasmosis and there are serious risks for their fetuses. Moreover, in order to prevent and control toxoplasmosis, seminars and educational classes could be effective.

Keywords: Acute Toxoplasmosis, IgG Avidity, Pregnant Women, South-Eastern Iran.
PP-3

Evaluation of Anti-Malaria Effect of Hydroalcoholic Extract of *Olea Europea L.* in Mice

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**Background:** Evaluation of medicinal plants has shown potential Anti-Malaria effects which introduced many drugs with antibiotic properties. As there were controversies about Anti Malaria action in the literature, this study evaluates the Anti-Malaria effect of Hydroalcoholic Extract of Olea Europea L.

**Methods:** In this experimental study, extraction of *Olea Europea L.* was performed by the percolation method using hydrocolloid solution. Then, 30 mice were infected with *Plasmodium Berghei* and treated with different concentration of *Olea Europea L.* extract (200, 300, 400, 500 mg/ml) for four consecutive days.

**Results:** The results indicated that, although all the four concentrations of the *Olea Europea L.* extract significantly reduced parasitemia in the infected Mice, the 500 mg/kg solution showed optimal effectiveness on the parasites in comparison with other concentrations.

**Conclusion:** Scientific developments and increasing international attention have promoted our ability to work with and understand the Anti-Malaria drug. The results concluded that the ethanolic extract of *Olea Europea L.* is a potential natural Anti-Malaria agent, however its effect is dependent on the source and extraction method.

**Keywords:** Malaria, Mice, Hydroalcoholic Extract, *Plasmodium Berghei*
Prevalence of Intestinal Parasitic Infection among working children, in Tehran, Iran

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Abstract:

Background: The limited available data indicate that working children often suffer from poor health. In this study prevalence of intestinal parasitic infection in working children related to Sobh-e Rooyesh school in Tehran, Iran was evaluated for the first time.

Methods: Stool samples were collected from 144 working children associated with Sobh-e Rooyesh school in Tehran and transferred to Research Center of Pediatric Infectious Diseases, Institute of Immunology and Infectious Diseases, Iran University of Medical Sciences, between February and September 2018 and examined by wet mount examination and formalin ether concentration. The permanent trichrome staining was performed for more confirmation.

Results: The results showed that prevalence of parasitic infection was 69/144(47.9%). Prevalence of Blastocystis hominis as the most prevalent parasites was 52 (36.1 %) followed by 14(9.7%) related to Giardia lamblia and13 (9.3%)
samples were positive for *Entamoeba coli*. Prevalence of helminthic infection was 2/144 (1.4%) that related to *Hymenolepis nana*.

**Conclusion:** Prevalence of intestinal parasitic infections was relatively high among working children in Tehran. Prevalence of protozoan infection was more than that of helminth infection. It is suggested that additionally necessary treatment, health education and personal hygiene should be provided to prevent transmission.

**Keywords:** Parasite; Working children; Prevalence; Tehran
PP-5

Seroprevalence of toxoplasmosis and related risk factors in pregnant women, Tabriz, Iran

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Abstract

Background: Toxoplasmosis is a zoonotic infection caused by an obligate intracellular parasite. Infections in humans are often asymptomatic. Most of the complications of this infection are congenital transmission.

Aims: The aim of this study was to investigate the seroprevalence of infection and its related risk factors in Tabriz, Iran in woman of reproductive age.
Methods: A total of 1200 serum samples of reproductive-age women referring to the 29- Bahman hospital since 2017 were recruited for this study. Blood samples were tested for *T. gondii* IgG and IgM antibodies in participants using commercial available enzyme immunoassays IFA, ELISA, and Elisa avidity then analyzed by their socio-demographic information.

Results: Of the 1200 samples studied, 381 (31.7 %) and 41 (3.4%) subjects were positive for IgG and IgM antibodies, respectively. Among the evaluated risk factors, the relationship between seroprevalence of toxoplasmosis and education and history of vegetable consumption were not significant, but factors such as contact with the soil, cat and hand washing before meal have an effect on the prevalence of this infection.

Conclusions: According to the results, more than two thirds of reproductive-age women in Tabriz are vulnerable to toxoplasmosis infection and training should be provided to observe the above measures to prevent infection in pregnant women.

Keywords: *Toxoplasma*; Seroprevalence; Reproductive age woman, Risk factors; Cross-sectional study; Tabriz
In vitro comparative study on cytotoxic effect of antimicrobial peptide CM-11 and Metronidazole on *Entamoeba histolytica*

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**Background:** *Entamoeba histolytica* is an intestinal parasite that is located in the lumen of the human intestine and is able to attack the epithelium. According to the WHO, *E.histolytica* is the third cause of death among parasites. Metronidazole is the first line to treat intestinal infections caused by *E.histolytica*, which has unpleasant side effects. Consequently, searching for anti-parasite compounds with more activity and less toxicity is still a necessary goal. Antimicrobial peptides (AMPs) are one of a variety of antimicrobial compounds that are effective against a wide range of microorganisms.

**Methods:** In this study, the cytotoxic effect of chimeric peptide cecropin-melittin (CM-11) with concentrations of 0.75, 1.5, 3, 6, 12 and 24 μg/ml as well as metronidazole (40, 20, 10, 5, 2.5, 1.25 μg/ml) on Caco2 cell were assay using MTT and flow cytometry method, as well as examination of parasites exposed to various concentrations of peptide and metronidazole compared with control group.

**Results:** MTT results showed that in the highest concentration (24 μg/ml), toxicity of peptide on Caco2 cells were 49.82% and 44.32% in 24 and 48 h, respectively. The toxicity of metronidazole were 43.48%, 42.17% in the highest concentration (40 μg/ml) in 24 and 48 h, respectively. The most level of apoptosis determined by flow cytometry in 24 and 48 h was associated with the highest concentrations of peptide (24 μg/ml) and metronidazole. The results of toxicity of CM-11 in coculture revealed that highest mortality rate on trophozoites in 24 μg/ml. The toxicity of trophozoites were high in concentration of CM-11 (24 μg/ml) and metronidazole (20 μg/ml).
Conclusion: The results of this study showed that CM-11 compared with metronidazole has a very high toxicity on Entamoeba histolytica, and the use of antimicrobial peptides in the future can be considered as antimicrobial compounds.

Keywords: E.histolytica, Chimeric Peptide, Cecropin-Melittin, Antimicrobial peptides, CM-11
Genotyping of *Echinococcus granulosus* larval stage isolated from sheep in the Markazi Province based on Cox1 gene

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**Background:** Hydatidosis is a parasitic disease caused by the larval stage of the *Echinococcus granulosus*, which its prevalence has been increasing in recent decades. This parasite is a human pathogen and also, can cause economic damage to livestock. Since genotypic difference has an effect on antigenicity, immunogenicity and, other pathogenesis factors, the identification and categorization of native genotypes of this parasite is important in each region. The aim of this study was to determine the genotype of the larval stage of the *Echinococcus granulosus* isolated from the sheep based on Cox1 gene in Markazi Province.

**Methods:** In this study, 38 samples of hydatid cysts from sheep were collected from different slaughterhouses of Markazi Province and transferred to the laboratory. Then, protoscoleces or germinal layers were isolated and their DNA was extracted using a special kit (Roche; Germany) and amplified with specific primers for Cox1 gene. Finally, the PCR products were sequenced.
**Results:** From the 38 hydatid cysts, using PCR The most common genotype was G1 with 56.8%, followed by genotype G3 with 40.5% of the isolates.

**Conclusion:** The results of this study showed that the most frequent genotypes of *Echinococcus granulosus* larval stage isolated from sheep in Markazi Province were G1. also, the G3 genotype in this study were found. In the life cycle of this strain, the dog and the sheep are final and intermediate hosts, respectively. Therefore, parasite control in dogs and sheep can reduce the risk of transmission of infection to humans.

**Keywords:** *Echinococcus granulosus*, Hydatidosis, Cox1 gene, Genotype
PP-10

Antimalarial properties of hydroalcoholic extract of *Artemisia persica* against *Plasmodium berghei* in laboratory albino mice

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**Background:** Malaria is one of the most important tropical disease in Iran and world. The malaria agent is resistant versus chemical drugs that have several side effects. So, the use of various medicine plants, especially the different species of *Artemisia* herbal, is important significantly. Therefore, the aim of this study was antimalarial properties of alcoholic extract of *Artemisia Persica* herbal against *Plasmodium berghei* in vivo.
Methods: In this experimental study, the herbal different parts were collected, powdered and macerated in ethanol and dried by Rotary Evaporator. The toxicity of herbal extract were assessed on several groups of albino mice and its antimalarial efficacy were investigated in mice infected with *Plasmodium berghei*. This mice were divided to groups for extract that were treated with different concentrations of extract and one group treated with chloroquine current drug. A group was assigned as a placebo group without any drugs. The Data were analysed using SPSS software and Paired and student T-test.

Results: In the In vivo toxicity studies of the plant extract, there were no gross physical and behavioral changes: including, diarrhea, depression and abnormal secretion for 24h and no mortality occurred within the observation period of one month. Also, there were a statistical significant difference in parasitemia decrease in 150 mg/kg concentration of extract versus other concentrations. Comparatively, the ethanol extract of the *Artemisia Persica* showed lower antimalarial activity than chloroquine current drug.

Conclusion: This study showed that alcoholic extract of *Artemisia Persica* in 150 mg/kg mice weight concentration have a significant effect on *Plasmodium berghei* parasite.

Keywords: *Artemisia Persica*, Chloroquine, *Plasmodium berghei*, antimalarial properties, laboratory albino mice.
Comparative study of *Toxoplasma gondii* serprevalance in patients with dementia and normal population in Hamadan and Arak citys, 2017.

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**Background:** Toxoplasmosis is one of the common parasitic infections in the human population. It’s been estimated that every one of the three persons is infected with this organism. The role of toxoplasmosis in neurological disorders such as migraine, Schizophrenia, Parkinson, Alzheimer and recently in dementia has been investigated. Dementia has a wide prevalence in elderlies. This study was conducted to determine the probable role of *Toxoplasma* infection in dementia patients in Arak and Hamadan City, West of Iran.

**Methods:** In this case-control study, 100 dementia patients referred to Arak and Hamadan affiliated hospitals and 99 healthy controls under supervision of neurologists were selected. The blood samples were transferred to the Research
Laboratory of Arak University of Medical Sciences, under cold chain. Serum specimens were isolated and were frozen in -20°C until use. The *T.gondii* IgG and IgM in serum samples were analyzed by commercial Enzyme Linked Immunosorbent assay.

**Results:** The overall prevalence of *T.gondii* infection among dementia patients and healthy control group were reported to be 59% (59/100) and 39.3% (39/99) respectively. A statistically significant difference was observed between the seroprevalence of toxoplasmosis in patient and control group. (P=0.002). IgG seropositivity was higher among cases in Hamadan in comparison to Arak (68% versus 50%). IgM seropositivity was distinguished in 2 cases from Arak. There was a significant correlation between seroprevalence of toxoplasmosis and the presence of cats in their neighborhood as well as meat consumption.

**Conclusion:** The significant higher seropositivity of IgG level in dementia individuals compared to controls showed the possible impact of this parasite on dementia. It is imperative that control measures should be taken to prevent toxoplasmosis especially in people with disorders prone to dementia.

**Keywords:** Toxoplasma gondii, dementia, toxoplasmosis
The most common protozoan parasites in children with leukocytosis, in Lorestan province western Iran

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Background: Nowadays, it has been proven that protozoan parasitic infections are recognized as one of the most important socioeconomic and health problems worldwide. Here, we evaluated the frequency of the protozoan parasitic infections in children with leukocytosis referred to Lorestan Province, Iran.

Methods: This cross-sectional investigation was carried out from February 2016 to February 2017 on 92 children with leukocytosis referred to Health Centers of Lorestan Province, Iran. The microscopic analysis was performed on 92 stools using the the direct smear and formol-ether techniques as well as trichrome and modified Zeihl-Neelsen staining methods

Results: Out of the 92 children with hypereosinophilia, 8 (8.7%) children were infected with at least one or more intestinal parasites including Giardia lamblia, and Blastocystis hominis, respectively. Logistic regression analysis demonstrated
that some risk factors were significantly associated to the prevalence intestinal protozoan parasites included consumed raw or unwashed vegetables and fruits, gender, living in rural regions, and consumed raw or unwashed vegetables and fruits (p<0.05).

**Conclusion:** These findings suggested that intestinal protozoan parasites may cause leukocytosis in children.

**Keywords:** Intestinal parasites; stool; leukocytosis; children
Intestinal protozoan parasitic infections in children with hypereosinophilia referred to Health Centers of Lorestan Province, Iran

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Background: Intestinal protozoan parasitic infections are well-known as one of the most important socioeconomic and health problems around the world. The present study aims to evaluate the prevalence of the protozoan parasitic infections in children with hypereosinophilia referred to Health Centers of Lorestan Province, Iran.

Methods: This cross-sectional study was performed from August 2016 to March 2017 on 86 children with hypereosinophilia (>10%) referred to Health Centers of Lorestan Province, Iran. The microscopic analysis was accomplished on 73 stools by means of the direct smear, and formol-ether, and flotation methods.

Results: Out of the 86 children with hypereosinophilia, 11 (12.8%) children were infected with at least one or more intestinal parasites including *Giardia lamblia,*
Blastocystis hominis, and Cryptosporidium parvum, respectively. Statistical analysis showed that some risk factors were significantly associated to the prevalence intestinal helminthic parasites included gender (p<0.05), living in rural regions (p<0.001), hands washing habit (p<0.001) and consumed raw or unwashed vegetables and fruits (p<0.001).

**Conclusion:** These findings suggested that intestinal protozoan parasites can cause hypereosinophilia in children.

**Keywords:** Intestinal parasites; stool; eosinophilic; children
Efficacy and safety of *Curcuma longa* essential oil to inactivate hydatid cyst protoscoleces

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**Background:** Today, available chemical drugs have shown severe complications during hydatid cyst surgery. Here we investigated the efficacy and safety of *Curcuma longa* (C. longa) essential oil against hydatid cysts protoscoleces.

**Methods:** Collected protoscoleces from sheep livers with fertile hydatid cysts were exposed to different concentrations of the essential oil (50-200 µl/mL) for 5-30 min in vitro and ex vivo. Then viability of protoscoleces was evaluated using the eosin exclusion test (0.1% eosin staining). In addition, 48 male NMRI mice were used to determine the acute and sub-acute toxicity of C. longa essential oil.

**Results:** The mortality rate of protoscoleces was 100% after 5 min of exposure to the concentration of 200 µl/mL of C. longa essential oil. Moreover, after 10 min of exposure, the scolicidal activity of C. longa essential oil was 100% at the concentration of 100µL/mL. Lower concentrations of C. longa essential oil, but, indicated a postponed protoscolicidal activity. C. longa essential oil at the concentrations of 50, and 100 µL/mL did not show the similar effect in the ex vivo analysis. But, at the concentration of 200 µL/mL and an exposure time of 5 min, approximately 100% of protoscoleces were killed within the hydatid cyst. We found that after intra-peritoneal injection of the C. longa essential oil for 14
days, no significant difference (p > 0.05) was observed in the clinical chemistry and hematologic parameters at the doses 0.15, 0.3, 0.6 mL/kg.

**Conclusion:** The findings of the present research demonstrated that C. longa revealed the promising scolicidal effects against hydatid cyst protoscoleces in vitro and in vivo, of course, after additional tests; it might be considered as a natural scolicidal agent to reduce the risk of protoscoleces’ spillage during hydatid cyst surgery. However, further studies will be desired to prove these results by checking the essential oil as a new scolicidal agent in a clinical setting.

**Keywords:** GC/MS; cystic echinococcosis; Echinococcus granulosus; protoscoleces; turmeric
Assessment and comparison of Echinococcus granulosus genotype frequencies among slaughtered camels in Yazd and Isfahan province in year 2015 and 2016

Abstract:

Introduction: hydatid cyst infection or hydatidosis is one of the prevalent disease results from poor general hygiene affecting people in many developing countries. The consequence could be numerous economical costs and harms. Hydatidosis considers a common zoonotic disease which has been observed around the world and also has been seen among livestock in Iran vastly. The infection has been fairly widespread among people in the country.

Key problem in understanding the cycle of transmitting infection in hydatidosis is lake of clear morphological characteristic to differentiate between the strains. Analyzing of DNA sequencing shows this class has around 10 different types of genotype, therefore knowing the various genotype obtained from cases around the world is a very practical method for epidemiological assessment of hydatid cyst in order to understand the cycle of disease transmission and consequently prevention management and treatment. The information increases our knowledge about spreading of disease and the possibility of contamination by various animal strains. In addition, recognition of the strains could help the authorities in planning for control and prevention of the disease. Considering camel as an important intermediate host in transmission of the disease, the exclusive knowledge of the genotype for various country regions specifically contaminated region to this parasite is vital. The aim of the study was recognition and separation of Echinococcus granulosus genotype s among slaughtered camels in Isfahan and Yazd province with use of HRM analysis.

Key words: Echinococcus granulosus, Genotype, Hydatid cyst, HRM, camel, Yazd province, Isfahan province
Prevalence Strongyloides Stercoralis and Its Risk Factors of Infection in Babol City and suburbs, Iran

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Introduction: Strongyloidiasis is prevalent in Northern provinces in Iran and is a persistent human parasitic infection caused by the intestinal nematode, Strongyloides stercoralis. Infection usually remains asymptomatic. But, it could cause hyperinfection and dissemination in immunosuppressed patients, especially under corticoid therapy and would result in a high mortality rate.

Materials and methods: The study was conducted for a period from November 2017 to November 2018. Demographic data (e.g., age, sex, place of resident) were obtained from the main registry in Babol city and suburbs. Fresh fecal samples were collected from 4725 patients and examined. Microscopic examination was performed using direct techniques (saline and iodine wet mounts).

Results: Only 39 cases out of 4725 tested samples, found positive with S. stercoralis infection. 23 (59%) of patients were from rural area and 16 (41%) were from urban areas. Also the study population included 5 (12.8%) cancer cases and 6 (15%) of patients were treated by corticosteroids. The prevalence of strongyloidiasis infection was estimated to be 0.82 %. The prevalence of strongyloidiasis was increasing with the increase of age remarkably there was an
increase in the age group 41-80 years of age (75.5%). The prevalence rate of parasites in males and females were 56% (n=22) and 44% (n=17), respectively.

**Discussion:** This geohelmintic parasite can lead to a disseminated and fulminant hyperinfection syndrome in severely immunocompromised patients, especially those treated with high doses of corticosteroid therapy. Corticosteroid therapy is associated with a two- to three-fold increase in the risk of severe forms of clinical disease due to *S. stercoralis*. Since disseminated strongyloidiasis is fatal in 80% of its cases, it is recommended to diagnose and treat the asymptomatic infection due to *S. stercoralis* before long-term corticotherapy. Consequently recommend that all physicians develop a high level of clinical suspicion, especially regarding patients with unspecific gastrointestinal symptoms, prior to chemotherapy or steroid therapy to rule out the presence of *Strongyloides stercoralis* larvae in stool samples.

**Key words:** *Strongyloides stercoralis*, Babol, Corticosteroid Therapy, Immunosuppression.
PP-20

Genotyping of *Giardia intestinalis* among the food handlers of northwest Iran

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**Background:** *Giardia intestinalis* is a commonly distributed flagellated protozoan parasite, worldwide. Transmission to human occurs by accidentally ingested parasite cysts through contaminated drinking water and food. In human, giardiasis could manifest either as a self-limiting asymptomatic disease or occur in the form of an acute infection. Reports have shown that different genotypes are involved in the pathogenesis of giardiasis. The present study was aimed to investigate the genotypes of *Giardia intestinalis* among the food handlers in Qazvin, Iran.

**Methods:** A total of 1530 stool specimens were collected from the food handlers who visited Shahid Bolandian health center in Qazvin. Specimens were evaluated by microscopic and concentration methods. Out of total samples, 20 specimens with appropriate number of giardia cysts were selected followed by DNA
extraction. Determination of giardia genotypes was achieved through PCR and sequencing the glutamate dehydrogenase gene. The phylogenetic tree was drawn using the Mega7 software. Finally, the data was analyzed statistically with a p value <0.05 was considered as significant.

**Results:** Out of total samples, 20 (1.3%) were positive for giardia cyst. All positive specimens were obtained from male participants with abdominal cramp being their most common symptoms. The mean age of infected individuals was 32 years. Molecular characterization was successfully performed for 17 isolates and two genotypes A (AII, 65%) and B (BIII, 35%) were identified.

**Conclusion:** The most prevalent giardia genotypes among the food handlers in Qazvin were A (AII) and B (BIII) genotypes with A (AII) genotype as the dominant one in the region. Considering the direct association between food handlers and public health and the impact of geographical and host conditions on dispersion and pathogenicity of various genotypes and their zoonotic aspects, further investigations are necessary.

**Keywords:** Giardia, Food handlers, Glutamate Dehydrogenase Gene, Qazvin, Iran
Cutaneous Leishmaniasis as an increasing threat for Iranian travelers attending in a religious ceremony in Iraq

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Background: Iran is one of the most important endemic foci of Cutaneous Leishmaniasis (CL) in the world. Border regions of Ilam province in proximity of Iraq are one of the most common of CL in Iran. Annually, a large number of Iranian Shia pilgrims travel to Iraq from this area in order to participate in one of the most important religious ceremony called Arbaeen Hosyni. This trip has coincided with the seasonal activity of sand flies in recent years. So, CL could be a serious threat for pilgrims on this pilgrimages trip. Here, we report CL cases among people who participated in this trip during 2017.
Methods: Totally, 16 patients were referred to our laboratory in Dept. of Parasitology and Mycology at Qazvin University of Medical Sciences, Qazvin, Iran. The most of patients were drivers of the Qazvin Bus Company, as if transferring of the pilgrims to Arbaeen ceremony in border areas between Iran and Iraq. Location of deployment of these people was in a building in margin of Mehran city. Dermal scraping and stained slides preparing of lesions were used to morphological diagnosis. DNA extraction and PCR amplification were optimized to identification of leishmania species.

Results: All of the patients were infected with CL in microscopic survey, so the results were confirmed by molecular approaches, and also only Leishmania major was diagnosed among the patients.

Conclusions: Consequently, the pilgrimage of Arbaeen could be a potential threat to Iranian pilgrims who travel to Iraq in future years.

Key words: Traveler, Leishmania, Cutaneous Leishmaniasis, PCR, Mehran, Iran
Study on parasitic contamination of vegetable's farms in Shushtar, Iran during 2018

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**Background**: Intestinal parasitic infection usually carried out through eating contaminated water and food. Row vegetables are mostly infection agents because feeding of vegetable is a habit’s nutrition and receive food supplement.

**Method**: In this study carried out on 50 samples from 10 farms on four geography cardinal directions of the city: north, south, west, and east.

**Results**: Generally, sixty-four percent contamination was reported that Entamoeba spp. 84% (27 cases), Giardia cyst spp. 75% (24 cases), Blastocysts spp. 31.25% (10 cases), Hymenolypis nana 9.3% (3 cases) and Trichostrongylus spp. 3.1% (1 case) were found.

**Conclusion**: Based on our results, it is necessary education to people about correct methods for washing of raw vegetables such as using disinfectants and destroy of parasites before consumption them added to avoid feces of animal as manure by farmers.

**Key words**: Vegetable, Parasite, Contamination
PP-23

Genotyping of Giardia intestinalis from dogs in Zanjan province using glutamate dehydrogenase gene sequencing

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Background:

Dogs as animals that are involved with human life and environment harbor a number of important zoonotic parasites. Giardia duodenalis is an intestinal protozoan which infects a wide range of hosts, eg, humans, livestock and domestic animals such as dogs. Molecular studies of Giardia duodenalis has revealed eight major genotypes (Assemblages A–H). Assemblages A and B can cause infection in humans and dogs, so aim of present study was to evaluate the presence of zoonotic assemblages of Giardia in stray dogs of Zanjan.

Methods:

A total of 450 samples of dog fresh feces were collected from streets in urban locations as well as farms in rural areas of different parts of the province. All samples were examined by microscopic examination using formalin-ethyl acetate sedimentation concentration method. The DNA of positive samples with Giardia cysts was extracted using the QIAamp fast DNA stool Mini kit (Qiagen, Germany). PCR products were visualized under ultraviolet light (UVIdoc, England). PCR positive samples of G. duodenalis were subjected to DNA sequencing by Takapouzist company. DNA sequences were visualised using Finch TV 1.4.0 and aligned using BioEdit version 7.2.0.

Results:
The prevalence of G. duodenalis in dogs was 1.6% (7/450) by molecular method. Positive samples successfully sequenced, of which all of them were identified as G. duodenalis assemblage C.

**Conclusion:** Result of study showed the prevalence of G. duodenalis 1.6% and no zoonotic assemblage was detected in stray dogs of Zanjan province. However comprehensive studies with other housekeeping genes are needed.

**Keywords:**
Giardia duodenalis- Dog- Genotyping
Investigation of intestinal parasites in Patients referring to hospitals laboratories in Ardabil in 2018

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Background: Parasitic diseases are one of the health problems of all societies and are considered as barriers to progress socio-economic development, especially in most developing countries. This study compares the results of evaluation of protozoal and helminthic parasitic infections with direct, concentration and culture methods in stool specimens of patients referring to laboratories of hospitals affiliated to Ardabil University of Medical Sciences in 2018.

Methods: Total of 409 stool specimens were collected from laboratories in hospitals affiliated to the University of Medical Sciences and transferred to the parasitology lab of the Faculty of Medicine and Paramedics for a period of less than two hours. In the laboratory, samples were evaluated using direct, concentration and culture methods. Data were analyzed using SPSS version 21 software.

Results: In this study, 409 stool specimens were collected from Imam Khomeini and Boooli Hospitals. In total, 22 cases (5.4%) were infected with intestinal parasites. 5.3% of men and 5.4% of women were infected. The rate of infection to the protozoa and helminths was 3.7% and 1.7% respectively. Infection rate of intestinal parasites including Entamoeba histolytica 0.5%, Entamoeba coli 0.7%, Giardia lamblia 1.2%, Blastocystis hominis 1.2%, Dicrocoelium dendriticum 0.97%, Trichostrongylus sp. 0.24%, Enterobius vermicularis 0.24% and free living larvae 0.24%.

Conclusion: The present study showed that infection rate with intestinal protozoa, especially Giardia lamblia and Blastocystis hominis in Ardabil is high, which requires special control measures.

Keywords: Frequency, Intestinal parasites, Patients, Ardabil
Identification and phylogenetic classification of *Fasciola* species Isolated from sheep and cattle by PCR-RFLP in Zabol, in Sistan and Baluchestan Province, Southeast Iran

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**Background:** The detection of *Fasciola* species in various geographical regions is essential for health policy making. Here, we aimed to identify livestock (cattle and sheep) related *Fasciola* genotypes by restriction fragment length polymorphism PCR.

**Methods:** Seventy adult *Fasciola* flukes were collected from 70 infected livers of 35 cattle and 35 sheep slaughtered in Zabol abattoir. *Fasciola* species were determined based on molecular features. For molecular detection, *Fasciola* ITS1 region was amplified and sequenced. A 700 bp fragment was amplified. These were digested with RasI enzyme. *Fasola hepatica* specific fragments were 47, 59, 68, 104, and 370, while those related to *Fasciola gigantica* had 45, 55, 170, 370.

**Results:** Our results showed that, the two main species of *F. hepatica* and *F. gigantica* are responsible for fasciolosis in sheep and cattle in our region. From 35 *Fasciola* isolated from cattle, 3 and 32 were *F. hepatica* and *F. gigantica* respectively. From 35 *Fasciola* isolated from sheep, 4 were *F. hepatica* and 31 were *F. gigantica*.

**Conclusion:** All Seventy *Fasciola* samples from two different hosts (cattle and sheep) were identified as either *F. hepatica* or *F. gigantica* by PCR-RFLP. Genotypic variability of *Fasciola* species was high in our region. It is recommended to assess molecular variation of *Fasciola* isolates in other host livestock.
Keyword: ITS1 PCR-RFLP, Genotyping, *Fasciola hepatica*, *Fasciola gigantica*, Fascioliasis, Iran
Molecular identification of human Blastocystis subtypes in northwest of Iran

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Abstract

Introduction: Blastocystis sp. is a polymorphic intestinal parasite in humans and animals. The parasite has a worldwide distribution, especially in developing countries with poor sanitation, exposure to animals, and improper disposal systems. The aim of this study was to identify the subtypes of Blastocystis sp. among children of Qazvin, northwest Iran.

Methodology: Totally, 864 stool samples were collected from the children referred to Qods hospital in Qazvin, Iran. Fecal specimens were investigated by
formalin-ethyl acetate concentration method and trichrome staining as well as cultivation of all samples in clotted fetal bovine medium. DNA extraction of culture-positive specimens and PCR amplification of 18S ribosomal RNA gene region was performed. The sequences detected were compared with reference genes in the GenBank, and the sequences further deposited in the GenBank database. Statistically, data analysis was performed by Chi-square test while a p-value of < 0.05 was considered as significant.

Result: Of 864 isolates, 4.1% (36/864) were positive for Blastocystis sp. with infection rate insignificantly higher among the females than males. The highest infection rate was estimated at 6.8% in 6-9 years old age group with abdominal pain as the most common (33%) gastrointestinal sing. No statistically significant difference was found between the variables and Blastocystis infection. Molecular analysis clarified the presence of three subtypes of Blastocystis including ST1 (56%), ST2 (28%), and ST3 (16%) of among specimens with ST1 as the predominant subtype. A significant association between intestinal signs and the subtypes was not found.
Conclusion: Considering ST1 as the predominant subtype, it seems that zoonotic transmission is a main route of human infections with *Blastocystis* sp. in the study area.

**Keywords:** *Blastocystis*, Epidemiology, Subtype, Iran
Effects of selenium nanoparticles on acute toxoplasmosis in mice model

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Background: Today, the best medication used to treat toxoplasmosis is the concomitant use of pyrimethamine and sulfadiazine; however, studies in recent years have suggested the side effects of these drugs specially in immunocopromised individuals. In this investigation, the in vivo efficacy and safety of Biogenic Selenium Nanoparticles (SeNPs) were assessed against acute toxoplasmosis caused by Toxoplasma gondii (Sarcocystidae) in mice.

Methods: Here, male NMRI mice were orally treated with normal saline (control group) and SeNPs at the doses of 5 and 10 mg/kg once a day for 14 days. On the 15th day, the mice were infected with 10⁴ tachyzoites of T. gondii RH strain by intraperitoneal route. The mortality rate and parasite load were determined in the infected mice. Additionally, 24 mice were applied to examine the safety of SeNPS after treatment during 14 days. The mRNA levels of IFN-γ, IL10, IL12, and inducible nitric oxide synthase (iNOs) were also examined in the infected mice treated by SeNPs by quantitative real time PCR.

Results: the rate of mortality in infected mice receiving SeNPs at the doses of 5 and 10 mg/kg compared with the mice in control group was 100%, 9 and 10 days after administration. The average number of tachyzoites in infected mice receiving SeNPs at the doses of 5 and 10 mg/kg was 127 × 10⁴ and 56 × 10⁴ was significantly lower than those in control group (288×10⁴ tachyzoites). No significant difference (p>0.05) in the biochemical parameters between the mice
treated with SeNPs compared with mice in the control group. The results revealed that mRNA levels of IFN-γ (P<0.001), TNF-α (P<0.001), IL-12 (P<0.05), and iNOs (P<0.05) meaningfully improved in infected mice treated with SeNPs compared with mice in control group.

**Conclusion:** The findings of the present investigation showed the considerable efficacy of SeNPs with no important toxicity to remedy the acute toxoplasmosis in the mice model. However, further studies are needed to clarify the accurate anti-Toxoplasma mechanisms of SeNPs.

**Keywords:** Prophylactic; Selenium; *Toxoplasma gondii*; treatment; toxicity
A Serological and Molecular study on *Toxoplasma gondii* infection in type 2 diabetic patients in Khuzestan province south west of Iran.

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Abstract

**Background:** *Toxoplasma gondii* is an intracellular protozoan has arisen as an important opportunistic agent. Diabetes is one of the most silent with serious complication disease and type 2 diabetes accounts for 90% of cases of diabetes globally. This study was aimed to detect of toxoplasmosis in type 2 diabetic patients in Khuzestan province south west of Iran.

**Methods:** ELISA and PCR targeting B1 gene were used to analyse blood samples from 377 diabetic patients and 200 from non-diabetic persons during 2015-2017.

**Results:** In ELISA, prevalence of toxoplasmosis were 44.29% (167/377) and 32.5% (65/200) for case and control groups respectively (P<0.05). In case, 153 (40.58%) were seropositive for IgG and 14 (3.71%) were seropositive for IgM. In control, 62(31%) were seropositive for IgG and 3(1.5%) were seropositive for IgM (P<0.05).In nested PCR, 102 out of 167 (61.07%) and 28 out of 65(43.08%)
of the seropositive samples had DNA molecules of B1 gene in case and control respectively. In association of diabetes and toxoplasmosis, the results analysis indicated a positive correlation between disease duration and Toxoplasmosis prevalence.

**Conclusion:** The prevalence of toxoplasmosis antibodies and Toxoplasma gondii DNA in diabetic patients was significantly higher than in non-diabetic patients. Thus, it is recommended to check chronic and acute phases of toxoplasmosis in diabetic patients and repeat it periodically.

**Key words:** Toxoplasmosis, Diabetes, ELISA, Nested PCR
PP-29

Demographic presentation of referred cystic echinococcosis patients to Imam Khomeini hospital in Ardebil city during 2013-2016

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Background: Echinococcus granulosus is the causative helminthic agent of cystic echinococcosis (CE), an important neglected disease which is reported world widely in both humans and herbivores. CE considered as major public health problem due to high incidence of hydatid cyst in Ardebil province. There have been few demographic studies reporting the situation of CE in our area. we assessed characteristics of CE patients who referred to Imam Khomeini hospital over a period of 3 years (2013-2016).

Methods: In this descriptive retrospective study, data were collected from the medical records of CE patients in the archive of mentioned hospital. Information of 82 CE patient such as age, gender, cyst site and location were investigated by using STATA statistical software (version 13.1.).

Results: Average age of 82 patients (39 [47.5%] males and 43 [52.4%] females) was 47.18. The most common localization organ was liver (74 cases), lung (4), spleen (2), abdomen (1) and peritoneum (1). Additionally, 75% of patients were
from Ardebil, 5% Bilesavar, Meshkin shahr, KHalkhal, Germi, Pars Abad per each 2% and 7% other reigns of Ardebil province.

**Conclusion:** Hepatic CE frequently observed among females in Ardebil city. Liver hydatidosis is more common than lung and other organs.

**Keywords:** Hydatid cyst, Surgery, Demographic characteristics, Iran
Parasitic contamination analysis of vegetables in Iran
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Background: We aimed the Meta analysis study on prevalence of parasites transmitted by vegetables in Iran

Methods: In the current Meta-analysis study, by using key-words such as Iran, vegetable, Parasitic contamination, and using search engines SID, Iranmedex, Web of Science, Pub-Med and Google scholar. We did comprehensive data collection. All articles with no row data were excluded. According to inclusion criteria out of 25 articles 23 studies data were analyzed by using Meta analysis software

Results: In this systematic review, of 30 studies, totally 20 articles were included based on inclusion criteria which all had been performed during 2004 to 2017 in Iran. Overall 6777 Samples had been studied in these studies in which Entamoeba Coli, Giardia, Ascaris Egg, Taenia, Hymenolepis nana, Entrobius Vermicularis, Trichostrongylus Egg, Free larvae, Fasciola hepatica Egg, Dicrocoelium Egg Respectively, 29.7%, 21.57%, 18.4%, 11.2%, 7.4%, 11.25%, 5%, 82.75%, 3.5%, 4.14%

Conclusion: Regarding the findings of the present study, it is recommend to thoroughly perform parasite decontamination before the consumption of vegetables. Furthermore, the officials can prevent the parasitic diseases by careful monitoring of public food distribution centers and controlling the source of vegetables in the winter.
Evaluation of the effects of aqueous, alcoholic extracts of *Fumaria* on *Leishmania major* Promastigotes and Amastigote growth under In vitro and In vivo conditions

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**Abstract:**

**Objective:** Leishmaniasis is a collection of parasitic diseases that have widespread clinical symptoms such as Cutaneous *Leishmania*, Muco Cutaneous *Leishmania*, visceral *Leishmania*. Nowadays there are many advances in use of herbal medicines, because of the harmlessness, the cheapness, the availability, the resistance of parasites to the existing drugs in comparison with the chemical drugs such as Glucantime, Amphotericin B. In the present study the effect of aqueous and alcoholic extract of *Fumaria* which is a native Iranian herb (Anti-bacterial, Anti-fugal, Anti arrhythmic effects of the plant has been studied) on the promastigote and amastigot under In vitro and In vivo condition.

**Method and Material:** The aqueous and alcoholic extract of the plant was prepared, then, it was evaluated the effect of different concentration of (1,2,4 mg/ml and 500,250,125,62.5,31.25,15 microgr/ml) of aqueous and alcoholic extract under In vitro and In vivo condition, on the growth of the promastigotes stage of *Leishmania* and infected macrophage with amastigotes by direct count and MTT assay, ‘flow cytometry’.
In the test, each of the wells and microtubes containing culture media and parasites were considered the control group without drug. Also, the effects of aqueous and alcohol extracts of *Fumaria* ointment on lesions caused by *Leishmania major* in BALB/c mice were examined.

**Result:** The MTT and direct count results indicated a significant differences among the number of promastigotes in the control groups or the treated groups, with mentioned concentrations of aqueous and alcoholic extract of the *Fumaria* within 24-48 and 72 hours after parasite culture. The MTT result indicated that aqueous and alcoholic extract of the *Fumaria* is not effective in killing macrophage. The flow cytometry results indicated that in the concentration of 4mg/ml of alcoholic extract, it has the highest amount of apoptosis and necrosis on parasites, 72 hours after parasite culture. Also, it was investigated the destroying effect of *Fumaria* extract on the infected macrophage with amastigotes. In this study, 20 BALB/c mice (5-8 weeks) were randomly classified into 5 groups. Group 1: untreated control, Group 2: Glucantime injection, Group 3: treated with 4 mg/ml alcoholic extract, Group 4: treated with 4 mg/ml aqueous extract the ointment was administered on ulcer for a month. The group treated with alcoholic extract (as ointment) wound diameter was not increased and was approximately constant. These findings were statistically significant different with the control group between 2-4 weeks.

**Conclusion:** The aqueous and alcoholic extracts of *Fumaria* is effective in killing *Leishmania major* promastigotes and infected macrophages with amastigotes In vitro and In vivo.

**Keyword:** *Fumaria, Leishmania major, Amastigote, Promastigote*
The Microscopic Detection of Species of the Plasmodium Parasite Affects Human Malaria

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Background: Malaria parasites are protozoa of the branch of the Api complex and of the Plasmodium dams. Species of the genus Plasmodium are human parasites, called plasmodium vivax, falciparum, malaria and oval, which are the first three species in Iran. The aim of this study was to investigate the diagnosis of the genus of plasmodium in Mazandaran University of Medical Sciences from 1996 to 2018.

Methods: All suspicious febrile patients and Afghan refugees were prepared from thin finger and thin layer on the lam. After drying, diluted with methanol alcohol was fixed, then both were expanded by Giemsa method, and with optical microscope and magnification of 800-1000 times more parasite searches in the blood than in the last three years with R.D.T Species were determined by microscopic examination.

Results: 897 positive patients were diagnosed in Mazandaran province from 1996 to 2018 which were detected by microscopic examination of thin parasite species. 97.9% of the vivax and a very small percentage of plasmodium falciparum (1.7%) were malaria (0.1%) and mixed species (0.2%)

Conclusion: Microscopic diagnosis is still a golden diagnostic method. Given the prevalence of Vivax's disease, hypnozoite should be treated to prevent recurrence of malaria, that is, 8 weeks of treatment.

Key words: Microscopic, Plasmodium, Malaria
Investigation the diseases of malaria in pregnancy

Fariba Abdollahi

Malaria is one important problem of healthy in our country, Iran. This disease is the most tropically prevalence and that transfers plasmodium parasites, by anopheles' sting. It appears with specific clinical and Para clinical symptoms. It has bad effects such as killing, economic and irreparable on patients. It can affect about 50% of on the world's population, directly or indirectly. About 10% of people are living in contaminated areas, that mortality rate is 1.5-3 millions.

In this study we regurd two groups, pregnant mothers and newborns that are the most vulnerable to disease. They need to quick and emergency care. When the danger reaches to critical point, the healthy services are very important and critical. In 2008, there are 11140 patients with Malaria in Iran. In 1991, the affected number were 40000, that 69% of these were habited in Sistan- Baloochestan. 12%-15% of pregnant mothers or newborns are prone to disease.

The pregnant mothers and newborns are vulnerable because of the weak immune response. This may lead to miscarriage or death, respectively.

One of the most important notes is the "low weight of newborn" with infected mothers. Finally it will be more sever when the parasites passes through placenta to embryo. It will causes mental and physical retardation in newborn.

Preventive factors such as mosquito-net, anti fly sprays and avoid from emigration, can be impacting on prevalence and propagating of disease.
Keywords: Malaria, Pregnancy, immune response, low weight, newborns
PP-34

Distribution and genetic characterization of *Blastocystis* subtypes in Qazvin province, Iran

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Abstract

Introduction: Blastocystis is a common intestinal parasite of human and animal hosts. The parasite has 17 subtypes, among those nine subtypes (ST1-ST9) were found in human hosts. The aim of the present study was to investigate the presence of different subtypes of Blastocystis sp. among the patients referred to Velayat hospital of Qazvin province, Iran.

Methodology: Overall, 864 stool samples were examined by using formalin-ethyl acetate concentration method and Trichrome staining. All of positive specimens were cultured in clotted fetal bovine medium. Later, DNA extraction and PCR amplification of 18S ribosomal RNA gene region was conducted and phylogenetic tree constructed.

Result: The results revealed 7.8% (68/864) of the study population were infected with Blastocystis. The prevalence rate of infection was 8.8% in >70 year old age
group which was higher than other age groups. Intestinal symptoms were observed in 61% (36/59) of individuals positive for Blastocystis, with abdominal pain in 58% (21/36) of cases which was more frequent than other intestinal signs. No significant relationship was observed among the study variables. By molecular and phylogenetic analysis, three subtypes ST1 (45%), ST2 (30%) and ST3 (23%) of parasite were identified. There was no statistically significant correlation between intestinal symptoms and the three subtypes.

Conclusion: This study showed ST1 subtype was the predominant subtype among the positive specimens, meanwhile the highest haplotype and nucleotide diversity were clarified in ST3 subtype. The results suggest the presence of a potentially zoonotic transmission route (cycle) in the study area.

Keywords Blastocystis, subtype, Phylogenetic analysis, Iran
Prevalence of the Toxoplasma gondii IgM and IgG antibodies in hemodialysis patients in selected hemodialysis centers of Tehran city in 2017

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Background:

Toxoplasmosis is a common disease among humans and animals, that is caused by the infection of the intracellular protozoan parasite, Toxoplasma gondii. Infection by this parasite is generally without any clinical symptoms, but it can have severe effects in people with immune deficiency, such as those experiencing chemotherapy, transplantation, cancer and AIDS, as well as dialysis patients. Considering the high prevalence of parasites in different parts of Iran, we decided to study the prevalence of toxoplasmosis in hemodialysis patients, in selected centers of Tehran.

Materials and Methods:

In this descriptive cross-sectional study, 260 hemodialysis patients attending 5 dialysis centers in Tehran in 2016 were studied. The serum samples were analyzed for anti-Toxoplasma IgG and IgG antibodies by the ELISA method.

Results:
In this study, 175 (67.3%) of the hemodialysis patients tested positive for anti-Toxoplasma IgG antibodies and 18 (7%) tested positive for anti-Toxoplasma IgM antibodies.

**Conclusion:**

Considering the high prevalence of toxoplasmosis in hemodialysis patients in Tehran compared to other control people in this region, and considering the fact that this infection is one of the most important risk factors in hemodialysis patients, regular screening and detection of antibodies against Toxoplasma gondii is necessary in these patients. Keywords: IgM and IgG, Toxoplasma gondii, Hemodialysis patients, Selected Hemodialysis centers of Tehran.

**Keyword:** Toxoplasma gondii, Hemodialysis, Iran
PP-36

Toxocara spp. infection and risk of childhood asthma: a systematic review and meta-analysis

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Background: Asthma is one of the most common chronic respiratory disease worldwide. There are some evidences to suggest that Toxocara infection is a neglected risk factor for childhood asthma. We performed a systematic review and meta-analysis to further understanding of this relationship.

Methods: Five databases include PubMed, Science direct, Scopus, Web of Science, and Google scholar were searched to identify the relevant studies. We used random-effects meta-analysis model to estimate the Pooled odds ratio (OR) and 95% confidence intervals (CI).

Results: A total of 17 studies including 11 studies with case-control design (1139 patients and 1023 controls) and six studies with cross-sectional design (a total of 5469 participants, 872 asthmatics and 4597 non-asthmatics children) met the eligibility criteria. An increased risk for asthma was observed in children with Toxocara infection seropositivity (OR, 1.91; 95% CI, 1.47–2.47). In sub-group analysis, the pooled ORs were (OR, 2.13; 95% CI, 1.43–3.15) and (OR, 1.73; 95% CI, 1.23–2.44) for case-control and cross-sectional studies, respectively. Moreover, considering to specific IgE seropositivity, a pooled OR of 2.36 (95% CI, 0.93–5.98) was observed. Conclusion: In conclusion, this meta-analysis revealed that children infected with Toxocara spp. are more likely to have asthma compared to non-infected children.

Keywords: Toxocara spp, childhood asthma, meta-analysis
Prevalence of intestinal parasites among food handlers in Iran: a systematic review

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Background: Intestinal parasite infection is one of the most common infections in humans, due to the transmission of parasites through water and food, food handlers can cause transmission and spread of parasitic infections if they do not comply with health principles. This review study was conducted to determine the prevalence of parasitic infections among food handlers in Iran.

Methods: Our study is based on a Systematic review that published databases and journals such as PubMed, Google Scholar, Science Direct, Scopus, ISI, Studies conducted on food handlers from 2001 to 2018 in Iran. Searches were performed based on keywords, entry and exit criteria, then the data were analyzed by descriptive statistics using SPSS 20 software.
Results: A total of 73988 food handlers, 8.07% (5971) were infected with intestinal parasites. 80.09% (4782) of the infection was related to the protozoan infection and 19.91% (1189) was the worm infection. Finally, 9 types of protozoa and 4 types of the worm were reported including: Giardia intestinalis 4.39%, Entamoeba histolytica/E.dispar 1.13%, Blastocystis Spp. 0.40%, Entamoeba coli 0.36%, Iodamoeba butschlii 0.06%, Dientamoeba fragilis 0.05%, Endolimax nana 0.02%, Chilomastix mesnili 0.001%, Cryptosporidium spp. 0.006%, Hymenolepis nana 1.13%, Ascaris lumbricoides 0.51% and Taenia saginata 0.001%.

Conclusion: The Prevalence of worm infection in Iran has decreased but the protozoan infection is significant, while it is less than other countries. Also, the rate of worm infection was lower than in other countries. Extending knowledge about the prevalence of intestinal parasites among foods handlers also their treatment and control can play an important role in reducing the incidence of parasitic infections.

Key words: Intestinal parasites, Prevalence, food handlers, Systematic review, Iran.
PP-38

Prevalence of intestinal parasites in food handlers of the Saqqez in 2016

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Background: This study was aimed at determining the prevalence of parasitic infections among the food handlers of Saqqez County in 2016.

Methods: Stool samples collected from 1530 food handlers. All samples were examined by both direct technique and sedimentation technique using formalin-ethyl acetate for detecting the intestinal parasites.

Results: Of total participants, 1462 (95.6\%) were male and 62 (4.4\%) female. Intestinal parasitic infections were found in 92 (6.01\%) individuals. The highest infection rate was due to Giardia lamblia (4.1\%) and the lowest associated with Endolimax nana, Iodamoeba butschlii, and Hymenolepis nana (0.1\%). No significant correlation between the intestinal parasitic infections and age, gender, education level, gastrointestinal signs and symptoms, and the type of profession, was established.

Conclusion: The results of the present study revealed that only a small number of food handlers in Saqqez County were infected with intestinal parasites with \textit{G. lamblia} as the most common cause of infection. More strict health control for those working in food industries is of vital importance and continuous education to improve the level of general health in these people is undoubtedly considered as a key determinant towards lower number of parasitic infections.

Keywords: Prevalence, Intestinal parasitic infection, Food handlers
Prevalence of intestinal parasites and bacterial pathogens in servants of Seyed-al-Shohada hospital of Farsan (October to December 2018)

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Background: Hospital servants, including food handlers, are in close contact with patients. Screening of these group for parasitic and microbial infections is a health necessary important. This study was conducted to investigate the intestinal parasites and bacterial pathogens contamination in these groups.

Methods: One hundred and fifty-eight stool of 60 servants(41 male and 19 female) were collected. The samples were examined for pathogen bacteria and intestinal parasites following standard procedures. Direct examination with Lugol's iodine and the normal saline solution were used for assessment of parasitic agents. The portion of specimens was transferred to liquid and solid culture media for recognition of the bacterial pathogens.

Results: The age of the participants was 37.63±10.02 years. Overall, 7.5% of participants were positive for intestinal protozoa include, Blastocystis hominis cyst (6.3%), Entamoeba coli cyst (0.6%) and Giardia lamblia cyst (0.6%). We did not find any eggs of parasitic helminths in samples. None of the participants was positive for Salmonella species and Shigella species in respect of their stool contents.
Conclusion: The results of this study showed, most of the found organisms were non-pathogenic. It seems that this group of people also be evaluated for intestinal pathogens in the warm seasons.

Keywords: Intestinal protozoa, *Blastocystis hominis*, *Giardia lamblia*, food handlers
The relationship of maternal chronic toxoplasmosis with serum free testosterone, malnutrition, height and weight of newborns

Abstract

Toxoplasmosis is a widespread zoonotic protozoan infection. One of the possible effects of *Toxoplasma* on the host's body is the increase in testosterone levels. One of the effects of testosterone on pregnancy is a change on the sex ratio. The present study has investigated the relationship between chronic toxoplasmosis, free testosterone levels and male birth in pregnant women. In this study, two-stage cluster sampling was conducted from health centers of Hamadan city in 2013 and 2014. After obtaining informed consent from the volunteers, blood samples were taken from each of them and their serum was tested by IgG ELISA, IgM ELISA and IgG avidity tests. Pregnant women with chronic toxoplasmosis were selected as case group and non-infected women with toxoplasma as a control group. Then, serum free testosterone was measured in both groups and after delivery, the newborns height, weight and sex were recorded. Data were analyzed by independent t-test, Pearson correlation coefficient, Chi square ($X^2$) and Fisher's exact tests. The results showed that testosterone levels were significantly higher in pregnant women with chronic toxoplasmosis than in women without toxoplasmosis ($P = 0.001$). But there was no significant relationship between maternal toxoplasmosis and weight ($P = 0.093$) and height ($P = 0.089$) of infants and also sex ($P = 0.109$). Moreover, the statistical analysis showed no significant correlation between maternal testosterone level and height, weight and sex of the infant. In the present study, the male birth in women with chronic toxoplasmosis
was higher than non-infected women. However, this significant difference was not observed. Further studies are needed on the possible role of factors affecting the male birth in mothers with toxoplasmosis, including changes in hormone levels or modifications in the immune system.

**Keywords:** Toxoplasmosis, Testosterone, Malnutrition, Newborns
Preparation of monoclonal antibody with hybridoma technology against Leishmania amastigote antigens to use in diagnosis

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Objective: Leishmaniasis is widely distributed around the world and they are greatly important for human as a parasite of serious infectious diseases. It is one of the important contagious diseases caused by parasites of the genus Leishmania which is common throughout the world and Iran. Visceral Leishmaniasis if not recognized in appropriate time, could result in death. The aim of this study was to apply different methods to production of monoclonal antibodies against amastigotes forms of Leishmania.

Methods: At first, standard strains were cultured and axenic amastigotes antigens of L. infantum were obtained. After that, immunization of Balb/c mice and determining of antibody titer were conducted. For hybridoma cell formation, Isolated lymphocyte cells from spleen of immunized mice and myeloma cells were fused in the rate of 10 to 1 ratio at presence of polyethylene glycol and limiting dilution method was applied for monoclone determining.

Results: About, over than 25 positive mono clone were Hybridoma obtained that 4 clones have optical density over than 1. We named these clones as 8D2 FVI6, 8D2 FVI3, 6G2 FV4 and 6G2 FV3 which were selected for limiting dilution. From these hybrids, Anti-Amastigotes L. infantum monoclonal antibodies were obtained. The result of Isotype determination, showed in IgG2b position and did not show any antibodies in IgG1, IgG2a & IgA position.

Conclusion: The only way to counter Leishmaniasis is treatment of it. The first step in its treatment is diagnosis of it in appropriate time and distinction of the host from other diseases. This study produced monoclonal antibody against amastigotes of Iranian strain of L. infantum for the first time. It seems that these
antibodies have appropriate reactivity against Iranian strain of *L. infantum* and could be used in tests for research and in diagnosis.

Key word: monoclonal antibody, hybridoma technology, *Leishmania* amastigote
In Vitro studies of Anti leishmanial effect of Artemisia Fragrance extract on Leishmania major

Introduction: Artemisia plant is used as a traditional medicine in Asia for the treatment of inflammatory and infectious diseases as like parasitic. The alternative therapies using natural products are inexpensive and have few or any adverse reaction. These reasons are sufficient to investigate the new natural therapeutic for leishmaniasis. We evaluated the anti leishmanial activity of Artemisia Fragrance on Leishmania major promastigote and amastigote forms.

Material and method: in this study Promastigote and macrophage cells viability were evaluated using the MTT method. Promastigotes (1×10⁵ parasites/100 ml/well) from a logarithmic growth phase culture were seeded into 96-well tissue culture microplates. Artemisia Fragrance extract diluted in series from 400 µg/mL to 25 µg/mL in a 96-well culture plate. After 24 and 48 h incubation at 25 C, 10 µg/mL of MTT were added to each well. The result was measured at a wavelength 450/650 nm using a spectrophotometer plate reader. The lethal dose (LD50) was defined as the dose of the extract that reduced the survival of Leishmania parasites by 50% compared with untreated parasites. J774 macrophages was adjusted to (1×10⁴ cell/100ml/well). Next, 100µl of extract concentrations were added to per well and plates were incubated for 24 and 48 h at 37°C, 5% CO₂. The cytotoxicity concentration (CC50) was defined as the dose of the compound that reduced 50% of the survival of macrophages.

Results: Fewer than 50 µg/ml concentrations of A. Fragrance extract were no appreciable effect on the parasite. According to MTT, the toxic effect of extract on L. major promastigotes increased with increasing drug concentration.

Conclusion: This study revealed that Artemisia extract has a little toxic effect on macrophages. According to the MTT results, this extract can be suggested as an appropriate drug for in vitro antileishmanial study.

Key words: Leishmania major, Artemisia Fragrance, MTT method, In vitro, Parasite
Hyper eosinophilia in worms parasitic infections

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Background:

Eosinophilia often has significant role which can be suggesting parasite infection. This phenomenon is more noticed in worm parasites (Helminthes) than protozoa, specially if tissue invasion by parasite accures but the degree and severity differs from patient in fresh infection than chronic infection by may have associated to other factors like allergic diseases or other predisorders, as collagen diseases. The purpose of this study was to investigate the relation between eosinophilic and parasitic infection.

Methods:

In this study, ten percent of population from hill stations and villages of flate area of sari township with direct and flouting methods, intestinal parasites were examined. 539 patients were positive and 161 negative blood samples were collected from the fingertip and examined after fixation with methanol and staining with giemsa.

Results

From 700 people under investigation, blood film was prepared to study eosinophilia, out of these (N=539) cases wew positive and 161 cases were negative, of the 539 positive people 172 has eosinophili (31.9%) and 367 people were non eosinophilic (68.1%) on the basis of chi-squers equation between eosinophilic and infection with intestinal parasite, there is meaningful reason on the other hand.

Conclusion

The parasitic infection can be one of the reasons of eosinophilic (P<5%). From the studied intestinal parasite the highest rate of eosinophilia (31%-40%) belonged to
trichostrongylus but the highest average (70.3%) also the personal eith mixed infection of ascaris plus trichocephal showed more eosinophilia.

Eosinophilia can be one of the important diagnostic factors in parasitic infections especially worms. When the worms are immature and have no ability to spawn and Parasitic experiments not possible.

**Key words:** Hyper eosinophilia, parasitic, worms
Investigation of associated infections in AIDS patients: toxoplasma, HBSAg, HCVAb

Background:
Toxoplasmosis in immunocompetent people is generally asymptomatic but in immunocompromised patients including HIV/AIDS, cancer patients, and organ transplant recipients, etc. it can lead to serious pathological problems. The objective of current study was to determine HCV Ab and HBSAg and the seroprevalence of T. gondii IgG and IgM antibodies in HIV/AIDS patients using ELISA technique in Mazandaran Province, northern Iran.

Methods: Overall, 82 serum samples (61 males and 21 females) were collected from HIV/AIDS patients in Mazandaran Provinces, in 2013. Sera were surveyed employing ELISA assay. Data were analyzed using Chi-Square or Fisher exact test. In addition, before sampling a questionnaire was filled out for each subject.

Results: Overall seroprevalence of examined sera was 96.3% for IgG antibody but none of the sera shown IgM antibody against T. gondii. The seroprevalence of toxoplasmosis in males and females was 96.7% and 95.2%, respectively. An antibody titer of >1 IU/ml was considered as positive. Furthermore, none of the included variables statistically was significant. Also, 61 of the AIDS patients had hepatitis C infection, -four of them had hepatitis B virus.

Conclusions: Seroprevalence of chronic (latent) toxoplasmosis in HIV/AIDS patients in Mazandaran Province is high compared to toxoplasmosis in general population. Consequently, the risk of acquiring Toxoplasma encephalitis in examined seropositive HIV/AIDS patients of Toxoplasma is high. Therefore, there are viral and parasitic infections in HIV positive and cause the death of AIDS patients.

Keyword: associated infections, AIDS patients, toxoplasma, HBSAg, HCVAb

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Abstract

Background and Objectives: Cutaneous Leishmaniasis disease is one of the health problems in tropic and semi tropic regions like Iran. So therefore, this is so necessary to study the prevalence and identify the new focus of this disease in different region of Iran. This study was conducted to survey prevalence of Cutaneous Leishmaniasis in Behbahan County in 2011-2014.

Methods: In the present study, 300 Cutaneous Leishmaniasis's patients (dry and moisture) that look up to Behbahan center of health service were investigated in 2011-2014. For studding this disease, some parameters were noticed such as outbreak months, history of Patients tripe to the polluted area before outbreak of disease, job, the anatomic local of sore in patient's body, the number of sores, sex and type of sore (dry and moisture).

Result: The 300 suspected cases 2011 to 2014 came to the health center of city Behbahan city, Direct and spread test and existence Leishman body (amastigote) in the wound in 182 (60/60%) of patients were positive, that 136 (74.72%) were male and 46 (52.27%) of paitiens were female.

Conclusions: This study tooke place fpr the first time in Behbahan city in Kuzestan province to investigate various aspects of the epidemiology of cutaneous Leishmaniasis. There is a posiiibility of spread of the disease in unknown area, so
in addition to health centers, other centers should also be prepared to deal with the disease.

**Keywords:** Leishman body, Cutaneous Leishmaniasis, Behbahan
PP-49

Abattoir Study of Hydatid Cyst Infestation in domestic animals from region of Kohgiluyeh.

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Abstract:

Background and purpose: Survey the population of livestock to hydatid cyst, is most important in terms of the public health and economic perspective, Definitive diagnosis id by necropsy and or inspection after slaughter.

The aim of this study was to investigate the prevalence of hydatid cyst in domestic slaughtered animals in indudstrial slaughterhouse of Dehdasht, Kohgilouyeh and Boyerahmad province (February -July 2014).

Materials and Methods: In this study was investigated 5066 head of animals (sheep, cows and goats). Their carcasses were inspected using macroscopic method for hydatid cyst in livers and lungs. Data analysis was performed by Chi-square test and SPSS software (Version 20.0).

Results: The prevalence frequency of hydatidosis in slaughtered animals was 59 (1.3%). Moreover, 18(0.35%) infected lungs and 27(0.53%) infected livers and 14 (0.27%) liver and lung simultaneously were found. On the seasonal bases, the surveys showed that maximum spread of the disease was in spring.

Conclusion: The prevalence of hydatid cysts of parasites is relatively high which in addition to imposing high economic losses due to the deleting of infested organs of animals and decrease in livestock products, indicates the existence of conditions for health risks for residents which requires more inclusive and
comprehensive sanitary and control measures due to this parasite's life cycle and transmission

**Key words:** Hydatid cyst, Slaughtered animals, Zoonoses, Human.
Epidemiological study of clinical hydatid cyst in Jahrom’s health centers between 2012 and 2017

Abstract:

Background:
Echinococcus granulosus is a rare parasitic infection causing Hydatid cyst which can be dangerous due to involving main body organs as brain, liver, and lung. This parasitic infection is a major health problem in Iran. Regarding the less attention paid to these parasites in Jahrom city (Fars province, Iran), we aimed to investigate the epidemiology and the economic impact of disease.

Method:
In this descriptive cross-sectional study, the files of 137 patients who were under the care and treatment of the final diagnosis of hydatid cyst were evaluated by a full-scale method and the information such as age, sex, occupation, place of residence was collected and analyzed by SPSS V19 software.

Results:
In terms of clinical symptoms, the main complaint at diagnosis, in all cases referring to the Jahrom Hospital was abdominal pain. Also, cough and fever were seen in 19.04% and 52.9% of them, respectively. Besides, 71.42% of the cases had liver involvement alone, 52.9% had lung involvement alone, 52.9% had both liver and lung involvement, and 4.74% had kidney involvement. There was no statistically significant relationship between age in the hospitalization time after diagnosis of hydatid cyst (P = 0.765).

Conclusion:
Hydatid cyst is an endemic disease in Jahrom city. Regarding the risk of hydatid cyst and its lethal side effects, it is necessary to pay attention to this disease and ways to prevent its harmful and economic consequences.
ASSOCIATION BETWEEN TOXOPLASMOsis AND TOXOCARIASIS WITH A RHEUMATOID FACTOR IN DIABETIC PATIENTS AND HEMODIALYSIS PEOPLE

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Keyword: Diabetic patients, Hemodialysis, Toxoplasmosis, Toxocariasis, Rheumatoid Factor.

Abstract
**Background:** In spite of the importance of toxoplasmosis and toxocariasis for the high-risk groups such as immunocompromised and autoimmune individuals, the infections is categorized as a neglected tropical disease by World Health Organization. In this study, we investigated seroprevalence and risk factors of toxoplasmosis, toxocariasis and their co-infection in diabetic patients and non-diabetic patients undergoing hemodialysis, referred to the Golestan hospital in Ahvaz city, southwest of Iran.

**Materials and Methods:** A total of 652 subjects comprising of both diabetic and non-diabetic patients undergoing hemodialysis were enrolled in this study. All sera samples were investigated for the presence of IgG antibodies against *Toxoplasma gondii* / *Toxocara* spp. and their Rheumatoid factor (RF) were examined by ELISA. Moreover, associated risk factors were obtained from participant’s responses to questionnaires. Data analysis for this study was performed using the SPSS software version 20.

**Results:** Seroprevalence of toxoplasmosis, toxocariasis and their co-infection among the diabetic patients was 38.69%, 10% and 4.78%, respectively and among individuals undergoing hemodialysis were 28.12%, 11.46% and 5.2%,
respectively. In our study, significant association was not found between rheumatoid factor and *T. gondii/Toxocara* spp. titration.

**Conclusion:** we believed a great need for more epidemiological studies to better understanding overlaps between *T. gondii* and *Toxocara* spp. in diabetic patients and undergoing hemodialysis individuals. Also, further studies will be necessary to clarify the pathogenesis of Toxoplasmosis/Toxocariasis in humans to understand whether these are two parasitic infections is a cofactor in the development of autoimmune diseases such as rheumatoid arthritis.

**Keywords:** Toxoplasmosis, Toxocariasis, Diabetes, Hemodialysis, Rheumatoid factor
Prevalence and Genetic Characterization of *Cryptosporidium* Species in Calves and Dairy cattle in Isfahan province, Iran

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**Background:** *Cryptosporidium* infection is the important intestinal protozoan with a different host range, having the capability to infect humans and different animals such as mammal, reptiles, birds, amphibians and fish. Among the different animals, cattle are considered to be one of major animal reservoir hosts of *Cryptosporidium*. *cryptosporidium* in cattle is of major concern due to the huge number of cattle and their economic importance. *Cryptosporidium* infections can be causes morbidity, weight loss and failure to thrive and especially sometimes mortality in young animals.

**Methods:** From October 2015 to June 2016, 174 bovine fecal samples were collected with and without diarrhea, from 11 dairy farms in Isfahan province, Iran. samples examined by microscopically for *Cryptosporidium spp*. All infected samples were also analyzed using nested-PCR method. A polymerase chain reaction (PCR)-restriction fragment length polymorphism (RFLP) analysis of the small-subunit (SSU) rRNA gene used to detect and identify *Cryptosporidium spp*. in PCR- positive samples.

**Results:** The overall prevalence of *Cryptosporidium* infection was 12.1% (21/174) which confirmed by PCR. Out of them, 17.03 % calves and 6.1% cattle were infected.

**Conclusion:** Our results shown that *C. parvum* is the major cause of infection in calves and Dairy cattle in Isfahan province and it could be as infection source in human.

**Keywords:** *Cryptosporidium*, PCR-RFLP, Calve, Dairy Cattle, Iran
Elevated serum level of IL-4 levels in Neuromyelitis Optica and Multiple Sclerosis patients

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Abstract

Background: Mediators have central roles in pathogenesis of neurodegenerative diseases. IL-4 is one of the most important cytokines which has regulatory impact on immune cells. We evaluated the level of IL-4 in new diagnosed Neuromyelitis Optica (NMO) and multiple sclerosis (MS) patients compared with healthy subjects.

Methods: In a case-control study we evaluated the IL-4 levels in new diagnosed untreated NMO and MS patients in comparison with age and gender matched healthy controls (each group consisted of 45 subjects). ELISA was used to measure levels of cytokines and data was analyzed by SPSS (ver.20).

Results: Elevated plasma level of IL-4 was seen in both NMO and MS patients compared with healthy people (P<0.001), but no significant association was found.
between MS and NMO patients (P=0.071). Furthermore, gender and AQP4-Ab had significant impacts on level of IL-4 in NMO patients (P<0.001).

**Conclusion:** Our results suggested that IL-4 could be a promised diagnosed marker for both MS and NMO disease and higher level of this cytokine compared to healthy controls is thought to have a possible regulatory role after attacks on immune cell such as macrophage as well as astrocyte.

**Keywords:** Interleukin-4, Neuromyelitis Optica, Multiple Sclerosis
PI-2

Evaluation of total salivary antioxidant level in smoker and non-smoker patients with chronic periodontitis.

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Background:

Periodontal disease is the most common inflammatory disease of the mouth and smoking is considered as a strong risk factor for it. Smoking can change immune response, oxidants and antioxidants capacity in saliva. So, in this study evaluated total salivary antioxidant level in smoker and non-smoker patients with severe chronic periodontitis attending to Zahedan Dental School in 2012-2013 academic year.

Methods:

63 patients with severe chronic periodontitis including 27 smokers and 36 non-smokers were selected as control group that had no systemic diseases. Samples of stimulated saliva were taken and transferred to the laboratory to determine the total antioxidant capacity of saliva. Data were analyzed by SPSS 18 software and statistical T-Test and ANOVA.

Results:

In this study, total antioxidant capacity of saliva in smokers with periodontitis (378.43±207.34 µm/lit) were lower than non-smokers (698.30±231.68 µm/lit) that
the difference was statistically significant (P=0.001). Total antioxidant capacity of smokers with use of more than 10 cigarettes were significantly lower than those who used less than 10 cigarettes per day (P=0.033). Total salivary antioxidant capacity in smokers had no significant difference based on duration of smoking (P=0.23). In this study, total antioxidant capacity of saliva was higher in women than men, and this difference was statistically significant (P=0.035). Total antioxidant capacity of saliva in patients with periodontitis in different age groups, was not significantly different (P=0.84).

Conclusion:
Total antioxidant capacity of saliva in smokers with generalized severe chronic periodontitis was lower than non-smokers with generalized severe chronic periodontitis. Therefore, Smoking causes changes in the antioxidant capacity of saliva and it can be involved in the pathogenesis of periodontal disease.

Keywords:
Periodontitis, Antioxidants, Saliva
PI-3

Evaluation of host CCR1 and CCR2 gene expression and expression of virulence CPF10 gene of *Mycobacterium tuberculosis* in patients with tuberculosis

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**Background:** Tuberculosis (TB) is the world’s second most common cause of death from all infectious diseases. A primary pathologic feature of *M. tuberculosis* infection is the formation of a granuloma. Immune cells migrate to the lung and then through the lung to the site of infection to form a granuloma. This structure contains the infection, and is often maintained for a long period of time. Since chemokines and chemokine receptors direct cells to specific sites within the tissues, it is plausible that these cells participate in granuloma formation. CFP10 (culture filtered protein 10) have been described as dominant antigens recognized by T-cells, which plays an important role in disease severity. In this project, we decided to evaluate the host/pathogen interactions in tuberculosis patients using assessment of gene expression of the chemokine receptors CCR1 and CCR2 in host and tuberculosis virulence factors, CFP10.

**Method:** Pronchoalveolar lavage (BAL) fluid samples were collected from pulmonary TB group (TB+) (14 cases) and non-TB lung disease group (TB-) (16 cases). After RNA extraction, cDNA synthesis and the gene expression of CCR1, CCR2 and CFP-10 was evaluated by Taqman Real Time PCR.
Results: Comparing the results of the TB + and TB - groups showed gene expression of CCR1 and CCR2 in TB + group was significantly greater than TB - group (3.55 and 1.64 times), respectively (p = 0.01). CFP 10 gene was expressed in all samples of TB + group (0.011± 0.03).

Conclusion: The results of this study showed that CCR1/ CCR2 expression in TB + patients was higher than the TB- group. Forasmuch as only CCR2 was essential to control high dose M. tuberculosis infection, in the case of active tuberculosis, the recruitment of active T cells will be less and thus the host immune system is not able to completely eliminate the infection.

Keywords: Mycobacterium tuberculosis, CCR1 ,CCR2, CFP-10
A study of the polymorphisms of pre-mir-499 rs3746444 T/C and pre-miR-146a rs2910164 C/G in the autoimmune diseases of rheumatoid arthritis and systemic lupus erythematosus in the west of Iran

Abstract

**Background:** In recent years, a great number of studies have focused on the potential effects of miRNA polymorphisms on susceptibility to many diseases. The present research is a case-control study to analyze the influence of pre-miRNA-146a rs2910164 and pre-miRNA-499 rs3746444 polymorphisms as candidate susceptibility factors for both rheumatoid arthritis (RA) and systemic lupus erythematosus (SLE).

**Materials and methods:** Polymorphism in Mir146 and Mir499 using ARMS-PCR was genotyped on 139 autoimmune disease (AD) patients (89 RA and 50 SLE) and 237 healthy control subjects.

**Results:** A significant increase in the likelihood of carrying the GC vs GG of pre-mir146-rs2910164 and T vs C allele of pre-Mir499-rs3746444 in patients with RA was found. On the contrary, it was observed that patients with RA were less likely to carry the TC + CC vs TT genotype and the C vs T allele of pre-mir499-rs3746444. In females with the GC vs GG and GC+ CC vs GG genotypes, a significant association was found with the increased risk of RA. Interestingly, it was shown that the genotypic combination of TC of the pre-mir499-rs3746444 with GG of pre-mir146-rs2910164 more strongly decreased the risk of RA. In patients with SLE, no notable associations were found between both pre-miRNA-146a rs2910164 and pre-miRNA-499 rs3746444 with risk of disease.

**Conclusions:** These findings indicate that genetic polymorphisms of Mir146 rs2910164 is associated with RA susceptibility especially in females.
Interestingly, it is suggested that there is a potential in Mir499 to reduce the risk with the protective effect of gene-gene interactions on Mir146 in RA disease.

**Keywords:** MicroRNA polymorphisms; mir146 rs2910164; mir499 rs3746444; rheumatoid arthritis; systemic lupus erythematosus
PI-5

Manipulating macrophage polarization and function using classical HDAC inhibitors: Implications for autoimmunity and inflammation

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Macrophages are an important player in defense against invading pathogens and their dysfunction is linked to most of inflammatory and autoimmune diseases. Inflammation is a normal and physiological response of the immune system against harmful stimuli such as infection and injury. However, when allowed to continue unchecked, under certain conditions it turns into autoimmune or inflammatory diseases, neurodegeneration, and carcinogenesis.

Currently, several safe and effective anti-inflammatory drugs are available with many more drugs in the development pipeline, among which are histone deacetylase inhibitors. Posttranslational modifications of histones influence the innate and, adaptive immunity through macrophage survival, proliferation, polarization and, functional responses. Also, Emerging classes of pharmacological agents which developed for use as anti-cancer agents, have been applied as anti-inflammatory drugs to treat macrophage-mediated inflammatory and autoimmune diseases.
Keywords:

Histone deacetylase inhibitor, Macrophage polarization, Autoimmunity, Inflammation
PI-6

Prokaryotic Influenza Virus Nucleoprotein induced specific antibodies in mice

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Introduction

Influenza is among the most well-known diseases that cause acute respiratory problems in patients, which may end to death. Because of constant antigenic changes in various strains of influenza viruses, researchers have concentrated on using protected/conserved antigens as influenza vaccine. In this study, the efficacy of NP supplemented with Alum is investigated as a universal subunit vaccine in Balb/c mice.

Materials and method

Pet28a-NP structure is expressed in prokaryotic host (E.coli). The recombinant NP protein was purified by Electro Elution method and injected to Balb/c in three doses, alone or supplemented with Alum. Negative control group was received phosphate buffer saline. Two weeks after the last immunization, mice sera were taken and investigated by Elisa assay.

Results
The results demonstrated that NP can be induced specific antibody responses with no adjuvant, but using this protein with Alum adjuvant would increase humoral antibody responses against NP antigen.

Conclusions

One of the main challenges for using recombinant subunit vaccines is limitations of transmission and immunization. So, we suggest using the Alum adjuvant to increase immune response against virus internal proteins like NP as an effective candidate vaccine.
PI-7

Decreased expression of ICAM-1, VCAM-1 and E-selectin by cultured human endothelial cell lines upon exposure to aqueous extract and saponin fraction of Tribulus terrestris L.

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Background: Atherosclerosis is a chronic inflammation that interferes blood arteries functions due to the accumulation of low density lipids and cholesterol. The aim of this study was to investigate the effect of aqueous extract and saponin fraction of Tribulus terrestris L. on the expression of Intracellular Adhesion Molecule-1 (ICAM1), Vascular Cell Adhesion Molecule-1 (VCAM1) and E-selectin in the Human Umbilical Vein Endothelial Cell (HUVEC) and Human Bone Marrow Endothelial Cell (HBMEC) lines in normal and lipopolysaccharide (LPS)-induced conditions (in vitro).

Methods: The HUVEC and HBMEC cell lines were cultured and induced with LPS. The effect of aqueous extract and saponin fraction of T. terrestris on the expression of endothelial cell proteins including VCAM-1, ICAM-1 and E-selectin were assessed using SDS-PAGE and Western blot techniques in the normal and LPS-induced conditions.

Results: Aqueous extract and saponin fraction of T. terrestris evidently affected protein pattern of HUVEC and HBMEC lines, thereby the expression of proteins with molecular weight of more than 90 and 65 KDa down-regulated. The findings also indicated down-regulation of the adhesion molecules (ICAM-1, VCAM-1 and E-selectin) in both normal and LPS-induced HUVEC and HBMEC lines.

Conclusions: Aqueous extract and saponin fraction of T. terrestris exerted anti-inflammatory activity on HUVED and HBMEC cell lines and decreased the expression of ICAM-1, VCAM-1 and E-selectin. However, anti-inflammatory
effect of aqueous extract was more than saponin fraction. In conclusion, *T. terrestris* could be a candidate for the treatment or prevention of atherosclerosis.

**Keywords:** Atherosclerosis, ICAM-1, VCAM-1, E-selectin, *Tribulus terrestris* L.
PI-8

In vitro reduction of adhesion molecule genes expression under the influence of aqueous extract and saponin fraction of Tribulus Terrestris L.

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Background: Atherosclerosis (AS), an inflammatory disease, is known as the major cause of mortality and morbidity in the industrialized world. Tribulus terrestris Linn. (TT) has been used since ancient times for treatment of various diseases. Due to the anti-inflammatory activity of the TT plant, the present study investigated the effect of aqueous extract and saponin fraction of TT on gene expression of Intracellular Adhesion Molecule-1 (ICAM1), Vascular Cell Adhesion Molecule-1 (VCAM1) and E-selectin expression in two human endothelial cell lines in vitro during normal and LPS-induced conditions.

Methods: Human umbilical vein endothelial cells (HUVEC) and human bone marrow endothelial cells (HBMEC) were cultured, stimulated by lipopolysaccharide (LPS), and treated with an aqueous extract and a saponin fraction of TT. Then, the expression of ICAM-1, VCAM-1 and E-selectin genes during normal and LPS-induced conditions was investigated through Real-Time PCR.

Results: The LPS-induced HUVEC and HBMEC cell lines treated with the aqueous extract and saponin fraction of TT, showed progressive decrease in expression of ICAM-1, VCAM-1 and E-selectin genes in comparison to control wells.

Conclusions: Taken together, our data suggest that TT may have an anti-inflammatory effect, however the extract showed more anti-inflammatory effect than the saponin fraction. More anti-inflammatory effect of the extract may be due
to the presence of other chemical constituents such as flavonoids and alkaloids. Studying in vivo anti-inflammatory effect of this herb may provide new insights into the development of herbal drug for prevention/therapy of atherosclerosis.

**Keywords:** Atherosclerosis, Tribulus Terrestris Linn., ICAM-1, VCAM-1, E-selectin.
Review of Relationship between Intestinal Microbiota and Development of Multiple Sclerosis

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Background: Microbiotas are the microorganisms living in different points of the human body including the skin, intestine, genital system, and nose. These microbes have complicated communications with the immune system and are often active for developing hemostasis. The human intestine is a very good place for living of a large number of microbiota and a different range of microbiotas live in the intestines of different individuals. Also these microbes are able to secrete a specific substance that leads to immune responses in a particular direction such as inflammatory and non-inflammatory directions. Studies show that one of the reasons for the autoimmunity and inflammation of the immune system is gastrointestinal microorganisms. Multiple sclerosis or MS is one of the autoimmune diseases that is developed by attack of pathogenic auto-reactive T cells to the central nervous system (CNS). Current study aims at providing a brief overview of effects intestinal microbiotas effects on immune system function in the development of multiple sclerosis and its resulting inflammation.

Methods: This review study was conducted with search in library resources as well as databases such as PubMed, Google scholar, Elsevier, and Magiran.
Results: Studies on the patients with autoimmunity indicate changes in the combinations and intestinal microbiotas of these individuals compared to healthy ones, which leads to inflammation and activation of autoimmune cells. Because auto-reactive cells with high affinity against auto antigens of CNS are present also in the healthy individuals, but do not pass the blood-brain barrier and remain silent. However, sometimes these cells are activated in environmental tissues such as the lungs and intestines. In development of MS, TH1 and TH17 cells are the main pathogenic factors. In addition, animal studies and evidence have shown that the compounds and the intestinal microbiotas are highly effective in transformation of these pathogenic T cells from inactive state to effector and the production of inflammatory cytokines such as Interleukin17. Other reports indicate presence of dysbiosis in the intestinal microbiota in these patients. On the other hand, these patients have fewer bacteriuroids, parabacteriosides, Prevotella and Lactobacillus gemera than normal people and have a higher rate of Akkermansia, Blautia, Ruminococcus and Bifidobacterium. Studies have also shown that a non-microbial mouse is highly resistant to MS, but if intestinal microbiota of a patient with MS is transmitted to a non-microbial mouse, it causes inflammation and MS disease in the mouse.

Conclusion: Intestinal microbiota seems to be very effective in maintaining tolerance, and if the combination of bacteria out of balance, it can cause inflammation. In fact, the microbiota range of the intestine can change the proportion of cells that are effective during an autoimmune disease such as MS. In patients with MS, microbiota can activate the autoimmune cells.

Keywords: Intestinal Microbiota, Multiple Sclerosis, autoimmune disease.
Prevalence of vitamin D deficiency and its associated factors in in Kashmar city in 2017

Background: Vitamin D deficiency health threats are evident since a century. Nowadays, vitamin D deficiency became a global pandemic with over one billion people affected in all age groups and both genders. Furthermore, vitamin D deficiency was found to be a potential contributing cause of death in patients with cardiovascular diseases, cancers. Prevention and early diagnosis and treatment of vitamin D deficiency are identified as key tools to reduce its health burden and promote health notably in the elderly.

Methods: This study aimed to determine the prevalence of vitamin D deficiency and insufficiency and related risk factors among healthy adults in Khashmar. A representative random sample of 4000 adults was taken in 2016-2017. Vitamin D and calcium complement and were collected via a brief interview. Blood samples were collected and serum level 25 (OH) D3 were measured using ELFA method with mini vida. Data analysis was performed using SPSS 21 software. The participants were divided into four categories according to their serum concentrations of 25-hydroxyvitamin D and also their age.

Results: Only 15% of the population had a “sufficient” serum 25(OH)D level 30-100 ng/mL, whereas 35% had “insufficient” [serum 25(OH)D level 10-30 ng/mL], 30% had “deficient” [serum 25(OH) ng/mL D level <10 ng/mL], and 10% had “intoxication” [serum 25(OH)D level >100 ng/mL].

Conclusion: The prevalence of vitamin D deficiency was greater among male 15-50 years old lower among people who use calcium complement and in female >75 years old.

Keywords: level of vitamin D, Prevalence, deficiency,
PI-11

The effect of metformin on the viability of gastric cancer cell line (MKN-45)

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Background: metformin, is a drug used for type 2 diabetes, may also have anticancer effects. In this study we want to examine the effect of metformin on gastric cancer cell line (MKN-45) viability.

Methods: 15× 10^3 gastric cancer cells/well were cultured in a 96-well plate for 24h, prior to treatment with various concentration of metformin (1mM, 5mM and 10mM) for 24. Subsequently MTT solution was added to each well and the plate was incubated for 3 hours. The medium was then removed and 100µl DMSO was added. Absorbance was read at 540nm using the ELISA reader.

Results: According to obtained results, the percentages of cell viability were 92%, 85% and 82% in cell cultures that was treated with 1mM, 5mM and 10mM respectively. Two higher dose of 10 and 5 were significantly (P≤0.05) different between test and control (non-treated).

Conclusion: as a result, we revealed that metformin inhibited the growth of gastric cancer cells in a dose dependent manner. It seems that metformin induces cell death by apoptosis induction.

Key words: gastric cancer, metformin, MKN-45
PI-13

Serum Hepatitis B Surface Antigen Quantitative Test versus Hepatitis B Virus
Polymerase Chain Reaction in Detection of Hepatitis B

Background: Hepatitis B virus polymerase chain reaction (HBV PCR) is a test that
used in evaluation and treatment of hepatitis B but this test is pretty expensive and
may be not available everywhere. Serum hepatitis B surface antigen (HBsAg)
quantitative test may be surrogate test that was available and much low price. The
aim of this study was to compare the accuracy of two tests.

Materials and Methods: HBsAg positive patients that referred to Yazd Bouali lab,
Iran for HBV PCR test during two years were selected. The subjects divided into
three groups for initial diagnosis inactive carrier (Group I), beginning of treatment
(Group II) and on treatment (Group III), and thirty in each group. 5mL blood
sample was obtained from each subject. HBV PCR was performed using real time
PCR method with senility of 150 Copy/ml. HBsAg and HBeAg levels were
measured by Electrochemiolance LIASION device. Level of upper than 0.025 Iu/mL
was considered positive for HBsAg.

Results: Serum HBsAg level was significantly different between group I
(1.7367×10^5 Iu/mL) and group II (5.6707×10^5 Iu/mL) also, between group I and
group III (6.1042×10^5 Iu/mL) (p=0.001). Viral load was significantly different
between groups (P<0.05). Serum HBsAg level and viral load showed positive
correlation (P=0.001, R=0.527). There was a correlation between HBsAg and viral
load in group I (P=0.017, R=0.431) and group II (P=0.023, R=0.427). Serum HBsAg levels and viral loads were different between HBeAg positive and negative (P=0.002 and 0.001 respectively).

**Conclusion:** HBsAg quantitative measurement may be a surrogate test for evaluation of hepatitis B patients that more simple and economic.

**Key words:** HBsAg, HBV PCR, HBeAg, HBV
Hydrogen sulfide improves anxiety in a murine model of chronic asthma induced by ovalbumin

Abstract

Objectives: Comorbidity of anxiety has been reported to aggravate the control of asthma symptoms. According to the important role of oxidative stress in the pathophysiology of asthma and anxiety, this study investigated whether hydrogen sulfide (H2S) as an antioxidant agent, has anxiolytic effects in a murine model of chronic asthma.

Materials and Methods: BALB/c mice were randomly divided into 4 groups (n = 8): control, asthma, NaHS (sodium hydrosulfide, a donor of H2S) and ascorbic acid (as a positive control). All animals except in the control group were sensitized and challenged with ovalbumin. In the NaHS group, 14 µmol/kg NaHS was intraperitoneally given 30 min before each challenge. In the ascorbic acid group, mice received 130 mg/kg ascorbic acid by gavage 30 min before each challenge. On the day of the last challenge, animal body weight and anxiety-related behaviors were evaluated.
**Results:** Induction of asthma resulted in significant decreases in the percentages of open arm entries and spending time in open arms in the elevated plus maze as well as the spending time in the light side in the light-dark transition. In addition, asthma caused a decrease of the animal body weight significantly. Administration of NaHS as well as ascorbic acid attenuated anxiety-related behaviors and improved the body weight in asthmatic mice.

**Conclusion:** The present study indicated that NaHS improves anxiety-related behaviors in chronic asthma induced by OVA similarly as ascorbic acid, a strong antioxidant. Thus, NaHS seems to be useful for managing the comorbidity of anxiety with asthma.

**Key-words:** Asthma, Anxiety, Oxidative stress, Hydrogen sulfide, Ascorbic acid
The Mechanisms Underlying Helicobacter Pylori-Mediated Protection against Allergic Asthma

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Abstract
Helicobacter pylori, a gram negative pathogen, infects the stomach and gastrointestinal tract and causes pathological damage to these organs. H. pylori infection is more prevalent among people living in developing countries. Allergic asthma is a chronic inflammatory disease of the airways. Hyperinflation, hyperresponsiveness, and abnormal immunological and inflammatory processes in respiratory airways typically occur during an asthma attack. The results of recent studies have suggested an association between H. pylori and asthma risk. However, the role of H. pylori infection in the pathophysiology of asthma is still a matter of debate. The results of some studies indicate an association between H. pylori infection and protection against allergic asthma. Exposure to infectious agents might educate the immune system and provide protection against allergic diseases. H. pylori inflammation also changes gastric hormonal levels and could influence the autonomic nervous system. T-reg could be influenced by the immunological response to H. pylori and then inhibit the Th-2-mediated allergic response. Therefore, H. pylori might play a protective role against asthma. H. pylori can also reduce gastro-esophageal reflux, which is an asthma stimulator. High loads of H. pylori are not always present during infection. It is not definitely clear whether H. pylori is a pathogen or simply an opportunist. It has been suggested that early exposure to H. pylori prevents development of pediatric asthma. Therefore, it is possible that therapeutic products made from H. pylori can be used for the treatment or prevention of asthma.

Key words: Helicobacter pylori, Allergic Asthma, Protection
PI-16

**Th2 cells in immunosuppressive protocol containing combined use of Tacrolimus and sirolimus in renal allograft recipients: a cohort study**

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ABSTRACT

**Background:** Long-term use of calcineurin inhibitors (CNI) (e.g. Tacrolimus (TAC)) is associated with nephrotoxicity, which is an important cause of renal dysfunction. Therefore, CNI-minimization strategies which decrease the CNI nephrotoxicity under the protection of additional immunosuppressant drugs have been developed. Th2 cells and their related cytokine IL-4 through activation of B cell can induce endothelial damage and thrombus generation leading to graft destruction and thereby transplant rejection. Therefore development and/or utilizing a potent and appropriate immunosuppressive protocol containing reduced dose of tacrolimus (TAC) for suppressing function of the effector Th2 cells in preventing allograft rejection is necessary. The aim of current cohort study was to assess the effect of immunosuppressive protocol containing reduced dose of tacrolimus (TAC) in combination with sirolimus (SRL) and prednisolone on the frequency of Th2 cells and their associated cytokine (IL-4) level in renal allograft recipients.

**Methods:** In this study, renal transplant recipients who received induction therapy (Antithymocyte globulin) and were also on triple immunosuppressive therapy were included which composed of 10 patients who received TAC, SRL and PRED. The frequency of Th2 cells in the peripheral blood mononuclear cells (PBMCs) of the patients was analyzed by flow cytometry before and 4 months after transplantation. In addition, IL-4 concentrations in PBMC culture supernatants of patients before and 4 months after transplantation were quantified by ELISA.

**Results:** The results of our study showed that Th2 cells and and IL-4 concentration were significantly decreased after transplantation in patients who had received SRL,TAC and PRED.

**Conclusion:** In conclusion, the data of the current study suggest that using reduced dose of TAC in SRL, TAC and PRED protocol is in favor of allograft survival; however a cohort study with larger sample size is needed for confirming our results.
Keywords: Kidney transplantation, Th2 cells, tacrolimus, mycophenolate mofetil, prednisolone, sirolimus

Abbreviations: SRL, Sirolimus; CNIs, calcineurin inhibitors; TAC, Tacrolimus, prednisolone; PRED
PI-17

Common infections and target organs associated with Chronic Granulomatous Disease (CGD) in Iran

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Abstract
Recurrent severe bacterial and fungal infections are characteristic features of the rare genetic immunodeficiency disorder chronic granulomatous disease (CGD). The disease usually manifests within the first years of life with an incidence of 1 in ~200,000 live births. The incidence is higher in Iran and Morocco where it reaches 1.5 per 100,000 live births. Mutations have been described in the five subunits of NADPH oxidase, mostly in gp91phox and p47phox, with fewer mutations reported in p67phox, p22phox, and p40phox. These mutations cause loss of superoxide production in phagocytic cells. CYBB, the gene encoding the large gp91phox subunit of the transmembrane component cytochrome b558 of the NADPH oxidase complex, is localized on the X-chromosome. Genetic defects in CYBB are responsible for the disease in the majority of male CGD patients. CGD is associated with the development of granulomatous reactions in the skin, lungs, bones, and lymph nodes, and chronic infections may be seen in the liver, gastrointestinal tract, brain and eyes. There is usually a history of repeated infections, including inflammation of the lymph glands, skin infections, and pneumonia. There may also be a persistent running nose, inflammation of the skin, and an inflammation of the mucous membranes of the mouth. Gastrointestinal problems can also occur, including diarrhoea, abdominal pain, and perianal abscesses. Infection of the bones, brain abscesses, obstruction of the genitourinary tract and/or gastrointestinal tract due to the formation of granulomatous tissue, and delayed growth, are also symptomatic of CGD. The prevention of infectious complications in patients with CGD involves targeted prophylaxis against opportunistic microorganisms such as Staphylococcus aureus, Klebsiella species, Salmonella species and Aspergillus species. In this review we
provide an update on organ involvement and the association with specific isolated microorganisms in CGD patients.

**Key words:** CGD, Infection, Aspergillus
PI-18

Mycophenolate mofite in Tacrolimus based therapy promotes regulatory T cell expansion in kidney transplant recipients

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Background: Accumulating evidence suggests that Regulatory T cells (Tregs) have a crucial role in immune tolerance and long-term graft survival. However,
The influence of immunosuppressive drugs on the level of Tregs has not been fully understood. Therefore we prospectively analysed the effect of calcineurin inhibitor (CNI)-based immunosuppression protocol on Tregs frequencies.

Methods: This clinical trial study (IRCT code: IRCT2016062528620N1) included 14 renal transplant recipients who received induction therapy (Antithymocyte globulin) and were on triple immunosuppressive therapy; Tacrolimus (Tac), mycophenolate mofetil (MMF) and prednisolone (P). The frequency of circulating Treg cells were analyzed by flow cytometry before and 4 months after transplantation.

Results: The levels of CD4\(^+\) CD25\(^+\) FOXP3\(^+\) Treg cells were significantly increased 4 months (4.14±0.93) after transplantation compare to baseline (3.16±1.25, P=0.02). But, the frequencies of CD3\(^+\)CD8\(^+\)CD28\(^−\) Tregs didn’t change significantly at the end of follow up (8.37±5.75) compare to before transplantation (7.37±3.59, P=0.4).

Conclusions: Our results suggest that Tac/MMF containing immunosuppressive regimen promotes renal allograft survival in association with CD4\(^+\) CD25\(^+\) Foxp3\(^+\) regulatory T cell expansion.

Keywords: regulatory T cells, renal transplantation, calcineurin inhibitor, mycophenolate mofetil, clinical trial
Mycophenolate mofetil combination therapy with Tacrolimus augment frequency of plasmacytoid dendritic cells in kidney transplant recipients

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Background/Aim: In recent years, there has been much attention to dendritic cells (DCs), because of their major role in the initiation of immune response. Some DC subsets such as plasmacytoid DCs (pDC) have tolerogenic properties while myeloid DCs (mDCs) have immunogenic properties. Recent studies show that immunosuppressive agents affect activities and frequencies of human DCs. Herein we aimed to compare the effect of mycophenolate mofetil (MMF) in combination with Tacrolimus(TAC) immunosuppressive therapy on the frequency of pDCs and mDCs in kidney transplant recipients.
Methods: In this clinical trial study (IRCT2016062528620N1), we enrolled 14 adult transplant recipients who received Anti-thymocyte globulin (ATG) as an induction therapy and MMF in combination with TAC and prednisolone (PRED) as a maintenance immunosuppression. Peripheral blood samples were obtained at two time points: 24-48 hours before transplantation and 4 months after transplantation. The frequency of DC subsets were analyzed by flow cytometry before and 4 months after transplantation.

Result: MMF treated renal allograft recipients showed a significant increase in pDC % and decrease in mDC1 frequencies at the end of follow up period compared to before transplantation.

There were no statistically significant difference in frequency of mDC2 compared to before transplantation.

Conclusion: MMF in combination with TAC induces an increase in circulating pDCs with a reduction of mDC1, which was in favor of better allograft survival.

Keywords: Kidney Transplantation, plasmacytoid dendritic cells, myeloid dendritic cells, Micofenolate Mofetil, Clinical trial
PI-20

Provides an ELISA-based diagnostic screening system for the diagnosis of enterohemorrhagic bacteria

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Background: Diarrhea is one of the most important factors in the delayed physical growth of children and their susceptibility to other diseases. Several factors, including viral, bacterial and parasitic agents, can cause intestinal infections. Among bacterial agents that are effective in the development of intestinal infections, there are various species of *Escherichia coli*, *Vibrio*, *Campylobacter*, *Shigella* and *Salmonella*. *Escherichia coli* EHEC is a major contributor to endemic and epidemic diarrhea through poison production around the world.

Methods: In this study, a chimeric protein containing *E. coli* enterohemorrhagic EHEC was used to design the ELISA kit.

Results: Thus, the recombinant protein was purified after expression in host *E. coli* BL21 (DE3) and immunization of mice and rabbits was performed to produce antibodies against protein.

Conclusion: After confirmation of immunity and the presence of specific immunoglobulins against this protein, purified IgG immunoglobulins were used in ELISA design. The results show that the designed alaitic sandwich can detect the toxin of all three bacteria.
Keywords: Diarrhea, immunological diagnosis, *E. coli* enterohemorrhagic
Design of an ELISA-based diagnostic screening system for the detection of *E. coli* enterotoxigenic bacteria

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**Background:** Diarrhea caused by various intestinal pathogens is one of the greatest global health problems. The route of transmission of these infections is usually from the stool from the patient to the other person through the fecal-oral, it can be transmitted through water, contaminated food or directly. Among bacterial agents that are effective in the development of intestinal infections, there are various species of *E. coli*, *Vibrio*, *Campylobacter*, *Shigella* and *Salmonella*.

**Methods:** In this study, a chimeric protein containing the enterotoxigenic bacteria ETEC was used to design the ELISA kit.

**Results:** Thus, the recombinant protein was purified after expression in host *E. coli* BL21 (DE3) and immunization of mice and rabbits was performed to produce antibodies against protein.

**Conclusion:** After confirmation of immunity and the presence of specific immunoglobulins against this protein, purified IgG immunoglobulins were used in ELISA design. The results show that the designed ELISA sandwich is able to detect the toxin of all three bacteria.

**Keywords:** Diarrhea, immunological diagnosis, ELISA kit, *E. coli* enterotoxigenic
Activated Natural Killer Cells Can Be a Promising Therapeutic Approach for Immunodeficiency disorders

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Background: Natural killer cells (NK cells) are a type of cytotoxic lymphocyte critical to the innate immune system. NK cells are identified by expression of different cell-surface receptors. NK cell deficiencies is one of the main reasons in progression of many different diseases. Using activated NK cells as a promising therapeutic approach have been reported recent published studies. In this comprehensive study, we assessed the relationship between NK cell deficiency and immunological syndromes.

Methods: Relevant English-language literature were searched and retrieved from PubMed search engine (200-2018). The following keywords were used: "Natural Killer Cells" and "Immunodeficiency ".

Results: Some of immunodeficiencies that affect NK cell function or numbers are X-linked inhibitor of apoptosis deficiency, bare lymphocyte syndrome, familial hemophagocytic lymphohistiocytosis types 2, 3, and 4, Hermansky-Pudlak syndrome, Papillon-Lefevre syndrome, nuclear factor kappa-beta essential modulator deficiency, severe combined immunodeficiencies, UNC13D, STX-11, X-linked lymphoproliferative disease, Griscelli syndrome, Chediak-Higashi syndrome and Wiskott-Aldrich syndrome.
Conclusion: Based on Published and ongoing projects in Royan Institute on using NK cell therapy for different diseases and our comprehensive study on different disease and finding their reasons, using these cell can be a suitable approach for treatment of Immunodeficiency disorders due to their altered or low number of NK cells.

Keywords: Natural Killer Cells, Immunodeficiency disorders, Immunotherapy.

*Presenting Author is underlined and Corresponding Author is indicated by *. 
PI-23

The new promising immunotherapy approaches for prevention and treatment of atherosclerosis in the primary stages: A systematic review

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Introduction:

Atherosclerosis is the main cause of cardiovascular disease that is chronic inflammation of the large or medium arteries wall. In the early stages LDL deposit and convert to ox-LDL that activate endothelial cells to produce cytokines and chemokines that have a widespread regulatory role in different stages of the atherosclerosis. So we try to identify cytokines and chemokines that are effective in the early stages to target them and control promotion in the early stages.

Methods and materials:

PubMed, Scopus and Google scholar was searched for this systematic review article. 35 articles found from the years 2014 to 2018 that we chose 15 of them.

Results:

Studies have been demonstrated that chronic inflammation and both innate and adaptive immune system have important role in pathogenesis of the atherosclerosis. Differentiation of monocytes Ly6C<sup>high</sup> to M1 macrophages is influenced by IFN-γ and IL-1β that produced by T-helper1 (TH1) and also monocytes Ly6C<sup>low</sup> differentiation to M2 is influenced by IL-4 and IL-13 that
produced by Th2. M1 produce pro-inflammatory cytokines (IL-12, IL-6 and TNF-α) but M2 produce anti-inflammatory cytokines (IL-10 & TGF-β) that imbalance between pro and anti-inflammatory cytokines can result in some inflammation disorder like atherosclerosis. Furthermore CCL2, CCL5 & CX3CR1 are important chemokines in recruitments of monocytes.

**Conclusion:**

Results show that we can use cytokines (IL-10) directly or use IL-4 & IL-13 to stimulate the production of IL-10 and TGF-β indirectly as anti-inflammatory cytokines, to regression the plaques. Monocytes-macrophages are important in atherosclerosis too, so blocking the receptors of CCL2, CCL5 or CX3CL1 (especially CCL2) may cause the regression of the plaques via decreasing monocytes recruitment. We suggest using CCR2-Neutralizing antibody and reduction of risk factors during the healing period, might be a useful method to prevent the promotion of the atherosclerosis plaque in the early stages.

**Keywords:** chronic inflammation, cytokines, chemokines, atherosclerosis, CCR2-Neutralizing antibody
**PI-24**

**Association of vitamin D receptor polymorphisms with severity of Multiple Sclerosis: A systematic review**

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**Introduction:** Multiple sclerosis (MS) is a complicated inflammatory central nervous system (CNS) disease. MS is characterized by demyelinating recurrently and neurodegeneration of probable autoimmune origin. Vitamin D deficiency might play a role in MS pathogenesis. Polymorphisms in vitamin D receptor (VDR) genes are considered as an outstanding risk factor associated with MS, which play an important role in vitamin D metabolism and adjustment.

**Methods:** In this systematic review, the PubMed, Scopus databases and Google Scholar search engine were searched by keywords: ("Multiple Sclerosis", "Vitamin D receptor", "polymorphism") in English language from 2010 to 2018. A total of 37 studies were selected which 17 of them were used for writing of this article with inclusion criteria “best match keywords/article abstracts” and selection of “original articles”.

**Results:** According to accumulative documents, the assessment of results was highly dissimilar, even inside areas or countries. In some studies kinds of correlation could be seen between VDR polymorphisms and MS. In contrast, in
other studies no evident association was observed among them. Various efficacies of each VDR gene (TaqI, ApaI, FokI and BsmI) polymorphisms have been shown in different MS patients, which can have probable relation with the severity and progression of MS. In fact, these different results associated with their various latitude of domicile, ethnicity and other environmental and genetic factors.

**Conclusions:** Our studies represent that the polymorphism of different VDR genes in various MS patients with ethnic and geographical differences, may determine the severity and progression of MS disease. Thus, individual position of each patient along side ethnic and environmental factors should be considered in follow-up treatment. Ultimately, association between VDR gene polymorphisms and MS disease remained unclear.

**Keywords:** Multiple sclerosis, Vitamin D receptor, polymorphism.
**PI-25**

**Effect of Aquatic Extract of *Ferulago angulata* Boiss With Aerobic Exercises on Serum Levels of Interleukin-10 and C-Reactive Protein of Obese Males**

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**Background:** The aim of the present study was to evaluate the impacts of chavir aquatic extract (*Ferulago angulata* Boiss) along with aerobic exercises on serum levels of interleukin-10 (IL-10) and C-reactive protein (CRP) of obese males.

**Materials and Methods:** In this study, 40 males with body mass index (BMI) >30 kg/m² and average age of 33.63 ± 4.78 years were randomly categorized into 4 groups of 10 individuals as control, combination (using the aquatic extract of chavir along with aerobic exercises), consumption of chavir aquatic extract, and aerobic exercises. The aerobic exercises in both groups of combination and aerobic exercises consisted of running on treadmill for 20 minutes in 60%-70% maximum oxygen uptake (VO2max). The aquatic extract consumption and the combination groups had to take 50 mg/mL/d of chavir aquatic extract every time. The control group received no intervention.

**Results:** Based on intragroup comparisons, body weight and BMI significantly decreased in the combination group; the content of body fat and waist-hip ratio (WHR) also reduced significantly in the aerobic, combination, and aquatic extract groups. In intergroup and intragroup comparison, CRP faced with a significant decrease in all groups (aerobic exercises, Ferulago aqueous extraction, and combination groups) and a considerable increase was also observed in the combination group regarding IL-10 variable.
Conclusions: Therefore, the effectiveness of the combination group regarding increasing IL-10 and decreasing CRP is more than other groups. As a result, using aqueous extract of *F. angulata* and doing aerobic exercise for 3 months reduced risk factors – cardiovascular, body composition, and increasing anti-inflammatory in obese men. Consequently, the effect of combination group to reduce the proinflammatory indexes and body factors of obese males was more compared to that of the other groups.

Keywords: Aerobic exercises, Chavir, IL-10, CRP, Obesity
PI-26

The relationship between sera levels of tumor markers in Patients with hepatitis B

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Background: Chronic infections with hepatitis B virus (HBV) is well-recognized risk factors for cirrhosis and hepatocellular carcinoma. Information about tumor markers in patients with HBV and HCV population is limited. Therefore, the aim of this study was to determine the serum levels of tumor markers  α-fetoprotein (AFP), carcinoembryonic antigen (CEA), cancer antigen (CA) 19-9, CA 125, CA 15-3 in HBV positive patients.

Methods: In a cross sectional analytical study, serum samples were collected from 61 patients with hepatitis B who referred to university hospitals. Clinical data and routine laboratory tests including liver functional test (SGOT, SGPT), were examined for evaluation of liver fibrosis. Serum level of tumor markers was measured by ELISA method in all included subjects. Statistical analyses were conducted using multivariate logistic regression.

Results: Increased CA15-3, CA19-9 and AFP levels were correlated significantly with liver fibrosis (P value was 0.049, 0.047 and 0.021 respectively). We did not find a significant increase in serum level of CA125, CEA in patients (P > 0.05).
Conclusion: This study showed that the sera level of tumor markers CA15-3, CA19-9 and AFP had increased in patients with HBV. Moreover, this concept offers, routine clinical evaluation serum tumor markers may be useful in early detection and screening of liver fibrosis.

Keywords: AFP, CA 125, CA 15-3, CA 19-9, CEA
PI-27

Multiple Biomarker Profiling; Great Diagnostic Opportunities for Acute Respiratory Infections (ARIs); A Systematic Review

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Background: Acute respiratory infection (ARI) which includes acute uncomplicated bronchitis, pharyngitis, rhinosinusitis and the common cold, is the most common reason for antibiotic prescription in adults and physicians visitors. It is important to detect type of infection for deciding to use antibiotics. As it can affects quality of life and early detection is necessary for treatment, we purposes to investigate biomarker profile for ARI early diagnosis.

Search Method: This systematic review study was performed to identify studies using 5 key words published in Scopus and Google Scholar database in 2014-2018 time interval. From initially 173 identified articles, 47 articles were totally included after removing duplicates and scanning the titles and abstracts.

Results: It was obtained that different kinds of molecular signaling pathways and different types of biomarkers (proteins, cytokines, microRNAs) in ARI microenvironment are known as predisposing factors for ARI progression and
severity. Inflammation and airways remodeling are known as pathogenic mechanisms of respiratory infection. All in all, interferon-α induced protein 10 (IP-10) associated with inflammation, infection, its severity and duration of the disease, interleukin 25 (IL-25) associated with inflammation and Procalcitonin (PCT) is as special factor for bacterial infection, are known as appropriate biomarkers in diagnosis and prognosis of ARI.

**Conclusion:** Despite efforts on ARI diagnosis improvement, it will be reasonable to identify of associations between biomarkers and ARI progression, encouraging basic clinical scientists to further investigations on targeting IP-10, IL-25 and PCT as profile for modulation in ARI microenvironment and contributing to specialists’ diagnosis qualification.

**Keywords:** Acute Respiratory Infection, IP-10, IL-25, PCT, Clinical applications
Importance of Multiple Biomarker Profiling; Diagnostic Opportunities for Psoriasis; A Systematic Review

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Background: Psoriasis is a Th1 related disease affected 2-3% of the white population worldwide. In this disease, the production and secretion of some inflammatory cytokines are increased and causes lesions. Surround investigations to focus on the role of different molecular pathways in psoriasis microenvironment, may be efficient for biomarker utilization perspectives in psoriasis early detection based strategies. So, in this study, we purpose to investigate the appropriate diagnostic biomarkers profile for psoriasis.

Search Method: This systematic review study was performed to identify studies using 5 keywords published in Scopus and Google Scholar database in the 2015-2018 time intervals. From initially 374 identified articles, 43 articles were totally included after removing duplicates and scanning the titles and abstracts.

Results: It was obtained that different kinds of molecular signaling pathways in psoriasis microenvironment are known as predisposing factors for psoriasis.
progression. It is demonstrated that cytokines, chemokine’s, growth factors, proteins have a characteristic role in psoriasis inflammatory pathogenesis. Interleukin 17 (IL-17) as a pro-inflammatory cytokine, interferon-α induced protein 10 (IP-10) associated with psoriasis severity and Th1 related inflammation, CC chemokine ligand 20 (CCL-20) a major Th17-attracting chemokine, is known as appropriate biomarkers in diagnosis and prognosis of psoriasis.

**Conclusion:** Despite efforts on psoriasis diagnosis improvement, it will be reasonable to identify of associations between these kinds of biomarkers and psoriasis progression, encouraging basic clinical scientists to further investigations on targeting IL-17, IP-10 and CCL-20 biomarker profile for modulation in psoriasis microenvironment and contributing to specialists’ diagnosis qualification.

**Keywords:** IL-17, IP-10, Psoriasis, Profile of biomarkers, Clinical applications.
PI-29

miRNAs: new diagnostic, prognostic and therapeutic agent in ischemic stroke: a systematic review

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Background: Stroke is the third cause of disability in the world that is classified into two categories of hemorrhagic stroke and ischemic stroke. Ischemic stroke with more than 80% prevalence has more victims. Since the disease can have irreversible complications, it requires appropriate methods for timely diagnosis, early prognosis, and safe treatment. Micro RNAs (miRNAs) are small non-coded RNAs with post-transcriptional gene expression function. Several studies have found out the results of using miRNAs in ischemic stroke diagnosis, prognosis, and treatment. Hence, it is hoped that they can be used for best management of stroke.

Methods: Data of this comprehensive article required from Google Scholar, science direct, PubMed databases and search engines since 2010 by using 6 keywords. We found 46 articles and finally, 22 related were selected based on our inclusion and exclusion criteria.

Result: In various studies, different roles are implied for miRNA in stroke. One of these roles is their association with the risk of ischemic stroke, including miR-126, miR-130a. Also, some other known as a prognostic factor such as miR-126 and miR-335 that associated with the severity of the disease.
miR-21 and four other have been known as Atherosclerosis-Related Circulating microRNAs that are related to stroke recurrences. On the other hand, some of the miRNAs can be therapeutic agents in ischemic stroke by rolling as oxidative stress antagonist.

CONCLUSION: Given the high costs of imaging and appropriate result of miRNAs in ischemic stroke diagnosis, prognosis, and treatment, utilizing these agents is recommended.

Key word: Ischemic stroke, miRNA, Prognosis, diagnosis, Therapy
PI-30

MiR-214 as a key player in Endometriosis (A Systematic Review)

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Background: Endometriosis is one of the most common diseases, which is characterized by the occurrence of ectopic foci of endometrial tissue growth in the pelvic cavity. Poor knowledge on endometriosis etiology will be more problematic when is accompanied with infertility and dysmenorrhea. So, this study aims to investigated clinical values of miRNA evaluation in women with endometriosis. miRNAs play an important role in the development of endometriosis lesions due to their regulatory functions in endometriosis, which include hypoxia, inflammation, tissue repair, TGF-β regulated pathways, cell growth, cell proliferation.

Search method:

We searched articles in the PubMed, Google Scholar and Science Direct databases between 2014 to October 2018. About 35 articles were found; of these, 10 articles related to our study that were investigated.

Results: Different miRNAs interact with these processes, such as miR-15b, 16, 199, 221, 222 and miRNA-214, which plays an important role in fibrous diseases. The fibrotic process is the first feature of the pathology of endometriosis. it has been observed that increased expression of miR-214 inhibits the fibrotic process in endometriosis. Connective tissue growth factor (CTGF) is known to be a
critical miR-214 fibrinogen mediator, which results in reduced collagen 1α, CTGF, and other fibrogenic markers in response to fibrotic stimuli due to increased miR-214 products. In addition, the reduction expression of miRNA-214 in ectopic endometrial stromal cells (ESCs), in comparison with healthy ESCs, can express the role of miR-214 in fibroblastic endometriosis. Thus, miRNAs can act as a potential regulator of gene expression in endometriosis and Reproductive-related diseases.

**Conclusion:**

Due to limited findings in the field of diagnosis, treatment, and follow up of endometriosis, hope that miRNA-214 may be used as a marker for the diagnosis and follow up of endometriosis patients

**Keywords:** Endometriosis, miRNA-214, Pathogenesis, Diagnosis
PI-31

B cell modulation strategies in transplantation

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Transplantation is the final treatment for graft failure, however recent progression in surgical techniques and development of various immunosuppressive drugs leads to long-term graft survival but the Immunological processes continue to be a deterrent to a successful transplantation.

Many efforts were made to modulate the immune system, for instance, several investigations were performed to attenuate the reaction of T cells and their interactions against transplanted allograft to avoid rejection.

In addition to T cells as an important part of the immune system, it has been shown that B cells have a key role in transplant rejection by several functions such as antibody production, antigen presenting, helping for T cell activation, forming the germinal center and tertiary lymphoid organs and etc.

Therefore, B cells modulating seems to be very considerable in these cases. Today several methods are available for this purpose and some of them routinely used for transplant recipients like deleting antibodies and eliminating B cells by monoclonal antibodies such as rituximab.
However, there are some efficient medications that disrupts B cell functions and induces tolerance in autoimmune disease or B cell malignancies, but they are not used in transplantation yet, some of these medications include epratuzumab and Inotuzumab ozogamicin (IO) that are anti-CD22 agents and induce the inhibitory effects of CD22 on B cells and are used for lupus and leukemia patients.

In this article, we reviewed the different methods for modulating B cells function and activity that are used for transplant recipients, or some other methods used in other diseases that can be useful in induction of transplantation tolerance.

**Keywords:** B cells, transplantation, tolerance
PI-33

drug regulation of TBK1 gene expression in relapsing-remitting multiple sclerosis patients

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Background: Multiple Sclerosis (MS) is known as a neuroinflammatory autoimmune disease. Disease-modifying drugs such as interferon-beta (IFN-\(\beta\)) are administered to reduce the number of relapses and slow disease progression in some patients. NF-kB and IFN signaling cascades deduced production of proinflammatory agents. TBK1 have key regulatory role in this signaling and modulation of this kinase may be useful in the treatments of diseases associated with inflammatory mediators.

Methods: In This study we compared the expression level of TBK1 in relapsing-remitting (RRMS) between different groups of patients with normal individuals in Iran. The RNA was extracted from blood of 50 RMSS patients (sort in 2 different groups, own group taken IFN-\(\beta\) treatments and other group new cases without any treatment) and 25 normal controls. Groups were matched in age and gender. Quantitative SYBR Green RT-PCR was performed to measure expression of TBK1 gene.

Results: Our result demonstrated The expression level of TBK1 gene was significantly upper in Not treated patients (NP) than their normal counterparts (\(P=0.005\)). Also no significantly change was observed in expression level of TBK1 gene between normal groups and Treated Patients (TP) (\(P=0.17\)). In
addition we found significantly down-regulated in TBK1 gene expression in TP compare NP (P=0.002).

**Conclusion:** Our findings suggest a possible contribution of IFN-β in the upregulation of TBK1 in not treated patients. Additionally, TBK1 downregulation can be considered as a potential indicator of a positive response to interferon beta treatment in multiple sclerosis patients.

**Keywords:** TBK1, Multiple sclerosis, IFN-β
PI-34

Improvement of immunotherapy with the help of diagnostic and monitoring biomarker in Glioblastoma: systematic review

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Introduction: Glioblastoma (GBM) is the most common malignant tumor of the central nervous system in adults, which the best condition, 3-5% of Glioma patients can survive for nearly 5 years. Today, evaluation and use of Glioblastoma specific biomarkers can develop the efficacy of the treatment in Glioma patients. The most important aspect of studying Glioma biomarkers is recognition of the features of this group of molecules to help with therapeutic strategies according to the patient's biology characteristics that it can be.

Methods: In this systematic review, relevant articles were collected from databases Science Direct, PubMed, Elsevier, and Google Scholar from 2013 to 2018. The result of this Searching in the mentioned databases, 37 articles were obtained, which 15 articles were reviewed and used.

Results: Today, for the diagnosis, monitoring, and prognosis of Glioblastoma, a number of biomarkers (MGMT, P53, PTEN and EGFR) associated with this cancer are used. These biomarkers allow accurate categorization of the tumor and awareness of the consequences of Glioma in the patient and predict the patient's condition. Understanding the functional mechanisms of biomarkers in Glioblastoma improves the design of immunotherapy-based therapies and activates the immune system to eliminate tumor cells and increase uncomplicated
survival. Among the results of using these biomarkers is the recognition of the actual progression of false development in the tumors, the diagnosis of the primary phase and the Glioblastoma and the specific molecular abnormality. In addition, best diagnosis of prognosis and prediction of response to treatment such as chemotherapy and radiotherapy are among the other advantages of using these biomarkers.

Conclusion: Progress in the effective use of biomarkers and immunotherapy can ultimately lead to the proper management of Glioblastoma and increase the efficacy of treatment. The acquaintance of the functional mechanisms of biomarkers can lead to efficient targeted of them in designing new therapeutic strategies.

Keywords
Prognosis, Predictive, Diagnostic, Biomarker, Immunotherapy, Glioblastoma
PI-35

Promising use of diagnostic and predictive biomarkers to novel treatment of Multiple Sclerosis: systematic review

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Introduction

Multiple sclerosis (MS) is a chronic and demyelinating autoimmune inflammatory disease, which is associated with a variety of factors, including genetic factors, environmental factors, and pathogens. This complex heterogeneous disease characterized by inflammation and demyelination of neurons and its diagnostic criteria include symptoms, the results of MRI, and differential diagnosis and biomarkers. Despite the advances made in diagnostic fields such as MRI, due to the high degree of heterogeneity in the various characteristics of the disease, we need to use biomarkers that incorporate different aspects of this heterogeneity, which are used to help better understanding of MS pathogenesis, prognosis, diagnosis, prediction of response to treatment and the development of novel treatments.

Methods

This systematic review is the result of data collected from the PubMed, Google Scholar, Scopus, and Science Direct databases. Initially, 27 articles were found that among the 14 selected articles from 2014 to 2018 were studied.

Results
According to studies, various biomarkers including cerebrospinal fluid biomarkers such as NfL, serum biomarkers such as GFAP, as well as miRNAs, that are short and non-coding RNA sequences, and other biomarkers have been identified that can lead to the design of immunotherapy-based therapies. Ever-increasing advances in the scope of biomarker recognition can provide a more accurate and personalized assessment of the specific biological characteristics of patients with MS; However, despite these advances, there are still many gaps in the understanding of reliable biomarkers that they could end up as a bridge to provide personalized medicine medications, leading to the discovery of novel and much more effective treatments.

**Conclusion**

Consequently, with respect to the features of the biomarkers mentioned, to improve treatment approaches, today we need extensive research on the identification of new and efficient biomarkers.

**Keywords**

Multiple Sclerosis, Diagnosis, Predictive, Biomarkers, Novel treatments
PI-36

Effect of 50Hz magnetic fields with various densities on serum IL-1β, and IL-23 and expression of BLIMP-1, XBP-1 and IRF-4 genes

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Abstract

Study investigated effect of 50 Hz magnetic fields (50Hz-MFs) on IL-1β and IL-23 at two phases of pre- and post-immunization of the immune system. In addition, expressions of three important genes in the humoral immunity i.e. B lymphocyte-induced maturation protein-1 (BLIMP-1), X-box binding protein-1 (XBP-1), and interferon regulatory factor-4 (IRF-4) were evaluated at post-immunization phase. Eighty adult male rats were divided into four exposed and a control groups. The exposed groups received 50Hz-MFs with densities of 1, 100, 500 and 2000μT, 2h/day for two months. The animals were injected by human serum albumin (100μg/rat) on Days 31, 44 and 58 of exposure. Serum level of IL-1β was decreased at pre-immunization phase after exposure to 1 and 100μT. In contrast, level of IL-23 was increased at post-immunization phase in 100μT group. Furthermore, exposure to 50Hz-MFs with density of 100μT down regulated expression of BLIMP-1, XBP-1 and IRF-4. In conclusion, exposure to 50Hz-MFs may decrease inflammation at short time and increase it at longer time exposures. In addition, 50Hz-MFs exposure may decrease the humoral immune responses. It is seems that 50Hz-MFs cause more alteration in immune system at lower compared with higher densities.
Keywords Interleukin-1β, Interleukin-23, 50 Hz magnetic fields, BLIMP-1, XBP-1, IRF-4
Interleukin-12 properties and roles in Immunotherapy of Glioma; Systematic Review

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Background:
Glioma is one of the most invasive tumor of nervous system. The common therapeutic methods for glioma are surgery, chemotherapy and radiotherapy. However, the mortality rate is about 12-15 months. Over time, some novel therapeutic strategies have been introduced. Immunotherapy is one of the novel cancer treatment methods. It applies substances which is produced in in vivo or in vitro to improve immune system against tumor microenvironment. One of these substances is cytokines. The cytokines which is used in tumor immunotherapy are the pro-inflammatory cytokines such as interleukin-12 (IL-12). The purpose of this study was to perform systematic review determine the immunotherapeutic role of IL-12 in glioma.

Methods:
This systematic review was performed to identify studies that were published in Pubmed, ScienceDirect, Scopus databases and Google Scholar search engine, in 2000-2018 time interval by using 3 keywords (Glioma, Interleukin-12, and
Immunotherapy). Of the 73 articles initially identified, 36 were selected to distinguish the role of IL-12 in glioma.

**Results:**
According to accumulative documents, IL-12 is an immune regulating cytokine which involved both innate and adaptive immunity. Studies have demonstrated that IFN-gamma and secondary pro-inflammatory cascade which is induced by IL-12 and anti-angiogenic mechanism of it would be beneficial in chronic inflammatory microenvironment of tumors.

**Conclusion:**
Result of this study show the potential immunotherapeutic role of IL-12 in cancer microenvironments. The pro-inflammatory mechanisms of IL-12 would make it a candidate for glioma immunotherapy.

**Key words:** Glioma, Interleukin-12, and Immunotherapy.
PI-38

Evaluation of Serum Free Light Chains (FLC) a new marker for the diagnostic in Patients with Amyloidosis Disease

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Background and objectives: free light chains (FLC) often increased in inflammatory disease in patients with plasma cell dyscrasias such as Amyloidosis. Amyloidosis disease often is difficult to diagnose because of its wide range of signs and what often are unclear symptoms. Polyclonal FLC have not been evaluated in patients with Amyloidosis disease yet can play an important role in pathologic disease. This study describes for the first time polyclonal FLC in patients with Amyloidosis.

Patients and Methods: Design, setting, participants, & measurements: A sensitive, quantitative immunoassay was used to analyze serum FLC in 52 patients with Amyloidosis

Results: Serum κ and λ chains concentrations augmented progressively with Amyloidosis patients (P < 0.001) and powerfully correlated with markers of liver function, such as alkaline phosphatase (κ: R 0.8 P < 0.02; and λ: R 0.69 P < 0.04). FLC concentrations were completely correlated with their parallel serum concentration creatinine and cystatin C (markers of renal function) (λ: R 0.64; κ: R 0.79; both P < 0.002).
Conclusions: This study shows significant abnormalities of serum polyclonal FLC in patients with Amyloidosis. These data offer the basis for studies that evaluate the contribution of polyclonal FLC to progressive liver injury and systemic inflammation (renal function) in patients with Amyloidosis disease.

Keywords: Free light chains, Amyloidosis, Inflammatory disease

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Provisional Title: PI-39

Evaluation of effects of general anesthesia induced with sodium thiopental on gene expression of interleukin-4, interleukin-10, and indoleamine 2,3-dioxygenase in leukocytes

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Abstract

The effects of anesthetic drugs on patient’s immune system can be considerable. These drugs may suppress immune responses. Various anesthetic drugs suppress immune responses directly or indirectly. Interleukin (IL)-4, IL-10 and indoleamine 2,3-dioxygenase (IDO), an intracellular enzyme that catalyzes the tryptophan degradation along the kynurenine pathway, have critical roles in suppression or regulation of immune responses. The aim of this study was evaluation of the effects of anesthesia induced by sodium thiopental, a short acting barbiturate, on expression of IL-4, IL-10 and IDO in leukocytes. General anesthesia was induced in BALB/c mice by intraperitoneal injection of sodium thiopental (50 mg/kg) and mice were kept at deep anesthesia for 4 h by repeated injection of sodium thiopental. After five periods of anesthesia with three-day intervals, leukocytes were during surgery and expression levels of IL-4, IL-10 and IDO were measured by real-time RT-PCR technique. Gene expression analysis showed that thiopental sodium did not significantly alter IL-4 and IDO gene expression levels, but it decreased IL-10 expression levels (p>0.05). These findings indicate that sodium thiopental may affect immune responses by altering gene expression of some cytokines in leukocytes during long-term deep anesthesia.
Keywords: General anesthesia, Sodium thiopental, Leukocytes, Gene expression, IL-4, IL-10, IDO.
PI-40

Pyroptosis block to prevent CD4 cell death in Acquired immune deficiency syndrome: a systematic review

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**Background and objectives:** Acquired immune deficiency syndrome (AIDS) is a severe loss of the body's cellular immunity. AIDS is a potentially life-threatening condition caused by the human immunodeficiency virus (HIV). AIDS is a global pandemic. As of 2016, approximately 36.7 million people have HIV. There is currently no cure or effective HIV vaccine. Treatment consists of highly active antiretroviral therapy (HAART) which slows progression of the disease. Studying the relation of new antiretroviral drug (caspase-1 inhibitor) and aids treatment is a main goal.

**Methods and materials:** This essay was a systematic review of English articles published in PubMed, Nature and Science since 2010. Being up to date, matching with keywords and accessing the full text were incoming metrics.

**Results:** The papers address a mystery: why immune cells die in people with HIV. A 2010 study showed that HIV does not directly kill most of these cells, called CD4 cells. Instead, the cells often self-destruct. They found that most of the cellular suicide occurs via a process called “pyroptosis”. A key protein involved in pyroptosis is caspase 1, and an experimental caspase-1 inhibitor made by Vertex Pharmaceuticals (VX-765) had already been tested in humans as a potential treatment for epilepsy. The drug, failed to help epileptics, but studies suggested that it was safe. Scientists tested VX-765 in HIV-infected cells cultured from human tonsils and spleens, and found that it blocked pyroptosis and prevented CD4 cell death.
Conclusions: The approach could one day provide an alternative to the antiretroviral drugs currently used by 9.7 million people worldwide to manage HIV infection. HIV infection causes a mass suicide of immune cells a process that can be halted by an experimental drug such as VX-765 that blocks cellular self-destruction.

Keywords: AIDS/HIV treatment, pyroptosis, caspase-1 inhibitor, Vertex Pharmaceuticals (VX-765)
PI-41

Detection of New Delhi metallo-β-lactamase-1 (NDM-1) among *Klebsiella pneumoniae* strains isolated from hospitalized patients in Iran

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Abstract

The global spread of New Delhi metallo-β-lactamase (NDM) is of significant public health concern. The aims of this study were the phenotypic detection of β-lactamases and molecular characterization of NDM in *Klebsiella pneumoniae* isolates at Tehran, Iran. From March 2014 to February 2017, 120 *K. pneumoniae* isolates were collected from hospitalized patients admitted to Tehran Hospitals, Tehran, Iran. Antibiotic susceptibility tests were accomplished using Kirby-Bauer disc diffusion and Broth Microdilution methods, according to Clinical and Laboratory Standards Institute (CLSI) guidelines. Detection of metallo-β-lactamase (MBL) activity was performed using the Combined Disc Diffusion Test (CDDT) and carbapenemase production was screened using the Modified Hodge Test (MHT). NDM gene was detected by PCR and Sequencing methods. The resistance of *K. pneumoniae* isolates to tested antibiotics was 82(68.335%) to cefotaxime, 74(61.66%) to ceftazidime, 12(10%) to ertapenem, 12(10%) to doripenem, 12(10%) to meropenem, 12(10%) to imipenem, 48(40%) to gentamicin, 35(29.1%) to amikacin, 90(75%) to ciprofloxacin, 112(93.4%) to cefpodoxime, 120(100%) to ampicillin, 10(8.3%) to fosfomycin, 90(75%) to cotrimoxazole, 51(42.5%) to levofloxacin and 6(4.9%) to colistin. Of the 120 strains, 92(76.6%) were identified
as ESBL-producers. Of 12, five were MBL-producing strain and 2 of them were detected as *K. pneumoniae*, carrying NDM-1 gene. The coexistence of NDM-1 with other antibiotic resistance genes is also of concern because of limited treatment options. Therefore, it is extremely important to think reasonably about infection control in hospital settings.

**Keywords:** *Klebsiella pneumoniae*; Antibiotic resistance; carbapenemase; NDM-1
PI-43

The role of Magnesium in different inflammatory diseases

Abstract

Magnesium deficiency (MgD) can cause inflammation in human body. The known mechanisms of inflammation caused by MgD include activation of phagocytic cells, opening of calcium channels, activation of the N-Methyl-D-Aspartate (NMDA)-receptor, and activation of nuclear factor (NF)-κB. In addition, MgD causes systemic stress response through neuroendocrinological pathways. The inflammation caused by MgD can result in pro-atherogenic changes in the metabolism of lipoproteins, endothelial dysfunction, and high blood pressure. Studies suggest that magnesium may play an important role in the pathophysiology of some inflammatory diseases. Several clinical trials and laboratory studies has been done on the functional role of magnesium. In this study, we review some inflammatory disease, in which the magnesium has a role in their pathophysiology. Among these diseases, diabetes, asthma, preeclampsia, atherosclerosis, heart damage, and rheumatoid arthritis have been highlighted.

Keywords: Magnesium deficiency; inflammation; asthma
Manipulated mesenchymal stem cells applications in neurodegenerative diseases

Abstract

Mesenchymal stem cells (MSCs) are multipotent stem cells that have multilinear differentiation and self-renewal abilities. These cells are immune-privileged as they express no or low level of class-II major histocompatibility complex (MHC-II) and other costimulatory molecules so they can be considered as great candidates for regenerative medicine. MSCs can be affected by a variety of situations so that their therapeutic applications are enhanced. Using different agents to pretreat MSCs with, obtaining extracellular vesicles from MSCs, and genetically manipulating them are the most common and practical ways to strengthen their survival and potency. Improved MSCs can have significantly enhanced impacts on diseases compared to MSCs not manipulated. In this review, we describe some of the most important manipulations that have been exerted on MSCs to improve their therapeutic functions and their applications in ameliorating three prevalent neurodegenerative diseases including Alzheimer's disease, Parkinson's disease, and Huntington's disease.
Interferon regulatory factors: Where to stand in transplantation.

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Interferon regulatory factors (IRFs) are implicated in regulating inflammatory responses to pathogens and alloantigens. Since transplantation is usually accompanied by ischemia reperfusion injury (IRI), acute and chronic rejections, as well as immunodeficiency due to immunosuppressive drugs, IRFs seem to play a considerable role in allograft outcome. For instance, IRF-1 has been shown to be involved in pathogenesis of IRI; however, IRF-2 exhibits an opposite function. Some IRF-3 and 5 SNPs are associated with better or worse graft survival rates. Of note, IRF-4 inhibition has resulted in improved transplant outcomes. Herein we review available studies about IRFs influence on various stages of transplantation.

\textbf{KEYWORDS:} Interferon regulatory factor; Ischemia reperfusion injury; Rejection; Transplantation
Evaluation of the Serodiagnosis efficacy of IgM anti-whole cell *Brucella abortus* S99 antibodies in human serum

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**Background:** Brucellosis is one of the most common zoonotic diseases worldwide. Serologic tests, which could be performed in any standard laboratory, would help to obtain definitive early diagnoses of Brucellosis. The use of new and feasible antigens in ELISA method seems to be of great importance for resolving the diagnostic obstacles. In the present study, we evaluated the usefulness of an indirect ELISA based on whole cell *Brucella abortus* S99 lysates for detection of IgM anti-Brucella antibodies in human serum for serological diagnosis of brucellosis.

**Materials and Methods:** Indirect ELISA, coated whole cell *Brucella abortus* S99 lysates in the plate, was used to demonstrate IgM anti-Brucella antibodies in human serum from brucellosis patients. Serum samples were obtained from 252 different groups of patients: positive Wright tube test \(n = 102\) and negative wright tube test \(n = 150\). Receiver operating curve (ROC) was used to calculate the cut off value and
comparison between brucellosis and non-brucellosis groups were done by the chi-square test.

**Results:** The indirect ELISA method, using a whole cell lysates, yielded 82% sensitivity (95% confidence interval (1) 67 to 93%) and 86% specificity (95% CI, 57 to 98%) for the diagnosis of brucellosis. The serum positivities for whole cell lysates in cases of positive and negative brucellosis patients were 96% (23/24) and 79% (82/104) respectively. The best cut-off point of ELISA-IgM was 10.78 IU/ml which produced the maximal sensitivity and specificity for the diagnosis of human brucellosis.

**Conclusion:** The detection of IgM anti-Brucella antibodies in sera from brucellosis patients by indirect ELISA using whole cell Brucella abortus S99 lysates is suitable for routine diagnosis of brucellosis and also for epidemiological surveys and can be used to develop an immunodiagnostic assay with increased sensitivity and specificity.

**Keywords:** Indirect ELISA, whole cell lysate, Brucella abortus s99, Brucellosis
PI-47

Evaluation of the LTBP1 and Smad6 genes expression in lung tissue of sulfur mustard exposed individuals with long-term pulmonary complications

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ABSTRACT

Introduction: Short and long-term complications of sulfur mustard gas affect different organs such as the lung. Transforming growth factor beta (TGF-β) has the main role in altering fibroblast activities linked to airways remodeling. Latency TGF Beta Binding proteins (LTBP1) facilitates localization of TGF-β in the extracellular matrix. Smad6 negatively regulates TGF-β signaling, thus establishing a main negative feedback loop. In this study, we investigated the expression of LTBP1 and Smad6 in the lung tissues of SM-exposed and control individuals.

Materials and methods: Lung FFPE blocks of SM-exposed (20 samples) and control groups (20 samples) were collected from archival pathology department of the general hospitals. The total mRNA of lung FFPE tissues was extracted. Quality of the extracted mRNA was evaluated by an Agilent Bioanalyzer and RNA was quantified using a NanoDrop. LTBP1 and Smad6 expression levels were evaluated by real-time RT-PCR.

Results: There were no significant increases in LTBP1 expression levels between the two groups (p-value= 0.086), but Smad6 expression levels were
significantly higher in SM-exposed individuals compared to the control group (p-value = 0.001).

Discussion: Our results revealed that Smad6 may be involved in lung tissue remodeling process in SM induced individuals. Smad6 regulates fibrotic alterations in lung tissue and its function as negative feedback mechanisms in TGF-β.

**KEYWORDS:** Sulfur mustard; LTBP1; SMAD6; Transforming Growth Factor β

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PM-1

New methods of evaluation of Pneumocystis Jirovecii and reporting of three cases in the Broncho alveolar fluid (BALF) of patients admitted to Mashhad hospitals due to acute respiratory tract infection referred to the laboratory.

BALF was collected on 50 patients who were hospitalized due to respiratory infections in Mashhad hospitals and samples were sent to the laboratory for diagnosis of TB by smear, culture, and PCR as well as culturing for mycotic germs. In the meantime, three cases of Pneumocystis jirocii have been found, which show a high prevalence. We therefore decided to report these three cases and, by presenting new diagnostic methods of Pneumocystis jirovecii, we would draw the attention of colleagues to the diagnosis of this parasite. Detection of this parasite can easily will be missed in labs due to lack of familiarity of laboratory colleagues.
PM-2

_Pichia fermentans_ detected in a patient with vulvovaginal _candidiasis_ affected to endometrial cancer in Northeastern Iran, Mashhad: A novel case report

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**Background:** One of the most common malignancies in the genitalia is _uterine cancer_ (endometrial cancer). This cancer is mainly caused in elderly women aged 55-70 years old. On the other hand, approximately 95% of cases of vaginitis are caused by one of _Cadida albicans_, _Trichomonas vaginalis_, and _Gardnerella_
vaginalis. Some species of Pichia are part of Candida species. Pichia species are reported as abnormal flora of the clinical specimens.

**Case presentation:** The present study described the isolation of *P. fermentans* from a case of vulvovaginal candidiasis in a 63-year-old female with endometrial cancer. The patient complained of complications such as vaginal bleeding and abdominal pain and leg pain and has a history of nine pregnancies, diabetes, birth control pills using and hypertension. One year ago, she was treated with enoxaparin, and was hysterectomized. The result of the pathology of the endometrial carcinoma was STAGE 1B. Then, vaginal discharge was cultured in sabouraud dextrose agar with chloramphenicol, and transferred to incubator 35°C for 48 to 72 hours. The genomic DNA of colonies was extracted and the isolate identified by PCR sequencing for ITS region. Subsequently, a drug-susceptibility test was carried out on ketoconazole, fluconazole, itraconazole and voriconazole using disc diffusion method.

**Discussion:** Some causes of vaginitis due to lack of accurate diagnosis and microbial resistance become chronic, which should definitely be recognized. Candidiasis is one of the factors that can contribute in this field.

**Conclusion:** *P. fermentance* reported of a patient with vulvovaginal candidiasis affected to endometrial cancer as the first report from Iran. Ketoconazole was more effective than other antifungals.

**Keywords:** Vaginitis; *Pichia fermentans*; Uterine cancer; *Candida*
PM-3

Interspecies differences of candida species causing recurrent vulvovaginal candidiasis in response to fluconazole treatment

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Background: Looking at the increased incidence of recurrent vulvovaginal candidiasis and refractory resulting from such non-albicans Candida species in recent decades, this study was performed aiming the use of rapid biochemical and molecular detection of drug-resistant Candida species in response to fluconazole in patients with vulvovaginal candidiasis and recurrent vulvovaginal candidiasis.

Methods: The cross-sectional study was performed at Kowsar Gynecology Center, Motahhari educational hospital and Medical Mycology Center, Faculty of Medicine, Urmia, Iran, from October 2013 to July 2015. Those patients referred to the clinic with symptoms of vaginal discharge, itching or burning that swab samples from endo-exocervix and distal fornix discharge were taken. The vaginal discharge samples submitted to Medical Mycology Center, Urmia School of Medicine for the direct microscopic examination and cultures. Identification at the level of species was performed using CHROMagar Candida and Corn meal agar media. The molecular test polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP) used for confirming culture results. For the susceptibility assay, disc diffusion method was performed with fluconazole and clotrimazole.
**Results:** In these study 198 samples collected from patients with symptoms of vulvovaginal candidiasis, 77 vulvovaginal candidiasis cases were identified. Candida species are common in primary and recurrent cases in terms of frequency, Candida albicans (85.7%), Candida krusei (10.2%) and Candida glabrata (4.1%) were identified respectively. Total of 27 cases of recurrent vulvovaginal candidiasis, 10 cases were resistant to both clotrimazole and fluconazole (37%) was observed that the most common species are resistant to treatment were Candida albicans by (82.1%), Candida krusei (14.3%) and Candida glabrata (3.6%) respectively. Drug resistance in Candida albicans, Candida krusei and Candida glabrata causing recurrent vulvovaginal candidiasis included 69.1%, 75% and 100% respectively.

**Conclusion:** Our findings have shown frequency of resistant non-albicans Candida species to fluconazole and clotrimazole is increasing. There is a considerable difference between Candida albicans and non-albicans species, Candida glabrata for the resistance to fluconazole and clotrimazole.

**Keywords:** candida, cross-sectional studies, fluconazole, vulvovaginal candidiasis
PM4

Effects of Cumin and Ginger on the protein pattern Alternaria alternate in vitro

Fungi are one of the environmental factors, Alternaria strains including fungi that have global distribution and can be found in most parts of Iran and they are easily separated from all ecosystems and crumbling materials (3,1). Among Alternaria species, Alternaria alternata is as an allergic fungus in the worldwide, that it has several allergic antigens like Alt a1-Alt a22 (3-5).

Several studies indicated that some plants or their products could be useful for controlling infection due to Alternaria fungus (2). Ginger (Zingiber officinale Roscoe) belongs to the Zingiberaceae family that has a wide range of pharmacological application (15-20). In other hands, Cuminum cyminum .L known as cumin which belongs to the family Apiaceae that could be used for many medicinal properties (10-19).

Material method: we perpetrated the extract of Alternaria fungal isolates .after that the effect of fungal extract was tested on the protein pattern of the Alternaria strains by SDS-PAGE.

Result: the protein content did not relation with amount of the colony mass. The results showed that the highest reduction in protein content was the effect of ginger on isolate 40. The results showed that the plant extracts was effective on the protein pattern of the Alternaria strains.
**Keywords:** Cuminum cyminum, Zingiber officinale, Alternaria alternate, protein pattern
PM-6

Diagnosis of invasive fungal infections: Current challenges and perspectives

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Invasive fungal infections are a serious threat, especially for people with immune deficiency. Traditional diagnostic methods, such as direct microscopic examination, histopathology and culture, which are still considered golden standards, are low in sensitivity and require the development of new tools for the diagnosis of fungal infections. New developed serological and molecular techniques are currently under clinical evaluation. Detection of galactomannan in aspergillosis, β-glucan in invasive candidiasis, polysaccharide capsules antigens in cryptococcosis and ... have been identified as important diagnostic methods in diagnosis of these infections. On the other hand, molecular methods such as PCR, (MALDI-TOF MS) and hybridization (FISH) have a promising role in the diagnosis of invasive fungal infections and should be standardized to be more widely used in diagnosis. The purpose of this study is to describe the various diagnostic methods currently used or being developed for invasive fungal infections, and the characteristics of the function and the associated challenges in using them.
PM-7

Induction of antifungal resistance within expression the Cyp51C gene in Aspergillus flavus due to different CO₂ levels

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Background: Aspergillosis is one of the most common opportunistic fungal diseases in immunocompromised. Due to changes in the concentration of CO₂ in some pathogens encounter during the infection process, the evaluated of changes in antifungal susceptibility patterns and the expression in the Cyp51C gene of in A. flavus in the effect of variable CO₂ concentrations.

Materials and Methods: A. flavus strain was cultured and incubated under the 1%, 3%, 5% and 12% of CO₂ concentrations, each time in one, two, and four weeks. Antifungal susceptibility tests were performed according in the Clinical and Laboratory Standards Institute (CLSI, M38-A2) and evaluated the expression the gene of intervener in Cyp51C with Real Time PCR protocols.

Results: The induction of antifungal resistance of susceptible strains to itraconazole and voriconazole increased after expose with 12% concentration of CO₂ and four weeks of incubation. The MIC value for itraconazole and voriconazole, were 8mg/ml and 2mg/ml respectively in A. flavus, these values in
comparison for control groups were 1mg/ml and 0/5mg/ml. Also, the results were showed increase the expression in the Cyp51C gene in A.flavus.

**Conclusion**: Exposure to different CO$_2$ concentrations inducted a significant increase the MIC values with increasing expression in the Cyp51C gene of in A.flavus.

**Key word**: *Aspergillus flavus*, Voriconazole, Itraconazole, Carbon dioxide
Natural Occurrence of Aflatoxin and Ocheratoxin A Contamination in Commercial and Unpacked Spices in Shiraz

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Abstract

Background: The Middle East boasts of a rich cultural heritage of traditional food, of which spices are an integral constituent. However, it has been reported that these spices might be contaminated with heat-stable mycotoxins that cannot be neutralized by cooking. Hence, in this study, the fungal contamination of spices with toxicogenic fungi and mycotoxins that include AFs such as B1, B2, G1, and G2 as well as OTA in red pepper, black pepper, turmeric, and cinnamon was examined.

Methods: A total of 20 samples of each spice, including both commercialized and unpacked in markets such as Vakil bazaar of Shiraz were extracted and treated with immunoaffinity columns. The prevalence of AFs and OTA was then determined using high-performance liquid chromatography (HPLC) with a fluorescence detector (FD). Simultaneously, a sample of each spice was cultured in SDA and Aspergillus agar to isolate and identify fungal contamination.

Results: The results depicted that 53 samples (65.4%) were contaminated with Aflatoxin and 63 samples (77.8%) with Ochratoxin A (OTA). The highest contamination by Aflatoxin was found in red pepper (100%), of which 50% of the samples revealed the level of contamination to be higher than the standard level of >0.005 µg/kg. OTA contamination was found in all black pepper samples (100%), and all their values exceeded the standard level of >0.015 µg/kg. The species of
fungi isolated belonged to 5 genera. Aspergillus species were the predominant species isolated, followed by *Penicillium*, and finally *Mucor*.

**Conclusion:** Considering the high levels of fungal and mycotoxin contamination found in commercial and unpacked spices, it is suggested that imported spices be scrutinized regularly by FDA offices, especially when being received at the incoming ports.

**Keywords:** Aflatoxin; Ochratoxin A, spices; HPLC;
Evaluation of fungal air contamination in ICU unit of two Hospitals in Qazvin, Iran

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Background: Inhalation of fungal spores by patients with underlying illness and immune deficiency Hospitalization can lead to a different range of hospital infections. Most common airborne fungi causing nosocomial infections are mainly by filamentous fungi.

Methods: The Samples were collected from the ICU of two hospitals in Qazvin city. Air sampling was performed using open Petri-dishes containing the Sabouraud dextrose agar. Plates were incubated at 27 °C for 7 to 10 days. Fungal isolates were identified using the macroscopic features of colony and microscopic characteristics in slide cultures.

Results: A total of 158 plates collected from the ICU of Velayat and Rajaei Hospitals, 169 colonies were isolated. Aspergillus spp. (43.19%), Cladosporium spp. (15.38), Penicillium spp. (9.46%), Alternaria spp. (7.69%), Rhizopus spp. And Acrimonium spp. (7.31%), Scopulariopsis Spp. (6.5%) And Fusarium Spp. (3.4%) obtained from two hospitals.

Conclusion: According to the results of this study, the frequency and diversity of fungal spores in hospitals ICU were different. In addition, since the fungal contamination in the hospitals environment are affected by various environmental factors and the efficiency of ventilation systems, some of the ICU require better ventilation system as well as regular monitoring to remove these fungal bio aerosols in order to maintain the health of patients and health care workers.
Keywords: filamentous, fungi, bio aerosols
PM12

The Survey of Antifungal Susceptibility of Planktonic Cells and biofilm forming in Candida species isolated from onychomycosis infection

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**Background:** Candida albicans is the second most common cause of onychomycosis after dermatophytes. The present study aimed to provide information about the virulence factors including biofilm formation, and azole susceptibility of Candida species isolated from onychomycosis.

**Methods:** Samples were obtained from 130 patients suspected of onychomycosis. After identification of the isolated strains using RFLP-PCR methods, biofilm forming ability was determined using the microplate method and crystal violet staining. Susceptibility of the candida species to fluconazole, itraconazole, ketoconazole, and voriconazole were determined by microdilution method.

**Results:** In this study, out of 130 subjects, 90 (69.23%) were identified as candidal onychomycosis. C. parapsilosis was the most common species 36 (40%) detected from the nail specimens, followed by C. albicans 31 (34.4%), C. krusei 8 (8.9%), C. tropicalis 8 (8.9%), C. glabrata 6 (6.7%) and C. kefir 1(1.1%). Out of isolates, 18 (20%) isolates were able to produce biofilms, of which 16 (88.88%) isolates had 1 <OD <2; 2 (11.11%) isolates had OD > 3; and C. parapsilosis complex had the highest biofilm production. Our results indicated that 6.5% (n=2), 25% (n=2) and 2.8% (n=1) of C.albicans, C. krusei and C. parapsilosis complex
isolates were resistance to itraconazole respectively (MIC≥1 μg/ml). For fluconazole 12.5 % (n=1) of C. krusei strain was resistant (MIC≥64 μg/ml).

**Conclusion:** The results of this study showed that only one species of C. parapsilosis complex with the highest biofilm production (+3) showed resistance to itraconazole, however other biofilm production species were not resistant to antifungal agents. In this study, most of the planktonic cells were susceptible to antifungal. Therefore, further studies are needed to comparison of planktonic and sessile susceptibilities of biofilm-forming Candida isolates and the relationship between antifungal resistance and the mechanisms of virulence in candidal onychomycosis.

**Keywords:** biofilm, planktonic cell, Antifungal
PM-14

TLR-2, IL-10 and IL-17-mediated immunity in experimental chemotherapy murine model of systemic candidiasis; cyclophosphamides’ impact and roles

Running title: Cyclophosphamide and immunity in systemic candidiasis

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Background: The majority of immune components such as Toll-like receptor (TLR)-2, interleukin (IL)-17, neutrophils, and IL-10 play pivotal roles in immunity to Candida albicans (C. albicans) through identifying and launching inflammatory and regulatory responses. Chemotherapy is one of the most potent risk factors for systemic candidiasis through inducing immunosuppression (mostly cyclophosphamide induced immunosuppression) and there is a sensible lack of study around the immunity to C. albicans in such a situation.

Methods: In this study, following the establishment of infection and immunosuppression in Balb/c mice model, the mRNA/protein levels of TLR-2, IL-10, IL-17, and Myeloperoxidase (MPO) in serum/kidney were measured using Real-time PCR and ELISA respectively. The survival of mice was checked daily and organ fungal burden was calculated and the histology samples were prepared.

Results: Results indicated that the mRNA and protein levels of IL-10, IL-17 and MPO were significantly elevated in immunosuppressed-infected mice (P<0.05).
Conversely, the mRNA level of TLR-2 in these mice were significantly decreased ($P<0.05$).

Conclusion: We conclude that, I. cyclophosphamide could induce only a minor state of immunosuppression through depletion of serum neutrophils. II. TLR-2 does not have important roles in developing immune responses in immunosuppressed mice model of systemic candidiasis. Our findings can be applicable for further experimental investigations on patients in clinics for deep understanding of pathogenesis of systemic candidiasis, which could be useful to further broaden our insights for targeted therapy, especially targeting TLR-2 and IL-17, based on siRNA, miRNA or monoclonal antibodies.

**Keywords**: Systemic candidiasis; cyclophosphamide; chemotherapy; immunosuppression; immune response
In Vitro Interactions between Aureobasidin A and fluconazole against Candida albicans growth

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Background: In recent years, the incidence of deaths caused by important fungal infections (such as candida albicans) has been increased due to the inherent or acquired resistance to common antifungal drugs. The emergence of C. albicans strains with reduced susceptibility confuse the management of these infections. Combination therapy is one approach that could be used to develop the efficacy of antimicrobial therapy for the treatment of fungal infections, mainly those caused by drug-resistant fungi. Aureobasidin A (AbA) is a cyclic depsipeptide antibiotic, isolated from the filamentous fungus Aureobasidium pullulans R106, which is toxic to yeast at low concentrations.

Method: In this study, antifungal activity of AbA determined according to a standardized broth microdilution method (M27-A2), against fluconazole resistance C. albicans ATCC 10231, in comparing with fluconazole. The interaction between AbA and fluconazole against C. albicans strain was tested by a microdilution checkerboard technique. To evaluate the drug combination interactions, for each combination the fractional inhibitory concentration (FIC) were calculated.

FIC of ≤0.5 was defined as Synergism, FIC of >0.5 ≤1 was defined as Indifferent (no antagonism), whereas FIC of ≥4 was defined as antagonism.
**Result:** The MIC50 and MIC90 of AbA and fluconazole were assessed in range 2 and 0.25 and 128, 512 (µg /ml) Against *C. albicans* ATCC 10231, respectively. FICI values for AbA plus fluconazole ranged from 0.445 to 0.125 for *C. albicans* strain. AbA was found to have a fungicidal and a synergistic effect when combined with fluconazole.

**Conclusion:** By itself, fluconazole has little or no effect on the tested strains. However, when it was combined with AbA, a potent effect was revealed. Our findings demonstrate a potential role for combination therapy with AbA and azoles to enhance activity against resistant *C. albicans*.

**Key words:** *Candida albicans*, Aureobasidin A, Antifungal, Minimum Inhibitory Concentration (MIC), microdilution checkerboard technique
Species identification and in vitro antifungal susceptibility testing of *Aspergillus* isolated from ICU of two hospitals

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**Background:** *Aspergillus* species are the most important fungus isolated from the environment of hospital which in patients with immune deficiency, creates a wide range of hazardous human diseases. In addition environmental *Aspergillus* species can harbor various antifungal susceptibility patterns. The aim of this study was to molecular identification and determine the susceptibility pattern of environmental *Aspergillus* species.

**Methods:** The Samples were collected from *Aspergillus* isolated were identified by using the PCR-sequencing of the b-tubulin gene. Furthermore, the susceptibility of isolates to three antifungal drugs, including itraconazole, voriconazole and amphotericin B, were tested according to CLSI M38-A2. The phylogenetic dendrogram was constructed using the maximum likelihood method (ML) with PAUP*.

**Results:** The majority of isolates were identified as *A. fumigatus* (36/51, 70.5%), *A. flavus* (11/51, 21.56%), *A. sydowii* (2/51, 3.9%) and *A. terreus* (2/51, 3.9%). Our results indicated that 8.3% (n=3) and 50% (n=1) of *A. fumigatus* and *A.
terreus isolates were resistance to Itraconazole respectively (MIC≥1 µg/ml). Voriconazole and Amphotericin B were highly active against Aspergillus species (100% susceptible at an MIC of ≤1 g/ml).

**Conclusion:** The targeted surveillance of environmental of Aspergillus species can be helpful to define epidemiology patterns. Our results indicated that a small number of A. fumigatus and A. terreus isolates isolated from ICU hospitals were resistant to itraconazole. Due to the invasive fungal infections with environmental Aspergillus species in Immunocompromised patients and increasing Antifungal resistance, accurate identification of the isolates and the determination of Antifungal susceptibility is important.

**Keywords:** Aspergillus, Antifungal, b-tubulin gene
PM-17

Rhinocerebral mucormycosis in patients with hematologic malignancies.

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Background: The patients with hematologic malignancies are at high risk for rhinocerebral mucormycosis that is a life-threatening infection caused by saprophytic fungi due to the severe and prolonged neutropenia related to high-dose chemotherapy. The objective of this study was to describe the Clinical characteristics of rhinocerebral mucormycosis in patients with hematologic malignancies.

Methods: Based on clinical findings and history of 34-year-old male patient with acute myeloblastic leukemia a provisional and differential diagnosis of rhinocerebral mucormycosis were made.

Results: Biopsy under local anesthesia was planned and specimen was obtained from the left and right nasal and left maxillary sinus mucosal and, on histopathological examination, such as Periodic acid–Schiff (PAS) and Grocott's silver methenamine (GSM) staining showed necrotic and hemorrhagic
background with acute inflammatory reaction and some fragmented non septated hyphae suggestive of a mucormycosis.

**Conclusion:** Mucormycosis is important causes of death in acute myeloblastic leukemia especially during intensive induction therapy and in relapsed-refractory disease. As the disease progresses with disturbing rapidity, quick and aggressive therapy is crucial. Successful treatment of mucormycosis consists of aggressive and repeated surgical debridement of necrotic tissue, systemic antifungal therapy, and immediate control of the underlying systemic diseases.

**Keywords:** Rhinocerebral mucormycosis, acute myeloblastic leukemia, Periodic acid–Schiff, Grocott's silver methenamine.
PM-18

Prevalence of *Pneumocystis jirovecii* in the transplant patient

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**Background:** *Pneumocystis jirovecii* are a fungal opportunistic agent that causes pneumonia in patients with impaired immunity. Definitive diagnosis of PCP in the transplant patient is essential given the need for early therapy to secure a successful outcome and the potential toxicities of most of the agents used to treat infection. The aim of this study was to detect the prevalence and risk factors of pulmonary colonization with *Pneumocystis jirovecii* in the transplant patient.

**Methods:** In the present study, 50 sputum specimens were obtained from the Imam Reza and Shahid Gazi hospitals in 2018. Specimens were collected from transplant patients. We investigated sputum of transplant patient for the presence of *Pneumocystis jirovecii* using Grocott's Methenamine Silver stain (GMS) method.

**Results:** Among 50 transplant patient, *pneumocystis jirovecii* detected in 8 (16%) patient.

**Conclusion:** Patients with impaired immune system display colonization with *Pneumocystis jirovecii*. Clinicians should be aware of this and ensure that they
consider the possibility of PCP when pulmonary symptoms arise in these patients.

**Keywords:** pneumocystis jirovacii, transplant patient, Methenamin silver staining
PM-19

Prevalence of Candida species in the transplant patient

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Background: The opportunistic microorganism Candida normally colonizes mucosal surfaces of humans. Candida can germinate in the respiratory tract upon entering the lung via inhaled air, by dissemination into the lungs via the bloodstream. Candida in the alveolar compartment are a serious threat transplant patients. The frequency of opportunistic fungal pathogens has increased significantly over the past two decades. This study was undertaken to provide information on the rate of colonization of candida species in respiratory tract. Isolation and identification of the infecting organisms are extremely important for the proper management of infections due to the less common opportunistic fungi.

Methods: The present microbial study was carried out for the duration of nine months. We investigated sputum of 50 transplant patient undergoing protocol treatment in the Emam Reaz & Shahid Gazi Tabriz hospital for the presence of candida albicans using CHROMagar Candida medium.

Results: Among 50 sputum specimen we detection 25 (50%) case candida species. All the species of Candida, namely, Candida albicans 4 (16%) case, Candida glabrata 10 (40%) case, Candida dubliniensis 1 (5%) case, Candida krusei 5
Candida parapsilosis 1 (5%) case and Candida tropicalis 4 (20%) case isolated in the transplant patient

**Conclusion:** candida species was common in respiratory tract of transplant patient and C. glabrata was the predominant species. The results thus only partly confirmed our hypothesis and a further studies are warranted in this area.

**Keywords:** candida, transplant patient, CHROMagar Candida.
PM-20

Antifungal activity of Aureobasidin A against Cryptococcus neoformans

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Background

Cryptococcus neoformans is an opportunistic fungi which can cause invasive fungal infections as an important problem in patients with profound immunosuppression. Due to the increasing incidence of invasive fungal infections and antifungal drug resistance in response to common causative agents, finding of novel drugs is an important alternative in the treatment of fungal diseases. Aureobasidin A, an antifungal peptide agent, is produced by Aureobasidium pullulans which is toxic to yeast at low concentrations. In the present study Antifungal activity of Aureobasidin A peptide was evaluated against C. neoformans, with special focus on determining MIC values compared to fluconazole.

Material and Methods:

Standard strain of C. neoformans (93-589) was obtained from Pasteur Institute of Iran. The MICs of fluconazole and Aureobasidin A were determined according to a standardized broth microdilution method (Clinical and Laboratory Standards Institute (CLSI) document M27-A2).

Result:

Our results was shown that the MIC90 and MIC50 of Aureobasidin A (4 µg/ml and 1 µg/ml) were less than the inhibitory effect of fluconazole (8 µg/ml and 4 µg/ml) against fungal growth, respectively.
Conclusion:

In this study, Aureobasidin A exhibited an appropriate antifungal effect against the standard strain of C. neoformans. Further research on this peptide including the effect of morphological alterations, changes of cellular superficial charges and cellular toxicity are suggested.

Keywords: Cryptococcus neoformans, Antifungal activity, Aureobasidin A
PM-21

In vitro Antifungal susceptibility testing of Echinocandin and Azoles in *Candida parapsilosis* isolates. *Candida parapsilosis* isolates were Resistance to Itraconazole.

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Background: The rate of nosocomial fungal infections due to non-albicans Candida species are increasing and among them, Candida parapsilosis is the third most common Candida blood isolates. Although fluconazole have been the main choice for therapy against invasive candidiasis, but several new antifungal
agents (e.g., echinocandins) have emerged as therapeutic alternatives. *Candida parapsilosis* has an intrinsically reduced susceptibility to echinocandins and resistance to fluconazole has reported recently. In this study investigated the activity of two class of antifungal (azoles & Echinocandins) in *candida parapsilosis* isolates the mechanism of drug resistance by screening the SNPs in genes responsible for drug resistance, *FKSI* and *ERG11*.

**Methods:** One hundred and five isolates of *C. parapsilosis sensu stricto* were investigated. In vitro antifungal activities of azoles and Echinocandin and two newazole drugs, loliconazole and lanoconazole were determined using the broth microdilution reference method according to CLSI M27-A3 and M27-S4 document. The *ERG11* and *FKSI* genes for resistant and susceptible isolates were sequenced and multi-aligned using MEGA6 software.

**Results:** Itraconazole resistance were observed in 89.5 % of *Candida parapsilosis* isolates and multi azoles resistance were observed 3.8 %. Amino acid substitution Y132F identified in *ERG11* in multi azoles resistance *Candida parapsilosis* isolates. The rate of resistance in Echinocandin drugs was similar to the azoles, so
that 3.8% of isolates were multi-Echinocandin resistant. The common P660A amino acid substitution was observed in both Echinocandin -resistant and -susceptible isolates and no more substitutions was detected.

**Conclusion:** Understanding the mechanisms responsible for drug resistance in *C. parapsilosis* is not only crucial for the development of new antifungals but is also important in choosing appropriate antifungals for patients at the earliest stages.

**Keyword:** Candida parapsilosis, FKS1, ERG11, Echinocandin
PM-22

Evaluation of Antifungal Effect Eugenol Extract Against Cryptococcus neoformans by Micro Broth Dilution Method

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Background and Aim: Cryptococcus neoformans is a relatively frequent cause of serious fungal infections in immunocompromised patients. Two varieties of C. neoformans have been distinguished: C. neoformans var. neoformans and C. neoformans var. grubii. Cryptococcosis is a worldwide infection especially in North America and sub-Saharan Africa. Cryptococcal infections have been infrequently reported from Iran. The first published data is related to study from 1970. Most of the antifungal agents are classified in theazole antifungal drugs, especially fluconazole and echinocandins drugs. In recent years, increased levels of resistance to antifungal drugs have been observed, so other treatments that are more effective and safer than new treatments are being studied, including the use of herbal extracts.

Methods: The inhibitory effect of: Eugenol extract against Cryptococcus neoformans was evaluated by micro broth dilution (CLSI, M-38) methods in comparing with fluconazole.

Results: The results showed that the minimum inhibitory concentration (MIC) of: Eugenol and fluconazole for fungi growth was 2 And 16μg/ml and MIC 50 for these compounds was 1 and 8 μg/ml, respectively.

Conclusion: The results of this study showed that: Eugenol is an effective factor that inhibit Cryptococcus neoformans growth and can be considered as a target for antifungal design methodology.

Keywords: Eugenol, Cryptococcus neoformans MIC, Antifungal effect
M-23

Effect of Thimus Kotchyanus extract on expression of CDR1 and CDR2 genes of Resistant to fluconazole Candida albicans isolets by Real time PCR

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Background: Candida albicans is an opportunist yeast which changes into fungus infection in humans with immunity system deficiency when the required conditions are present. It may cause fatal infections. The Thimus kotchyanus ammoniacum is anti-fungus plants whose effects on CDR1 and CDR2 expression have been studies. The two genes are important in resistance against Fluconazole.

Methods: The alcohol essence of Thimus kotchyanus is prepared through drying the plants in Percolation method and then their 500, 250, 125, 62.5, 31.2, 15.6, 7.8, 3.9, 1.95 and 1 mg/lit concentrations of the solution are prepared and evaluated with .5-2.5×10⁵ clinically isolated Candida albicanses and the neighboring standard species and the MIC and MFC. Then the clinical samples of Candida albicans were treated using the plants MIC. The clinical samples' RNAs were extracted before and after treatment with the plants and then they were cDNA synthesized and the real time PCR was conducted.

Results: The results revealed that the alcoholic essences of Thimus kotchyanus had MIC value was 0.125 µg/ml and MFC value were 0.062 µg/ml for C. albicans isolates. Also, C.albicans ATCC (10231) had MIC and MFC value about 0.062 and 0.031 µg/ml respectively. The qPCR result shown that the Thimus kotchyanus was able to inhibit the CDR2 & CDR1 genes in clinical isolates of Candida albicans. Moreover,

Conclusion: Today, application of the plants with anti-microbial qualities which have less side effects is increasing; because of drug resistances. With regard the
present study's findings, the Thimus kotchyanusis effective in reduction of CDR2& CDR1 expression which in turn plays a basic role in resistance against Fluconazole. Therefore, the plant may be used as a suitable alternative for drugs and introduced as an efficient anti-fungus factor.

**Keywords:** *Candida Albicans*, Anti-fungal, CDR2, CDR1
PM-24

Signature Polymorphisms in ITS rDNA and LSU Fragments for the Differentiation Species of the *T. interdigitale* and *T. mentagrophytes*

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**Background:** In the last two decades, infections caused by dermatophyte species becoming remarkable public health problem due to increasing number of cases particular in immunocompromised patients. Identification of dermatophytes at the species level is an essential factor to treat patients. Identification of this closely related group of fungi classically is based on phenotypical and physiological characteristics (29, 30). Therefore, because of the high degree of morphologic similarity between several dermatophyte species, identification mistakes are inevitable. Several molecular methods have been developed for precise identification of dermatophyte species. Ribosomal genes ITS and partial LSU are sequenced as standard. Based on latest classification anthropophilic *T. mentagrophytes* should now be relabelled as *T. interdigitale*. To the best of our knowledge, no data have been published on precise differentiation of
dermatophytes spp. by the ITS and LSU sequences according to the new classification of dermatophytes in Iran. Therefore, the present study was designed to compare the discriminatory power of the ITS and LSU sequences.

Methods: 95 scales were inoculated into mycobiotic agar (SCC). Reference strains of *T. rubrum* (PFCC 51431), *T. mentagrophytes* (PTCC 5054), *T. tonsurans* (CBS130924) and *E. floccosum* (CBS767.73) were included in the study. DNA was extracted from the fresh colony of four-five days culture for amplification of the ITS rDNA and LSU fragments using the primers ITS1/4 and NL-1/NL-4, respectively. Phylogenetic analysis was carried out using Bayesian analysis and the CIPRES Science Gateway. Finally, comparative the ITS and LSU trees were performed.

Results: The results of the ITS sequencing showed that *T. rubrum* was 20, followed by *T. tonsurans* 29, *T. interdigitale* 21, *T. mentagrophytes* 6, and *E. floccosum* 23. Analysis dataset of ITS indicated that six isolates belonged to *T. mentagrophytes* and twenty-one isolates were known as *T. interdigitale*. While LSU sequences failed to discriminate them. Interestingly, a complete overlap was observed between both methods in case of remaining isolates. Dermatophyte species, mostly well-resolved using DNA sequences of ITS.

Conclusion: Surprisingly and in conflict with most other groups of filamentous fungi, best resolution (highest number of supported clades) was obtained with ITS. According to the new classification of dermatophytes, the LSU sequence fails to differentiate between *T. interdigitale* and *T. mentagrophytes* species.

Keywords: LSU, ITS, discriminatory power
PM-25

Comparison of antifungal activities of Allium cepa and fluconazole against Aspergillus fumigatus

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Introduction: During recent decades the incidence of opportunistic fungal infections have seen a significant surge. The cause of anti-fungal drug resistance has been the main driving force behind formulating an effective strategy against said diseases in the field of medical mycology. Both man and animal are constantly exposed to inhaling numerous fungi spores. Aspergillus Fumigatus is one of the most common saprophytes inhabiting the air. This fungus is currently known as the cause of the most common opportunistic fungal infection the world over. Considering the increased resistance to azoles and echinocandins; plant-derived antifungal substances are shaping up to be one of the main counter measures ever to be considered viable by researchers all over the globe.

Method: Dilution method was used in liquid culture medium(SDB) to evaluate the antifungal activity of the extract. MIC fluconazole and alcoholic extract of Allium sepa were determined.

Result: Concentration of 1.1 mg/ml EAC (MIC50) inhibited 50% growth of A. fumigatus. In addition, the concentration of 9.1 mg/ml of EAC was completely inhibited the growth and colonization of A. fumigatus. Of the extract MIC fluconazole and alcoholic extract of Allium sepa were determined.

Conclusion: According to the results of this study, Effects of Allium cepa is more than fluconazole in A. fumigatus Invitro examination.

Keywords: Allium cepa, Aspergillus fumigatus, MIC,
PM-26

Genome sequencing reveals novel fungal agent with high frequency and different antifungal susceptibility in otomycosis patient

**Background:** Otomycosis is a superficial infection of the ear caused by a spectrum of various fungal agents. Black aspergilli (*section Nigri*), particularly *Aspergillus niger* is the most prevailing causative agents. However, using morphological criteria alone, **discrimination of species within section Nigri** - A number of different species whose morphological features resemble those of *A. niger*- cannot be reliably achieved. **Due to different susceptibility patterns to antifungal agents and appropriate treatment,** species delimitation is issue of great importance. The aim of this study was to determine the frequency of otomycosis and determination the susceptibility pattern of a set of black aspergilli isolated.

**Methods:** A set of 412 subjects with a suspicion of external otitis were included. Yeast isolates and black *aspergillus* were identified using PCR-RFLP and the PCR-sequencing of the β-tubulin gene respectively. The susceptibility of isolates to fluconazole (FLU), clotrimazole (CLT), and nystatin (NS).

**Results:** 117/412 (28.4%) included patients were diagnosed with otomycosis including 64 (54.7%) males and 53 (45.3%) females. The highest prevalence age range was found 46-55 (30.77%). Pruritus (89.74%) and auditory manipulation (83.76%) were the predominant predisposing factors. Black aspergilli (n=43,
34.1%) were the most common etiologic agents and *Candida glabrata* (n=25, 20%) was the predominant isolated yeast. 16 cases of mixed otomycosis were identified due to *A. niger* and *C. glabrata* (seven cases). While, with sequence-based methods the majority of black aspergilli isolates were identified as *A. tubingensis* (32/43, 74.42%) followed by *A. niger* (11/43, 25.58%). The lowest minimum inhibitory concentration (MIC) were observed for NS. CLT showed wide MIC ranges and a statistically significant inter-species difference FLU was inactive against both species.

**Conclusion:** *A. tubingensis* is the most prevalence cause of otomycosis. Considering the low and variable activity antifungal drugs, empirical treatment can result in treatment failure. Accurate identification and antifungal susceptibility testing of isolates is recommended.
PM-27

Evaluation of Fungal Air Contamination in Meat Sales Centers of Zahedan

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Abstract

Background: The growth of fungi on chicken and meat could endanger the health of consumers. Therefore, in this study we aimed to evaluate and identify fungal air contamination in Zahedan meat supply centers.

Method: In this descriptive study, 59 media plates samples were collected and placed in the exposure for 15 min at a height of 120 cm from the ground of indoor air and around the centers of market offering chicken and meat in Zahedan, Iran. After 3-7 days of incubation, the direct smear from the plates (in triplicates) were prepared and stained with lectophenol cotton blue to identify their microscopic characteristics.

Results: A total of 177 colonies with 3 genus of fungi including Penicillium (62.0%), Aspergillus (32.7%), and Alternaria (29.9%) were identified, respectively.

Conclusion: In the present study, the type of fungal contamination of the centers and markets offering chicken and meat were roughly the same, but their rates were different. Penicillium, Aspergillus, Alternaria were identified as the most...
common fungi. These are considered toxigenic and infective which may endanger human health.

**Keywords:** Fungus, contamination, markets, meat
A Survey on the Prevalence of *Tinea Capitis* in Patients Referred to Bu-Ali Hospital in Zahedan

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**Background:** *Tinea capitis*, as one of the common infections with the prevalence rates of approximately 40% in some societies, caused by dermatophyte fungi. The aim of this study was to investigate the epidemiology of Tinea capitis among patients referred to Bu-Ali clinical laboratory in Zahedan.

**Methods:** In this descriptive, cross-sectional study, a total of 75 patients suspected to *Tinea capitis* were selected from December 2017 to December 2018. Samples were examined by direct microscopic examination of wet mount with 10% KOH (potassium hydroxide), and were cultured in the SCC media at 25 °C in four weeks, and then the data were analyzed using SPSS software Ver. 22.

**Results:** Out of 75 patients (36.8% female and 61.3% male) suspicious to *Tinea Capitis*, a number of 65 cases (86.6%) were positive. Clinical manifestations of *Tinea capitis* indicated that the frequency of each type of *Tinea capitis* was as follow, respectively: Ecthotrix 43.9%, Endothrix 25.3%, Favus 17.3%.

**Conclusion:** The findings indicated that there are cases of *Tinea Capitis* in this area of country, so it seems essential to take special measures to prevent and control its prevalence.

**Keywords:** Prevalance, Ecthotrix, Endothrix, Favus
Antifungal activity of aqueous extract of *Salvia rhytidea* Benth against *Candida parapsilosis*, *Candida krusei* and *Candida lusitaniae*

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_Background:_ *Candida* species such as *Candida parapsilosis*, *C. krusei* and *C. lusitaniae* are known as the main hospital-acquired pathogens and cause superficial cutaneous, mucocutaneous and systemic infections. Antifungal therapy with topical or systemic agents can be effective in the control and treatment of candidiasis. However, the treatment of candidiasis with the currently available antifungal drugs is associated with increasing resistance among *Candida* spp. *Salvia rhytidea* Benth (*S. rhytidea*) has been used since ancient times in medicine and subjected to extensive pharmacognostic research. It has significant biological activities in medicine including antifungal activity. The present study was planned to evaluate the antifungal activities of the aqueous extract of *S. rhytidea* against various *Candida* isolates such as *C. parapsilosis*, *C. krusei* and *C. lusitaniae*.

_Methods:_ The aqueous extract of *S. rhytidea* in various concentrations was prepared. Minimum inhibitory concentration (MIC) and the minimum fungicidal concentration (MFC) values of aqueous fractions of *S. rhytidea* extract were performed by Broth microdilution.
Results: The MIC and MFC of aqueous *S. rhytidea* fraction were, 200 μg/mL and \( \geq 200 \) μg/ml for *C. parapsilosis, C. krusei*. While, MIC and MFC for *C. lusitaniaes* were 100 and \( \geq 200 \) μg/ml, respectively.

Conclusion: The aqueous extract presented strong antifungal effect on *C. lusitaniaes* than *C. parapsilosis, C. krusei*.

Keywords: Salvia rhytidea, Candida parapsilosis, Candida krusei, Candida lusitaniaes
PM-30

**In vitro activities of eight antifungal drugs against a national collection of clinical Candida parapsilosis complex**

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**Introduction:** *Candida parapsilosis* has been emerged as the most common non-albicans *Candida* species, which generally isolated from bloodstream infections with high mortality rate. However, so far there is no systematic study on their antifungal susceptibility profiles. Therefore, the aim of this study was evaluate the in vitro activities of eight antifungal agents against a national collection of *C. parapsilosis* complex.

**Methods:** A collection of 87 clinical isolates of *C. parapsilosis* complex consisted of *C. parapsilosis sensu strict* (n= 75), and *C. orthopsilosis* (n= 12) were verified by MALDI-TOF MS assay. According to recommendations stated in the Clinical and Laboratory Standards Institute (CLSI) M27-A3 and M27-S4 document, minimum inhibitory concentration (MICs) were determined.
Results: Posaconazole (MIC$_{90}$: 0.016 μg/ml) and voriconazole (MIC$_{90}$: 0.031 μg/ml) had excellent activities. Fluconazole showed the widest MIC range (0.25-8 μg/mL) and highest MIC$_{90}$ (2 μg/mL) value against all C. parapsilosis species complex. Three echinocandin drugs were used in this study and all isolates were susceptible to these drugs. C. orthopsilosis were less susceptible to itraconazole compared to other antifungal agents.

Conclusion: Due to differences in antifungal susceptibility profile, further studies to warrant discrimination of the species and monitoring the distribution and antifungal susceptibility to achieve appropriate therapy should be performed. The clinical effectiveness of these medications in the treatment of C. parapsilosis complex infection should be determined in the future studies.

Key words: C. parapsilosis complex, Antifungal susceptibility, Iran.
Identification and antifungal susceptibility pattern of *Candida* species isolated from patients with nosocomial candiduria

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Abstract

**Background:** Nosocomial candiduria could be due to cystitis, pyelonephritis, or fungus ball in urinary tract system. Several reports also imply to candidemia and upper urinary tract involvement as the complications of candiduria. The aim of this study is the assessment of nosocomial candiduria; identification of *Candida* isolates and determination of their drug susceptibility pattern.

**Methods:** Urine samples of 115 hospitalized patients were collected during five months. *Candida* species were isolated and identified using conventional and molecular (PCR-RFLP) diagnostic methods. Antifungal susceptibility profiles for
amphotericin B and fluconazole were performed using broth microdilution method based on CLSI M27-A2 guideline.

Results: Nosocomial candiduria was diagnosed in 5 (4.3%) patients. Isolated Candida species identified as Candida albicans (n: 4) and C. glabrata (n: 2). Two strains of C. albicans, and C. glabrata strains were resistant to fluconazole.

Conclusion: Similar to several reports, the results of this study indicated that C. albicans is the main Candida species causing nosocomial candiduria and drug resistant Candida species are causative agents of candiduria in hospitalized patients.

Key words: Nosocomial, Candiduria, Candida species, PCR-RFLP, Fluconazole.
PM-32

Survey on the prevalence of scrotum in patients referred to BoAli Hospital in Zahedan (December 2017 - Dec. 2018)

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Abstract

Background: Tinea capitis disease of the cryptanal tissues of the hair and is caused by a group of keratinophilic fungi called dermatophytes. Alopecia head an infection common fungal around the world. The goal of this research was to study the epidemiology of Tinea capitis among patients referred to Buali clinical laboratory in Zahedan. Review and study fungal infections of view of public health and prevention anywhere in each population of the country is very important.

Methods: In this descriptive and cross-sectional study a total of 75 patients suspected to Tinea capitis. Samples were examined by direct microscopic examination of wet mount with 10% KOH (potassium hydroxide), to determine the species culture in the environment SCC and then the data were analyzed by SPSS-22 statistical software.

Results: The 75 patients (36.8% female and 61.3% male) that waste suspicious hair and shell head was 65 samples (86.6%) positive. Clinical manifestations Tinea capitis for ecthotrix 43.9%, endothrix 25.3%, mycilia were seen in the hair shaft 17.3%.

Conclusion: this study showed that the fungal diseases in particular Tinea capitis an important contribution in between the skin diseases area have.

Keywords: Tinea capitis, Zahedan, Epidemiology
PM-33

Hepatic Candidiasis in immunocompromised Patients: A review study

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Background: Candida species, in particular Candida albicans, are serious causes of fungal infections in immunocompromised patients. Hepatic Candidiasis is a type of candidiasis in immunocompromised patients as a challenge for these patients. In the 50-75% of the immunocompromised patients with candidiasis, the liver is damaged. It is very difficult to diagnose this disease before the liver biopsy. About 50 percent of the Blood cultures are negative and biochemical parameters of liver damage may not have a non-specific value. Generally, liver lesions cannot be detected by ultrasound or computed tomography until the patient’s neutrophil count returns to normal. Even when proper diagnosis and treatment is performed, the prognosis is often not satisfactory.

Methods: In the present study, the collection of materials was done by searching the keywords (Hepatic Candidiasis and immunocompromised Patients) in the google, PubMed, SID, Iran Medex databases.

Results: The clinical laboratory results and radiological findings of immunocompromised patients, as well as patients with leukemia, with Hepatic candidiasis, showed that liver and blood cultures were usually negative. An increase in alkaline phosphatase levels was significant in comparison with the increase in transaminases, bilirubin and gamma glutamyl transferase. Despite the
negative cultures, computed tomography of the liver biopsy revealed the yeast and hyphae forms. The presence of Candida species in the liver tissue sections was confirmed. In one patient of five patients, Candida albicans was reported. The response to treatment in immunocompromised Patients was found in only 13 out of 22 cases. In leukemia patients, the response to treatment (conventional treatment with amphotericin B) was poor, about 34.4% of the patients died.

**Conclusion:** Recent studies on autopsy and clinical specimens of immunocompromised patients reveal the liver involvement with Candida agent, which is a challenge in immunocompromised Patients with invasive candidiasis, especially in neutropenic patients. Due to the many problems associated with the treatment of Hepatic candidiasis, the prevention management of disease should be considered. For this purpose, oral antifungal prophylaxis is suggested. It seems that the most appropriate strategy to reduce the incidence of candidiasis in immunocompromised patient populations is Preventive or prophylactic therapies.

**Keywords:** Candidiasis, immunocompromised, fungal
PM-34

The role of molecular methods for identification of fungal pathogens; report of rare case

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Coelomycetous fungi, a set of extremely divergent genera and species, are experiencing an increasing trend as human pathogens. Species of the genus Didymella are coelomycetous fungi which are rarely reported as human pathogens. Didymella microchlamidospora is a member of this genus with no
report of human pulmonary infections. Here, we present the first report of infection due to this pathogen 50-year-old patient, which was identified using the molecular methods. Pathological examinations of tissue sections were reported as invasive candidiasis, however the results of culture and direct examination were not in line with this report. Microscopic features of the isolated filamentous fungus were compatible with species of the genus Nattrassia and Phoma, however when the isolate was subjected to sequence analysis of several molecular markers, it was identified as Didymella microchlamydospora. The patient was successfully treated with voriconazole.

Keywords: Didymella, uncommon fungi, pulmonary infection
Synergistic effect of fluconazole with echinocandins against azole-resistant clinical isolates of *Candida parapsilosis* complex

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**Background:** The *Candida parapsilosis* complex has been described as one of the most common yeast species isolated from patients with bloodstream infections worldwide. This complex consists of three species: *C. parapsilosis* sensu stricto, *C. orthopsilosis*, and *C. metapsilosis*. Although *C. parapsilosis* strains are usually susceptible to azoles, recent reports indicate the emergence of invasive infections due to fluconazole (FLC) resistant *C. parapsilosis* complex isolates and all species show elevated MICs for the echinocandin class drugs relative to other *Candida* species. We therefore investigated the efficacy of fluconazole with echinocandins against clinical *candida parapsilosis* complex isolates.

**Methods:** *In vitro* susceptibility to fluconazole and echinocandins of *C. parapsilosis* (n=80), *C. orthopsilosis* (n=20) and *C. metapsilosis* (n=3) was tested using CLSI broth microdilution M27-A3 methodology. The *in vitro* interactions between fluconazole and echinocandins (micafungin, anidulafungin) determined against fifteen triazoles resistant and high MICs echinocandins *C. parapsilosis* complex strains by use of a microdilution checkerboard technique.

**Results:** The combined interaction by fluconazole with micafungin (FICI range: 0.2-0.5) and fluconazole with anidulafungin (FICI range: 0.2-0.5) provided
synergic interaction. No antagonism and indifferent interactions was observed for any combination.

**Conclusion:** The combination of echinocandins with fluconazole exhibited synergistic activity against clinical *Candida parapsilosis* complex isolates suggesting an alternative approach to overcome antifungal drug resistance. The further studies in addition to determination of the underlying mechanism of this synergistic action will be need for using of this combination therapy in the *in vivo*.

**Keywords:** *Candida parapsilosis*, Azoles, Echinocandins
Mean platelet volume: a possible prognostic parameter in Immune thrombocytopenic purpura patients

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Background

Immune thrombocytopenic purpura (ITP) is a bleeding disorder which is caused due to presence of auto antibodies produced against platelet glycoproteins (GPs). These auto antibodies cause destruction of platelets in peripheral blood (PB), impairment of thrombopoiesis in bone marrow (BM) and increased risk of bleeding. ITP can be seen in both males and females at any age.

Methods

Relevant English-language literature was searched and retrieved from PubMed database (2000-2018). The following keywords were used: "Immune Thrombocytopenic purpura", "Platelet", "Mean platelet volume ", and "Thrombocytopenia".

Results
Most of ITP patients produce IgG antibodies (and rarely IgM or IgA) against platelet GPs specially GP IIb/IIIa and GP Ib/IX. ITP has three phases: newly diagnosed occurring within 3 months since diagnosis, persistent phase which can last to 12 months after diagnosis and chronic phase with lasts for more than 12 months since initial diagnosis. Currently there is no any definitive diagnostic/prognostic biomarker available for patients.

**Conclusion**

Studies before, indicated that larger platelets are more metabolically active. So hypothetically said, a higher mean platelet volume (MPV) in ITP patients can be interpreted as good prognostic parameter since it shows compensative activity of BM (releasing platelets to PB earlier) and more metabolic activity of platelets which is beneficial for patients because of reducing risk of bleedings.

**Keywords:** Immune thrombocytopenic purpura; Platelet; Mean platelet volume; Thrombocytopenia.
PH-4

Study on the significance correlation between CEBPA and Calreticulin at mRNA level diagnosed in de nevo AML patients

Abstract

Objectives: Calreticulin (CALR) and CCAAT/enhancer binding protein (C/EBP) alpha (CEBPA) are two important multifunctional proteins which play different roles in regulation of hematopoiesis. Expressional changes of these genes were related to the malignancy.

Methods: The present study aimed to investigate the expression levels of CALR and CEBPA genes in 96 de novo AML patients compared to 18 normal people as the control group through the Real-Time-PCR.

Results: Results of the present study revealed that the expression of these genes was significantly higher in patients with AML than the normal group (P <0.0001). Furthermore, there was a significant and positive correlation between CALR and CEBPA (P= 0.001 and r= 0.348).

Discussion: Higher level of CALR expression was expected, but the over-expression of CEBPA was on the contrary to its well-known role in the myeloid maturation. Based on the studies, CALR probably played roles in the expression of oncogenic CEBPA and it repressed the CEBPA translation in tumor suppressor gene (TSG).

Conclusion: The present study first indicated the over-expression of CALR in AML patients and compared it with the healthy normal control group and also
found a positive relationship between CALR and CEBPA expression in the AML patients.

**Keywords**

Acute myeloid leukemia (AML), CEBPA, CALR, Oncogene, Malignancy
PH-5

Transcription factors LEF1, PU.1 and IRF8 have decreased expression levels in majority of de novo acute myeloid leukemia patients

Abstract

The lymphoid enhancer-binding factor 1 (LEF1), PU.1 and interferon regulatory factor 8 (IRF8) are three important differentiation genes that are commonly defective and associated with the development of leukaemia. Alternations in the expression of these genes can be resulted in malignancy. In this study the expression levels of the genes mentioned were analysed using Real Time PCR with SYBR Green and the ΔΔCT method within 96 patients with acute myeloid leukaemia (AML) and 16 healthy subjects as a normal control. The results presented in this study revealed that PU.1 and LEF-1 gene expression was significantly lower and IRF8 gene expression levels were significantly higher in patients with AML in comparison with the normal control group (P < 0.0001). Furthermore, Analysis determines that the three genes have moderate positive correlation with each other; correlation between PU.1 and IRF-8 is R: 0.378, P < 0.0001, expression of PU.1 and LEF-1: R: 0.399, P < 0.0001 and the expression of IRF8 and LEF1: R: 0.320, P: 0.001 in patients with AML. In our study, the relatively strong positive correlation between these genes was observed which is supported by other studies. It can be indicated in this study that when malignancy for unknown reasons that new connections between transcription factors occur...
which can affect the malignancy process. Our observations suggest that examining the oncogenic role of these genes and discovering new molecular mechanisms formed in the process of malignancy in each of these differentiation genes can play a role in the design of novel diagnostic methods, monitoring and treatment of patients with acute myeloid leukaemia.

**Keywords:** IRF8, PU.1, LEF1, gene expression, AML
Changes of AML 1 and P53 tumor suppressor gene expression in patients de novo acute myeloid leukemia

Abstract

P53 and AML1 are two important tumor suppressor genes in the regulation of hematopoiesis with a critical role in keeping a balance between proliferation and differentiation. Alternations in the expression of these genes can result in malignancy. The present study investigated the expression levels of P53 and AML1 genes in 82 de novo AML patient specimens against 12 normal control group using Real-Time-PCR. The results presented in this study revealed that AML1 gene expression was significantly higher and P53 gene expression levels were significantly lower in patients with AML in comparison with the normal control group (P = 0.016 and P = 0.002). Furthermore, the correlation between P53 and AML1 was significant and positive (P= 0.037 and r= 0.231). The lower levels of P53 expression were expected and in line with the normal role of this gene as a tumor suppressor gene, however, AML1 overexpression was in contrast with of its well-known role in myeloid maturation. However, these findings suggest that despite the current established role this genes in myeloid cell differentiation, the oncogenic form of AML1 (AML1a) has possibly increased and high expression of this isoform may act as an inhibitor for other normal AML1 isoforms and P53 as well.

Key words: Acute myeloid leukemia (AML); P53; AML1; oncogene; malignancy
Methylation Status of SOX17 and RUNX3 Genes in Acute Leukemia

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Background: Several studies have examined the presence of DNA methylation of CpG islands in leukemia. Methylation of SOX17 and RUNX3 genes may play a role in leukemogenesis through silencing tumor suppressor genes. We investigated the methylation status of SOX17 and RUNX3 genes in patients with acute leukemia.

Methods: In this case-control study, peripheral blood samples from 100 AML and 100 ALL patients and 100 healthy controls were collected. Isolated DNA was treated with sodium bisulfite and methylation status was examined by methylation specific PCR (MS-PCR) with primers specific for methylated and unmethylated sequences of SOX17 and RUNX3 genes.

Results: The frequency of hypermethylation of SOX17 and RUNX3 genes were 36% and 28% in patients with acute myeloid leukemia (AML), and 21% and 22% in patients with acute lymphoblastic leukemia (ALL), respectively. Aberrant methylation of these genes was found in all FAB classifications of AML and ALL. Hypermethylation of SOX17 (P=0.055) and RUNX3 (P=0.003) genes were associated with FAB-M0 and M1 subtypes of AML, respectively. Also, aberrant methylation of RUNX3 gene was associated with FAB-L1 subtype of ALL (P=0.053). There was not any significant association between hypermethylation of SOX17 and RUNX3 genes and clinical parameters of patients with leukemia including sex, age, WBC, and platelet counts.

Conclusion: Hypermethylation of SOX17 and RUNX3 genes was seen in patients with acute leukemia. Moreover, no significant association was observed between hypermethylation of SOX17 and RUNX3 and induction of remission.
Keywords: Acute myeloid leukemia, Acute lymphoblastic leukemia, RUNX3, SOX17, DNA Methylation
Correlation Between C677T and A1298C Mutations on the MTHFR Gene With Plasma Homocysteine Levels and Venous Thrombosis in Pregnant Women at Risk of Thrombosis

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Background: Deep venous thrombosis (DVT) is a common disease with a high morbidity, mortality and increase in miscarriages. The purpose of this study was to assess the correlation between C677T and A1298C mutations on the methylenetetrahydrofolate reductase (MTHFR) gene with total plasma homocysteine levels and deep venous thrombosis in pregnant women at risk of thrombosis.

Methods: In this case-control study, 120 pregnant women with risk of DVT and 100 pregnant women without risk of DVT were included in the study. Assay for identification of MTHFR mutations was carried out by PCR-RFLP. Total plasma homocysteine was measured by ELISA method.

Results: Homozygous (MM) mutations of MTHFR C677T and A1298C were not associated with DVT in pregnant women with and without DVT, respectively. Plasma homocysteine levels were significantly higher in pregnant women with DVT (18.3 ± 5.9 μmol/L) than in the pregnant women without DVT (8.9 ± 6.4 μmol/L) in C677T and A1298C mutations on the MTHFR gene, respectively (P = 0.021).

Conclusion: Our results showed that MTHFR C677T and MTHFR A1289C polymorphisms are not connected with total plasma homocysteine levels in pregnant women with and without DVT. Also, plasma homocysteine levels were significantly higher in pregnant women with DVT.
Keywords: Mutations, Homocysteine, Deep Venous Thrombosis, Pregnant Women
Cancer Stem Cell Research In Intestinal Disease

Cancer Stem cell (CSC) ideas was raised up 160 years ago. But demonstrated in 1997 for the first time. Scientist have been identified cells that are able to self-renewal, proliferation, differentiation, tumor formation and expansion. This theory suggest a small population of adult stem cell are located in some tissues. Drug resistant is another feature of CSCs. Intestine, is one of the CSCs location. These are located in the base of intestine between crypt cells in a limited count and responsible for repairing the intestine epithelial cells after cell damage. Increasing in the number of stem cells, along with their migration from the base to the top of the crypts, is a signal for stem cell expansion and tumorigenesis. Clone cancer is one of the fourth most lethal cancer in the world. The result of the studies showed the presence of Intestinal Cancer Stem Cell (ICSC) role in initiating and expansion of colon cancer. Immunohistochemical, Quantitative PCR, Laser Micro Dissection and Laser Endomicroscopy, are techniques for studying in CSC markers and signaling. The presence of cell markers including CD133, CD166, CD44, Lgr5, etc. on their surface and the Wnt-β catenin signaling pathway that is controlled by Lgr5-Rspondin, are important findings of these cells in intestine. According the role of CSCs in the development of tumorigenesis and drug resistance and the role of this cells in colon cancer, studying on these cells will play an important role in the design of anticancer drugs and disease control.
PV-7

Frequency of hepatitis C infection in HIV infected patients in Ahvaz, Iran

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Background: Hepatitis C (HCV) prevalence still appears on the rise in HIV-infected patients worldwide. HIV and HCV share the same transmission rout; therefore, co-infection is frequent. Compared with HIV mono-infected patients, the mortality among HCV co-infected patients with HIV remains markedly increased because of multiple risk factors, in particular among drug users. HIV patients co-infected HCV remains an important clinical problem that requires a
multidisciplinary approach including direct-acting antivirals for those at risk of liver-related death.

**Methods:** This study comprised 78 HIV-infected patients. The sera were collected from patients whom were referred to Rzai hospital and counseling health center of Ahvaz. All the patient sera were tested for anti-HCV antibody by Enzyme Linked Immuno-Sorbent Assay (ELISA). The sera of positive anti-HCV antibody, were assayed for 5'-UTR and core regions of HCV genome by Nested RT-PCR. The HCV genotyping was determined by sequencing based on 5'-UTR and core region.

**Results:** A total of 78 HIV-infected patients followed in 2016, 67(85.89%) males and 11 (14.1%) females. The male patient ages were from 25 to 51 years with mean age 33.66 ± 6.31 years and the female patient ages were from 21 to 33 years with mean age 29.27 ± 3.92 years. Overall 25/78(32%) of patients showed positive for HCV Antibody. Whereas 19(24.4%) were positive for 5'-UTR and core regions by nested-PCR. HCV genotype 1a was the most prevalent (60%), followed by genotypes 3a (40%).

**Conclusion:** The distribution of HIV patients co-infected HCV was significantly higher in male patients compared to females (p=0.029). To improve treatment and to prevent cirrhosis and hepatocellular carcinoma, the screening of HCV infection by molecular technique such as PCR and HCV genotyping should be implemented for all patients with HIV infection.
Keywords: Frequency, HIV patients, Co-infected HCV
PV-8

Frequency of hepatitis C virus genotypes in people with HCV infection and HCV-HIV infection in Isfahan province

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Background: Hepatitis C virus has a high genetic diversity and is divided into six types of genotypes and over 70 different types (a, b, c, d, etc.). The variation of these genotypes is different in different parts of the world and there is a significant difference in response to treatment with alpha interferon and progression to chronic infection among different hepatitis C genotypes. Infection with hepatitis C in HIV-infected people and specially injecting drug users is one of the most important problems that causes liver damage and death. The aim of this study was to determine the frequency of hepatitis C virus genotypes in people with HCV infection and those with HCV-HIV co-infection that are referred to the Isfahan Counseling Center for Behavioral Illnesses in 1396.

Methods: This is a descriptive and cross-sectional study. Of the 530 patients referring to Isfahan Counseling Center for Behavioral Illnesses in 1396 who were suspected of having hepatitis C, 95 patients with positive HCV regarding to and RT-PCR and serological results were included in the study. The amount of viral
load and determination of hepatitis C genotype in patients were evaluated using Real Time PCR.

**Results:** In this study, 95 patients with hepatitis C with RT-PCR were tested. The most common genotype was genotype 3 in all patients (50%), while in HIV-HCV-coinfected individuals, genotype 1 was the most common (25%).

**Conclusion:** Regarding the high prevalence of genotype 3 in Isfahan and considering the high cost of treatment for hepatitis C drugs and the fact that the duration of treatment of genotypes 3 is less than other genotypes and better treatment response and longer SVR, it seems it would be better to evaluate patients regarding to genotype before treatment for hepatitis C.

**Keywords:** HCV, HIV-HCV co-infected, genotypes
PV-9

Experimental close contact transmission of A/H9N2 viruses in guinea pig models

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Background:

Following initial plan for the elimination of chickens and eggs infected and vaccination attempts with killed vaccines, there is still an enzootic disease in Iran. Information is limited on A/H9N2 human infections cases in Iran, indicating the need of further studies. Guinea pigs are considered as suitable models to study the transmission potential of A/H9N2. The aim of this study was to evaluate the close contact transmission of A/H9N2 in guinea pig’s models.

Methods:

Thirty days old specific pathogen free (SPF), viral antibody free (SPF/ VAF) Dunkin-Hartley strain of guinea pigs (\textit{Pasteur Institute, Iran}), were used for the study. Virus isolation, titration of A/H9N2 (TCID50 assay) and Reverse transcription-polymerase chain reaction (RT-PCR) were performed. Following experimental A/H9N2 infection of guinea pigs, euthanasia was performed at prescribed time points. Lungs were collected in 10% neutral buffered formalin.
and embedded in paraffin wax. Sections were then cut at 5μm and stained with Hematoxylin and Eosin for histopathological examination.

**Results:**

We found that A/H9N2 virus was able to replicate in low titers in the nasal turbinate and lung of guinea pigs and also transmit through close contact from infected guinea pigs to sentinel guinea pigs. Mild to moderate macroscopic changes both experimentally infected and close contact animals were observed in the lungs. Histopathological examination in infected animals showed mild lymphocytic& Macrophage perivascular and peribronchial. focal mild intraalveolar edema with Neutrophil& Macrophage infiltration mild bronchopneumonia lymphocytic pneumonia infiltration.

**Conclusion:**

The results of this study showed that prevalent avian A/H9N2 influenza viruses in Iran have the potential for transmission to guinea pigs. There is also the possibility of close contact transmission of the A/H9N2 virus among animal models.

**Keywords:**

A/H9N2, guinea pig, TCID50, close contact, risk assessment
PV-10

Evaluation frequency of cccDNA in Chronic Hepatitis B patients

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Introduction: Hepatitis B virus (HBV) infection is a serious health problem in the world and increases the risk of progression to cirrhosis and hepatocellular carcinoma. Considering the cccDNA in replication cycle of HBV has an important role in the development of chronic infection and developing to HCC. Aim of this study evaluated the incidence of cccDNA in the chronic infection with hepatitis B virus.

Materials and method: In a retrospective cross-sectional study 96 blood samples 64(66.7%) Males and 32(33.3%) females, were collected from patients with chronic Hepatitis B virus infection during July 2017 – April 2018. cccDNA, HBV load and other serological markers were determined in these samples.

Results: Out of 96 samples of CHB infections, there were 25 samples (26%) positive for HBeAg. There was a significant relation between serological markers (HBeAg, HBsAg) and cccDNA and HBV DNA levels, that means cccDNA plays an important role in progression of HBV infection from acute to chronic phase.

Discussion: The increased levels of cccDNA and HBV loads in chronic hepatitis B patients were associated with positive serum HBeAg. Since high levels of this molecule and HBe Ag positive were indicative of active and transcriptional activity of HBV, these findings indicate that the level of cccDNA and HBV load can affect the course of chronic HBV infection. In this study, there was no
relationship between the levels of cccDNA and gender in patients with chronic HBV infection.

**Keywords:** Hepatitis B virus, Chronic Infection, cccDNA, Hepato cell carcinoma
PV-11

An Evidence-Rate Study of BK Virus Prevalence among Iranian Renal Transplant Recipients
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Abstract

Background: Reactivation of BK virus (BKV) is a major risk factor for renal transplant recipients. It is crucial to investigate the prevalence of BKV in those patients. The aim of the present study is to summarize our current knowledge about BKV status in Iranian renal transplant recipients.

Methods: PubMed, GoogleScholar, and Iranian scientific databases were scavenged with specific terms. Quality of data was assessed and processed for further analysis. I² and Cochran’s Q-value have evaluated for heterogeneity. I² more than 25% was implicated heterogeneity. Evidence rate was investigated with the confidence interval (CI) of 95%. Publication bias has also been double-checked with eye through funnel plot and statistically with Egger’s and Begg’s tests. P-value less than 0.05 was considered as significant.

Results: twelve studies were found to be illegible for the study. Further data were extracted for sub-group analysis. Accordingly, four groups of BKV detection, including real-time PCR, PCR, double PCR and semi-nested PCR, and light microscopy examination were extracted from included studies. According to heterogeneity, random model was used for analysis. The overall evidence rate in the random model was 0.347 (CI 95%, 0.225-0.493, p-value=0.04). Random evidence rate for Double PCR method was 0.287 (6.96E-2-0.685, p-value>0.05). For Light microscopy, the overall evidence rate was 0.131 (0.014-0.618, p-value>0.05). For PCR and Real-time sub-groups, evidence rate was 0.287 (0.121-0.54, p-value>0.05) and 0.465 (0.252-0.692, p-value>0.05). Heterogeneity was
also observed in sample type sub-groups. This group was composed of Biopsy (0.515 (0.154-0.86), p=0.0001), Plasma (0.279 (0.106-0.557), p=0.0001), Urine (0.343 (0.179-0.556), p=0.0001).

**Conclusion:** Evidence rate of BKV among renal transplant recipients is 34.7% (ranged from ~10-60%) in Iran. The rate of BKV is higher than that reported from other parts of the world. Organ transplant donors need to be screened for BKV.
PV-14

Presence of CCR5Δ32 Mutation in HIV-infected Patients, Individuals who were at High Risk for HIV Infection, and Healthy Controls

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Abstract:

**Background:** The C–C chemokine receptor 5 (CCR5) is known as a co-receptor for human immunodeficiency virus-1 (HIV-1) attachment and entry to T lymphocytes. The 32-base pair deletion on CCR5 (CCR5Δ32) is recognized as a protective allele against to HIV infection and immune system disorders. This study was designed and implemented to clarify the CCR5Δ32 allele frequency in healthy controls, HIV-infected people, and individuals who were at high risk for HIV infection.

**Materials and Methods:**

From April 2016 to October 2018, 140 healthy people as controls, 71 individuals who were at high risk for HIV infection, and 76 HIV infected people were enrolled in this cross-sectional research. The peripheral blood mononuclear cells
(PBMCs) were isolated from the whole blood by a standard protocol of Ficoll–Hypaque gradient centrifugation, and then the genomic DNA was extracted from the PBMC specimens of studied participants. The CCR5 gene was amplified using polymerase chain reaction (PCR) technique, and then the PCR products were sequenced.

**Results:** The allele frequency of the CCR5Δ32 in healthy people as control group were 1.4%, in high risk group for HIV infection were 4.2%, and in HIV-infected people were 6.6% for heterozygous genotype. It is noteworthy that none of the groups had the homozygous genotype of the CCR5Δ32.

**Conclusion:** Based on the findings of this research, it seems that the CCR5Δ32 allele does not exist in Iranian society and Iranians similar to neighbor countries are susceptible to HIV infection.

**Keywords:** Human Immunodeficiency Virus-1 (HIV-1); Chemokine Receptor, CCR5Δ32, AIDS, Iran
Molecular prevalence of human papillomavirus infection among Iranian women with breast cancer.

Ghaffari H, Nafissi N, Hashemi-Bahremani M, Alebouyeh MR, Tavakoli A, Javanmard D, Bokharaei-Salim F, Mortazavi HS, Monavari SH.

Abstract

BACKGROUND:

The etiology and molecular mechanisms involved in the development of breast cancer still remain poorly understood. Some epidemiological studies have shown an association between human papillomavirus (HPV) and breast cancer. However, the findings are controversial.

OBJECTIVE:

Our study was aimed to investigate the presence of HPV DNA in breast carcinomas of Iranian women.

METHODS:

In total, 72 samples of formalin-fixed paraffin-embedded (FFPE) tissues of breast cancer collected between December 2014 and April 2016 were examined. HPV DNA detection was performed by nested-PCR assay. Next, positive samples were subjected to genotyping by the CLART HPV2 microarray system. All statistical analysis was carried out using SPSS v.18.0.

RESULTS:

HPV DNA was detected in 4/72 (5.55%) samples. Clinical factors were not statistically associated with HPV presence. However, CLART HPV2 microarray assay failed to determine the genotype of any positive samples.
CONCLUSION:

The low frequency of HPV detected in our study does not support an association between breast carcinoma and HPV infection. However, it is possible that HPV may be responsible for breast carcinogenesis only in small percentage of all breast cancer.

KEYWORDS:

Breast cancer; Breast carcinoma; HPV; Human papillomavirus; Iran
PV-16

No Evidence for Human Papillomavirus in Patients with HIV in Iran
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Abstract
Background and Aims: Human Papillomaviruses (HPVs) have an established role in the development of cervical cancer. However, the presence of underlying conditions such as HIV/AIDS is a factor for the development of this malignancy. This study was aimed to evaluate the prevalence of HPV DNA in plasma samples from HIV-positive patients in Tehran, Iran.

Materials and Methods: Plasma specimens from 95 patients diagnosed with HIV infection from Tehran’s hospitals were examined for the presence of HPV DNA by means of a Real-Time polymerase chain reaction (PCR) assay with the amplification of a fragment of L1 region of the HPV genome. Furthermore, HIV viral load testing was performed for all patients using the COBAS TaqMan assay.

Results: Out of 95 patients, 59 (62%) and 36 (38%) of the cases were males and females, respectively. The mean age of the patients was 37.42 ± 11.25 (range 2–69) years. The mean HIV viral load of all patients with HIV was 73010.754 copies per ml. None of the 95 HIV positive patients tested had HPV DNA detected in their plasma by Real-Time PCR assay.

Conclusions: Previous studies have suggested that patients with HIV infection are at risk for acquiring HPV infection. However, we have shown no evidence of HPV DNA in plasma samples of patients with HIV.

Keywords: HPV, Human Papillomavirus, HIV, Human Immunodeficiency Virus, Iran
The Role of Human Papilloma Virus in Breast Cancer Pathogenesis

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Abstract

Background: Breast cancer is the most common malignancy among women worldwide. Recent studies have been shown that the role of human papillomavirus (HPV) infection in breast cancer. The aim of this study was to determine the possible role of HPV in breast cancer development.

Methods: Breast tissues samples were collected from 85 patients with breast cancer and 53 healthy controls. The detection of HPV was examined by
polymerase chain reaction (PCR). Also, ELISA and Real-time PCR were used to measure the expression level of inflammatory cytokines and some of cellular genes including anti-carcinogenic genes (such as p53, retinoblastoma (RB)), BRCA1, and BRCA2.

**Results:** The HPV DNA was detected in 61.7% and 22.6% of breast cancer and healthy tissues respectively. The association between HPV infection and breast cancer was significant (P<0.05). The expression of mentioned cellular genes was decreased in patients in comparison to healthy controls (P<0.05). Also, the expression of these genes was decreased in patients with positive HPV than negative ones (P<0.05 for all of them).

**Conclusion:** The current study indicated that HPV infection has a role in pathogenesis of breast cancer and can be considered as an important agent in the breast tumor development.

**Keywords:** Inflammation, HPV, Cancer Development
The roles of FOX proteins in virus-associated cancers

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Abstract

Forkhead box (FOX) proteins play a crucial role in regulating the expression of genes involved in multiple biological processes, such as metabolism, development, differentiation, proliferation, apoptosis, migration, invasion, and longevity. Deregulation of FOX proteins is commonly associated with cancer
initiation, progression, and chemotherapeutic drug resistance in many human tumors. FOX proteins deregulate through genetic events and the perturbation of posttranslational modification. The purpose of the present review is to describe the deregulation of FOX proteins by oncoviruses. Oncoviruses utilize various mechanisms to deregulate FOX proteins, including alterations in posttranslational modifications, cellular localization independently of posttranslational modifications, virus-encoded miRNAs, activation or suppression of a series of cell signaling pathways. This deregulation can affect proliferation, metastasis, chemotherapy resistance, and immunosuppression in virus-induced cancers and help to chronic viral infection, development of gluconeogenic responses, and inflammation. Since the PI3K/ Akt/mTOR signaling pathway is the upstream FOXO, suppressing it can cause FOXO function to return, and this can be one of the reasons for patients to recover from the infection of the viruses used to treat these inhibitors. Hence, FOX proteins could serve as prognosis markers and target therapy specifically in cancers caused by oncoviruses.

KEYWORDS : cancer, forkhead box proteins, viruses
PV-21

Evaluation Epstein-Barr virus in children under 5 years suspected mononucleous city of Sanandaj

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Introduction: Epstein-Barr virus of the herpes virus family and is the subfamily Gamma herpes Virinae. Infection with the virus is common in the whole world. In developing countries, more than 90% of children, up to 6 months old, become infected. The virus causes infectious mononucleosis, which is associated with the involvement of b-lymphocytes and symptoms such as headache, restlessness, fatigue, and sore throat.

Methods: Out of 18 children with suspected cases of infectious mononucleosis, blood samples were taken from the medical examination laboratory of Hosseini Nasab in Sanandaj And their serum was separated after 15 minutes of centrifugation. Then they tested IgM anti–VCA by the closed system Alegria company ELISA was performed. To confirm the positive cases, Monotest (rapid method) and the method of observing the patient's blood smears, under the microscope, are used to observe the presence and amount of large lymphocytes (activated T cells) known as atypical cells. These cells are found in viral infections such as mononucleosis, mumps, cytomegalovirus, and hepatitis, also can be seen in drug reactions and pertussis, and brucellosis.

Results: In 10 cases (16.67%) of boys and 8 patients (13.34%) of the girls, who had mononucleosis symptoms IgM test was positive (30% total n = 18). Rapid
serologic testing (Monotest) was positive in all of them (100%). In peripheral blood smear, there were atypical lymphocytes with an average of about 3.2 atypical cells per patient.

**Conclusion:** As can be seen, all of these tests are good confirmation tests and Performing a Monotest and observing atypical cells can help in cases of positive antibodies IgM EBV and suspicion of infectious mononucleosis. But it must be said that for the final diagnosis of infectious mononucleosis, especially in acute cases, other tests, such as WoW and Nenenen, are necessary with new methods and techniques and closed systems.
PV-23

Molecular Detection of Occult HCV Infection in Iranian Injection Drug Users with HIV Infection

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Abstract

Background:

One of the pathological form of chronic hepatitis C is occult HCV infection (OCI), in which there are no detectable HCV-RNA in serum or plasma in the presence of HCV-RNA in peripheral mononuclear cells (PBMCs) and liver biopsy specimen. There are 2 kinds of OCI, seronegative OCI: no Anti-HCV antibody in
serum/plasma, and seropositive OCI: the existence of anti-HCV antibody in serum/plasma. The aim of this study is to estimate prevalence of OCI in HIV positive among people who inject drugs.

**Material and Methods:**

From April 2015 to August 2018, 161 Iranian IDUs with established HIV infection were enrolled. The viral RNA was extracted from the plasma and PBMC samples of studied participants, and the presence of HCV-RNA was examined using RT-nested PCR by primers from two conserved regions (5´-UTR and NS5B region). HCV genotyping was performed by RFLP method. To confirm the results of genotyping, the amplified PCR products were sequenced.

**Results:**

Of the 161 patients, 134 (83.2%) were positive for anti-HCV antibody, and HCV-RNA was detected in the plasma specimens of 84, and in PBMC samples of 98 (60.9%) subjects. Therefore, 14 (8.6%) subjects suffering from OCI. The result of HCV genotyping of the cases with OCI was as follows: 5 patients (35.7%) were infected with subtype 1a, 8 patients (57.1%) were infected with subtype 3a, and 1 patient (7.1%) was infected with genotype 4.

**Conclusion:**

Thus it seems that the existence of OCI in HIV positive IDUs is an extremely intricate and may postpone the global eradication of HCV infection until 2030.
Key words:
Hepatitis C virus; Intravenous drug users; Occult HCV infection; Peripheral blood mononuclear cells (PBMCs); Iranian.
PV-24

The frequency of hepatitis c virus Genotypes in the patients of the Azerbaijan republic referring to Tabriz metropolitan therapeutic centers

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Background: Generally, hepatitis C has been identified as one of the major health issues that about 3 percent of the world’s population have been threatened and affected by it (about 170 million people) and also it can be considered as a factor in acute and chronic hepatitis.

Methods: The aim of this study is to determine the prevalence of HCV genotypes in Azerbaijan patients. In this study, sampling was done on the referred patients to the treatment centers. RNA was extracted after isolation of plasma and then after the synthesizing of CDNA the sample was carried out to the laboratory for performing the Real-time phase in order to determine the genotype.

Results: The evaluation of HCV genotypes in positive plasma samples showed that dominant subsets were remarkable and the mean age of the patients was 37.3±11.8 (In the age range of 2-63). Among the 235 patients, 139 of them (59.1%) were male. Statistically, the average number of women was more than men (T. test. p<0.05). 1b genotype type was reported 70% in the patients above 40 years old and also it was reported as 71/6% in the patients under 40 years old that wasn’t statistically significant. The incidence of serotype 3a was higher among the patients younger than 40 years old (3a was 18.1% vs. 15%), and this serotype was prevalent among men (3a was 18.7% vs. 14.6%), which was statistically significant.

Conclusion: The findings indicate that among the Azerbaijan’s patients with chronic hepatitis C, 1b (71.1%) and 3a (17%) genotypes were dominant.
Keywords: Hepatitis C, Genotype, Infection
PV-25

Prevalence of Rubella antibodies in pregnant women of Mahshahr city, southwestern Iran

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Background: Rubella is a member of Togaviridae and it causes a mild infection with fever and rashes. The most significant issue about it is causing the congenital rubella syndrome which leads to dangerous disorders on embryo forming especially in early periods of pregnancy. This virus infection dramatically can lead to abortion or if the pregnancy go on the child will be born with cardiac anomalies, mental retardation, blindness, lost of hearing and cataracts. According to the WHO in 2014, only 46% of newborns can develop immunity. So we decided to evaluate the immunity of pregnant women in Mahshahr who had been examined in different laboratories for almost 3 years.

Methods: We studied all the pregnant women (2473 person aged from 17 to 43 years old) who referred to different laboratories to be checked for IgM and IgG Rubella antibodies with different ELISA kits.

Results: We found that all the women who had been examined for Rubella antibodies were immun with high IgG titers and negative for IgM antibody.

Conclusion: As all tested women were immune to rubella, we understand that they had been vaccinated and need no more dosage of vaccine.

Key words: Rubella, pregnant women, Mahshahr
PV-26

Molecular detection of Genogroup I of Noroviruses in patients with acute gastroenteritis from Tehran and Alborz provinces

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Introduction:

Human Noroviruses (NoVs) are the leading cause of gastroenteritis in all age groups worldwide. NoV is a small, non-enveloped virus that belongs to the family Caliciviridae and is characterized by high infectivity and stability. NoVs are genetically and antigenically diverse and have been divided into seven genogroups (GI-GVII) on the basis of nucleotide and amino acid sequences and each genogroup can be further divided into genotypes. The aim of this study was to determine the presence of Genogroup I NoVs in samples from Tehran and Alborz provinces residents with acute gastroenteritis symptoms.

Material and methods:

A molecular epidemiological study of NoVs prevalence was performed in two provinces of Iran (Tehran and Alborz) from November 2017 to June 2018. A total of 296 stool specimens were collected from hospitalized patients with acute gastroenteritis and stored at -70°C until use. Viral RNA was extracted and reverse
transcription Nested-PCR was employed to amplify and detect NoV genome. The N-terminal/Core region of NoV genome was amplified, then the nucleotide sequences were determined and phylogenetic analysis was performed.

**Results:**

The study population comprised of 131 males (44.3%) and 165 females (55.7%). The average age is 11.24 ± 16.20. Main clinical symptoms were diarrhea, fever, vomiting, abdominal pain and headache. Totally, 3 of 296 samples (10.1%) were positive for GI NoVs infection. The number of genogroup GI in negative samples were 0 and in positive samples were 3 and no difference in GI NoVs infection frequency was observed between male or female groups. (5.7% vs 9.1% respectively, P value=0.316).

**Discussion:**

The findings indicate that GI NoVs is one of the most important etiologies of acute gastroenteritis among patients from Tehran and Alborz provinces but the prevalence of gengroup GI is lower than GII. Although the prevalence of GI NoVs is lower than other developing countries, promoting public health education and preparation of health care setting for controlling the Norovirus sporadic cases and outbreaks are strongly recommended.

**Keywords:** Acute gastroenteritis, Noroviruses, Genogroup I, Molecular detection
PV-27

Effects of medicinal plants for the treatment of respiratory viral infections

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Abstract

Since available antiviral regimens have unsatisfactory clinical outcomes, suggesting the need for novel antiviral drugs. It also, the refractory viral infections resistant to available antiviral drugs are alarming threats and a serious health concern. Medicinal herbs are used as traditional medicine for the treatment of various diseases, including viral infection. They are widely accepted as nature gift and powerful agents for treatment of infectious diseases. The aims of this study are to assemble the facts and to conclude the therapeutic potential of medicinal
plants in the eradication and management of various viral diseases especially respiratory viral infections. The articles, published in the language since 2000 to 2018, were included from Web of Science, Cochrane Library, AMED, CISCOM, EMBASE, MEDLINE, Scopus, and PubMed by using relevant keywords. The data mainly focusing on plant extracts and herbal products with therapeutic efficacies against respiratory viral infections were included in the study. Several of plant extracts with antiviral effect were recognized.

CONCLUSION: In conclusion, herbal medicine can be as a promising and innovative treatment option for the treatment of viral infections. In this study we investigated the effects of Radix Ginseng, Maoto, Licorice roots, Antiwei, North American ginseng, Berries, Echinacea, plants extracted carnosic acid, pomegranate, guava tea, and Bai Shao in treatment of Viral infections and we recognized that all of them had positive effects in treatment of viral infections such as HIV, HSV, HCV and specially respiratory viral infections like Influenza.

Keywords: herbal medicine; respiratory viral infections; treatment
CD32-a as a novel biomarker for HIV reservoir diagnosis and treatment; True or False? a systematic review

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Background:

Human Immune Deficiency Virus (HIV) has remained one of the most important health issues for more than three decades affecting more than 40 million individuals. Conventional treatment of HIV includes antiretroviral therapy (ART); however, recurrence after ART renders HIV resistant to treatment. Various efforts have been conducted to identify reservoir CD4+ T cells from the intact cells. CD32-a was introduced as an HIV reservoir cell marker in 2017; however, new studies have released contrasting results. In this review, we will discuss CD32-a as an opportunity and obstacle for the eradication of HIV.

Search method:

PubMed, Google Scholar, Scopus, Elsevier, and Embase were searched in English with the keywords: HIV, CD32-a, reservoir, eradication, and diagnosis from 2012 to December 2018. 40 articles were found based on our inclusion criteria, and 13 articles were selected and included in our study based on exclusion criteria.

Results:

One of the most important obstacles that hinder the efficacy of ART are the latent HIV reservoirs. Therefore, identification of new markers for reservoir cells could open a new opportunity for HIV diagnosis and eradication.
In 2017, Descours et al. published an article in *nature journal* which introduced CD32-a as a novel marker for CD4$^+$ T cells as the most important reservoir of HIV infection. Subsequently, other studies were published which questioned this hypothesis. In 2018, Christa et al. and Badia et al. published two similar papers that indicated CD32-a as a marker of T cell activation, but not reservoir marker.

Conclusion:

Identification of novel biomarkers for HIV could pave the way to designing novel treatment strategies for HIV. The potential of CD32-a as an HIV reservoir marker has been questioned recently; however, more studies are recommended for evaluation of this concept.

Keywords:

HIV, CD32-a, reservoir, eradication
PV-29

Assessment of the immunogenicity of foot and mouse disease vaccine produced by Razi Institute against types of A13, A15 and O2010 of FMD virus

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Abstract

Background: Foot-and-Mouth Disease (FMD) is a highly contagious infectious disease of livestock which has made a barrier to hygiene providing and production of livestock and their products due to severe economic losses. FMD leads to a sharp reduction in the livestock production and also plays the main role in the livestock trade and raw products.

The aim of this study was assessment of antibody response against viral types A13, A15 and O2010 and also the evaluation of humoral system status with FMD virus after the injection of FMD vaccine produced by Razi Institute.

Methods: twenty non-vaccinated healthy calves were purchased and their health was evaluated. In order to ensure the absence of antibodies against FMD virus of
all types, the blood of them was sampled and all were cooperated to serum neutralization test (SNT).

The SNT method was performed by the micro-neutralization test. Serum samples were tested before and after vaccination. Six wells of dilutions, 1/8 to 1/256 of serum were prepared and after adding the FMD virus they were incubated and then were added to the cell culture. After 48 hours the CPE was checked.

**Results:** The mean serum titers of antibodies against all three viral type Average A13, A15 and O2010 prior to vaccination was equal to 0.6. One week after the injection, the antibody titer increased especially against A15 in a significant difference (p value=0.017) compared to two other types. The increase in the three virus type was continued a month after injection. Since then the A13 and A15 type antibody titer underwent increasing but declined against O2010 type. In the second month after the injection, the titer against A13 and A15 remained in stationary state and declined against O2010 type. The statistical analysis showed that the antibody level against the viral types was significantly different in 7 days, 1, 2, 4, 6 and 7 months after the injection.

**Conclusion:** The FMD vaccine produced by Razi institute showed the ability to protect animals become dependent on test conditions, the type O2010 for 6 months and for the type A15 and A13 for 7 months after vaccination.

**Key words:** foot and mouth disease virus, vaccine, antibody response
PV-31
A systematic review of the evidence on the effects of Cytomegalovirus on Abortion

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Abstract
Background: Cytomegalovirus (CMV) is a species of Herpesviridae, which has no clinical symptoms in early infection in pregnant women. Nevertheless, it can be transmitted to the baby through saliva, body fluids, blood and cervical secretions. The aim of this study is a systematic review of the effects of CMV on abortion.

Method: Data was collected from Web of Science (ISI), PubMed, Scopus, Ovid, and EMBASE databases by May 2018. The keywords used included abortion, current abortion, B19, Cytomegalovirus, spontaneous abortion, and placenta. The National Institutes of Health's Quality Assessment Tool was used for quality assessment.

Results: 15 papers from 1993 to 2018 were reviewed. 11 out of 15 were descriptive-analytic and 6 were case-control studies. In case-control studies, the control group consisted of healthy pregnant women with no history of abortion. The case group comprised women who experienced abortion and recurrent abortion. The maximum sample size included 779 and the minimum included 17 cases of abortion. The highest incidence of CMV infection in abortion was 100%, reported by Saraswathy and 97% in the study of Tarokhian. The lowest incidence was observed by Oliveira with 0.04% and Rubina with 16%.

Conclusion: The results of most studies indicate that CMV infection can lead to abortion by transferring through body fluids, as well as activating the uterine inflammatory response and immune response, and transferring into embryonic tissues.
Keywords: Cytomegalovirus; Pregnant women; Abortion; Recurrent abortion
A Nonglycosylated 27 KDa Molecule as Common Antigen between Human Breast Cancer and *Echinococcus granulosus* Hydatid Cyst Wall

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Abstract

Background: Hydatid cyst, which has anti-cancer activities, outwardly is covered with the cyst wall. It is in close contact with the host tissues and its molecules presented to the immune system. In this work immunological reaction of the sera of breast cancer patients with the hydatid cyst wall antigens have been investigated.

Method: For this purpose, sera of patients with breast cancer, hydatid cyst and normal human sera were collected and their reaction with hydatid cyst wall antigens was tested using western immunoblotting technique.

Results: All sera of patients with breast cancer, hydatid cyst and also human normal sera reacted with a band in western immunoblotting. However, sera of patients with breast cancer showed reaction with a 27 KDa band.

Results of this work also revealed that this band was not glycosylated and may express only in some stages of breast cancer development.

Conclusion: Sera of patients with breast cancer cross reacted with a nonglycosylated antigen of hydatid cyst wall. However, more work is recommended to find if this band involves in anticancer activity of the hydatid cyst.

Keywords: Breast Cancer, Cross Reaction, Hydatid Cyst
PC-2

Monoclonal Antibodies Production against 40KDa Band Antigen of Hydatid Cyst and Their Effects on Breast Cancer Cells

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Introduction: Hydatid cyst is the larval stage of the tapeworm Echinococcus granulosus. Hydatid cyst fluid, cyst membrane and Protoscolices, contain a complex mixture of antigens that can induce immune responses in the host. Anti-cancer properties of Protoscolices and hydatid cyst fluid has been shown. In order to identify antigens of hydatid cyst fluid that have anti-cancer effect, in this study production of monoclonal antibodies against one of the hydatid cyst fluid band (40KDa) that has cross reaction with sera of patients with breast cancer has been investigated.

Methods: In this experimental study, 40KDa band of hydatid cyst fluid was used as antigen. A group of mice were immunized with this antigen, and then their spleen cells were extracted and fused with SP2 cells. Monoclonal antibodies production was checked in wells using ELISA and western blotting. The reaction of the produced monoclonal antibodies with breast cancer cells was tested using flow cytometry method. Finally effect of the monoclonal antibodies on growth of breast cancer cells was investigated in vitro.

Results: The results of this study showed that monoclonal antibodies antibody against 40KDa were detected in several wells. The produced monoclonal antibodies reacted with the surface of breast cancer cells. However, they had no significant effect on growth of breast cancer cells in culture medium.
Conclusion: Produced monoclonal antibodies against hydatid cyst fluid 40KDa band reacted with the surface of breast cancer cells but had no significant effect on growth of these cells.

Key Words: monoclonal antibodies, hydatid cyst fluid antigens, anti-tumor effect
Inhibition of cancer cell proliferation and the effect of oleoropine in the expression of DNA methyltransferase (DNMT) gene

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Background: The cytosine methylation in the CpG islets in the promoter region is an important mechanism in regulating the expression of genes, and this arrangement can play a role in the developmental and evolutionary stages and, by binding to TLR9, produces IL12, and produces IFN gamma that results in stimulation Cytotoxicity of NK cells, or after evolution, can be a factor in silencing the expression of genes, especially in some cancer cells.

Materials and Methods: In the intestinal cancer cells, the most important marker for the methylation of the promoter is the CA19-9 gene. In this study, different concentrations of nano-oleoropine on the expression of the gene expression in DNMT were investigated using Real Time PCR.

Results: The results showed that the relative expression of DNMT1 gene was significantly reduced by the action of 33ppm nano-aluoropine in the intestinal cancer cell line.

Conclusion: Obviously, by reducing the expression of the MT gene, methylation can be reduced, and the expression of exonenced genes may be re-performed.
Evaluation of the pri-miR-34b/c rs4938723 polymorphism and its association with breast cancer risk

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Background: Evaluation of the pri-miR-34b/c rs4938723 polymorphism and its association with breast cancer risk in a sample of the Iranian population

Methods: The present study is a case-control investigation, with 263 breast cancer (BC) patients and 221 control women, which examined the potential association of the pri-miR-34b/c rs4938723 polymorphisms with BC susceptibility. The polymorphisms were genotyped by the polymerase chain reaction restriction fragment length polymorphism method.

Results: The association between the pri-miR-34b/c rs4938723 variant and clinicopathological characteristics, including age, body mass index (BMI), tumor size, tumor stage, tumor grade, lymph node metastasis, estrogen and progesterone receptors (ER and PgR), and human epidermal growth factor receptor 2 (HER2). The results showed a significant association between the pri-miR-34b/c rs4938723 variant and grade, PgR and HER2 status of BC patients (P<0.05). No significant association was identified between the rs4938723 polymorphism and
age, BMI, tumor size, lymph node metastasis, stage and histological type of BC patients (P>0.05).

Conclusion: In conclusion, no significant association was identified between pri-miR-34b/c rs4938723 polymorphism and the risk of BC. However, the present findings indicate that this variant may be associated with clinic-pathological characteristics. Population-based studies with larger sample sizes of different ethnicities and long-term follow-up are required to confirm this finding.

Keywords: pri-miR-34b/c, breast cancer, polymorphism
Study of Mir-22 and Mir-335 Expression in Peripheral Blood Mononuclear Cells of Breast Cancer Patients

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Abstract:
Background: Breast cancer (BC) is the most common malignant tumor as well as the leading cause of cancer mortality in women worldwide. Early diagnosis of BC can lead to a more effective management and consequent improved overall survival of BC in patients. Mir-22 and Mir-335 play important roles in cellular DNA damage response (DDR) system and their dysregulation have been related to various types of cancers including BC.

Materials and Methods: In this study we aimed to compare the expression changes of Mir-22 and Mir-335 in peripheral blood mononuclear cell (PBMC) of 60 women diagnosed with stage I/II of invasive ductal carcinoma (IDC) BC with 30 matched normal controls using Real time PCR. PBMCs were isolated from EDTA treated whole blood using Ficoll gradient. Mir-16 was selected as endogenous control. We used Livak method to analyze obtained data and t- test analysis was used to determine the statistical significance between studied groups.

Results: We found that Mir-22 was significantly down regulated ($2^{\Delta\Delta Ct_{patients}}=252.43$, $2^{\Delta\Delta Ct_{controls}}=2299.08$, Expression Ratio: 0.110) in patients in comparison to normal sample ($P$-value: 3.80E-51). The comparison of patients and normal groups also showed that Mir-335 was significantly down regulated in our study as well ($2^{\Delta\Delta Ct_{patients}}=56.11$, $2^{\Delta\Delta Ct_{controls}}=128.91$, Expression Ratio: 0.44, $P$-value: 0.020).

Conclusion: Results indicate that these two studied miRNAs can be used as potential biomarker in early diagnosis of BC. Results also indicate that Mir-335 and Mir-22 both may play as a tumor suppressor miRNA in BC. Both of our
studied miRNAs are playing important roles in DDR system and their down regulation can cause failure in DNA repair system in BC patients.
PC-8

Epstein–Barr virus and Human papilloma virus detection in Iranian patients with colorectal cancer

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Abstract

Background: colorectal can affect by different type of risk factors such as infection agents. It has been showed that human papilloma virus (HPV) and Epstein–Barr virus (EBV) are associated with emerging and progression of various cancers. It has proved, these viruses are related to some cancers, but the relationship with colorectal cancer is unclear. In our study, we investigate the prevalence of HPV and EBV in colorectal cancer.

Methods: 74 tumorous and 63 their adjacent paraffin-embedded tissues were collected from Modares hospital in Tehran between 2011 and 2017. Extracted DNA was confirmed by GAPDH . To identify HPV (L1) with MY and GP primer,
Nested PCR have been employed, and also PCR with 2 pairs of primers was carried out to detect EBV.

Result: Overall, in 137 healthy and cancerous tissues, 18 and 14 adjacent normal ones have got HPV DNA, but neither healthy, nor tumorous tissues have EBV. We did not find any relationship between HPV and EBV with age and sex of patient.

Conclusion: We suppose, because of insignificant meaningful different number of HPV in healthy and tumorous samples, HPV and EBV may have not an effect on colorectal cancer progression. Since studies have different results, more studies are required.

Key words: HPV, EBV, CRC
Overexpression of the growth arrest-specific-2 (GAS2) gene in colorectal cancer tumor tissues, and its relationships with disease progression and poor prognosis

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Background: Dysregulated expression of the growth arrest-specific-2 (GAS2), a gene prerequisite for cell cycle regulation, proliferation, and apoptosis, are frequently shown to be involved in colorectal cancer (CRC) tumorigenesis. Accordingly, in this study, we sought to realize whether the gene contributes to CRC progression and prognosis.

Methods: In this study, the expression level of GAS2 was measured by a quantitative real-time PCR method in 40 CRC tumor tissues along with the matched adjacent normal tissues. Subsequently, the expression changes of the gene in CRC tumor tissues in relation to the clinicopathological characteristics and overall survival of patients were further investigated.

Results: It was uncovered that GAS2 expression level was higher in tumor tissues compared with those in paired adjacent normal tissues of CRC patients (P=0.00001). The overexpression of the gene in CRC tumor tissues was resolved to be significantly correlated with tumor size (P=0.03), TNM stage (P=0.01), tumor grade (P=0.01) and reduced overall survival time (P=0.0001). Furthermore, univariate and multivariate analyses indicated that the higher expression levels of GAS2 was appeared as an independent predictor of poor prognosis in CRC patients (P=0.041).

Conclusion: The current data indicated that the high expression levels of GAS2 was associated with the progression of CRC and may serve as a novel independent prognostic biomarker in patients with CRC.

Keywords: Colorectal cancer, GAS2, Tumor tissue, Prognosis
PC-10

The Antitumoral activity of Zataria multiflora methanolic extract on acute promyelocytic leukemia cell line; NB4

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Background: Zataria multiflora is a plant that belongs to the Laminaceae family with several therapeutic effects. Acute promyelocytic leukemia is a distinct subtype of acute myeloid leukemias with dominancy of promyelocytes in bone marrow and blood stream. The aim of this study was to investigate the anticancer effects of Zataria multiflora extract on acute promyelocytic leukemia cells.

Materials and methods: Acute promyelocytic leukemia cell line, NB4 cells were treated with different concentrations of Zataria multiflora methanolic extract. Cell viability and metabolic activity of NB4 were investigated using trypan blue dye exclusion test and MTT assay 24 hours. Additionally, the expression of hTERT was studied using Real-time PCR.

Results: Acute promyelocytic leukemia NB4 cells were treated with different concentrations of Zataria multiflora extract. The viability and metabolic activity were decreased in a dose dependent manner. Gene expression analysis showed 59% ± 4% decrease in the expression of hTERT.

Conclusion: It was shown that Zataria multiflora significantly decreased the viability and metabolic activity of NB4. The expression of hTERT showed more than 50% decrease compared with control group. Therefore, Zataria multiflora methanolic extract potentially has anticancer effect on acute promyelocytic leukemia cells through down regulation of hTERT. Further investigations are needed to explore other mechanisms of actions and the pure extract.
Keywords: Zataria multiflora, hTERT, Acute promyelocytic leukaemia, NB4
PC-11

Analysis of the Bach2 and HDAC3 genes expression in Iranian acute myeloid leukemia patients

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Background: Acute myeloid leukemia (AML) is a hematopoietic malignancy that results from abnormal proliferation and accumulation of myeloid progenitors and is the most common form of acute leukemia in adults. Previous reports have demonstrated the increased levels of some immune system checkpoints such as PD-1, TIM-3 and TIGIT on T cells of AML patients. This status may be related to the elevated expression of Blimp-1 transcription factor. There are some evidences that show Blimp-1 coding gene, Prdm1, is negatively regulated by Bach2 and Bcl6 transcription factors together with some epigenetic factors, including HDAC3 and NCoR1. In the present study, we aimed to investigate the changes in the expression levels of Bach2 and HDAC3 genes in peripheral blood samples of Iranian AML patients.

Methods: 24 de novo AML affected patients and 15 healthy controls were recruited to the study. Total RNA was extracted from peripheral blood samples and relative expressions of Bach2 and HDAC3 genes were determined by quantitative Real Time PCR. The data were analyzed using Graphpad prism7 software.
Results: Comparison of relative gene expression in controls and patients revealed that Bach2 and HDAC3 are down-regulated in AML patients by 7.78 and 7.11 folds, respectively ($p=0.002$ and $p=0.0056$).

Conclusion: The reduction in the expression levels of Bach2 and HDAC3 genes in AML patients may explain increased levels of Blimp-1 and also immune checkpoints in affected cases.

Keywords: Acute Myeloid Leukemia, Gene Expression, BACH2, HDAC3.
PC-12

Oncolytic Reovirus Titer Determination in Exposure to Low-intensity Ultrasound

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Background: Over the past two decades, researchers have discovered a promising biological treatment called a cancer virotherapy as an attractive strategy. The reovirus is as an oncolytic virus, enters the cell cytoplasm by endocytosis and is released at the end of the cell cycle by inducing death and destroying the membrane. Reovirus is used because of its specific characteristics, including high infectivity, the absence of significant human disease to kill cancer cells and treat them. For enhancement of entry and function of the oncolytic virotherapy, low-intensity ultrasound can be used as one of the delivery systems. The purpose of this study was to investigate the oncolytic reovirus in the presence of low intensity ultrasound for investigation of destruction caused by virus propagation.

Methods: L929 cells and CT26 colorectal cancer cells were cultured with DMEM and FBS. The cells were infected with reovirus (MOI=1) and exposed to low intensity ultrasound (1 MHz frequency, 20% duty cycle intensity, distance from probes:2 cm) for a minute. At different hours, the effects of infected supernatant dilution were investigated in permissive host cells.

Results: The effects of low intensity ultrasound in infection pattern of inoculated reovirus were investigated in L929 cells. Based on the result the titer of virus was increased in comparison with untreated cells by ultrasound.

Conclusion: It seems that the low intensity ultrasound has respectable potential to increase the oncolytic effect of virus for killing cancer cells.

Keywords: Oncolytic reovirus, colorectal cancer, low intensity ultrasound
PC-13

The impact of simultaneous administration of oncolytic reovirus and irinotecan for cancerous cell death

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Background: Oncolytic virotherapy is one of the appropriate methods used to kill the cancer cells. Among oncolytic viruses, we used reovirus. Reovirus is an anticancer oncolytic virus that belongs to the Reoviridae family. Irinotecan is a semi-synthetic drug that acts on a topoisomerase I enzyme to provide a specific kill in the S stage of cell cycle, results in a stop/delay in the G2 stage of the cell cycle.

The purpose of this study is to investigate the synergistic effect of reovirus on the cells treated with irinotecan individually or simultaneously.

Methods: L929 cell was cultured in DMEM medium containing FBS. The irinotecan resolved in PBS and the L929 cells were seeded into a 96-well plate. After 48 hours of incubation, the plate was divided into 3 groups and evaluated 2 times after 48 and 72 hours for different treatments. The first group was treated with irinotecan alone with 3 concentrations (80, 120, 160 μg/ml), the second group was treated with irinotecan and reovirus (MOI=1) simultaneously, the third group was treated with reovirus (MOI=1) alone. After 48 and 72 hours the MTT test was performed.
Results: Based on the results of the MTT test, in the first group, the cell viability at concentrations of 80, 120, 160 μg/ml after 48 hours were 92.1%, 90.1%, and 58.4% respectively, and after 72 hours were 48.71%, 30.3%, and 24.3%. The results for the second group after 48 hours decreased to 56.42%, 48.7%, and 56% and after 72 hours decreased to 18.81%, 15.67%, and 18.31% whereas, for the virus inoculated group after 48 hours was 67.2% and after 72 hours was 52.3%.

Conclusion:

According to the results, Reo oncolytic virus and irinotecan can be used together in order to increase cell death in treatment of colorectal cancer cells.

Keywords: Irinotecan, Oncolytic reovirus, Cancer
PC-14

Role of mesenchymal stem cells in regenerative medicine

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Background: Mesenchymal stem cells (MSCs) are non-hematopoietic progenitor cells, which they are capable to differentiate into cell lineages and self-renewing capacity. They increasing tissue repair by immune responses modulation, anti-inflammatory activity and express several different anti-tumor molecules. Therefore, they could lead to various therapeutic possibilities such as tissue regeneration. In this review, we discuss the potential involvement of MSCs in regenerative medicine.

Method: Relevant literature was identified by a Pubmed search (2000-2018) of English-language papers, using the terms “Mesenchymal stem cells”, “Regenerative medicine”, and “Therapy”.

Results: MSCs involved in cell migration, homing process, and integration into the damaged tissues by express bioactive molecules such as cytokines and growth factors, which support the expansion of hematopoietic and embryonic stem cells. So MSCs transplantation may have a high capability to develop the desired outcome in clinical therapies due to their paracrine function.

Conclusion: Given the important role of MSCs in multi-potentiality, self-renewal, anti-inflammatory, immunomodulatory and anti-tumor effects by expression of several different anti-tumor molecules, accordingly, MSCs transplantation are hopeful tools for tissue engineering, gene therapy, immunotherapy, a choice to deliver anti-tumor agents and regenerative medicine.

Keywords: Mesenchymal stem cells, Regenerative medicine, Therapy.
**PC-15**

Programmed death-ligand 1 as a novel marker for early diagnosis of Multiple myeloma

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Introduction: Multiple myeloma is a systemic malignant disease of the blood, in the most cases incurable. The World Health Organization (WHO) counts it among the lymphoproliferative B-cell diseases. Multiple myeloma is characterized by the uncontrolled proliferation of monoclonal plasma cells in the bone marrow, leading to production of nonfunctional intact immunoglobulins or immunoglobulin chains. The identification and validation of diagnostic, prognostic and predictive biomarkers are essential for directing and optimizing personalized therapy. Programmed death-ligand 1 (PD-L1) is a membrane-bound protein primarily expressed on dendritic cells (DC) and monocytes. Its receptor, Programmed cell death protein 1 (PD-1), is expressed on activated T cells and B cells, DC, and monocytes. Blood levels of soluble programmed death-ligand 1 (sPD-L1), a checkpoint-relevant protein, might predict treatment response and survival outcomes in MM patients. Thus, sPD-L1 represents a marker with numerous potential clinical applications as a diagnostic and/or prognostic tool in Multiple myeloma.

Methods: The current review has been achieved by using an organized search of the scientific data published on molecular biology of prostate specific antigen in
women from various databases, including PubMed, ScienceDirect, Scopus, Scielo, SciFinder and Google Scholar.

Results: The results of the present study showed sPD-L1 could be a good candidate as a prognostic factor to early diagnosis of Multiple myeloma.

Discussion: sPD-L1 has been reported to be a potential biomarker of Multiple myeloma. Given the dire need for tumor markers, only further studies can establish the utility of sPD-L1 in the detection and treatment of Multiple myeloma and provide irrefutable evidence for its diagnostic and/or prognostic use as a new weapon against Multiple myeloma.

Keywords: Programmed death-ligand 1, marker, Multiple myeloma
PC-16
9-tBAP from spiroaminopyrimidones family decreases cell proliferation and Down-regulation of survivin concomitant with induction of apoptosis in NB4 leukemia cells

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Introduction: It has been recently reported the activity of aminopyrimidone family to induce apoptosis in human cancer cells. In this study, we reported an active compound from spiroaminopyrimidone family with apoptotic activity against NB4 acute promyelocytic leukemia cells.

Methods: The cells were seeded in 96-well plates at 1×105 cells/well and treated with 10-150 μM of the 2, 4-Diamino-1, 3-diazaspiro [5.5]-9-tert-butyl-2, 4-diene-5- carbonitril (9-tBAP). This compound was found to be highly active cell growth inhibitor with IC50 of 30±3.5 μM as determined by MTT assay. Evaluation of survivin expression in NB4 cells treated with 9-tBAP was performed by real time PCR.

Results: 9-tBAP decreases cell proliferation of the NB4 cells in a dose- and time-dependent manner. The IC50 value following 72 h exposure was found to be 30
μM for the cells. Furthermore, real time PCR analysis revealed that the treatment with the compound down-regulated the expression of survivin in a time dependent manner.

Discussion: These data further suggest that 9-tBAP may provide a novel therapeutic approach for the treatment of leukemia.

Kew words: Survivin, 9-tBAP, NB4 cells, Apoptosis
Expression of miR-155 in Cancers (review article)

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Background: Micro-RNAs are a group of non-coded small protected RNAs that play an vital role in important cellular processes, including proliferation, differentiation, apoptosis and metabolism through post-transcriptional regulation in gene expression. Changes in the expression of microRNAs have been reported in many human cancers. The changes in the expression of miR-155 have been proven in many malignancies and its association with diseases. The purpose of this review study was to investigate the expression of miR-155 in human cancers. In order to know the changes in the expression of this micro RNA, it can be used in the diagnosis, treatment and estimation of the minimum residual disease (MRD).

Methods: This is a review study by searching English articles on pubmed databases and Google Scholar.

Results: In a study by Eis et al., The increase in miR-155 expression in B cell lymphoma has been shown. Jingtian et al.’s study has shown a reduction in miR-155 expression in colorectal cancer. The study of GUO and colleagues revealed increased expression of miR-155 with increased PSA expression in prostate cancer. Volinia and colleagues have shown increased expression of miR-155 in breast, colon and lung cancer. Studies by Lee et al. Have shown an increase in miR-155 expression in ductal adenocarcinoma. The O’Connell study showed that miR-155 expression in M4 and m5 subtypes of acute myeloid leukemia increased. Also in Fulci studies, increased expression of miR-155 in chronic lymphocytic leukemia has been shown. In studies by Rokah et al., Reduction of miR-155 expression in chronic myeloid leukemia has been demonstrated.
Conclusion Studies have shown that miR-155 is declining in a number of malignancies, and in some of them there is an increase in expression. This micro-RNA can be used as a biological factor to detect and predict these malignancies. Further studies are needed to find out the exact role of these micro RNA genes in their disease.

Keywords: miR-155, micro RNA, chronic myeloid leukemia, breast cancer.
PC-18

cytotoxicity effect of cold atmospheric plasma on B16 and L929 cell lines

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Background: Cancer will be an important disorder in the world and melanoma cancer is one of the deadliest cancers with 74% of the mortality of skin cancers and in recent years it is developing more rapidly than skin cancers. Common therapies of cancer have side effects and work as non-selective and die normal cells in addition to cancer cells. The cold atmospheric plasma (CAP) is a new research topic that is important in biological and medical applications. One of the hope applications of CAP is using of it for cure of cancer. Therefore, in this study, a cold atmospheric plasma was used to investigate the growth inhibition of melanoma cancer cells (B16) and to investigate growth inhibition of this cell line compared to the growth inhibition of normal fibroblast cell line (L929).

Methods: In this study, a Cold atmospheric plasma device that have Argon gas was used for treatment of B16 and L929 cell lines at time ranges of 20,30,40 and 50 seconds and viability of cells was studied using MTT test and data were analyzed using SPSS V23 and One Way ANOVA method.

Results: Results shows that viability of cancer cell line (B16) are treated with cold atmospheric plasma significantly was reduced than untreated cancer cells (p<0.01)
and optimal time for cancer cells is 40 seconds. While plasma had no effect on the % viability of normal cell line (L929).

Conclusion: This study proved that cold atmospheric plasma can be used for cure of melanoma cancer because of its excellent cytotoxicity to cancer cells and its high selectivity that kill cancer cells and can't kill normal cells.

Keywords: cold atmospheric plasma, melanoma cancer, cytotoxicity
Serum Alkaline Phosphatase and Lactate Dehydrogenase activities application to favorable prognosis and staging of Hodgkin Lymphoma

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Background and Objectives: Hodgkin's disease (HD), is a neoplastic disorder originating in lymphoid tissue, which spreads to lymphoid structures and ultimately nonlymphoid tissues. Because of membrane cell damages, Lactate Dehydrogenase (LDH) and Alkaline phosphatase (ALP) activities in blood are increased. The aim of this study was to compare Lactate Dehydrogenase and Alkaline phosphatase activities in children with different stages of Hodgkin's Lymphoma (HL).

Methods: In the present study, the sera of 30 patients who suffered from HD and referred to children's Medical center of Tehran and 30 normal subjects were collected. LDH and ALP activities were measured by use of kinetic method and colorimetric methods orderly. Data were analyzed by use of pearson correlation coefficient and t-test.

Results: The mean of age was 7.5 years in patients and 6.8 years in normal subjects. Stages III, IV disease (advanced-Stages) were Occurred in 61.4% of the patients. LDH activity of patients was statistically increased in comparison with controls (P<0.01). Similary it was significant increase in ALP activity of patients.
in comparison with controls (P<0.05). A comparison between both LDH and ALP levels of advanced stages (III, IV) with initial stages (I, II), revealed important elevated LDH and ALP activities among advanced stages (P<0.001).

Conclusion: The results of present study propose LDH and ALP activities as independent predictors of HD severity.

Key words: Lactate Dehydrogenase, Alkaline phosphatase, Hodgkin's Disease.
Long non-coding RNA based cancer assessment

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Background: Cancer diagnosis have mainly relied on the incorporation of molecular biomarkers as part of routine diagnostic tool. The molecular alteration ranges from those involving the DNA, RNA, non-coding RNAs (miRNAs, LncRNAs,) and proteins. The long non-coding RNAs (LncRNAs) are recently discovered non-coding endogenous RNAs that critically regulates the development, invasion and metastasis of cancers. They are altered in cancers and have the potential to serve as diagnostic markers for cancer.

Methods: A comprehensive published original articles in the most common types of cancer was searched in PubMed between the years 2000 and 2018 with the following keywords, “long non-coding RNA”, diagnosis, prognosis, detection, biomarker, “biomarker discovery, cancer, “body fluids such as blood, plasma, serum, urine and saliva” and circulating in combination or alone.

Result: in this review article we reported the current biomarker base cancer detection in most 8 common cancers and also the LncRNAs which can be used in cancer detection. LncRNAs are release outside of the cells in the body fluids which makes them to use as a non-invasive method in order to cancer detection or prognosis for example PCA3 in urine, Lnc-PCDH9-13:1 in plasma and saliva, MALAT-1 in plasma of prostate cancer (PCa), Hepatocellular carcinoma (HCC) and Lung cancer (LCs). Besides, some of them have specific tissue expression pattern are more valuable for cancer detection for example PCA3, UCA-1.

Conclusion: in the field of malignancies we face with two major problems, 1-lack of proper methods or biomarker for early detection and 2-the drug resistance of
cancer cells. the current biomarkers for cancer diagnosis do not have proper sensitivity and specificity and may increase the rate of false positives and false negatives.
PC-23

The Convenient and Economical method to Collect Adipose Mesenchymal Stem Cells

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Abstract:

Background: Enzymatic digestion is an essential stage to collect and culture Mesenchymal Stem Cells (MSC) in order to apply these cells as a therapeutic agent. Several factors such as being cost-benefit, efficiency, safety, yield and amount of produced cells are determined using the type of enzyme. Collagenase as a conventional type are used commonly, however others like trypsin and even combination of them used as an alternative types in different situations.

Materials and Methods: Abdominal subcutaneous adipose tissue was obtained from male BALB/c mice and digested under two different enzymatic processes: collagenase and collagenase/trypsin. Cell culture process include of washing, centrifuging, incubating under standard situation was performed and after the 3rd passage cell growth was assessed and characterization was performed by flow cytometry.
Results: In this study, we have investigated two different enzymatic methods to digest adipose-MSCs of BALB/c mice. The morphology of cells is pretty different and was more homogenous in collagenase group. Also the yield of cells is varied in two groups. Furthermore the obtained data from flow cytometry for negative and positive cluster of differentiation (CD) markers, revealed that adipose-MSC were positive for PE-CD90 (70%), PE-CD29 (98%), APC-CD105 (52%) and negative for FITC-CD45 (>2%)

Conclusion: The application of different enzymes is depends on the condition; it reveals that, although use of trypsin in isolation protocol is cost-benefit, but it can be just an alternative method whenever if limited number of cells are needed. However, collagenase as a well-known and conventional method to isolate a large amount of cells to several proposes.

Keywords: Mesenchymal Stem Cell, Adipose, Collagenase, Trypsin
Exosomes as a promising approach in Cancer Diagnosis and Therapy

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Background: Exosomes offer a new perspective on the biology of cancer with both diagnostic and therapeutic concepts. Due to the cell-to-cell association, exosomes are involved in the progression, metastasis, and therapeutic efficacy of the tumor. They can be isolated from blood and other body fluids to determine the disease progression in the body, including cancer growth. In addition to being reservoirs of biochemical markers of cancer, exomes can be designed to restore tumor immunity. Tumor exosomes interact with different cells in the tumor micro-environment to confer beneficial modulations, responsible for stromal activity, angiogenesis, increased vascular permeability, and immune-evasion. Exosomes also contribute to the metastasis with the aim of epithelial transmission to the mesenchyme and the formation of pre-metastatic niches. Moreover, exosomes protect cells against the cytotoxic effects of chemotherapeutic drugs and prevent the transmission of chemotherapy resistance to adjacent cells. Therefore, exosomes are essential for many fatal cancer agents, and understanding their origins and role in cancer is important.

Conclusion: In this article, we attempted to clarify the potential of exosomes for application in cancer diagnosis and therapy.

Keywords: Exosomes, Cancer, Diagnosis
PC-25

Expression of the BCL-2 gene in primary breast cancer and its relationship with prognostic factors

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Abstract

Background: Breast cancer is the most common malignancy in women. Over the past 50 years, the incidence of breast cancer has increased significantly in different parts of the world. The emergence of Bcl-2 occurs in more than half of breast cancers. Excess Bcl-2 is associated with the acquisition of cancer and programmed cell death. Investigating cell death factors can help diagnose and treat diseases. Bcl-2 is one of the important factors of apoptosis, and its expression is a response to cell destruction. The aim of this study was to determine the incidence of Bcl-2 gene in breast cancer and its relationship with malignancy, tumor stage and lymph node involvement.

Materials and methods:
The study was conducted in 85 breast cancer patients at Imam Khomeini Hospital in Ardabil (1392-96). The study was conducted in 85 breast cancer patients at Imam Khomeini Hospital in Ardabil (1392-96). After preparation, the tissue is excised from the sample. One of the tumors and lymph nodes was stained with
lymphoid haematoxylin and eosin. Another lamb was tested to determine the expression level of Bcl-2. All lambs were examined by the pathologist of the unit. The data was analyzed using Chi-square, Mann-Whitney and SPSS software.

**Results:** The mean age of the subjects was 54.1 years and the standard deviation was 52.22 years. 69.3% of patients had lymph node involvement and 41.3% had Bcl-2 positive. There was no significant correlation between the incidence of Bcl-2, tumor stage, and lymph node involvement. There was a significant correlation between the appearance of bcl2 and the degree of malignancy (P <0.006).

**Conclusion:** It seems that Bcl-2 is an effective factor in the prognosis of breast cancer. In order to obtain conclusive results and determine the role of Bcl-2 in the prognosis of breast cancer, it is valuable to evaluate other tumor markers at the same time.

**Keywords:** Breast cancer, Bcl-2, Malignancy degree, Tumor stage.
PC-26

Association research between polymorphism of the insulin gene and colorectal cancer

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Abstract

Back ground: Colon cancer is considered the third most diagnosed as the third most common cancer in the world. Its prevalence is related to age, diet and historical family, smoking, exercise, etc. One of the polymorphisms involved in colorectal cancer is related to the insulin signaling pathway. The aim of this study was to evaluate the prevalence of insulin gene polymorphism (rs689) in the Iranian population and to assess the role of polymorphism in increasing the risk of colon cancer.
Materials and methods: In this case-control study, 130 colon cancer patients by PCR-RFLP method in blood samples were collected to assess the polymorphism rate of rs689 genes in case and control samples.

Results: There was no significant difference in the incidence of mutant alleles between patients and controls (OR = 1.59 95% CI = 0.99-2.39, Pe = 0.058).

Conclusion: These findings indicate that the insulin gene polymorphism (rs689) is not associated with an increased risk of colorectal cancer.

Keywords: Colon cancer, Polymorphism, Insulin rs689
Evaluation of serum level of haptoglobulin by Capillary zone electrophoresis in patients with multiple myeloma stage I

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Background: Acute phase proteins are synthesized mainly by the liver and macrophages in an inflammatory conditions as a result of some trauma and malignancies. Increased levels of these proteins have been reported in many cancer tumors and multiple myeloma as an important indicator of prognosis of malignancies. Because of importance of this issue, we investigate the serum level of haptoglobulin in multiple myeloma stage I.

Materials and methods: The serum level of haptoglobulin was measured 30 in patients with multiple myeloma stage I and 30 persons as a control group. Patients aged 69 years. measuring haptoglobulin by using Capillary zone electrophoresis and high resolution (HR) method and total protein by biuret method. The data were analyzed by SPSS program.

Results: The values obtained from results of the test and statistical calculations in two groups of patients and control showed that serum haptoglobulin level in multiple myeloma stage I (0.75±0.13) compared to the control group (1.07 ± 0.27) was decreased. The reduction was significant. (P=0.0001)

Discussion and Conclusion: The results of study indicates the reduction of serum level of haptoglobulin in stage I patients compared to control group, which is inconsistent with previous studies in this field. This protein may considered as...
specific prognostic and diagnostic factor in multiple myeloma stageI. However, further studies are needed to assess accurate results.

Keywords: Multiple myeloma, acute phase proteins, haptoglobin.
PC-28

Hsp90-β as a novel marker for diagnosis of lung cancer

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Introduction: Worldwide, lung cancer is the most common malignancy and the most common cause of cancer deaths in the past few decades. The identification and validation of diagnostic, prognostic and predictive biomarkers are essential for directing and optimizing personalized therapy. Heat shock proteins (Hsps) are evolutionarily conserved proteins. One member of the Hsp family is Hsp90, a highly abundant protein in eukaryotic cells that is involved in many important cellular processes. Heat shock protein 90 (Hsp90) has been shown including two major cytoplasmic isoforms, namely, Hsp90-alpha and Hsp90-beta. Studies show that Hsp90-beta is highly expressed in some cancer tissues including lung cancer and breast cancer. On the other hand, studies show that Hsp90-beta overexpression in serum and tissues of patients with lung cancer was associated with malignant behavior of lung cancer. Thus, these data suggest that Hsp90-beta could be a clinically useful biomarker as a diagnostic and/or prognostic tool in lung cancer.

Methods: The current review has been achieved by using an organized search of the scientific data published on molecular biology of Hsp90-beta from various databases, including PubMed, ScienceDirect, Scopus, Scielo, SciFinder and Google Scholar.

Results: The results of the present study showed Hsp90-beta could be a good biomarker as a prognostic factor to diagnosis of lung cancer.

Discussion: Hsp90-beta has been reported to be a potential biomarker of lung cancer. Given the dire need for tumour markers, only further studies can establish the utility of Hsp90-beta in the detection and treatment of lung diseases and provide irrefutable evidence for its diagnostic and/or prognostic use as a new weapon against human lung cancer.
Estradiol, des-acylated, and total ghrelin levels are associated with ovarian cancer

Saba Fooladi

Abstract

Purpose: The present study aimed to investigate the association between estradiol, acylated, des-acylated, total ghrelin levels along with pathological parameters and ovarian cancer (OC) risk.

Materials and methods: A case-control study was carried out on 45 OC patients and 33 age-matched post-menopausal women as the control subjects. Plasma levels of estradiol, acylated, des-acylated, and total ghrelin were measured by ELISA method.

Results: Estradiol’s plasma levels were significantly higher in OC patients compared to control subjects ($P < 0.001$). Although acylated, des-acylated, and total ghrelin levels were not associated with OC in conditional logistic regression models, estradiol levels were significantly related to the increase in OC risk (OR: 1.083, 95% CI: 1.037-1.13, $P < 0.001$). However, estradiol levels in the two first quartiles ($Q_1$, $Q_2$) were associated with decreased risk of OC (OR: 0.011, 95% CI: 0.001-0.118, $P < 0.001$, and OR: 0.030, 95% CI: 0.003-0.284, $P = 0.002$, respectively). For those patients in the third quartile of plasma des-acylated and total ghrelin compared to those in the highest ($Q_4$), the multivariate odds ratio of OC were respectively 0.192 and 0.25.
Conclusion: In conclusion, higher baseline concentrations of des-acylated and total ghrelin were associated with the decreased OC risk. Furthermore, lower and higher baseline levels of estradiol were reported to be associated with the protective and risk effect on OC, respectively. Further studies are required to confirm the present findings and to explore the role of estradiol and ghrelin in the etiology of OC.

Keywords: Acylated ghrelin; Des-acylated ghrelin; Estradiol; Ghrelin; Ovarian cancer.
PC-30

Anti-tumor activity of amitriptyline on human leukemia K562 cancer cell line

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Background: Cancer is one of the leading causes of morbidity and mortality worldwide. Chronic myelogenous leukemias (CML) is a clonal hematopoietic stem cell disorder that accounts for 15-20 percent of adult leukemia. It has been found that Amitriptyline (AMI), a widely used antidepressant drug, possessed antitumor roles in a variety of cancers including Melanoma, Glioma, Osteosarcoma, Lung Cancer, Cervical Cancer, Hepatoma and Multiple myeloma. In this study, we provided evidence that AMI had a potent antiproliferative activity in the (CML).

Materials and Methods: K562 cell lines were cultured in RPMI-1640 medium containing 10% FBS and 1% penicillin. Then, the cells were treated with different concentrations of AMI for 24 hours. MTT assay was used to determine
the viability of cells. DAPI staining and DNA electrophoresis were used for apoptosis analysis.

**Result:** Based on the results of MTT assay, AMI dose dependently decrease K562 cell growth. The results of DAPI staining showed that DNA fragmentation was increased in the treated cells. DNA electrophoresis analysis revealed that AMI induced apoptosis.

**Discussion:** As the results showed, AMI inhibited the cell growth and induced apoptosis in K562 cells dose-dependently. However, further investigation of its cytotoxic effects against tumor cells, both in vitro and in vivo, is recommended.

**Keywords:** K562 cell line; apoptosis; amitriptyline
PC-31
Antiproliferative activity and Apoptotic Properties of Dorema aucheri against human colorectal cancer cells

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Introduction

Background & objectives

Colorectal cancer is one of the most prevalent malignancies in the world. Dorema aucheri is rich in phenolic compounds with antioxidant and antimicrobial activities. According to the side effects of current chemical chemotherapy and cytotoxic effects of Dorema aucheri, in the present study, the anticancer effects hydroalcoholic extract of Dorema aucheri (HEDA) on two colorectal cancers (SW48 and SW1116) cell lines were investigated.

Methods: The cells were exposed to different concentrations of extracts as well as Vincristine for 24 hours. Cytotoxic activity of HEDA in colorectal cancers (SW48 and SW1116) was determined by the MTT assay at various concentrations. Apoptosis cells were stained with FITC-Annexin V and propidium Iodide (PI) and
assessed by flow cytometry. Quantitative real-time polymerase chain reaction (qRT-PCR) amplification was performed. The expression of the EGFR gene of HEDA was measured. The statistical analysis was carried out using analysis of variance (ANOVA).

Results: The IC₅₀ values, of HEDA and vincristine, were determined 478.5 and 60 μg/mL in SW1116 cell line and 531.8 and 90 μg/mL in SW48 cells, respectively in 24 hours (P<0.05).

The rate of apoptosis in HEDA and vincristine was determined 21.8% and 15.5% in SW1116 cell line and 62.5% and 41.4% in SW48 cell line, respectively (P<0.05).

The expression of the EGFR gene in both cell lines treated with HEDA and vincristine was lower than that of the control group(P<0.05); The reduction rate of SW48 cell line was more than SW1116 cells(P<0.05).

Conclusion: The present results recommend that HEDA possess important anti-proliferative property. The viability of SW48 and SW1116 cells was reduced after treatment with HEDA, and apoptosis in human colon carcinoma cell lines (SW48 and SW1116) was enhanced which suggested for further phytochemical analysis and mechanistic evaluation.

Keywords: Dorema Aucheri, MTT, Apoptosis, colon cancer cell line SW48 and SW1116, EGFR gene
Study of hsamiR-515-5 gene expression in Hepatocellular carcinoma

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Background: Hepato cellular carcinoma (HCC) is the most occurrence form of human liver cancer, and main reason of worldwide cancer death. HCC as a malignancy, is well considered and associated with tumor progression and metastasis. The molecular pathway of formation and progression of HCC are not clear. Various studies have been made to unravel the molecular pathway and that consists of cancer invasion process and metastasis. Searching in liver cancer molecular targeted therapies for further molecular agents has developed patient survival. New molecular targets such as miRNA have benefits that progresses the molecular pathogenesis of HCC. Both physiological and pathological processes such as development and can be altered by function and expression modifying of miRNA. Studies have been noticed that miR-101, miR-106, miR-623, miR-515-5p, miR-199a, and miR-34a-5p which have a considerable connection with tumor size in HCC patients.

Methods: We selected 40 FFPE HCC blocks, and 40 normal liver FFPE tissues from the archives of the pathology department Imam Reza hospital Medical School, University of Tabriz. We used 5 microns in thickness histological sections from each block according to protocol specifications. For gene expression Real-time PCR we used the Real QPlus ampliqon. Prime Script RT kit (Takara) was used, either with a primer mix composed of random and oligo-dT primers with oligo-dT primer For cDNA synthesis.
Results: Gene expression in case group is significantly different as of control group. miR-515-5p was 3.8 fold of control group.  
Conclusion: Our results indicate different level of miRNA in case and control groups. A reason of highlight of biomarkers in diagnosis of cancer. Different profile of miRNA in HCC led to vesting of robust miRNAs and precise analysis for diagnosis purposes.  
Key words: miRNA, HCC, FFPE
PC-34

**HsamiR-623 gene expression in Hepatocellular carcinoma FFPE tissues**

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Methods: We selected 40 FFPE HCC blocks, and 40 normal liver FFPE tissues from the archives of the pathology department Imam Reza hospital Medical School, University of Tabriz. We used 5 microns in thickness histological sections from each block according to protocol specifications. For gene expression Real-time PCR we used the Real QPlus ampliqon . Prime Script RT kit (Takara) was used, either with a primer mix composed of random and oligo-dT primers .with oligo-dT primer For cDNA synthesis.
Results: Gene expression in case group was significantly different as of control group. miR-623 was 2.57 fold of control group.

Conclusion: Our results indicate different level of miRNA in case and control groups. A reason of highlight of biomarkers in diagnosis of cancer. Different profile of miRNA in HCC led to vesting of robust miRNAs and precise analysis for diagnosis purposes.

Key words: miRNA, HCC, FFPE
Applicable of CLEC12A in Acute Myeloid Leukemia

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Background: Acute Myeloid Leukemia(AML) is one of the malignancies that, despite the many advances made in recognizing and developing chemotherapy, is still a difficult-to-treat malignancy, Because most patients do not survive more than 2-5 years after the diagnosis due to recurrence. In this regard, it is necessary to identify more specific targets for the development of an effective treatment against malignant cells.

Methods & Results: Recent studies at Pubmed sites showed that the antigen that is called CLEC2A and does not express in hematopoietic stem/progenitors cell, Considerably (77.5 to 92%) on the surface of leukemic blast cells and stems AML patients expressed. Assessments of the severity of expression of this antigen during the stages of diagnosis, treatment, and relapse of AML patients showed that the level was consistently stable. On the other hand, the expression of this marker with characteristics such as complete remission and event-free survival and overall survival of AML patients has a direct relationship and with favorable-cyto genetic abnormalities such as CEBPA has a reverse relationship.

Conclusion: It can be concluded that the evaluation of CLEC2A, as a prognostic factor and diagnostic factor, can applicable in predicting the survival rate and MRD monitoring of AML patients. in addition to, due to the lack of achievement in current therapies, CLEC2A itself can also be used as a potential Target for chemotherapy of AML patients.

Keywords: CLEC2A, AML, Diagnosis, Prognosis, Treatment
The Expression of CD Markers in Solid Tumors: Significance in Metastasis and Prognostic Value

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Background: The clusters of differentiations (CDs) are among the surface markers expressed on different cells in the body, which are involved in the communication of cell with each other and the induction of signaling. Moreover, the evaluation of the ectopic expression of these markers in solid tumors has led to the detection of disease in early stages. In this paper, we have examined the effect of CD markers expression on the function of cancer cells, as well as their importance as the diagnostic and prognostic factors for monitoring the progression of solid tumors.

Methods: Relevant literature was identified by a PubMed search (1988-2017) of English language papers using the terms “CD markers”, “diagnostic”, “prognostic”, “predictive marker” and “solid tumors.”

Results: Finally, it can be stated that the evaluation of CDs is not only of diagnostic value at disease onset, but these markers can be used as prognostic and predictive markers to contribute to the treatment of disease and predict its relapse.

Conclusion: Monitoring of tumors progression through CDs expressed on circulating tumor cells could be a new diagnostic and prognostic factor in the future.

Keywords: CD Marker, Solid Tumors, Diagnosis, Prognosis, Predictive
PC-37

PD-1/PD-L1 as a Prognostic Factor in Leukemia

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Background: PD-1 receptor is a component of the immune system that is recognized as a negative regulator of immune responses together with its ligand (PD-L1). In this study, we review the role of the immune system on leukemia cells through PD-1 and its ligand.

Material and methods: Relevant literature was identified by a Pubmed search (1995-2016) of English-language papers using the terms "PD-1", "PD-L1", "leukemia", and "prognosis".

Results: PD-1 is an inhibitory receptor of CD28 family. Although initially introduced as a driving factor of apoptosis in activated T-cells, pre-clinical studies revealed the importance of this molecule as a checkpoint in ambient tolerance immune system. The ligand of this molecule is widely expressed on malignant cells in leukemia and inhibits the T cytotoxic lymphocytes. Therefore, targeting PD-1/PD-L1 can sensitize the malignant cells to chemotherapy and increase patient’s survival as a therapeutic approach.

Conclusion: Recently, immunotherapy has shown promising results in preclinical studies using antibodies against PD-1/PD-L1 against different cancers and it is hoped that the application of these antibodies in combination with other treatments (including chemotherapy) could inhibit leukemia cells and improve the patient’s conditions.

Keywords: Leukemia, Lymphoma, PD-1, PD-L1, Prognosis
The significance prognostic of MMP-7 promoter polymorphisms in lung cancer

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Background: Matrix metalloproteinase-7 (MMP-7) plays an important role in metastasis behavior of cancer cells, and overexpression of MMP-7 has been associated with poor prognosis in non-small cell lung cancer. However, the contribution of various genotypes of MMP-7 has not yet been investigated in lung cancer in Iran. Therefore, this study aimed to investigate the association of MMP-7 genotypes with lung cancer risk among the Iranian.

Methods: In this hospital-based case-control study, genotypes and distributions at two promoter sites of MMP-7, A-181G and C-153T, were determined, and their association with lung cancer risk in Iran was evaluated among 358 lung cancer patients and 228 age- and gender-matched healthy control individuals. In addition, the interaction of MMP-7 genotypes and smoking status were also examined.

Results: The percentages of variant AG and GG at MMP-7 A-181G in the lung cancer group were similar to the control group (12.8% and 2.3% vs. 11.3% and 1.5%, respectively; p=trend=0.5294). The allelic frequency distribution analysis showed that the variant G allele at MMP-7 A-181G conferred non-significant elevated lung cancer risk compared to the wild-type A allele [odds ratio (OR)=1.18, 95% confidence interval (CI)=0.85-1.66, p=0.2289]. As for the genotypes of MMP-7 C-153T, all the studied Iranian population was of CC genotype. Furthermore, there was no obvious joint effect of MMP-7 A-181G genotype and smoking status on the lung cancer risk. No statistically significant correlation was observed between MMP-7 A-181G genotype distributions and gender.
Conclusion: There was no evidence that the genotypes of MMP-7 A-181G may act as a biomarker in determining personal susceptibility to lung cancer in Iran.

Keywords: Lung cancer, MMP, polymorphism.
Targeting ketone bodies sensitize cancerous cells to chemotherapy

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Manipulation of the energy productive signaling pathways has been shown to increase cancer cells sensitivity to chemotherapy in cancer patients. Restriction of glucose intake in cancer patient’s diet could diminish energy production of cancer cells and thus slow cancer progression. Recently, ketogenic diets have been studied as an adjuvant to cancer therapy. A fat rich, low-carbohydrate diet in cancer patient’s regimen is to reduce circulating glucose levels and induce ketosis such that cancer cells are starved of energy while normal cells adapt their metabolism to use ketone bodies as an alternative source of energy and survive, however it depends on the type of tumor. Ketone bodies exhibit several unique characteristics such as glycolysis inhibition, altering the expression of oncogenes and tumor suppressor genes and etc. that support their use as a metabolic therapy for cancer. Therefore ketone bodies could be to retard the growth of tumors and sensitize some of the cancer cell types to chemotherapy.

Keywords: energy metabolism, Ketone bodies, Cancer
The cytotoxic effects of *Eucalyptus* extract on lung Cancer Cell Line (A549) and Healthy Fibroblast Cells (HFF2)

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Background: Lung cancer (Lung cancer) is a disease that is characterized by the uncontrolled growth of cells in lung tissue. If this condition is not treated cell growth can be treated in a process called metastasis to the lung from expanding out, today the use of medicinal herbs in the treatment of cancer are of great importance. Eucalyptus (*Eucalyptus spp.*) is one of the most famous medicinal plants that have been the effect of the anti-microbial that limelight, this herb is rich in Polyphenols and Terpenoids. The aims of research investigating the properties of eucalyptus extracts on lung cell lines and compare it with normal cells.

Methods A human cell line A549 (ATCC: CCL-185) and a human normal fibroblast cell HFFF2 (NCBI: C163) of the Pasteur Institute of Iran was purchased. This is the category of cell culture DMEM containing 10% cow serum (FBS) was cultivated. 1/10/100/1000 µg/ml concentrations of extract of *Eucalyptus* were in 24 and 48 hours were used to examine its cytotoxicity activity. MTT method was used to evaluate its effectiveness.

Results: IC50 was obtained: 110.4 µg/ml and 34.85 µg/ml for HFFF2 in 24h and 48 h respectively and 88.23 µg/ml and 22.63 µg/ml for A549 in 24h and 48 h respectively also.

Conclusion: The results obtained from the cellular toxicity test, indicating the increasing effect of plant extracts on both cellular categories can be fitted. This
increase is dependent on concentration and time, and with increasing concentration and time of patients in both the cell survival rate category, fitted cut cell. As well as forklift data indicates the sensitivity of cancer cells to extract more fitted.

Keywords: *Eucalyptus*, Lung cancer cell line, Cytotoxic
PC-42

Evaluation of anticancer activity of Camellia sinensis against colorectal cancer cell line Caco-2

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Abstract:

Background: Colorectal cancer (CRC) is widespread as the third most common cancer, and is managed by antineoplastic agents and a combination of agents. Cells of vital organs such as the kidney, lungs, bladder and nervous system may be affected by conventional anticancer treatments, and there is a need to search for alternative drugs. Medicinal plants and other natural yields have been used from ancient times up to now for the treatment of several diseases and illnesses. Camellia sinensis whose leaves are used to produce green tea, is a native plant of Iran and in the current work it is used for evaluation of its anticancer effects.

Materials and Methods: The hydroalcoholic extract of camellia sinensis young leaves was prepared by percolation technique. The effects of Camellia sinensis were assessed on the carcinoma colon (Caco-2) cell line and mouse normal fibroblast cell line L929, and cytotoxicity was evaluated by MTT assay. Aquaporin 5 was detected as a biomarker for colorectal cancer using immunofluorescence microscopy.
Results: MTT assay with hydroalcoholic extract of Camellia sinensis shows considerable anticancer activity on Caco-2 cell and had little beat significant value on L929 cell.

The results indicated that Concentration of 800 μg/ml with P<0.05, was significantly effective against Caco-2 cells comparison with the cis-platine. The results also showed the protein levels of aquaporin-5 decreased in Caco-2 cell culture following green tea extract treatment. Conclusion: According to the results of the current study, Camellia sinensis is a potent anticancer agent without any side effects.

Key words: Tea ; Caco-2 Cells; Cisplatin; Aquaporin 5
PC-43

Anti-CTLA4 CAR T cell: Auxiliary treatment in cancers

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Introduction

Based on this point that some of the cancers do not appropriately respond well to conventional therapy or there is the possibility of relapse, immunotherapy is currently under investigation. One of its new branches is treatment with T cells that change their receptor. The research on these cells is generally according to the design of a receptor against a specific tumor antigen. But this review attempts to show that by targeting the regulatory T cell (Treg), as an important immune cell in the tumor microenvironment, good effects can be seen.

Methods

This review article has been prepared with electronic search based on keywords related to the aim of this paper. we use scientific databases such as scholar, PubMed, science direct and springer. almost all the articles that were used, are for the last 5 years.
Results

For targeting Treg, CAR T cell is recommended to be designed. The leukocytes must be collected by leukopheresis method and then T cells are isolated. CAR is a construct that expresses the receptor against a specific antigen in the tumor. It is a difficult way to design CAR T cells so tumor infiltrative lymphocytes (TILs) can be isolated from the beginning using existing methods. Then these cells are grown in vitro. Anti-CTLA4 receptor in TILs alone or in conjunction with an anti-NRP1 receptor are used which requires their simultaneous expression in TILs so that only special types of them that do not produce IFN-γ are detected. In addition to the above mentioned, a receptor CCR4 anti-chemokine CCL17, CCL22 within the tumor environment is required. After that, cloning and transferring to lentiviruses, then transferring this anti-CTLA4 and anti-NRP1 to memory T CD8+ must be done. Functionality, cytotoxicity and other assays should be evaluated. Finally, this CAR T is injected into a patient with a solid tumo.( Figure)

Conclusion

Tumor environment factors consist of blood and lymphatic vessels, extracellular matrix, activated fibroblasts, macrophages and other immune cells. They can be the most important factors in the progression of tumor, metastasis, and suppression of immunity and resistance therapies. Therefore, in this method therapeutic care should pay attention to the tumor environment. Chemokines are also important factors that can influence tumor immune cell infiltration and regulate angiogenesis, proliferation, and survival of tumor cells. The targeting of chemokines, if accompanied by existing treatments for cancer, can have synergistic effects for immune responses.

There are new methods of immunotherapy, including the use of checkpoint inhibitors, bispecific antibodies, and CAR T cell, each of which can be used in certain conditions, and in some cases it is possible to use a combination of them to increase the efficacy of the drug together or sometimes with existing therapies. Regarding the above, it can be said that sometimes there is a need for personalized treatment for the optimal use of the drug.
In this review, we try to introduce the effective methods with respect to the tumor and its environment, as a new type of CAR T cell that will have higher efficacy.

Many characteristics of the CAR T cell, such as its sustainability, are being investigated. To improve the stability of T and overcome the T cell exhaustion, T memory can be used that has better stability and protects the patient for a longer period against recurring diseases. IL-15 and IL-12 result in memory phenotypes and increased susceptibility. Checkpoint inhibitors against PD1-PDL1 or CTLA4 can also be used to further stabilize the T cell within the body. In this study, it is also thought that durability of CAR T may be high due to the use of T-memory and drug-resistant checkpoint. Also, toxicity would decrease significantly when the iCas9 system was designed to prevent the hyperactivation of T cells. Because of the bi-specificity of the receptor, the probability of binding to the non-specific antigen was low.

Of course, some of the problems with such a treatment are definitely its design, that probably results in considerable cost, because there are certainly many problems with the many factors involved in making a drug, but the effectiveness of the drug will certainly be higher and simultaneous use of other drugs can occur only when the condition of the patient is followed by an impairment in the recovery of the disease.

C: Keywords: chimeric antigen receptor T cell, CTLA4, Regulatory T cell
Intestinal microbiota and its association with colorectal cancer

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Colorectal cancer (CRC) is the third most common cancer in populations with about 1.36 million of new cases per year. Epidemiological studies have revealed that fiber and vegetable rich diets, coffee and physical activity are associated with reduced rates of colon cancer, while consumption of red and processed meat, or alcoholic beverages, and overconsumption as reflected in obesity are associated with increased rates (1,2). Recently a central role for the microorganisms in the gastrointestinal tract in colon cancer development is being probed, and it is hypothesized that the microbes may integrate diet in the etiology of the disease. The modulation of the gut microbiota by strategies can have a beneficial impact on the dialogue between the gut, the immune system and the microbiota. In addition, increasing evidence shows that gut microbiota manipulation can exert a protective effect against CRC (3,4). This review focused on the current knowledge of the association of diet and intestinal microbiota with colorectal cancer.

Keywords: Colorectal cancer, diet, gut microbiota
PC-45
Association of epithelial to mesenchymal transition and pancreatic cancer

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Pancreatic cancer (PC) is one of the poorest prognosis malignancies with 6 months survival rate after diagnosis (1,2). Epithelial-mesenchymal transition (EMT) is essential for proper embryonic development. Physiologically, EMT occur in adults during tissue regeneration, wound healing, and cancer progression (3). The activation of epithelial to mesenchymal transition (EMT) process is related to properties of stem cell exclusivity for both normal and neoplastic cell (4,5) Cells with an EMT phenotype effect molecular characteristics of cancer stem cells (CSCs); CSCs also express an EMT phenotype. This phenomenon showed that EMT and CSCs are closely related (6). According to the last studies, pancreatic cancers are associated with a CSC population. CSCs are resistant to chemotherapeutic drugs, and escapes chemotherapy and promotes tumor recurrence. Cancer cell EMT is associated with generation of CSCs, metastasis, and treatment resistance in pancreatic cancer (7). Several areas are needed for investigation to find out the role of EMT mechanism in physiological and pathological processes.

Keywords: Pancreatic cancer, EMT, CSC
Clinical Role of Breast Ultrasound: A Systematic review

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Background: Early detection and diagnosis of breast disease, especially breast cancer. However, excessive follow-up or unnecessary biopsy digestion is the greatest challenge of mammography. Physical examination and mammography to increase diagnostic accuracy and to reduce unnecessary surgical biopsy. This article is to review the indication of breast ultrasound examinations as well as merits and limitations compared to mammography.

Methods: This systematic review study, in 2018, searches for keywords such as Breast Ultrasound; Breast cancer; Diagnosis was performed on valid data databases such as PUBMED, Clinical Key, ISI. In a large search, there were 67 articles related to literature that, after using the Prism check list, 42 articles were selected.

Results: Breast ultrasound is a valuable adjunctive to mammography for the identification and characterization of palpable and nonpalpable abnormalities. With the advances of ultrasound techniques over the past 10 years, the role of ultrasound has evolved from differentiation of benign from malignant masses, evaluation of mammographic abnormalities, and guidance modality of interventional procedure to preoperative evaluation of lesion extent, follow-up after operation, and screening method for high-risk women. It can also be used as a supplemental modality of a physical examination and mammography to increase diagnostic accuracy and to reduce unnecessary surgical biopsy.
Conclusion: The current indication for breast ultrasonography is clinical signs Evaluation of abnormalities of breast or mammography, Evaluation, and induction of biopsy. However, Malignancy, post-operative follow-up, and high-risk screening. Breast ultrasound is used for physical examination, mammography, etc. Together, it improves the diagnosis rate of breast cancer, Biopsy can be reduced. The accuracy of breast ultrasonography And the quality of the inspection equipment, diagnosis should be done by proper and proper equipment Can be achieved.

Keywords: Breast ultrasound, Breast cancer, Diagnosis
The types of immunotoxins and their use in cancer treatment

Saber Soltani

Immunotoxins are two functional which crossing the cell membrane and enters the target cell and destroy the cell. Toxin-based treatments are a widespread research field and can have broad applications in the biology and public health. Immunotoxins act selectively against cancer cells and have a good potential for detecting and targeting cancer cells. Specific immunotoxins to target immune cells due to the selection type antibody and antibodies are responsible for the identification of the target cells. Cancer is becoming a major cause of death in most developed countries. In order to have a strong factor in cancer repression, that agent must target the cancer cells directly and specifically. Often, but not always, immunotoxins are produced for disabling and killing cancer cells, that this issue is one of new therapeutic approaches in recently. Clinical aims to designing and create new cancer therapies focused with this approach, a lot of information about the toxin and intracellular pathways have been obtained. So, toxins in medicine are useful for the treatment of human disease and study of professional cellular functions. So, immunotoxins have a high potential for cancer treatment. Other applications of immunotoxins, including immune system regulation and treatment of viral diseases and parasites diseases. More research is needed to improve the immunotoxin effects and to reduce their side effects. On the whole, with design creative, clever and experienced programs, many human diseases, particularly cancers can be in a short period of time and faster than other methods of treatment that the treatment of long, to be treated. Following the design and implementation of clinical trials, the effects of immunotoxins on animal tumorigenic models were performed. In fact, in this study, we focus on the use of protein-bound toxins with bacterial and herbal sources and more specifically Pseudomonas immunotoxins which attached to antibodies to target cancer cells.
Evaluation of Anticancer Activity of Camellia Sinensis in the Caco-2 Colorectal Cancer Cell Line

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Abstract

Background: Colorectal cancer (CRC) is widespread across the world. While conventional anticancer treatments can help the affected patients, cells of vital organs such as the kidney, lungs, bladder and nervous system may suffer from side effects of chemotherapeutic drugs, so that it is necessary to search for alternatives. From ancient times, attention has focused on medicinal plants and natural products. In the current work, Camellia sinensis, whose leaves are used to produce green tea was evaluated for anticancer effects in cell culture. Materials and Methods: A hydroalcoholic extract of Camellia sinensis young leaves was prepared by percolation and compared with Cisplatin as a known anticancer drug for effects on two cell lines: Caco-2, colon carcinoma cells, and mouse normal fibroblasts (L929). Cytotoxicity of 50, 100, 200, 400 and 800 μg/ml of Camellia sinensis extract was evaluated by MTT assay and aquaporin 5 (AQP5), detected as a biomarker for surviving cells using immunofluorescence microscopy. Results: MTT assays with hydroalcoholic extract of Camellia sinensis showed considerable inhibition of growth of Caco-2 cells, significant at 800 μg/ml (P<0.05), with little effect on L929 cells. Levels of aquaporin 5 protein decreased in Caco-2 cell culture following green tea extract treatment. Conclusion: According to the results of the current study, Camellia sinensis is a medicinal plant with potent anticancer influence which might be specific. Keywords: Tea- Camellia sinensis- Caco-2 cells- Cisplatin- Aquaporin 5
Adoptive cellular immunotherapy (ACT) employing engineered T lymphocytes expressing chimeric antigen receptors (CARs) has demonstrated promising antitumor effects in advanced hematologic cancers, such as relapsed or refractory acute lymphoblastic leukemia, chronic lymphocytic leukemia, and non-Hodgkin lymphoma, supporting the translation of ACT to non-hematological malignancies. Although CAR T cell therapy has made remarkable strides in the treatment of patients with certain hematological cancers, in solid tumors success has been limited likely due to heterogeneous antigen expression, immunosuppressive networks in the tumor microenvironment limiting CAR T cell function and persistence, and suboptimal trafficking to solid tumors. Here, we outline specific approaches to overcome barriers to CAR T cell effectiveness in the context of the tumor microenvironment and offer our perspective on how expanding the use of CAR T cells in solid tumors may require modifications in CAR T cell design. We anticipate these modifications will further expand CAR T cell therapy in clinical practice.

Keywords: CAR T cell, solid tumors, immunotherapy
Chimeric antigen receptor (CAR) γδ T cells: A new therapeutic platform for adoptive T cell cancer therapy

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Excitement is growing for therapies that harness the power of patients' immune systems to combat their diseases. One approach to immunotherapy involves engineering patients' own T cells to express a chimeric antigen receptor (CAR) to treat advanced cancers, particularly those refractory to conventional therapeutic agents. Although these engineered immune cells have made remarkable strides in the treatment of patients with certain hematologic malignancies, success with solid tumors has been limited, probably due to immunosuppressive mechanisms in the tumor niche. In nearly all studies to date, T cells bearing αβ receptors have been used to generate CAR T cells. In this review, we highlight biological characteristics of γδ T cells that are distinct from those of αβ T cells, including homing to epithelial and mucosal tissues and unique functions such as direct antigen recognition, lack of alloreactivity, and ability to present antigens. We offer our perspective that these features make γδ T cells promising for use in cellular therapy against several types of solid tumors, including melanoma and gastrointestinal cancers. Engineered γδ T cells should be considered as a new platform for adoptive T cell cancer therapy for mucosal tumors.

Keywords: γδ T cells; Chimeric antigen receptor; Cancer immunotherapy
PC-51

Gene-editing chimeric antigen receptor (CAR) T cells: Two chimeras come together to fight cancer

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Recently clinical trials utilizing genetically engineered T cells expressing a chimeric antigen receptor (CAR) that is half monoclonal antibody and half T-cell receptor have demonstrated remarkable response in patients with advanced cancers like relapsed or refractory acute lymphoblastic leukemia (ALL) and lymphoma. Moreover, emerging chimeric genome editing tools such as zinc-finger nucleases (ZNFs), transcription activator-like effector nucleases (TALENs) and clustered regulatory interspaced short palindromic repeat (CRISPR)/Cas composed of sequence-specific DNA binding module(s) linked to a non-specific DNA cleavage domain have made possible to dramatically expand the ability to manipulate cells aim to treat and/or study a wide range of diseases including cancer. Here, we will discuss how joint application of these two chimeras will help us to manipulate CAR T cells aiming to enhance the efficacy of CAR T cell therapy in preclinical and clinical settings.

Keywords: Chimeric antigen receptor T cells, Chimeric nucleases, Cancer immunotherapy
Immunotherapy of patients with HM by vaccination

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Background:
Vaccination is a powerful immuno-therapeutic method in HM (Hematological Malignancies) that results in prominent immunological responses and minimal clinical effects. HM is an immunosuppressive medium that is diagnosed by resistant dendritic cells, increased inhibition cells, regulators of checkpoints, and immune-suppressive solution inhibitors. TME, in the lymph nodes or bone marrow (BM), creates a suppressive immune system that by using resistant dendritic cells (DCs), an increase in the amount of suppressor cells such as the T-cells (Tregs) and suppressing cells Myelogenous, the regulation of tumor and peripheral tumor site control inhibitors, and T cell and TNF inhibitors (NKs). The effect of the vaccine depends on the successful activation and progression of the specific T cells of the tumor. Selected ages for vaccine development are identified based on selective expression patterns, which are more expressed by malignant tumors than normal cells. Cancer vaccines are based on the assumption that tumor antigens that are stimulated simultaneously can provide tumor-specific immunity and are selectively targeting malignant cells.

Material and Methods:
Cellular and non-cellular vaccines have been investigated for the treatment of HM types by changing clinical effects. A novel strategy for the design of the vaccine involves the identification of neo-antigens derived from tumor-dependent mutations, which these neo-antigens have been tangled with T-cells that have not been centralized. During this research and search on medical science databases, a number of articles related to the subject of the study were studied and studied.

Findings:

WT-1 is used as a tartrate of cytotoxic T lymphocytes, with high specificity for anterior CML cells. The combination of T cells with CD3/CD28 ligand-release methods leads to the spread of tumor lymphocytes. A series of clinical trials have shown that vaccination is associated with stimulation of cellular immune responses and homoral anti-idiotypic responses that potentially target the remaining disease with standard chemotherapy. Successful treatment with dendritic cell vaccines has also shown that in patients with B-CLL vaccination with pulsed DCs or tumor cell lysates led to a decrease in leukemia cells in a number of patients. The use of active or engineered T cells is a promising part of cancer immunotherapy. The peptide vaccination with LiTAAs/LiTAPs may be promising a new peptide vaccination method because of the widespread and repeated expression of antigen-peptides on the target cell population.

Conclusion:

With a better understanding of the immune system and HM immunobiology suppressing environment, reasonable combination therapies with vaccine to stimulate inherent immune responses that have a high potential for changing the pattern of HM treatment can be designed. More effective strategies for the heterogeneity of the tumor have been invented through polyclonal responses that are practiced by targeting multiple antigens and enhancing antigen presentations by professional APCs and immunotherapy therapies.

Key words: Leukemia vaccines, immunotherapy, immunosuppressive drugs, micro-environment around the tumor
Immunotherapeutic approaches for targeting ROR-1 in cancer cells

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Background: Being one of the most common health threatening challenges, cancer is forcing scientists to conduct different studies to cure and manage the disease. Despite traditional therapies, new therapeutic approaches including immunotherapy are considered to be alternatives.

Methods: ROR-1 is a tyrosine kinase receptor being expressed in different cancer cells and contains extracellular and intracellular parts that are good targets for new therapeutic strategies. Immunotherapy strategies utilized against ROR-1 include specific monoclonal antibodies and modified T cells (CART cell). This review aims at studying different types of cancer immunotherapy targeting ROR-1.

Conclusion: Presently, human and chimeric antibodies, as well as CARs T cells and modified T cells Bi-specific T cell engagers (BiTEs) are used to target the ROR marker while testing on cancer cell lines. Today, cancer immunotherapy can be regarded as a new and effective way of controlling and treating different types of cancer.

Keywords: receptor tyrosine kinas like orphan, immunotherapy, cancer.
PC-54

Evaluation of the effect of hydroalchoholic extract of *Achillea wilhelmsii* on the rate of cellular death and expression of four important genes in the HIIPPO signaling pathway in A549 non-small cell lung cancer cell line

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Background: Nowadays the use of plant compounds for prevention, control, and treatment of different cancers has received increasing attention. *Achillea wilhelmsii* is a medicinal plant that has been widely used for treatment and alleviation of different digestive, vascular, and neurological illnesses. The aim of the present study was to evaluate the effect of the hydroalchoholic extract of this plant on the survival and mRNA expression of *LATS1* and *LATS2* tumor suppressor genes and *TAZ* and *YAP1* oncogenes associated with the Hippo signaling pathway in the A549 lung cancer cell line.

Methods: After extraction of the hydroalchoholic extract of *Achillea wilhelmsii*, its effects on the A549 lung cancer cell line survival and mRNA expression of *LATS1*, *LATS2*, *TAZ*, and *YAP1* genes were assessed compared to the control group using MTT and RT-PCR, respectively.
Results: The survival rate was decreased significantly after 24 hours treatment with hydroalcoholic extract of *Achillea wilhelmsii* at concentrations of 200 and 1000 µg/ml and after 48 hours treatment at a concentration of 100-1000 µg/ml. The mRNA expression of *LATS1* and *LATS2* did not change while the expression of *TAZ* and *YAP1* decreased significantly compared the control group.

Conclusion: The results of this study showed that the hydroalcoholic extract of *Achillea wilhelmsii* decreased the expression of *TAZ* and *YAP1* oncogenes in A549 lung cancer cell line.

Key words: Lung cancer, Hydroalcoholic extract of *Achillea wilhelmsii*, MMT, HIPPO pathway, A549 cell line
Cell-Penetrating Peptides: An Ideal Candidate for Smart Targeting Cancer Treatment

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Background and Aim:

Cell-penetrating peptides (CPPs) were widely used as motifs for drug delivery to a specific target. These therapeutic peptides are a promising and novel approach to treat many diseases including cancer. They have several advantages over proteins: as they are (1) easy to synthesize, (2) have a high target specificity, and selectivity and (3) have low toxicity.

CPPs are 5–30 amino acid in length and can translocate through the plasma membrane and transport cargos ranging from small molecules to proteins and as such provide a promising mechanism for drug delivery. They are taken up by the cell unless by direct translocation or endocytosis and pinocytosis process. Newly the novel CPP has been designed which named BR2 which is 17 AA peptide based on the CPP motif of buforin IIb. This peptide has cytotoxicity upon HeLa cells, B16-F10 mouse melanoma cells and HCT116 human colon cancer cells, except not HaCat human keratinocytes, NIH 3T3 mouse fibroblasts, and BJ human fibroblasts. BR2 was conferred to cooperate with gangliosides on the cell lamina of these tumor cells. Also, CPPs can target markers such as receptors displayed on the tumor cell membrane. Targeting the integrin ανβ3 and ανβ5 protein which showed on the membrane of lung cancer, melanoma, brain tumors, ovarian carcinoma, and breast cancer cells has been performed successfully.

Methods:
We carried out a literature review utilizing PubMed and Web of Science for investigations on smart targeting cancer treatment between 2014 and 2018. The following keywords were used: “Cell-penetrating peptides”, “CPPs”, “Cancer treatment”, “Smart delivery” and “Targeted delivery”.

Conclusion:

CPPs can be invented to target nearly any protein of interest due to the easiness of synthesis and great target specificity and selectivity. These therapeutic peptides bind specifically to those target protein to which they are intended for. They provoke cell death in several cancer cells in vitro and in vivo. They exhibit selectivity in targeting cancer cells without damaging untransformed cells.

Keywords: Cell-penetrating peptides, Smart targeting, Cancer treatment,
PC-56

Blood-Based Molecular Markers for Breast Cancer Detection: A Systematic Review

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Abstract

BACKGROUND: The early diagnosis of breast cancer is associated with decreased mortality. One of the ways to diagnose this cancer is the detection of circulating tumor cells (CTCs). CTCs are the main factor in cancer metastasis and are a promising prognostic significance in cancer detection.

OBJECTIVE: This study aimed to review all articles that related to the biomarkers for the early detection of CTCs in peripheral blood by using molecular tests.

METHODS: We retrieved relevant articles from PubMed and Scopus, were published from January 1, 2000 to March 1, 2017.
Results: Of the 18 biomarkers reviewed, MGB and CK19 are two of the most widely studied markers and they seem to be the best markers for early detection of cancer. 100% sensitivity and 69% specificity for MGB and 100% specificity and 86% sensitivity for CK19 have been reported.

CONCLUSIONS: A small number of biomarkers don’t have the role in the early detection of CTCs; however, the use of some blood-based markers could improve significantly early detection of breast cancer.

Keywords: Breast cancer, CTC, early detection, metastasis
Bioreductive agents: a review of the solid tumor treatment

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Abstract

The Hypoxic tumor microenvironment is the characteristic feature in the most solid tumors which is associated with resistance to chemotherapy and radiotherapy. The most of the solid tumors have regions with low oxygen tension which are associated with resistance to chemotherapy and worsen prognosis. Recent biological studies demonstrated that these regions are a favorable target for cancer treatment. There are some compounds which activate in hypoxic regions and leads to the generation of the free radicals which damage to DNA. The main purpose of the hypoxia-activated prodrugs (HAPs) or bioreductive prodrugs is to eradicate hypoxic regions. These prodrugs are different in potency and in different phases of clinical trials. The effectiveness of some agents has been confirmed in several clinical trials but it is still controversial. The aim of this review article is to discuss targeting tumor hypoxia as a pivotal target of cancer treatment, focusing...
on the mechanism of bioreductive prodrugs activation and current clinical progressions.

Key words: bioreductive, solid tumor, hypoxia, cancer
MicroRNA 506 increase cell viability in T cell Acute Lymphoblastic Leukemia Cell Line (Jurkat)

Background: microRNAs (miRNAs) regulate gene expression through binding directly to the 3’UTR of protein coding genes. Any changing of miRNA expression may result in the creation of cancerous phenotypes. Therefore, for the first time, the aim of this study is investigating the effect of the over expression of miR-506 in the acute lymphoblastic leukemia of T cell (Jurkat cell line).

Method: Jurkat cell lines cultured in RPMI-1640 medium and was transfected at a final concentration of 50 and 100 nM with Lipofectamine 2000. The accuracy of transfection was assured by transfection of siRNA conjugated with FITC as a scramble. 48 hours after transfection, for test of MTT assay, 10 μl MTT (3-(4, 5-dimethylthiazol-2-yl)-2, 5-diphenyltetrazolium bromide) solution (5 mg/ml) was added to each well and the plates were incubated for a further 4 h. After removal of the medium, each cell was treated with 150 μl DMSO. The culture plates were shaken for 15 min and the optical absorbance values were read at 570 nm using an enzyme-labeled analyzer.

Result: Our data indicated that the viability of Jurkat cells was increased in comparison with the control group when the cells were treated with miR-506 50 and 100 nM miR-506 respectively. Moreover, the viability of 100 nM miR-506 was increased in comparison with 50 nM miR-506, but the difference was insignificant and survival of the scramble group was not significantly different from the control.
Conclusion: This study showed that miR-506 could play the role as an oncogenic microRNA in acute lymphoblastic leukemia cell line

Keywords: Acute lymphoblastic leukemia, Jurkat, miR-506
LIF gene expression can be considered as a prognostic index in breast cancer

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Nowadays, development of new accurate diagnostic methods for cancer prediction in the early stages is very important. Many genes have yet been presented as the tumor markers. In this study SDF-1α gene was introduced to MCF-7 cell line as a pcDNA3.1(+) -SDF-1α recombinant construction. In the next step, the effect of the recombinant gene increased expression on the expression profile of some selected genes was analyzed using real-time RT-PCR method. Also the scratch test aim to comparing the cell proliferation before and after transfection was carried out. The results of gene expression study revealed that LIF expression was increased more than 5 folds under this induction. Interestingly the scratch test demonstrates a 1.6 fold increase in cell proliferation rate of transfected MCF-7 cells compared to the control cells. These results propose that the regulatory system of LIF gene can be the first controlling system inducing by the cytokines. In other words over expression of LIF gene can be considered as an index factor confirming the effect of the growth factors in the tumor cells. Web mapping of the LIF and related genes verify LIF’s probable role in early stages of cancer and proliferative signaling pathways.

Key Words: LIF, SDF-1α, MCF-7, Gene expression, Tumor marker
PC-60

Cold Atmospheric Plasma (CAP), an alternative method for the death of mouse melanoma cells and metastatic inhibition

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Background: Metastasis is a key step in the progression of malignant melanoma, which indicates advanced stage and worse prognosis. Any mistakes from a metastatic cell results in the death of cancer cells during the cellular events. Therefore, the cell death regulation in melanoma cells is essential for survival during metastasis. Although Dacarbazine improves the mortality rate of cancer patients by melanoma cell death, But also due to high oxidative stress, it causes normal tissue disorder, which has significant side effects and therefore reduces the quality of life of patients. Cold Atmospheric Plasma (CAP) acts as an alternative method for inducing apoptosis in melanoma cells and inhibition of metastasis which has no side effects for healthy tissue.

Methods: Initially, inoculated B16 melanoma cells into Balb/c male mice. When tumor reached 20±5 mm³, mice were randomly assigned into 4 groups: tumor
control (untreated), Dacarbazine treatment, CAP treatment, combination of Dacarbazine and CAP treatment. Tumor volume (mm³) was measured during the 0, 5, 10 and 15 days after each treatment compared to the untreated tumor control group. Then, to investigate the melanoma cell metastasis, H&E staining was performed on the liver, kidney, spleen, lymph nodes and muscles. Also, the serum levels of TNF-α, IL-6 and IL-1β pro-inflammatory cytokines were measured in each group by ELISA assay.

Results: The tumor size was significantly reduced in the CAP group compared to the other groups. The amount of tight junctions in cell-cell and cell membranes in the CAP-treated group had not changed, but in the Dacarbazine and combination groups, these connections disappeared and the cells were severely degraded. Also in the CAP group, leukocyte infiltration and inflammation in the tumor site were significantly higher than other groups. The levels of TNF-α, IL-6 and IL-1β production in the CAP group were higher than the control group and other groups.

Conclusion: our results indicated that CAP not only can degenerate the tumor tissue, but also can recruit leukocytes in infected tissue and induce inflammation. It also prevents melanoma cell metastasis to vital tissues without affecting healthy tissue. Therefore CAP can be a safer option than chemotherapy for the treatment of melanoma.

Keywords: Mouse melanoma, Dacarbazine, Cold Atmospheric plasma (CAP), apoptosis, metastasis, H&E staining, ELISA assay.
Evaluation of miR-21 and miR-451a as a prognostic marker for non-small cell lung cancer (NSCLC): A systematic review

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Background: Recent studies demonstrated that microRNAs can be used as biomarkers for the prognosis and diagnosis of many human malignancies such as NSCLC. The aim of this study was to clarify the usefulness of microRNA-21 and microRNA-451a as novel biomarkers for the early prediction of recurrence and prognosis in non-small cell lung cancer patients.

Methods: We searched articles in the PubMed, KARGER, Google Scholar and Science Direct databases between 2017 to 2018. About 26 articles were found; of these, 8 articles related to our study that were investigated.

Result: The results of this study showed that the levels of serum/plasma and sputum mir-21 expression in patients with NSCLC, increases compared to healthy persons. And over expression of miR-21 in plasma exosomes of these patient
shows a generally poor overall survival, that sensitivity and specificity of this in the prognosis of NSLC patients are 73.8 and 71.1 respectively. Also miR-21 can be used to examine the brain metastasis of these patients, which is elevated in patients with positive metastasis. Furthermore, there is a direct correlation between serum levels of miR-21 and TNM staging (primary tumor size, the extent of lymph node involvement, presence of distant metastasis) and lymph node metastases in NSCLC patients. In addition, plasma exosomal miR-451a level in NSCLC individuals are higher than healthy persons. The expression of exosomal miR-451a has a direct relationship with lymph node metastasis, vascular invasion, disease stage, and recurrence. Furthermore patients with NSCLC who have a more expression of miR-451a, have less survival. Conclusion: Our review exhibited that miR-21 and miR-451a can be useful biomarkers for prognosis, survival rate, metastasis, and recurrence of patient with lung cancer (NSCLCS) as a non-invasive method. Keywords: non-small cell lung cancer, Prognostic marker, miR-21, miR-451a
PC-62

**Evaluation of miR-376c and miR-199a as a diagnostic marker for Gastric cancer: a systematic review**

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Background: According to the invasive methods (such as biopsy and endoscopy) and low sensitivity and specificity markers (such as CEA, CA19-9, CA72-4, CA125) used today for diagnosing gastric cancer, recent studies have shown that microRNAs have vital role in progression, invasion, metastasis of cancers and they have high stability in bio-fluids so they could be potential novel diagnostic markers for human cancers. In this review, the expression levels of miR-376c and miR-199a in some biological fluids and their diagnostic value were investigated.

Methods: We searched articles between 2016 to 2018 in PUBMED, SCIENCE DIRECT, KARGER, GOOGLE SCHOLAR databases and 29 articles were found that 10 articles among them were related to our review and were investigated.

Results: The results demonstrated that miR-376c level increase in plasma and urine in patients with gastric cancer. Increased plasma miR-376c occurs in the early stages of tumorigenesis of gastric cancer and with the progression of cancer, the level of it will not change. Increased level of miR-376c in urine of gastric cancer patients occurs with the presence of malignant tissue. Measuring the level
of miR-376c in plasma has sensitivity and specificity of 71% and 78%, respectively; evaluating the level of this miRNA in urine has sensitivity and specificity of 60% and 64%, respectively. Also the studies presented that miR-199a level increase in plasma of gastric cancer patients and the level of this miRNA enhanced with the progression of gastric cancer and depth of invasion. Measuring the level of miR-199a in plasma as a diagnostic biomarker has sensitivity and specificity of 92.9%, 71.4, respectively.

Conclusion: In this study results showed that miR-376C and miR-199a could be used as non-invasive markers for early diagnosis and staging gastric cancer.

Keywords: gastric cancer, diagnostic marker, miR376c, miR-199a
Evaluation the effects of Fibromodulin protein expression on NFkB and TGFβ signaling pathways in liver cancer cells

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Background: Liver cancer is one of the most common cancers in the world and is considered the most lethal gastrointestinal cancer. Fibromodulin (Fmod) is one of the best genes for treatment of cancer. The aim of this study was to investigate the effects of Fibromodulin protein expression on nuclear factor-κB (NF-κB) and Transforming growth factor-β (TGF-β) signaling pathways in liver cancer cells.

Methods: Fibromodulin was cloned in PET22 vector in JM109 Ecoil, and protein expression was checked with western blot assay. After that this gene was transfected in liver cancer cell line (huh-7) in 2 groups (treatment and control), and the expression of the gene is measured using Real Time-PCR and protein production by Western blot and ELISA. NFkB and TGFβ signaling pathways were measured with Real time –PCR.

Results: The Fibromodulin gene was cloned in PET22 vector and expressed protein in bacterial. This gene transfected in liver cell line and express protein in supernatant. Expression of NFkB and TGFβ signaling pathways were down regulation in treated group compare with control group (P≤0.05).
Conclusion: It seems Fibromodulin had anticancer effects in the liver cancer and can be used as an important therapeutic biomarker in liver cancer patients.

Key word: Liver cancer Fibromodulin, NFkB, TGFβ
PC-64

Analyzed and compared Effects of silymarin on liver cancer cells in animal model in mice Balb / c with liver cancer with standard drug

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Background: Liver cancer is one of the most common cancers in the world and is considered the most lethal gastrointestinal cancer. silymarin is one of herbal plan used for inflammation disease, infection disease such as HCV. This plan has special properties effect on cancer cell. The purpose of this study was to evaluate and compare the effects of silymarin on liver cancer cells in the animal model of Balb / c mice with standardized standard liver cancer.

Methods: The antiproliferative activity of Silymarin and Sorafenib on the cell line of liver cancer cells (Huh-7). We injected $10^6$ huh cell (subcutaneous of leg region) in balb/c mice and checked tumor in 10 days. Then we injected Silymarin and Sorafenib into the liver cancer model of the mouse in 2 groups. One group was control without treatment. The level of gene expression NF-kB pathway and Wnt / B- Catenin gene done with Real time-PCR and histological examination.
Results: Silymarin suppressed cell growth in Huh-7 cells via modulation of Wnt and NF-kB pathways. Silymarin was decreased liver cancer tumor. In the signaling pathways, Silymarin either significantly influences the NF-kB, Wnt/β-catenin pathway (P≤0.05).

Conclusion: We demonstrated the antitumor activity of Silymarin in a liver cancer, but further investigations are needed on the therapeutic potential of this novel anticancer agent in clinical trial as a complementary drug for the treatment of liver cancer.

Key word: Liver cell cancer, Huh-7, Silymarin, Sorafenib, Wnt/B- Catenin, NF-KB
PC-65

Overexpression of microRNA-630 in T cell Acute Lymphoblastic Leukemia cell line (Jurkat)

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Introduction

Acute lymphoblastic leukemia (ALL) is identified by the increase of cancerous B and T lymphoid precursor in bone marrow. It is considered as the most common cancer in children and often occurs at 2 to 5 years of age. Limited treatment and resistance to current therapies or relapse are occurred so finding novel remedies are extremely important. MicroRNAs, noncoding RNA molecules which can effect on biological functions such as cellular proliferation, differentiation and apoptosis as tumor suppressors and oncogenes. In some malignancies, the increased expression of miR-630 can cause invasion and metastases, and in other type of malignancy, it causes apoptosis of cancer cells, so this study has been investigated the effect of overexpression of miR-630 in T cell acute lymphoblastic leukemia cell line (Jurkat).

Method

In the experimental study, mature hsa-miR-630 transfection were performed by lipofectamine 2000 at concentrations of 50 and 100 nM in 96-well plate. After 48
hours, proliferation of cancer cells were analyzed with MTT assay and flow cytometry with Annexine V / 7-AAD staining. Also the expression of P53, P21 and Bcl2 genes in each Group by RQ-PCR were investigated. Transfected groups were compared with non-transfected cell line as a control and scramble. SPSS software v.16 were utilized for data analysis.

Result

MTT assay showed that the proliferation in concentrations of 100 nM was significantly higher than 50 nM and increased in both concentration in comparison with control. The secondary apoptosis and necrosis rates were significantly lower than control and there were decrease by elevating rate of miR transfection. In the treated group expression of pro-apoptotic genes (p53, p21) and anti-apoptotic gene (Bcl2) were significantly decreased and increased respectively.

Conclusion

MiR-630 could play as an oncogenic microRNA in Jurkat cell line. Overexpression of miR is caused to increasing of viable cancer cells.

Keywords

Acute lymphoblastic leukemia, Jurkat, miR-630, miRNA, Oncogene
PC-67

Video conferencing based lobectomy surgery to remove chest lung cancer

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Background: Lung cancer with clinical manifestations and symptoms of chest wall fracture is seen in 5% to 8% of patients with surgery and its treatment as a challenge for the medical staff. The surgical removal of the chest is currently the standard of care, and there is disagreement about the best surgical approach. However, the most appropriate approach is the use of video conferencing for lobectomy surgery, as well as clinical reports published on this kind of satisfactory visual surgery. The purpose of this study was to investigate the feasibility of videoconferencing-based lobectomy surgery to remove chest lung cancer.

Methods: The present study was a systematic overview with a comprehensive search of web sites, validated journals, Scopus, SID, Google Scholar, ISC and related articles in this field. Lobectomy surgery, video conferencing, and lung cancer were used to search the English input and keywords, and the combination of them was used and the time period from 2013 to 2018 was considered for the selection of articles. The articles were found in about 198 articles, of which about 130 articles were included in the study, and then these articles were evaluated in terms of title, abstract and full text. After removing repetitive and unrelated, about 91 related articles was selected by research.
Results: The results of the studies showed that videoconferencing video surgery is the most desirable and fastest method for lung cancer surgery, with increased acceptance over the past five years, demonstrating the high safety and security of this type of surgery. And also shows that the patient has less waist pain than other pulmonary surgeries after this type of surgery, as well as a quicker postoperative recovery of the patient.

Conclusion: The study and facial summaries from the study of the articles in this field showed that video-based surgery due to its high quality and quantity compared with other pulmonary surgeries is accepted by the medical staff of different countries. Because the use of this type of technology in clinical surgery reduces the risks and risks of surgery, and the cost of it is also significantly reduced.

Keywords: lobectomy surgery, video conferencing, lung cancer
PC-68

Evaluation of the therapeutic capability of nanoscale fluorescence imaging technology in cancerous ovarian tumor

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Background: Ovarian cancer is one of the most common types of cancer worldwide, according to studies conducted over the past decades by the World Research Committee. Nanoparticles are used as nanomedicine that are used to diagnose and treat various diseases, including cancer. Therefore, nanobiotechnology, a combination of diagnosis and treatment for ovarian cancer, is a crucial component of a new approach to dealing with such malignancy. The aim of this study was to investigate the therapeutic capability of nanoscale fluorescence imaging technology in cancerous ovarian tumors.

Methods: The present study was a systematic overview with a comprehensive search of web sites, valid journals, scopus, SID, Science Direct, ISC and Google Scholar search engine, as well as related books in this area. The Ovarian Cancer, Imaging, Nanotechnology, X-rays and their combination were used to search, and the time range from 2013 to 2018 was considered for the selection of articles. The articles were found in about 90 articles, of which about 60 articles were included in the study, and then these articles were evaluated in terms of title, abstract,
full text. After removing repetitive and unrelated, about 50 related articles was selected by research.

Results: The results of the studies showed that the use of nanoscale with a fast scan method, the distribution of a wide range of the main elements and elements present in the tumor nodes, is depicted in a non-destructive manner. In the study of cancerous tumors of the ovary, using a nanoscale fluorescence imaging, a map of small structures inside the building is also shown; these structures are nuclear nuclei, where the ribosomal synthesis takes place. The use of nanoscale in imaging also makes it clear the distinction between the outside of the nucleus and inside the nucleus.

Conclusion: According to the studies, we found that the non-destructive effects of using nanoscale fluorescence imaging and nanotechnology, especially when a wide range of analytical methodologies is used for a sample; to obtain maximum information very useful. In the study of cancerous tumors of the ovary by using X-ray fluorescence imaging, we can obtain a better and better resolution picture.

Keywords: Ovarian Cancer, Imaging, Nanotechnology, X-rays
Tumor growth and metastasis effects of nano-system containing curcumin and quercetin in gastric cancer cell line

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Background: Curcumin is a polyphenolic compound derived from Curcumin longa L. Quercetin, a plant flavonol from the flavonoid group of polyphenols, is found in many fruits, vegetables, leaves, and grains. There are growing bodies of evidences revealing the antitumor effect of curcumin and quercetin in different tumors; although the molecular mechanism behind of this inhibition cancer cell. Here we investigated the antitumor activity of curcumin and quercetin in gastric cancer cell line in monolayer cell cultures and spheroids models. Furthermore, we characterized affecting cell cycle perturbation, as well as apoptosis induction in gastric cancer cell line.

Methods: The antiproliferative activity of curcumin and quercetin was assessed in monolayer and spheroid models. The influence of the cell cycle and expression levels of NF-κB and Wnt/β-catenin pathway was checked.

Results: nano-system containing curcumin and quercetin suppressed cell growth in gastric canc cells via modulation of Wnt and NF-kB pathways. Moreover, cells developed an early G2/M cell cycle arrest followed by sub-G1 apoptosis and apoptotic bodies formation post treatment with nano-system containing curcumin and quercetin. In the core signaling pathways of GBM, nano-system containing curcumin and quercetin significantly influences the NF-kB pathway by decreasing
p-65 expression or significantly inhibits the Wnt/β-catenin pathway by declining cyclin D1 expression.

Conclusion: we have shown that nano-system containing curcumin and quercetin effectively prevent proliferation, and invasion of GBM cells through perturbation of Wnt/β-catenin and NF-κB pathways, suggesting further investigations on the therapeutic application of this novel anticancer drug in in vivo models.

Key Words: curcumin, quercetin, Anti-tumor effect, Keywords: Spheroid
Neutrophil lymphocyte ratio as a marker of cancer prognosis in murine breast cancer model

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Background: Despite many advances in the treatment of breast cancer, it is still the second most common cause of death in women. Several studies have shown the role of inflammation in enhance tumor growth, invasion, metastasis, and angiogenesis.

Methods: We established a model of stage IV breast cancer by injecting 5×10^5 4T1 tumor cells into the mammary of BALB/c mice. Total white blood cells (WBC) count was performed using Neubauer chamber. The blood smears were stained with Giemsa solution and viewed for the presence of the granulocyte, lymphocyte and monocyte populations. The overall survival analysis was also performed and tumor-free mice was used at the as a control.

Results: Higher Neutrophil lymphocyte ratio (NLR) levels were found in tumor-bearing mice (P=0.028), whereas Platelet lymphocyte ratio (PLR) had no significant relationship with survival (P = 0.732). The median overall survival in mice with an NLR of >17 was 35 days in those with an NLR of 8 to 17 was 44.5 days and NLR of ≤8 was >50 days.

Conclusion: Using 4T1 mammary tumor model that shares many characteristics with human breast cancer we demonstrate that NLR as useful independent prognostic marker for survival.

Keywords: Neutrophil lymphocyte ratio, breast cancer, Inflammation
PC-71

The Relationship between serum concentration of the vitamin D in the breast cancer patients)

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Background: Breast cancer is the most common cancer in women worldwide and the leading cause of cancer death among this patients. In Iran, the incidence of breast cancer is increasing. Also, several studies show that there is a high prevalence of vitamin D deficiency in Iranian women. Experimental studies have shown anti-carcinogenic effects of vitamin D due to participation in regulating cell proliferation, differentiation, and apoptosis in normal and malignant cells. Therefore, the aim of this study was the evaluation of relationship between sera concentrations of vitamin D and breast cancer risk in Iranian women.

Methods: In a case–control study, serum samples were collected from 39 women with breast cancer and 35 healthy women that matched according to age. Vitamin D status was assessed by measuring 25-dihydroxyvitamin D levels. Different levels of vitamin D deficiency were determined as normal (>30 ng/ml), insufficient (20–30 ng/ml), deficient (<20 ng/ml), and severely deficient (< 10 ng/ml).

Results: Overall 33% had sufficient vitamin D, insufficient 38%, deficient 26%, severely deficient 5%, with trend toward lower vitamin D levels among breast cancer group (15.6 ng/ml) compared to control group (24.3 ng/ml). Also, there is no statistically significant relationship between serum vitamin D and tumor grading, staging, or other paraclinical findings.
Conclusion: This study showed that vitamin D deficiency is common in our country but levels of this deficiency is significantly higher in women with in breast cancer compared to healthy women. This concept offers, routine clinical evaluation of serum levels of vitamin D might be an economical and safe way to reduce cancer incidence by adding vitamin D supplements.

Keywords: vitamin D, deficiency, breast cancer
Active immunotherapy for breast cancer: going toward to overcome immune ignorance and tolerance

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Breast cancer is the most common malignancy in women with high mortality and incidence of >1,000,000 cases occurring worldwide annually. There is no effective therapy for patients with invasive and metastatic breast cancer. The immune system is active in breast cancer, but the ability of tumor cells to evade the immune system and poor immunogenicity of self/tumor antigens prevent to formation of the effective immune response against cancer. Recent progress in fundamental understanding of tumor immunology and identification of tumor-associated antigens have opened a new avenue of cancer vaccines. Active Immunotherapy provides long-term immunologic disease control compared to conventional chemotherapy or chemoimmunotherapy. Hence, in this review, we have discussed recent progress in in the field of active immunotherapy under clinical and animal models investigation of breast cancer: peptide and protein based, DNA based, whole tumor cell based, dendritic cell based, and provides a determination of the best vaccine formulation, adjuvant selection, delivery system and strategies to overcome distinct immune tolerance pathways to self/tumor antigen.

Keywords: breast cancer, active immunotherapy, tolerance
MicroRNA based Molecular Diagnostic Strategies as a Biomarker Suggestion for Cancer Specialists

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Background: As one of the most critical challenges for health community services, cancer still comprises a high percentage of mortality rates. Therefore, it motivates clinical researchers to other measurements. Validation of fluctuations in circulating microRNAs (miRNA) expression, has opened a new promising cancer biomarker, for early diagnosis, prognosis and monitoring the treatment in metastatic tissues. So, this study aims to evaluate the clinical potentials of cancer-related miRNA.

Methods: This systematic review was conducted to outline comprehensive studies published in PubMed, Scopus, Science Direct and Google Scholar databases from 2014 to November 2018. 78 articles were screened and 50 articles were totally included based on our inclusion and exclusion criteria.
Results: Although clinical examination, magnetic resonance, and laboratory assessments are measured out for cancer dilemma. There is a wide array of reports on miRNAs post-translational gene expression regulation. Alterations in miRNA levels after physiological imbalance makes their implementation logical for cancer diagnosis, also increases the sensitivity and accuracy of detection rate up to 99%. It is highlighted that expression levels of miR-155, miR-210, and miR-21 in diffuse large B-cell lymphoma, miR-21 and miR-210 in prostate cancer, serum miR-500 in the hepatocellular carcinoma patients, plasma miR-184 in tongue Squamous cell carcinoma, miR-17-5p, miR-21, miR-106a, b in gastric cancer were significantly increased in comparison with healthy controls. Whereas let-7a in gastric and breast cancer, plasma levels of miR-195, miR-92a in acute leukemia were decreased compared with healthy controls. Mainly, the amount of miRNA reduces after surgery.

Conclusion: Despite meticulously efforts for health system improvement, cancer diagnosis criteria should have been revised. Optimistic insights on miRNA as non-invasive and low-cost strategy, makes coordination between physicians and laboratory scientists obligatory, clarifying disease progression and accrediting diagnosis based clinical outcomes.

Keywords: Molecular Diagnosis, Cancer Diagnosis, MicroRNAs, Clinical Advantages.
Background: Triple-negative breast cancer (TNBC) is heterogeneous that contain 10–20% of diagnosed breast cancer cases, characterized by lack of hormonal receptors (estrogen, progesterone, and Her2) with poor prognosis. So hormonotherapy is not appropriate in TNBC management. Different kinds of biomarkers have a role in pathophysiology and microenvironment of TNBC that these biomarkers detecting have appropriate indication for better cancer manage. Given the existing diagnostic and prognostic biomarkers that haven’t been able to detect this kind of breast cancer till now, we decided to make this systematic review study to introduce new biomarker for TNBC progression regulating.

Search Method: This systematic review study was performed to identify studies using 4 keywords (cd73 and triple negative breast cancer and diagnostic biomarker and immune microenvironment) published in Scopus and Google Scholar database in the 2015-2018 time intervals. From initially 284 identified articles, 45 articles were totally included after removing duplicates and scanning the titles and abstracts.
Results: We understood that CD73 is a glycosyl phosphatidylinositol (GPI) coded by the NT5E gene. It has an immunosuppressive effect by A2A adenosine receptors (surface proteins) activation. CD73 is expressed by epithelial tumor cells and immune cells such as TH17. CD73 expression has an association with chemoresistance and poor prognosis of TNBC. Overall, CD73 seems to be an appropriate diagnostic and prognostic factor in TNBC.

Conclusion: Our study shows that CD73 is as a new diagnostic and prognostic biomarker in TNBC management. So targeting this biomarker could be the appropriate method for TNBC therapy. Also, CD73 detecting could give promising opportunities for laboratory investigations and clinical applications in improving the relationship between lab and clinic.

Keywords: Triple negative breast cancer, CD73, Clinical applications, Diagnostic and Prognostic biomarker.
Ex Vivo Polyclonal T-cell Expansion for Cancer Immunotherapy Purposes

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Cancer is the second cause of death in the world and traditional treatments, such as chemotherapy, radiotherapy, and surgery fall short in cancer treatment. One new method in our arsenal is cancer immunotherapy, which is the manipulation of the immune system to destroy cancer. One important subtype of cancer immunotherapy is adoptive cell transfer (ACT). One effective approach of ACT is injecting the anti-tumoral lymphocytes into the patient’s body after ex vivo expansion. These T cells can be unmodified and derived from tumor sites or drained lymph nodes (tumor-infiltrating lymphocytes or TILs) or genetically modified peripheral blood T-cells with artificially integrated TCR (TCR T-cell) and CAR (CAR T-cell). Over the past years ACT has been recognized as a major breakthrough in the field of cancer immunotherapy with CAR T cell being approved by the US Food and Drug Administration (FDA). Importantly, a crucial step in this process is the ex vivo expansion of the desired T-cells to clinically-relevant numbers in the presence of proper stimuli and growth factors. First, T-cells are activated by an antibody that binds to TCR complex and stimulates T-cells. The activation step requires a co-stimulatory signal to enhance T-cell expansion, which is usually mediated through the stimulation of CD28. Other co-stimulatory receptors include CD40, 4-1BB (CD137), and OX-40. In addition, media and cytokines (e.g. IL-2, IL-7, IL-15) are essential factors that determine T-cell expansion. Each media performs differently based on their proliferation...
capacity and cell viability. Cytokines’ dosing and their combination are also determinants of T-cell expansion. Thus far, numerous methods have been devised for T-cell expansion, but a unanimous protocol specifically suitable for polyclonal T-cell expansion is lacking. Considering the importance of ex vivo T-cell numbers in immunotherapy, optimizing its expansion is pivotal in cancer treatment.

Keywords: T-cell, immunotherapy, cancer, cell expansion
PC-77

Potentiation effect of melatonin on radiation induced chromosomal aberration in G2-Lymphocyte of breast cancer patients.

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Background: Radiation therapy is a main modality for cancer treatment by inducing DNA damages, chromosomal aberrations and cell death. In this study we aim to evaluate the modulating effect of melatonin on radiation induced chromosomal aberrations in cells irradiated at G2 phase of the cell cycle.

Materials and Methods: G2 assay was performed on peripheral blood lymphocytes obtained from 15 breast cancer patient and 5 normal control. Whole blood culture was initiated in complete RPMI-1640 medium and cells were irradiated with 1 Gy gamma rays 4 h prior to harvesting. One group of the samples was irradiated alone, and the other group was treated with 800 µg /ml melatonin for 2 hour before irradiation. Cells were harvested 4h after irradiation; harvesting and slide preparation was done according to standard procedures. Cells were stained in 10% Giemsa and 50 well spread metaphases were scored for presence of chromatid type aberrations.

Result: Results show that radiation alone increased the frequency of chromatid type aberrations considerably compared to unirradiated samples (p≤0.01). Melatonin by itself increased background chromatid type aberrations, however addition of melatonin to cultures led to increased frequency of aberrations in irradiated cells (p≤0.05).
Conclusion: Despite that melatonin is a known antioxidant agent, but in combination with radiation led to an increased clastogenic effect. The mechanism by which melatonin enhanced radiation effect is not fully understood but may alter genes involved in DNA repair process leading to increased chromosomal aberration.

Keyword: Lymphocyte, breast cancer, ionizing radiation, melatonin, chromosomal aberration.
PC-78

Association between the XPD gene polymorphism and CML risk in Iranian population

The genetic polymorphism xeroderma pigmentosum complementation group D (XPD) repair gene may lead to genetic instability and leukemogenesis. The purpose of the study was to evaluate the association between XPD Lys751Gln polymorphism and the risk of developing CML in Iranian patients.

The case–control study was performed in 93 patients with CML on imatinib treatment and in 93 cancer-free controls for investigation the polymorphisms of the XPD gene. The DNA samples were genotyped by using of PCR- RFLP method. The variants’ frequencies in both groups were compared. Clinical information regarding to smoking status of patients and healthy control was collected from their clinical file.

A significant difference was observed in the variant genotype frequencies of the XPD Lys751Gln polymorphism between the patients with CML and control group. The XPD mutant allele and genotype frequency were higher in patients compared to controls ($X^2=6.1$, df$=2$; $P=0.04$), and were similar among patient males and females. Regarding to smoking, consumption rate was higher in patients compared to controls ($P=0.003$). we showed an association between XPD polymorphism, smoking status and susceptibility to CML development ($P<0.05$). These findings show the correlation between XPD genetic polymorphism and CML cancer risk and pattern their interactions with smoking as genetic modifiers in the etiology of CML disease in the Iranian population.

Keywords: CML, Polymorphism, XPD, Iranian population
Evaluation of effects of dexamethasone administration on tumor growth rate in a mammary tumor model

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Background: Early detection of cancer and optimizing of anticancer therapy modalities, including surgery, chemotherapy, and radiotherapy, have led to increased survival of patients with cancer. However, cancer still is a major cause of death in humans worldwide. Thus, optimizing efficacy of anticancer therapies is essential. Dexamethasone, a synthetic glucocorticoid, is widely used as an anti-inflammatory drug or as an immunosuppressive agent in autoimmune diseases and other disorders. Furthermore, dexamethasone is routinely used in some cancer patients. However, dexamethasone may affect antitumor immune responses of cancer patients. Since there are a little knowledge about effects of this drug on tumor growth in hosts with mammary cancer, we evaluated effects of administration of dexamethasone on tumor growth rate in a mammary tumor model.

Methods: Twenty-five inbred mice were divided into five groups. First group was healthy control group, second group was placebo control group, and the other three groups were drug-treated groups. Mammary tumors after propagation in culture medium were inoculated into mice and effects of administration of dexamethasone on tumor growth rate were assessed in comparison with tumor growth rate in control tumor mice.

Results: Repeated administration of dexamethasone led to enhanced tumor growth, but, this increasing in tumor growth rate was not significant when compared to tumor growth rate in control group (p>0.05).

Conclusion: These findings shows that dexamethasone may have harmful effects on mammary tumors.
Keywords: Cancer, Dexamethasone, Mammary tumor, Tumor growth rate.
PC-80

Unfavorable Toxicities Associated with Chimeric Antigen Receptor (CAR) T-cells

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Cancer is one of the leading causes of death worldwide. Immunotherapy is an alternative to traditional cancer treatment, especially hematological malignancies, that helped reduce cancer mortality. Immunotherapy is using our body's immune system to target cancer cells. Adoptive immunotherapy with genetically engineered T-cells expressing a chimeric antigen receptor (CAR-T) can induce a high response rate in patients with relapsed or refractory B-cell malignancies. However, an issue with this approach is toxicity, which can be life-threatening. The time and severity of toxicity can be different in various patients. This variation depends on CAR T-cell dose, CAR structure, the toxicity grading systems used, conditioning chemotherapy, level of certain cytokines, the host characteristics (including the age of the patient, type of malignancy, and disease burden). Serious toxicities may be observed after CAR T-cell therapies. Two of the most common toxicities are cytokine release syndrome (CRS) and neurotoxicity, known as CAR T-cell-related encephalopathy syndrome (CRES).
Manifestations of these toxicities are different. CRS manifests as signs of fever, hypoxia, hypotension, cytopenia, and coagulopathy. Neurotoxicities include symptoms such as encephalopathy, dysphasia, cognitive defects and seizures. Apart from mentioned toxicities, some cases of tumor lysis syndrome (TLS), macrophage activating syndrome (MAS), on-target off-tumor toxicity, and anaphylaxis may be observed. Managing toxicities associated with CAR T-cell therapy is a clinical challenge. Timely diagnosis, close monitoring, standardization of toxicity grading, assessment and management strategies are necessary to reduce toxicity and improve the efficacy, safety, and widespread applications of CAR T-cell therapy. All in all, efforts to overcome the toxicities associated with CAR T-cell therapy offer new hope in the cancer treatment.

Keywords: chimeric antigen receptor, toxicity, cancer, immunotherapy
The association of Cyclooxygenase expression with pathophysiology of Functional and Non-Functional Pituitary adenoma

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Background and aim: Pituitary Adenoma is one of the most common tumor-related inflammatory diseases in the young people that Approximately 2.5 million people in the world and about 35,000 people in Iran are afflicted. The etiology of this type of cancer is un-known and investigations are in progress to clarify the molecular mechanism of pituitary adenoma. It seems that the COX enzyme stimulates the cell proliferation, inhibits the apoptosis, increases the malignant cells’ invasiveness and induces the angiogenesis. The aim of the present study was to investigate the expression level of Cox in tumor tissue of patients with functional and non-functional pituitary adenoma and the relevance of the gene expression level with patient's clinic pathophysiology.

Materials and Methods: In this case-control study, 40 patients with pituitary adenoma with who were referred to the Firoozgar Hospital in Tehran were
participated. Tumor tissue samples were used to extract mRNA and cDNA, and to determine the gene expression of COX enzyme, the Real-Time PCR-based sybergreen method was used. The correlation of COX enzyme with patient's clinic pathophysiology features were evaluated. Finally, statistical analysis was performed using version 6 of GraphPad Prism software and independent t-test.

Results: Measurement of COX enzyme expression level in tumor tissues of patients with functional and non-functional pituitary tumor revealed that the level of this gene was significantly increased in patients comparing to healthy subjects and normal tissues. Also, the increased level of this gene was associated with elevated level of tumor grade and stage.

Conclusion: The results of the current study have shown that the COX enzyme can account as local bio marker in patients with functional and non-functional pituitary tumor due to the significant differences of the expression level in patients comparing to controls, it can be noticed as a possible biomarker for controlling disease.

Key Words: functional pituitary adenoma, non-functional pituitary adenoma, COX enzyme, cancer.
Undifferentiated pleomorphic sarcoma in brain whit New Mutation in P53 gene: Case Report

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Undifferentiated pleomorphic sarcoma (UPS) is an extremely rare tumor that occurs in the head and neck region. Here, we report a unique case of a primary undifferentiated pleomorphic sarcoma in the occipital bone region. She is 45-year-old woman with no previous history of surgery, skin malignancy, or radiation. Most studies have shown that there are association between the development and malignancy of brain tumors and tumor suppressor genes and oncogenes. The aim of this project is to investigate the P53 gene mutations in exon 8 in patients with UPS in brain.

The tumor was surgically removed and adjuvant radiotherapy was required after histological examination, which showed an undifferentiated pleomorphic sarcoma of the brain. The extraction of DNA from Undifferentiated pleomorphic sarcoma sample was performed by phenol-chloroform protocols. After PCR amplification of exon 8 of p53 genes, screening by SSCP (Single -Strand Conformation Polymorphism) was performed to detect the shift.

Those are that have shift were sequenced. In this study was detected three malignant novel missense mutation including TP53_g.13851A>G, Tp53_g.1386C>G and TP53_g.13835G>T. Also one synonymous mutation (TP53_g.13832A>G) was detected. There was no recurrence after 1 year of follow-up.

Though rare, undifferentiated pleomorphic sarcoma should be included in the differential diagnoses of brain tumors. Molecular Findings from this study were indicated that mutations in exon 8 of the P53 gene was in this case, this issue is important in diagnosis and gene therapy of UPS in brain.
Key word: pleomorphic sarcoma, Mutation, P53
PC-83

Biological and Molecular Diversity in Telomerase: Characteristics of hTERT in Human, Vertebrates and Yeast

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Abstract

hTERT (human telomerase reverse transcriptase) is the catalytic subunit of telomerase enzyme, and is essential for its functions. The aim of this review was to compare the TERT in human and other species including microorganism, vertebrates and mammals, in terms of its functions and regulation. According to literature, the catalytic subunit of telomerase in animals contains many conserved domains and residues, which have crucial roles in its functions. Moreover, the structure and biology of human telomerase seem to be more similar to that of dog compared other animals. Thus interestingly, unlike the mouse that is seemingly not a proper model for evaluation of telomerase activity and its regulation, dog may be an appropriate model for the experimental investigations of telomerase function and therapeutic strategies in cancer studies.

Keywords

Telomerase; hTERT; Human; Vertebrate; Yeas
The Study of Serum Catalase Level in Women Suffering from Breast Cancer in Disease Stage 1

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Introduction: Since early in 1980 breast cancer incidence has been increased among women of all races and nowadays it is one of the most prevalent cancers in developing countries. Breast cancer has the highest malignancy among Middle East women, having high among Iranian too, involving 21.4% of all malignancies among them. The main cause of breast cancer has not been still identified clearly and Different studies have reported that the role of stress oxidative, antioxidants in incidence of breast cancer. The aim of present investigation is to see plasma catalase activity changes amount in these patients’ in stage 1 of breast cancer.

Methods and materials: Enzyme catalase concentration in plasma of 15 patients suffering from breast cancer in stage 1 were selected as case group along with 15 healthy women were selected as control group. Age range of patients was 25-40 years. The catalase activity rate was measured with two H₂O₂ molecules changing to oxygen and two water molecules. Finally data were analyzed using SPSS software.

Result: experiments in both case and control group indicated that catalase activity rate in stage 1 of case increases compared to control group. Catalase activity rate for control group was $\pm 0.4 \text{ nmol/min/ml}$ and $\pm 3 \text{ nmol/min/ml}$ for case group determined and Significant changes observed. (P<0.05)

Conclusion and discussion: it has been found that stress oxidative plays crucial role in carcinogenes. The role of antioxidants has been studied widely in patients...
with breast cancer. Studies about catalase activity in breast cancer show controversial results. Considering the important role of catalase in neutralizing Reactive Oxygen Species, More studies are suggested about power of different cell antioxidants including catalase to prevent tumor development. Our finding indicated that catalase activity level increases in patients with breast cancer. Further study requirement in this subject for better understanding.

Key words: catalase, breast cancer, antioxidants
A Novel cancer therapy: Synthesis and optimization of nano drugs containing cisplatin as an effective chemotherapy drug

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Abstract:

Breast cancer is the most common cause of cancer in women and the fifth causes of death in the worldwide. Platinum-base is one of the most common drugs in chemotherapy,

Cisplatin and other chemotherapy drugs has a lot of side effects, For this reason, Nanoparticle drug delivery systems are suggested to reduce side effects, Liposome is one of the appropriate carriers. In this study, we presented the new
formulation of nano-cisplatin for more effective treatment and reduction of side effects of the drug.

1| Introduction

According to the latest World Health Organization World Cancer Report, breast cancer is the most common cause of cancer in women and the fifth causes of death in the worldwide. Most women with breast cancer are identified at an early stage. The traditional treatments for cancer include surgery, radiation therapy and chemotherapy. Platinum-based chemotherapy, such as carboplatin, particularly cisplatin and oxaliplatin, are the most active agents in Human malignances. Platinum agents mediate their cytotoxic effects by the inhibition of DNA replication and the transcription process, and induction of apoptosis and necrosis. However, cisplatin-compound are distributed non specifically in the body where they affect both cancerous and normal cells. Side effects of chemotherapeutic drugs include: Loss of hair, dry skin, immune suppression, nephrotoxicity and neurotoxicity. Several ways to reduce the side effects and the same increased treatment efficiency has been applied. Therefore, one of the key research in cancer therapy is to deliver anticancer drugs selectivity to tumors while decreasing aggregation in normal tissue. Nanoparticles such as liposomes, is one of the appropriate carriers in delivery applications and have been extensively applied to enhance the therapeutic efficacy of drugs. Liposomes are self-assembling closed globules structures composed of lipid bilayers especially phospholipids and have a spherical shape in which an outer lipid bilayer surrounds a central aqueous phase. Liposomes make it possible to load lipopolysaccharide (lipophilic) in a phospholipid dome and dissolve in water (hydrophilic) in medium fluid spaces.

For the preparation of nanoliposome, a certain proportion of lecithin, cholesterol and polyethylene glycol 2000 were mixed together and the cisplatin has been added to it. The mean diameter of cisplatin nano liposomes was calculated using Zeta-sized apparatus and the loading and release rates of the drug from the nano liposomes were done by dialysis method. Finally, the effect of
toxicity of the encapsulated drug in the liposome was investigated using MTT method.

Results: Mean diameter of pegylated nano liposome containing cisplatin was measured with the aid of a zeta-seizer device, which obtained 119.5 nm. The IC50 value after an MTT test showed in nano-drug cytotoxicity versus free drug.

Conclusion: This study showed that the cytotoxicity of the pegylated nano liposomal drug is greater than that of the free drug and it is suggested that this study be tested on animal models.

The aim of this study is to provide a new formulation of nanoliposomes containing cisplatin to improve its therapeutic index.

Keywords: Nano-based drug delivery systems, nano liposomes, cisplatin, MCF-7 cell line
PC-87

Urtica dioica have good potential to inhibits cell proliferation and induces apoptosis in human liver and colon cancer cell lines.

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Background: Cancer is the second serious cause of death in the worldwide. In spite of the great promotion that has been made in the cancer therapy, significant deficiencies for improvement of new treatments remain yet. Nowadays the use of herbal medicines such as plant-derived products has been extensively examined in the treatment of many types of cancer such as liver and colon cancer. Urtica dioica is a traditional herb that has many pharmacological and clinical effects and wildly used as a therapeutic agent in cancer. In this study, we have evaluated the effects of the different concentrations of methanolic extract of Urtica dioica on viability, death pattern, and expression of the apoptosis-related gene in normal human dermal fibroblast (HDF), liver cancer cell lines (HEPG2) and colon cancer cell line (HCT116).

Methods: Tow Cell lines (HEPG2 and HCT116) and HDF normal cell line were cultured in suitable media. After 24 h, different concentrations of the Urtica dioica methanolic extract (100, 200, 400 and 600 μg/ml) were added and after 24 and 48h Cells viability was assessed by MTT assay, and apoptosis was also evaluated at the cellular level by Annexin V/PI flow cytometry analyzing and AO/EB staining. Apoptotic gene expression such as BCL2 and BAX were assessed by TaqMan real-time PCR assay.
Results: Urtica dioica methanolic extract has a significant dose-dependent and anti-proliferative effects on HEPG2 and HTC116 cells after 48h with an IC50 value of about 182 and 200 μg/ml, respectively (P < 0.001). Apoptotic cells were observed in HEPG2 and HTC116 cells but not in HDF after 48 h of treatment. Furthermore, the increased level of the apoptotic BAX/BCL-2 ratio was observed in HEPG2 and HTC116 cells under treatment of different concentrations of Urtica dioica methanolic extract.

Conclusion: Our present study suggests that the Urtica dioica methanolic extract may influence liver cancer and colon cancer cell lines at specific doses and change their proliferation rate by changing the expression of apoptotic-related genes as well as BAX and BCL2. Finally we can say Urtica dioica have a good potential to used as a liver and colon cancer medicine.

Keywords: Cancer therapy, Herbal-medicin, Urtica dioica, liver cancer, colon cancer
PC-88

SCGB3A1 and APC as a novel epigenetic biomarkers for Breast cancer

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Background: Breast cancer is the most common malignant tumor in women worldwide. The absence of specific biomarker for early diagnosis makes it difficult to detect on-time diagnosis of breast cancer. Common tools to diagnosis it are mammography, MRI and biopsy but due to some disadvantages of these ways such as injury, bleeding, infection and DNA methylation, finding new strategies is important. Due to this problem, we aim to study new non-invasive biomarkers.

Methods: This systematic review was conducted to outline comprehensive studies published in PubMed, Scopus, Science Direct and Google Scholar databases from 2008 to November 2018 by using 4 keywords. 85 articles were screened and 45 were totally included.

Results: We assessed promotor methylation level of two gene panel, Apc & SCGB3A1, in breast cancer. Secretoglobin family 3A member 1 (SCGB3A1) is a protein in human encoded by SCGB3A1 gene and has several biochemical
functions such as cytokine activity. APC & SCGB3A1 disclosed 100% specificity for breast cancer detection. Also, SCGB3A1 is a tumor suppressor gene that is inactivated in the early stages of B.C. So it could be functional in diagnosis.

Conclusion: According to failure in common therapeutics, breast cancer progression has been remained as a dilemma, but we would like to introduce SCGB3A1 and APC as valuable biomarkers.

Keywords: Breast cancer, new biomarkers, DNA methylation, Diagnosis.
PC-89

Introducing exosomal biomarker for prostate cancer diagnosis

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BACKGROUND: Prostate cancer is the second most common cancer in men worldwide, and the eighth cause of cancer-related death. There are some tests such as PSA (Prostate specific antigen) blood test and DRE (digital rectal exam) to detect prostate cancer. The disadvantages of these strategies like to be invasive with uncomfortable examination with very little gain or even with a false positive result, leads us to find noninvasive and effective biomarkers. Lately, exosomes have appeared as a novel source of non-invasive cancer biomarkers.

METHODS:
This systematic review was conducted to outline comprehensive studies published in PubMed, Scopus, Science Direct and Google Scholar databases from 2008 to October 2018 by using 4 keywords. 93 articles were screened and 48 were totally included.

RESULT: TM256 (transmembrane protein) with 94% sensitivity, LAMTOR1 (regulator complex protein) with 81% sensitivity and ADIRF (adipogenesis
regulatory factor) with 81% sensitivity are biomarkers with 100% specificity, found only in the urine of males with prostate cancer which could be mentioned as a specific early diagnostic biomarker for prostate cancer.

CONCLUSION: Based on these studies, clinical researchers look for novel agents for early diagnosis. TM256, LAMTOR1, and ADIRF would be the 3 most promising diagnostic exosomal biomarkers in the early detection of prostate cancer.

KEYWORDS: prostate cancer, extracellular vesicles, exosomes, cancer biomarkers.
What makes microRNA profiling unique in early diagnosis of renal cell carcinoma?

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Background: Renal cell carcinoma (RCC) is the second-most common nephrological and kidney cancer in adults, responsible for approximately 90–95% of cases. The immune system is remarkably good at hiding the symptoms and as a result people with RCC often have advanced disease by the time it is discovered. So early diagnosis of RCC is challenging. Absence of specific biomarkers for detection and monitoring complicates the on-time diagnosis of the disease and relapse. So that identifying novel diagnostic and prognostic biomarkers is urgently demanded.

In recent years imaging tests, biopsy and body fluids (blood, urine and etc.) tests were some diagnostic ways of many cancers; But due to some disadvantages of these ways such as bleeding, infection and injury to other organs in providing biopsy, causing DNA mutation, cell necrosis and other threatening impacts in imaging tests, finding new ways is mandatory.

The study is a review of recent knowledge regarding potential clinical applications of microRNA profiling as a biomarker of RCC.

Methods: This systematic review was conducted to outline comprehensive studies published in PubMed, Scopus, Science Direct and Google Scholar databases from
2008 to October 2018 by using 5 keywords. 133 articles were screened and 52 were totally included.

Result: We comprehend that in RCC there is a stepwise decrease in expression of miR-141 and miR-200b in comparison to normal tissues. Also there are distinguishable levels of all microRNAs between malignant and benign RCCs. To distinguish RCC from normal kidney tissue miR-141 has 81.7% sensitivity and 100% specificity and miR-200b owns 97.5% sensitivity and 100% specificity individually. Interestingly, in combination of them 99.7% sensitivity and 100% specificity is observed.

Conclusion: Based on these studies, we would like to introduce miR-141 and miR-200b profile as valuable, stable and non-invasive biomarkers in distinguishing RCC from normal kidney.

Keywords: Renal cancer, carcinoma, biomarker, diagnosis, microRNA.
A Review of Cancer Immunotherapy

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Background: In the human body, millions of different cells of the body are made daily by various physical, chemical, biological and spontaneous factors (which can be the origin of malignancy). If the immune system does not have the ability to cope with these cells, it will increase the incidence of cancer. The use of conventional malignancies such as surgery, chemotherapy and radiotherapy can treat or control partly about half of the cancers. Cancer cells have the ability to escape the by using certain mechanisms, and they also use their peripheral biomolecules to supply the materials and signals they need to grow, therefore, immunotherapy will be very important in order to compensate for the immune deficiency in identifying and responding to cancer.

Key words: Immunotherapy, Cancer, Immune system
PC-92

Performance assessment of ARMS method for mutation analysis cancer in cds of cds1 gene

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Abstract

Background: One of important checkpoints of cell cycle control that activated upon genomics DNA injury was coded by cds1 gene. The regulation of these checkpoints changed in malignancies. In present study we evaluated mutation in coding sequence (cds) of cds1 gene by designing a molecular method in breast cancer samples.

Method: A total of 40 genomic DNA of whole blood (patients with cancer and control samples) with clinic-pathological characteristics were obtained from bio bank of IDRC center. The amplification refractory mutation system (ARMS) at annealing temperature 54°C was optimized for amplification of samples. Then data were statistically analyzed by special software.

Results: Electrophoresis results of used ARMS showed the validity of our bioinformatics designing and molecular experiments. This method can detect a mutant genotype in cds of cds1 gene. The results of detection mutant status were statistically significant (odd ratio: 3.9487, 95% CI: 1.9032-8.1925, z statistic: 3.688, p=0.0002).
Conclusion: Occurrences of mutations at the coding genes of cell cycle checkpoints have been validated in different diseases including breast cancer. Our technique was useful for detection of mutant status in the studied samples, and could be probably used in cancer diagnostic analysis, although more numbers of samples are proposed.

Key words: Breast cancer, cds, ARMS
Impact of HER2 status on chromosomal instability in breast cancer tumors
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Background: The chromosomal numerical abnormality is one of the most important factors in starting and becoming malignant of breast cancer. Chromosome abnormalities are due to molecular pathways and cell signaling as key parts of cell cycle regulation. HER2 signaling pathway change is one of the most common phenomena in breast cancer and it amplified in 20% of breast cancers. Determining the relationship of HER2 amplification to chromosomal instability can be helpful in evaluating prognosis and therapeutic strategies.

Methods: 40 tissue samples (FFPE) of patients with breast cancer (20 cases HER2 amplified and 20 cases not amplified) were used. HER2 amplification status was studied by IHC and was confirmed by CISH. Changes in a number of chromosomes 7, 8 and 17 were performed by CISH technique and centromeric probe and compared between the two groups. SPSS version 20 was used to analyze the data.

Results: Chromosome numerical abnormality frequency was 34% [p<0.001] and was higher in HER2+ than HER2- group. Among the three chromosomes examined, chromosome 17 showed more severe instability.

Conclusion: Our results showed that HER2 amplification resulted in chromosomal numerical abnormalities. Identifying pathways leading to chromosomal instability can lead to new therapeutic approaches.
Keywords: Chromosomal Instability, HER2, Breast cancer
Pro-Brain-Derived Neurotrophic Factor/ Brain-Derived Neurotrophic Factor as a New Index in Glioma Diagnosis; Systematic Review

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Background:

Glioma is one of the most invasive tumors of nervous system. The mortality rate is about 12-15 months. The precursor of Brain-Derived Neurotrophic Factor (proBDNF) and its receptor were reported to be high in glioma. BDNF is a member of neurotrophins family. It has a role in nervous system development and plasticity. The purpose of this study was to perform systematic review determine the diagnostic state of proBDNF/BDNF index in glioma.

Methods:

This systematic review was performed to identify studies that were published in Pubmed, ScienceDirect, Scopus databases and Google Scholar search engine, in 2000-2018 time interval by using 4 keywords (Glioma, Pro-BDNF, BDNF, and Diagnosis). Of the 117 articles initially identified, 62 were selected to distinguish the diagnostic role of proBDNF/BDNF index in glioma.

Results:
According to accumulative documents, the level of BDNF decreased in glioma patients which its mechanism is unknown. On the other hand, the levels of proBDNF and its receptor are upregulated in these patients. Studies have demonstrated the function of higher proBDNF levels is increment in differentiation and apoptosis and reduction in cell growth and migration. So, proBDNF would have a beneficial effect on the response of immune system.

Conclusion:
In attention to the alteration of proBDNF and BDNF levels in glioma patients, it is presumed that the proBDNF/BDNF index could be as a candidate for diagnosis and monitoring of glioma patients.

Key words: Glioma, Pro-BDNF, BDNF, and Diagnosis.
Crocetin, an important carotenoid extracted from the saffron, induces antiangiogenic and apoptotic activities in HCT-116 colorectal cancer cells

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Background: Colorectal cancer is the fourth and third most commonly diagnosed cancer in world and Iran, respectively. Crocetin, a glycosylated carotenoid, which has been shown to have anti-cancer properties. The aim of this study was to evaluate the antiangiogenic and apoptotic potential of crocetin on colorectal cancer cells.

Methods: In this study we analyzed VEGF (vascular endothelial growth factor) and caspase-3 mRNA expression in cells treated with various concentrations of crocetin. In order to investigate the anti-angiogenic and apoptotic effect of crocetin on HCT-116 cell line, RT-PCR was performed.
Results: Crocetin significantly decreased VEGF mRNA expression. Caspase-3 mRNA up-regulation at various concentrations of crocetin treatments were also significant.

Conclusion: Crocetin induces a VEGF-dependent antiangiogenesis and a caspase-3-dependent apoptosis in colon cancer cells. The study demonstrates the potential of crocetin for use in the treatment of colon cancers.

Keywords: antiangiogenic; apoptotic; vascular endothelial growth factor; caspase-3; HCT-116
Evaluation of the effect of fludarabine phosphate on the gene expression of inducible nitric oxide synthase in tumor tissue

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Background: Fludarabine is a fluorinated nucleotide antimetabolite analog of the antiviral agent vidarabine (ara-A) with antineoplastic activity. The aim of this study was evaluation of the effect of fludarabine phosphate on the gene expression of inducible nitric oxide synthase (iNOS) enzyme, a predictor of poor outcome in multiple cancers.

Methods: Breast tumor-bearing inbred mice were divided into two groups, one treatment group (n=5) and a placebo control group (n=5). The treatment group received 500 μg fludarabine phosphate two times at 7 days intervals. Two weeks later, mRNAs were extracted from tumor cells for gene expression analysis by Real-time RT-PCR.

Results: Fludarabine was able to suppress tumor cell growth in vitro. But, iNOS gene expression was not significantly altered in tumor tissues of mice in the treatment group compared to that in the control group in vivo.

Conclusion: This results show that fludarabine have no significant effect on gene expression of iNOS in breast tumor tissues in vivo.

Keywords: Fludarabine phosphate, Tumor tissue, iNOS.
PC-97

Cancer stem cell model of colorectal cancer cells associated with EMT markers

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Background

Epithelial-Mesenchymal Transition in colorectal cancer cell is a critical process which cells lost their epithelial properties and obtain mesenchymal characteristics resulting tumor cells and metastasis. In this study, we worked on cancer stem cell model of colorectal cancer cells associated with EMT markers and transcription factors.

Method

In this study, we used HT29 that is colorectal cancer cell line. Cells were treated for 48 hours with TGF-β in order to induce EMT in HT29. We used the Real-Time PCR for evaluating EMT markers and transcription factors. Flow cytometry applied to confirm whether HT29 turned into cancer stem cell line.

Results

Inducing TGF-β in colorectal cancer cells caused morphological changes. We showed that E-cadherin downregulates after induction of EMT with TGF-β. On the other hand, there were a significant increase in β-catenin, Vimentine and Snail
expression. CD133 and CD44 as surface markers showed a significant difference of these markers.

Conclusion

Understanding the molecular basis of tumor metastasis is critical for colorectal cancer treatment. Findings demonstrated morphological alterations in consequence of inducing EMT. This process affects EMT markers of E-cadherina, Vimentin, β-Catenin and Snail. This model wills helps knowing cancer and metastasis pathway and also could be use for drug screening procedures.

Key words: Cancer stem cells, colorectal cancer, Epithelial-Mesenchymal Transition
PC-99

Caffeic Acid Phenyl Ester, a potential sensitizer for cytotoxicity effects of NVP-BEZ235

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Background: The phosphoinositide 3-kinase/AKT (PI3K/AkT) pathway assumes a critical roll in the inception and advancement of human breast malignancies. Hyper activation of PI3K/AkT pathway lead to the uncontrolled development, movement and attack of breast malignant growth cells. The increased expression of TGF-β1 in human breast malignant growth tissue conceivably inspires tumor development, metastasis and protection from chemotherapy. We explored whether TGF-β1 expands breast disease cells protection from NVP-BEZ235 as well as caffeic acid phenyl ester (CAPE), a characteristic mixes, adds to improving remedial viability.

Methods: MCF-7 cells were exposed (for 14 days) to TGF-β1 and then were treated single or in combination of NVP-BEZ235 and/or CAPE. After that Cell viability, apoptosis and surface expression of CXCR4 were analyzed in all cultures by MTT, flowcytometry and Real time PCR.

Results: Constriction of PI3K/AkT pathway in blend with CAPE diminished apoptosis obstruction incited by means of TGF-β1 in bosom disease cells. Diminished CXCR4 articulation following NVP-BEZ235 presentation was described by flowcytometry measure, while Real time PCR affirmed that NVP-BEZ235 expanded the statement of CXCR4 in mRNA level.
Conclusions: Overall, our results suggest that combination of NVP-BEZ235 and CAPE decreased resistance induced by TGF-β1 and increase the therapeutic efficacy of breast cancer cells.

Keywords: Breast Cancer; NVP-BEZ235; TGF-β1; CXCR4.
PC-101

Evaluation of post-transcriptional modification in *TREB5* transcript in CRC samples

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Abstract

Background: Colorectal cancer is the third most common cancer after breast and lung cancer with incidence of 1.36 million people per year in the world. The genetic causes of this heterogeneous disease are the occurrence of changes in several genes and transcripts. Signaling transduction pathways responding stress is associated with cancers. In present study, we evaluated the post-transcriptional modification in *TREB5* transcript of stress pathway in CRC.

Method: A total number of 30 complementary DNA from tumor and non-tumor CRC tissue samples were used from our previous study. All samples had been collected during last 2 years. These samples have pathologic data details, which used as template in amplification tube with specific primers. The primers designed for amplification of spliced variant of *TREB5* transcript. The results of amplification reactions with P values of less than 0.05 were considered as statistically significant.
Results: The positive results of PCR indicated amplicons of *TREB5* transcripts that were spliced. Furthermore these data showed that total numbers of spliced variants in marginal tumors samples were 7.8 times more than tumor tissues samples (P<0.05).

Conclusion: Alteration of the gene expression in stress signaling pathways in cancer have been proven. Our results indicated that there is negative correlation between the splicing of the *TREB5* and CRC tumor status which can probably induced by stress pathway. However, it requires to gene expression analysis and examination of the number of samples from new surgical tissue.

Key word: CRC, TREB5, modification
PC-102

The quantification of the expression level of miR-126 in colorectal cancer cells

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Introduction

MicroRNAs (miRNAs) are the short noncoding RNAs molecules that have been occupied in the regulation of different cellular processes such as tumor angiogenesis, invasion, migration and regulation the expression of other genes post-transcriptionally. MiR-126 is a key regulatory human miRNA which contributes to colorectal cancer (CRC) and plays a pivotal role as a tumor suppressor through inhibition of vascular endothelial growth factor (VEGF) in CRC. In the current study, we evaluated the expression level of miR-126 in the panel of five CRC cell lines.

Material and Methods

The five human CRC cell lines (HCT116, HT29/219, SW742, Caco2, and LS180) were obtained from the National Cell Bank of Iran (NCBI, Pasteur Institute, Tehran). Cells were grown and cultured in RPMI 1640 supplemented with 10% FBS, 2 mM Gln, 100 U/ml penicillin, and 100 μg/ml streptomycin in a humidified 5% CO2 at 37 °C. Total RNA was extracted from CRC cells and the expression levels of miR-126 were analyzed using stem-loop quantitative real-time-PCR technique.

Result

Our results indicated that LS180 cells expressed the lowest levels of miR-126. Therefore, LS180 cells were used as a reference and set to 1.0. MiR-126 expression in all other cell lines were expressed as an n-fold difference relative to
the reference. The average level of miR-126 transcript in well-differentiated Caco2 cell line was significantly higher than those in other cell lines (p < 0.05). Quantitation of miR-126 showed that Caco2, SW742, HCT116, and HT29/219 cells, respectively, expressed 40, 34.8, 8.7 and 5.1 times more than that of LS180 cells.

Conclusion

Our results showed that miR-126 expressed in CRC cell lines in a cell-type specific manner. The association between miR-126 expression and clinicopathological features of CRC cell lines will be analyzed and used as a potential biomarker for tumors classification.

Keywords: MiR-126, gene expression, cell culture, colorectal cancer
Family relationship of mir-34 with the expression of gene and protein p53 in colorectal cancer

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Background: Multiple miRNAs, including the miR-34 family, are transcriptionally activated by p53. The CRC begins with an abnormal growth of the cells lining the colon and rectum leading to the formation of a non-cancerous growth or benign tumor known as a polyp. Ectopic expression of miR-34a leads to cell cycle arrest, apoptosis or senescence, mimicking p53 activation. Non-coding RNAs, most especially miRNAs, are attracting considerable interest, with increasing evidences on the role of miRNAs’ expression in CRC development and progression. This has led to the use of miRNAs as therapeutic targets.

Methods: To identify all relevant literature, we searched PubMed, NCBI for CRC, miRNA, expression profiling studies published between 2002 and 2017. Only miRNA expression profiling studies using tissue samples obtained from surgically resected colorectal cancerous tumors and corresponding noncancerous colorectal tissues were considered.

Each of published miRNA expression profiling studies\textsuperscript{14-20} comparing miRNA expression between the CRC and neighboring noncancerous colorectal tissues resulted in a list of differentially expressed miRNAs.

Result: Regular screening for CRC is essential and should be done to detect tumor early before it metastasizes. Recently, the involvement of 18–22 nucleotide to the foreknown miRNA, and its relation to dietary factors and tumorigenesis. Collectively, bioactive components from the diet modulate several miRNAs which are involved in cancer development and growth via several mechanisms. The link between miR-34, inflammation, and cancer is of particular importance considering that recent evidence has suggested a significant role of the loss of miR-34 in cancer.
Conclusion: With current evidence showing a large set of oncogenic mRNAs being targeted by miR-34, therapeutics involving replenishment of miR-34 has evolved into clinical trials following early discoveries of its role as tumor suppressor. This new and innovative therapeutic shows a promising future path towards becoming one of the effective therapies against cancer.

Keywords: P53, CRC, miRNA
PC-104

The status of VEGF gene expression in the colorectal cancer cells

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Introduction

Vascular endothelial growth factor (VEGF) is a potent angiogenic factor serves as an oncogenic gene in tumor invasion and angiogenesis. Moreover, it has been suggested that VEGF plays an important role in progression of colorectal cancer (CRC), and has a well-defined role in the formation of new blood vessels and expressed in approximately 50% of colorectal cancers. In the present study, we examined the expression level of VEGF in the panel of five CRC cell lines.

Material and Methods

In the current study, the five human CRC cell lines (HCT116, HT29/219, SW742, Caco2, and LS180) were obtained from the National Cell Bank of Iran (NCBI, Pasteur Institute, Tehran). Colorectal cancer cells were grown and cultured in RPMI 1640 supplemented with 10% fetal bovine serum, 2 mM Gln, 100 U/ml penicillin, and 100 μg/ml streptomycin at 37 °C in a humidified 5% CO2 atmosphere. Total RNA was extracted from CRC cells and the expression levels of VEGF were analyzed by quantitative real-time-PCR assay. GAPDH was used as an internal control gene and the relative expression levels of VEGF were determined using the 2-ΔΔCT standard method.

Result

Our results showed that SW742 cells expressed the lowest levels of VEGF. Therefore, SW742 cells were used as a reference and set to 1.0 and VEGF expression in all other cell lines were expressed as an n-fold difference relative to the reference. Quantitation of VEGF indicated that HCT116, LS180, Caco2, and
HT29/219 cells, respectively, expressed 27, 17.1, 11.85 and 5.3 times more than that of SW742 cells. Moreover, our results indicated that HCT116 significantly expressed VEGF transcript level in comparison to all other cell lines (P<0.05).

Conclusion

Our results indicated that VEGF expressed in CRC cell lines in a cell-type specific manner. However, the five CRC cells evaluated in this study varied in genetic heterogeneity. The association between VEGF expression and clinicopathological features of CRC cell lines will be analyzed and used as a potential biomarker for tumors classification. This study might provide significant insight regarding the role of VEGF gene expression in CRC development.

Keywords: VEGF, gene expression, colorectal cancer, cell culture
Investigation of different fractions of Juniperus excelsa on pre-B acute lymphoblastic leukemia cell line (Nalm-6)

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Introduction

ALL is one of the most common hematological malignancies in childhood. ALL typically affects children younger than 6 years but is also encountered in older children and in adult populations. The diagnosis is established by immunophenotyping, commonly by flow cytometry (FC). Chemotherapy agents have many side effects, such as diarrhea, nausea, vomiting, that these side effects are dose-dependent. Today, the use of traditional medicine drugs due to less toxicity and side effects for patients, has been considered. Juniperus excelsa is known as a medicinal herb which has been traditionally used to treat some problems. Previously, the apoptotic effect of this plant has been reported on various tumor cell lines. In this study, the effective fraction of the extract of this plant has been investigated on pre-B acute lymphoblastic leukemia cell line (Nalm-6).

Material and methods

The cytotoxic activity of different fractions of J. excelsa in Nalm-6 cell line was evaluated by Trypan blue and MTT assay. Apoptosis was assessed by caspase 3 activity assay and flow cytometry. The expression levels of some apoptosis-related genes, caspase 3, BAX, Bcl-2 were determined by Real-time PCR. Data were analyzed with one-way ANOVA.
Results

Different tests on J. excelsa showed that the lethal dose of chloroform fraction from Trypan blue and MTT assay was 2.5 μg / ml (IC$_{50}$ 2.5μg/ml). Apoptosis in the above dose were confirmed with AnnexinV-PI method by flow cytometry. Expression of CASP3 and BAX genes were significantly upregulated to compare with control group, while Bcl-2 gene was downregulated in Nalm-6 cell line (p<0.05).

Conclusion

Previous studies have shown that the apoptotic effects of some medicinal plants on various cancers are very important. Because of its naturalness and lower side effects, more studies are needed in the future to confirm its use as anticancer drugs.
Altered expression of MALATI IncRNA in chronic lymphocytic leukemia patients, correlation with cytogenetic findings

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Apoptosis Induction of Armeniacae Semen Extract in Human Acute Leukemia (NALM-6 and KG-1) Cells
PC-107

Apoptosis Induction of Armeniacae Semen Extract in Human Acute Leukemia (NALM-6 and KG-1) Cells

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Abstract:

Background: Prunus armeniaca is a member of the Rosaceae family. The most important ingredient of this family is amygdalin that is believed to have anti-tumor and analgesic properties. The aim of this study was to evaluate the anti-proliferative effects of Armeniacae semen extract on the acute leukemia, Nalm-6, and KG-1 cell lines, and investigate the effect of the extract on apoptosis of these cell lines and caspase-3 gene expression.

Methods: We prepared aqueous, ethyl acetate, and hydro alcoholic extracts of the Armeniacae semen. The Nalm-6 and KG-1 cell lines and mono nuclear cells were treated with different doses of the extracts for 48 hours; then, cell viability was investigated with the 3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide test. High Performance Liquid Chromatography was done for amygdalin identification. The percentage of apoptotic cells was determined using the
Annexin V-FITC/PI flow cytometric kit and caspase-3 gene expression was evaluated.

Results: 3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide test revealed that the strongest Inhibition Concentration (IC50) in KG-1 and Nalm-6 cell lines was related to the ethyl acetate extract. This extract did not have toxic effects on mono nuclear cells. Flow cytometric analysis showed that the ethyl acetate extract at its IC50 concentration led to almost 50% apoptosis in both cell lines after 48 hours. On molecular examination, a significant (P value: 0.0001) increase was seen in caspase-3 gene expression to the control.

Conclusion: Our data confirmed that the ethyl acetate extract of apricot kernels could reduce the proliferation of KG-1 and Nalm-6 cell lines probably by activating the apoptotic pathway.

Keywords: Armeniacae semen; Acute leukemia; KG-1; Nalm-6; caspase-3.
PC-109

Gamma-H2AX as a predictive molecular biomarker of tumor cell radiosensitivity comparing to colonogenic assay


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Background:
Colonogenic assay and surviving cell fraction following irradiation with 2 Gy (SF2) as a gold standard for identifying cellular radio-sensitivity, can be used to predict tumor response to radiotherapy. Despite the importance of so-called technique, it showed a serious limitation of long incubation time about two weeks. Considering this disadvantage, it might be a great need for using new rapid novel radio-sensitivity predictive assay. To address this issue, we investigated very sensitive biomarker of DNA double-strand breaks (DSBs) formation termed gamma-H2AX (γ-H2AX) as the phosphorylation of serine 139 of H2AX, known as an early molecular endpoint. Although there was no certain correlation between primary DSBs and cellular radiosensitivity, it was clear that unrepaired DSBs as the most destructive type of molecular damage resulted to cell death. So we compared colonogenic assay and H2AX foci formation in two different human tumoral cell lines; Hela and HN5 (Head and neck squamous cell carcinoma).

Methods:
To fulfill the aim of colonogenic assay post irradiation, defined numbers of two cell lines were seeded on 6-well plates in triplicate. After incubation for about 10 days up to two weeks based on doubling time of cell lines, the cells were fixed and stained with crystal violet and colonies of at least 50 cells were counted. The surviving fractions at 2Gy were Plating efficiencies of 2 Gy normalized to the corresponding unirradiated controls, yielding SF2. Gamma-H2AX assay performed 1hour post radiation and in brief included cell preparation and fixation with FA4%, PBS washing, premeabilization with triton x-
100, blocking using BSA1%, gamma H2AX antibody incubation for 2-hour in wet chamber, BSA1% washing, anti-mouse IgG FITC secondary antibody incubation for 45 min, final washing and Dapi staining. Foci were visualized by fluorescent microscopy, counted by eye qualitatively and mean foci per cell (FPC) was reported.

Conclusion:
Our observations indicated a significant difference between mean FPC of Hela and HN5 after 2 Gy comparing to control groups, which was in agreement with the results of colonogenic assay with statistically significant decrease in mean colony of cells after radiation (P< 0.05). Considering gamma-H2AX assay, Hela showed higher level of mean FPC in irradiated and unirradiated groups emphasizing on the more radiosensitivity of Hela. So the present study confirmed that the tumor cell radiosensitivity can be predicted by manifestation of gamma-H2AX foci after irradiation as an early sensitive marker and appropriate tool to anticipate radiation response in radiotherapy.

Keywords:
Radio-sensitivity, Colonogenic assay, Gamma-H2AX assay
Gene Expression Evaluation of in vitro Bystander cells in Spatially fractionated technique of Grid radiation therapy


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Background:
Based on the challenge of bulky tumors treatment considering the normal tissue tolerance, spatially fractionated grid radiation therapy (SFGRT) as a hypo-fraction technique could be an effective treatment of bulky malignant tumors. Many studies mentioned radiation-induced bystander effect (RIBE) as a radiobiological response of so-called technique. RIBE associated with the induction of radiation effects in non-irradiated cells via signaling of hit ones. DNA double-strand break (DSB) as a highly toxic lesion resulting to cell death plays a crucial role in bystander signaling. So in the present study, we evaluated expression change of non-homologous endjoining (NHEJ) and bystander genes in grid bystander regions.

Methods:
Based on the purpose of this study, RIBE was evaluated via specific protocols of media transfer and cell to cell contact following grid therapy. Two different human cell lines including Hela and HN5 (Head and neck squamous cell carcinoma) were irradiated by single radiation fraction of 10 Gy with available grid block attached to the linac head at Imam Khomeini hospital. Irradiation with Grid pattern of 145
circular fields, 13mm in diameter with 17mm center to center distance created the cell to cell contact of directly irradiated and bystander cells. Regarding media transfer strategy, bystander cells were irradiated by 1.5Gy receiving the conditioned medium of hit cells based on dosimetric data of Gafchromic EBT3 as well as TLD. To fulfill the aim of cell-cell contact, cells under hole (irradiated) and block part of grid (bystander) were scraped separately. Cells were harvested at 4 h after grid irradiation and were then centrifuged at 1200 rpm for 10 min. So the expression of DNA damage response genes: H2AFX and XRCC6 as NHEJ and bystander genes versus GAPDH as an internal control, has been analyzed in bystander and irradiated cells via q-PCR protocol including total RNA extraction, overnight incubation, reverse transcription with random hexamer primers and real time pcr. If a gene exhibited a fold-change greater than 1.5, it was considered as showing an “effect”. **Conclusion:**

In brief, a fold-change expression of DNA repair genes in both cell lines showed increase in grid adjacent as well as directly irradiated cells. H2AFX as a bystander mediated gene illustrated high expression in bystander cells which confirmed RIBE in grid therapy. Overall based on this study, the expression change of grid-induced bystander genes provided molecular evidence for possible mechanisms of high dose bystander damage signaling. **Keywords:**

Grid therapy, Bystander effect, DSB.
PC-111

Cold Atmospheric Plasma (CAP), as an alternative treatment to chemotherapy, Induce selective apoptotic cell death in B16 melanoma cells

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Background: Cancer treatment, especially malignant melanoma, has the highest levels of therapeutic resistance. Cold atmospheric plasma (CAP) therapy is a low-grade, fast-acting, lack of any side-effects to healthy cells, no impairment of immunity and post-treatment infections. In this study, we investigated invitro the effectiveness of CAP rather than Dacarbazine and combination therapy for the apoptosis of B16 melanoma cells.

Methods: initially, cytotoxic effects were evaluated in groups treated with CAP, Dacarbazine and combined therapy on B16 and L929 cells (as healthy control) by MTT assay. In order to showing percentage of apoptotic cells in the treated groups, flow cytometry analysis was performed by Annexin/PI staining and Then the expression of pro-anti apoptotic genes was measured by Real-time PCR.
Results: Using the MTT assay, our results revealed that the death rate in CAP-treated B16 cells was increased significantly compared to the Dacarbazine group and the combination therapy, also cell death in CAP-treated L929 cells was very low, while in the others, were observed a high cell death rate. Also, by flow cytometry analysis, we showed that the percentage of apoptotic tumor cells in the CAP group was significantly higher than other groups. Then, by examining the expression of pro-apoptotic and anti-apoptotic proteins (Bax/Bcl-2 and Caspase-3) in B16 cells, we showed that CAP significantly increased the expression of these proteins, but in CAP-treated L929 cells, there was no significant difference in compared to the control group.

Conclusion: This study indicated that the treatment of melanoma cells with Dacarbazine, either alone or in combination with CAP, induced a high death rate of cancerous and healthy cells, while the CAP selectively destroys only cancer cells. Therefore, it would be hoped that the CAP could be used as a therapeutic alternative to chemotherapy at the clinic.

Keywords: B16 cell line (melanoma), Dacarbazine, Cold Atmospheric Plasma (CAP), apoptosis, Flow cytometry, Real-time PCR.
PC-112

Combined effects of saffron and vitamin C on fetal amniocytes irradiated at G2 phase of the cell cycle.

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Purpose: Radiosensitivity of cells at different fetal stages is a known phenomenon. However, attempts were made to reduce clastogenic effects of ionizing radiation by means of chemical natural or synthetic radioprotectors. The aim of this study was to study the effects of herbal antioxidant saffron and naturally occurring antioxidant vitamin C on radiation induced chromatid type aberrations induced in amniocytes at G2 phase of the cell cycle.

Materials and Methods: Amnioctes were separated from amniotic fluid by centrifugation and cultured in amniogrow culture medium. Cells were maintained in a CO2 incubator, and grown with the use of trypsin –EDTA for preparing different cultures for treatments. DPPH assay was done to find appropriate dose of saffron and vitamin C with appropriate antioxidant properties. Cells were treated with vitamin C and saffron 2 hour prior to irradiation. Irradiation was done with a 6-MV linear accelerator at a dose of 2 Gy with a dose rate of 1 Gy/min. Following irradiation cells were incubated at 37 degree centigrade for 4 hours. 1 hour before harvesting cells was exposed to colcemid to inhibit cells at mitosis. After harvesting and slide preparation, cells were stained in Giemsa. Fifty – 100 well spread mitoses were scored for chromatid type aberrations under a light microscope with X1000 magnification.

Results: Results showed induction of considerably high frequency of chromatid breaks in amniocytes following radiation alone (in average 3 breaks/ cell). Saffron
and vitamin C alone induced a low level breaks compared to normal control by themselves. However, when either saffron or vitamin C was combined with radiation, the frequency of chromatid breaks in all samples increased significantly in a synergistic manner (P<0.01). Combined use of vitamin C and saffron did not reduce the frequency of radiation induced chromosomal aberrations.

**Conclusion:** The results imply that although both saffron and vitamin C are known and potent antioxidants, but in combination with radiation potentiate radiation effects and acts as a radiosentiziser. Therefore they are not acting as radioprotective agents at least for fetal cells.

**Keywords:** Amniocytes, G2 assay, chromatid breaks, Saffron, vitamin C, radiosensitization
Down-regulation of long non-coding RNA LY86-Antisense1 in type2 diabetic patients

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Background: Long non-coding RNAs (lncRNAs) are newly discovered non-coding RNAs. The potential roles of lncRNAs in the pathogenesis of type 2 diabetes mellitus (T2DM) are not well-known. In this study, we assessed the LY86-Antisense1 expression level in T2DM patients and control group.

Methods: In this case-control study, we acquired whole blood and serum samples from 100 diabetic and 100 non-diabetic individuals. Using Ficoll-density-gradient centrifugation, Peripheral blood mononuclear cells (PBMCs) were extracted from whole blood. Also, by using TRIzol LS reagent (GeneAll), we isolated total RNAs from the PBMC lysates of diabetic and non-diabetic subjects. Complementary DNA (cDNA) was synthesized with a Reverse Transcription Kit (Takara). Finally, for detecting our lncRNA expression level, quantitative real-time PCR (qPCR) was performed using the Rotor-Gene system (Qiagen).
Results: In this study, we found that LY86-Antisense1 expression level was significantly down-regulated in diabetic patients compared to non-diabetic participants. The REST results revealed that the expression level of GAPDH was 1.000, while it was 0.042 for LY86-Antisense1. Furthermore, in this study, the significant inverse correlation was observed between the expression of LY86-Antisense1 and FBS levels. Logistic regression test results demonstrated that for each unit increase of Δct LY86-Antisense1, the chances of T2DM raised by 19.6%. Receiver operating characteristic (ROC) curve analysis showed that LY86-Antisense1 with an area under the ROC curve (AUC) > 0.7 and P-value < 0.0001 could be considered as a potential novel diagnostic biomarker for type 2 Diabetes Mellitus patients.

Conclusion: Lowered expression of LY86-Antisense1 in diabetic patients and inverse correlation of this lncRNAs expression with FBS levels could possibly be associated with the pathogenesis of T2DM in Iranian population. Furthermore, based on ROC curve results, LY86-Antisense1 could be probably considered as a novel biomarker for diagnostic purposes.

Keywords: Long non-coding RNA, LncRNA, LY86-Antisense1, rs9502478, Type 2 Diabetes Mellitus
PBG-2

Impact of ATM and SLC22A1 Polymorphisms on Therapeutic Response to Metformin in Iranian Diabetic Patients

Metabolic syndrome and its pathological sequel, type 2 diabetes are considered as important global health problems. Metformin is the most common drug prescribed for patients with this disorder. Consequently, understanding the genetic pathways involved in pharmacokinetics and pharmacodynamics of this drug can have a considerable effect on the personalized treatment of type 2 diabetes. In this study, we evaluated the association between rs11212617 polymorphism of $ATM$ gene and rs628031 of $SLC22A1$ gene with response to treatment in newly diagnosed type 2 diabetes patients. We genotyped rs11212617 and rs628031 polymorphism by PCR based restriction fragment length polymorphism (RFLP) and assessed the role of this polymorphisms on response to treatment in 140 patients who have been recently diagnosed with type 2 diabetes and were under monotherapy with metformin for 6 months. Response to metformin was defined by HbA1c and fasting blood sugar (FBS) values. Based on such evaluations, patients were divided into two groups: responders (n= 63) and non-responders (n= 77). No significant association was found between these polymorphisms and response to treatment (OR= 0.86, [95% CI 0.52–1.41], P= 0.32) for rs11212617 and (OR= 0.45, [95% CI 0.64–1.76], P= 0.45) for rs 628031. The reported gene variants in $ATM$ and $SLC22A1$ are not significantly associated with metformin treatment response in type 2 diabetic patients in an Iranian population.

Key words: Metformin, type 2 diabetes, pharmacogenetic
Aminoguanidine induced Down-Regulation of Sphingosine-1 Phosphate Receptor-1 (S1PR1) in heart tissue of Diabetic Rat

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Background: Diabetes Mellitus is a metabolic disorder. Activation of Sphingosine -1 phosphate receptor -1 (S1PR1) triggers the intracellular signaling cascade, eventually leading to cellular responses such as angiogenesis and cellular survival. S1PR1’s dysfunction in diabetes is an important sign for cardiac microvessel complications. Aminoguanidine (AG) is an inhibitor of advanced glycation compounds and has an antioxidant effect. In this study, the expression levels of S1PR1 at mRNA level in the heart tissue of diabetic rats treated with AG, were assessed to determine its therapeutic value on diabetic animals.

Methods: The number of 34 rats in 8 different groups were prepared. After total RNA extraction from heart tissue, and cDNA preparation, the expression of S1PR1 and GAPDH genes were determined by quantitative Real-Time PCR. Finally, the fold change of S1PR1 expression was compared between diabetic mice treated with different doses of AG and the control groups using Pfaffl formula and Mann-Whitney non-parametric statistical analysis.

Results: Analysis of S1PR1 gene expression in diabetic mice without treatment showed a significant decrease compared with the control group. after AG
treatment, S1PR1 gene expression was increased in a dose-dependent manner compared with either untreated diabetic mice or the healthy control group which had already been treated by the same amounts of the drug (p<0.001, p=0.07, respectively). The expression of S1PR1 was significantly upregulated in diabetic rats treated by 200mg/kg of the drug vs. the other groups (P<0.001).

**Conclusion:** The expression of S1PR1 gene is decreased in diabetic rats compared to the normal ones. It seems AG has a positive influence on the expression level of S1PR1 in diabetic rats but not in normal ones. Therefore, the usage of AG may be beneficial for the prevention of the cardiovascular complications associated with diabetes.

**Keywords:** S1PR1, Aminoguanidine, Diabetes, Gene expression
Studies of the Association of Arg72Pro Polymorphism of P53 Gene with Type 2 Diabet

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Background: TP53 is an important tumor suppressor genes that plays a determinant role in maintenance of genetic stability as an transcription factor. The witnesses show that gene TP53 is inactivated in most cancers and diabetes type II diseases.

Methods: Diabetes is one of the common adult diseases in the world, according to estimates it is predicted that until future ten years this disease will be increased 122% and the number of patients will reach to 300 millions in 2025 from 135 millions in 1995. Type 2 diabetes is the result of interaction between environmental factors a strong hereditary component. We examine the effect of polymorphism TP53 gene in diabetes to in this research. This study was done on codon 72 polymorphism located in exon 4 of the TP53 gene.

Results: This research was done on 100 participants, for doing so, the blood sample in 59 patients with diabetes type II and 47 none diabetic (controls group) individuals and then DNA was extracted by K proteinase and using two pairs exclusive primers, PCR reaction was on DNA in two phases. The second PCR product was enzymatic digestion by using BsU1 enzyme, then agarose gel electrophoresis RFLP pieces and comparison with DNA marker the length of the pieces were determined.

Conclusion: In control group, genotype frequency Arg/ Arg=14% Pro/Pro=35% and Arg/ Pro=51% was obtained and genotype distribution in diabetes group was Arg/ Arg=0.05%, Pro/Pro=21% and Arg/ Pro=74% (p<0.05). As a result polymorphism Arg/ Pro codon 72 of exon 4 in TP53 gene has no effect in diabetes type II.
Keywords: Diabetes Type II, Gene TP53, Arg 72, Pro Polymorphism
Investigation of the relationship between G / C polymorphism of cyclooxygenase-2 gene and lung cancer in Ardabil population

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Abstract

Background:
There are two types of cyclooxygenase 1 and 2 enzymes in the human body, the activity of which produces prostaglandins. Prostaglandins play a role in a variety of activities, including the immune system, venous diameter regulation, cell division and angiogenesis. The report is based on increased expression of enzymes in the onset, expansion and metastasis such as laryngeal, gastric and colon cancers. The aim of this study was to investigate the role of the Gc-765 polymorphism in the lung cancer cyclooxygenase 2 promoter and its control group in the Ardabil population.

Materials and methods:
In this case-control study, 120 patients and 110 healthy people were evaluated by PCR-RFLP. Chi-square tests were used to compare the expected population of the...
observed genotypes with the Hardy Weinberg equilibrium. Differences between genotypes and alleles in the groups were tested using odds ratio (OR) analysis.

**Results:** The GC genotype of the patient polymorphism -765GC (62.5%) did not increase significantly (45.55%) compared to the control group (P > 0.6). There was a weak association between GG genotype and G / C polymorphism and metastasis when patients were divided into metastatic and non-metastatic groups (P < 0.04).

**Conclusion:** It appears that the cyclooxygenase 2 gene-765G / C polymorphism is not associated with the pathogenesis of lung cancer, but a weak link between polymorphism and metastatic activity is observed.

**Keywords:** Cyclooxygenase 2, PCR-RFLP, Determination of genotype, lung cancer
Evaluating the expression of XRCC5 gene and miR-223 in peripheral blood of diabetic patients

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Background: Diabetes mellitus is a chronic metabolic syndrome. T2DM is more common than T1DM, comprising 85–90% of total DM cases. Diabetes patients often show increased production of reactive oxidative species (ROS). Increased ROS cause chromosomal instability and reduce the binding affinity of KU proteins (encoded by the XRCC5 /6 genes), which are the proteins involved in the pathway for Non-homologous end joining. The expression of miR-223 (one of the target genes is XRCC5 gene), also changes due to stress. This study has investigated the expression of this gene and miR in diabetic patients and healthy people.

Methods: Peripheral blood samples were collected from 30 patients with type 2 diabetes and 30 healthy women, and kept in tubes containing EDTA anticoagulant. EDTA blood was used to extract total RNA and cDNA was made for examination of gene expression XRCC5 and miR-223 by RT-PCR technique using primers designed. Primer pairs specific for each gene were designed using primer3. Data from real-time PCR were analyzed using the ΔΔCt method. Statistical analysis was carried out using the SPSS statistical software. One-way analysis of variance (ANOVA) was performed to evaluate differences between gene and microRNA expression. A difference at a level of P < 0.05 was considered statistically significant. For miRNA, a receiver operating characteristic (ROC) curve was generated.
**Results:** Our results showed that the expression level of XRCC5 and miR-223 was significantly decreased in T2D patients compared to control group (P<0.05). The ROC curve showed that the level of miR-223 in plasma can be distinguished among diabetic patients with controls [AUC = 0.891].

**Conclusions:** These results might imply that the effect of increased ROS on reducing the expression of XRCC5 gene and microRNA-223. MicroRNA-223 can be as a candidate novel diagnostic biomarker in Diabetic patient.

**Keywords:** Type 2 diabetes; metabolic syndrome; microRNA;
Assessment of genomic instability in peripheral blood lymphocytes of diabetic patients by G2 chromosomal assay

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Background: Type 2 diabetes is the most common metabolic disorder worldwide including 90 to 95 percent of diabetic patients. Hyperglycemia is a sign of diabetes, causes glucose oxidation which is increased in several ways and produces free radicals (ROS). The presence of these ROS may lead to increased DNA damage and chromosomal instability in peripheral blood lymphocytes that may be revealed by the G2 assay.

Methods: To test genome instability in diabetic patients, peripheral blood samples were collected from 20 patients with type 2 diabetes and 20 healthy women, and kept in tubes containing heparin anticoagulant agent. Lymphocyte cultures were initiated using heparinized blood in RPMI-1640 culture medium supplemented with antibiotics, FBS and PHA was used as a mitogenic initiator of mitosis in resting T-lymphocytes. Bleomycin sulfate at a dose of 10 microgram/ml was used to induce DNA damage in G2 lymphocytes. After harvesting, slide preparation and staining of metaphase spreads, 50 well spread mitoses were analyzed for each sample. Frequency of chromatid type aberrations
were scored. Statistical analysis was done with SPSS software and P-value <0.05 was considered as significant level when two groups were compared.

**Results:** The results of the studies and statistical studies show that there is a significant difference (P <0.001) between induced chromatid instability and intrinsic chromatid instability in women with type 2 diabetes. The results and analysis of the data show that the intrinsic chromatid instability was significantly (P <0.001) higher in women with diabetes than control women. Also, induced chromatid instability in women with diabetes was significantly (P <0.001) more than control women.

**Conclusions:** These results may indicate the effect of increased ROS on chromatid instability in diabetic patients. Such changes might contribute to accelerated aging and atherogenesis in diabetes and to the microangiopathic complications of the disease.

**Keywords:** Type 2 diabetes; metabolic syndrome; genomic instability, G2 assay
PBG-11

**Relationship of rs6265 polymorphism of BDNF gene in susceptibility to tinnitus in men with this disease compared with control group**

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**Introduction:** Tinnitus is a sound sensation without external stimulation and is considered as an imaginary hearing perception. According to studies on twins, it has been somewhat determined, the genetic relationship and tinnitus .The frequency of polymorphisms is one of the factors that can be part of the answer for the cause of this disorder. Meanwhile, the brain-derived neurogenic factor (BDNF) is likely to be more important because of its effects on the auditory maturity process.

**Materials and Methods:** In this case-control study, after extraction of DNA from tinnitus men referring to Farrokhi hospital in Yazd, rs6265 polymorphism genotypes were determined by PCR-RLFP method and loaded on 2% agarose. Data were analyzed by SPSS software using t-test and chi square.

**Results:** After analyzing the results of enzyme digestion, genotypic percentages of AA, AG, GG in tinnitus patients were 6.7, 40, 53.3, respectively. In the control group, genotypic percentages were 3.5, 35.1, 61.4, respectively. After statistical analysis, there was no significant relationship between the patient group and the control group (p = 0.682).

**Conclusion:** The results show that rs6265 polymorphism is not associated with tinnitus susceptibility in the population under study. A study with more sample sizes is recommended in different populations

**Keywords:** tinnitus, syndrome, auditory, polymorphism
Investigation the effect of high body mass index on relative leukocyte telomere length in Iranian subjects

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Morbid obesity can accelerate normal aging. Leukocyte Telomere Length (LTL) is a biomarker of aging which shows high variability in different ethnicities and has an association with body mass index. In this matched-pairs study, we examined LTL of 53 morbidly obese subjects (18-65 years old, 85% women). Individuals with BMI>40 kg/m², who were candidate for bariatric surgery, and had a sibling from the same sex with age difference about ±5 years, were selected before surgery. By selecting siblings as controls, most important factors affecting LTL (age, genetic background, ethnicity, and sex) were highly adjusted for cases
and controls. All siblings (17-61 years old) were nonsmokers and clinically examined to have no sign of chronic infections, cancers, or cardiovascular diseases. LTL was measured by qPCR, based on relative standard curve method, using a mixture of 5 genomic DNA with different chronological ages as reference DNA, and K562 as quality control. Ratio of telomere to single copy gene (albumin) quantity was calculated and normalized by K562 for each sample. Data analysis showed that LTL was negatively correlated with age in both cases (p-value= 0.048) and controls (p value= 0.023). We compared LTL between 53 cases and 53 completely matched non-obese siblings by Generalized Estimating Equation method. Results showed that obese subjects have significantly shorter LTL than non-obese individuals (β = -0.6, P value = <0.001). According to well matching criteria between obese and non-obese subjects, these results strongly suggest that high body mass index can cause shorter telomeres, and increase the incidence of age related disorders.

Keywords: Telomeres, RTL, BMI, Obesity
Genomic instability in the G2 lymphocytes in peripheral blood of poly cystic ovarian syndrome patients

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Abstract

Objective: Polycystic ovary syndrome (PCOS) is the most common endocrine disorder of women in reproductive age and one of the main reasons of infertility, affecting 7 to 10 percent of women in fertile age. PCOS is a complex and heterogeneous disorder, so genetic and environmental factor are involved in the formation and incidence of this disease. In this study we aim to study genomic instability in patients with PCOS by G2 assay.

Materials/methods: G2 assay was performed on peripheral blood lymphocytes obtained by venipuncture from 20 PCOS patients and 20 normal control in tubes contain lithium heparin as anticoagulant. Blood culture was initiated and cells were treated with 10ng/ml bleomycin 5 h prior to harvesting. Colcemid was added and cells were harvested 1 hours after addition of colcemid. After metaphase preparations, slide making and staining in Giemsa, chromatid breaks such as deletions, gaps and translocations were scored in 50 metaphase spreads.

Results: The results of the studies and statistical studies show that there is a significant difference (P <0.001) between induced chromatid instability and intrinsic chromatid instability in the normal women group. There is also a significant difference (P <0.001) between induced chromatid instability and intrinsic chromatid instability in women with polycystic ovary syndrome. The results and analysis of the data show that the intrinsic chromatid instability was significantly (P <0.001) higher in women with PCOS than control women. Also, induced chromatid instability in women with PCOS was significantly (P <0.001) more than control women.
Conclusions: From this present work it can be concluded that chromatid breaks analysis in metaphase spreads with G2 assay can be effective biomarker for PCOS, along with increased chromatid breaks in lymphocytes as a sign of genomic instability. There is a hypothesis that chromosomal aberrations could have a predictive value for cancer. From this present work it can be concluded to some technique like G2 assay can be effective for diagnosis.

Keywords
PCOS; genomic instability; G2 assay; chromatid breaks
Evaluating the expression level of IRS-1 gene and MicroRNA-223 in peripheral blood of polycystic ovarian syndrome patients

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Abstract

Objective: Polycystic ovary syndrome (PCOS) is the most common endocrine disorder of women in reproductive age and one of the main reasons of infertility, affecting 7 to 10 percent of women in fertile age. PCOS is a complex and heterogeneous disorder, so genetic and environmental factor are involved in the formation and incidence of this disease. In this study we aim to investigate the expression level of gene (IRS-1) and also microRNAs (miR-223) in our target groups.

Materials/methods: Blood samples from 30 normal individuals and 30 PCOS patients were obtained by venipuncture and transferred to tube containing anticoagulant EDTA. Specific primers for IRS-1 gene and miR-223 were designed and used for measuring relative expression of IRS-1 and miR-223 by quantitative real-time RT-PCR. Efficiency of each primer was determined by the use of LinRegPCR Software.

Results: Data obtained from the real-time PCR for human IRS-1 and mir-223 were normalized respectively versus GAPDH and U6 as an inner gene control. A decreased level of IRS-1 mRNA was detected in the patient group (P<0.05). miR-223 expression was increased in patients compared than control (P<0.05).

Conclusions: PCOS is a heterogeneous group of disorders. Future studies need to characterize the endocrine and metabolic profile of the various subgroups. IRS-1 lower expressing and miR-223 overexpressing agents seem to be an effective diagnostic tool for a subset of patients, but not for all women with this syndrome.
Results of this study may be useful in the diagnosis-treatment management of the patients affected with PCOS. ROC graph shows the expression of miR-223 may be relatively well used to distinguish people with PCOS.

Keywords:
PCOS; IRS-1; miR-223; endocrine disorder; gene expression
PBG-16

Association of synergism between paraoxonase Arg 192 and the angiotensin converting enzyme D allele with severity of coronary artery disease

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Background: The concomitant presence of the ACE gene D allele and paraoxonase (PON1) codon 192 arginine (Arg) on the severity of CAD is less known. Regarding the high rate of CAD among Iranians the aim of present study was to examine the hypothesis of synergistic effects between ACE-D and PON1-Arg alleles on predisposition and the severity of CAD in our population.

Methods: The PON1 192 and ACE insertion/deletion (I/D) genotypes were detected by PCR-RFLP and PCR, respectively in 414 individuals undergoing their first coronary angiography. Patients were placed into one of two groups: CAD and control without CAD or diabetes.

Results: We mentioned the synergistic effects of both genes and not ACE gene alone is a risk factor for CAD. We found that PON1 Arg 192 and ACE D allele act synergistically to increase the risk of CAD (OR 1.3, P = 0.044). Our results showed a significant correlation between the possession of both PON1 192 Arg and the ACE D allele and the extent of CAD in CAD patients and CAD subjects without diabetes, represented by the increased frequency of three-vessel disease with OR 2.7, P = 0.046; \( \chi^2 = 4, P = 0.046 \) and OR 2.4, P = 0.051; \( \chi^2 = 3.8, P = 0.051 \), respectively.

Conclusion: We found that PON1 Arg 192 and ACE D alleles act synergistically to increase the risk of CAD in CAD patients and CAD subjects without diabetes from west of Iran, who have high frequency of three-vessel disease. Our data suggest that PON1 192 Arg and the ACE D allele in combination with each other.
can be important independent risk factor for severity of CAD in patients carrying both PON1 192 Arg and the ACE D allele in a west population of Iran.

Keywords: Paraoxonase, Coronary artery disease, Diabetes mellitus
PBG-17

Diagnosis of a case with Cri-du-chat syndrome, using Array CGH

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Abstract

Cri-du-chat syndrome is an autosomal deletion syndrome caused by a partial deletion of chromosome 5p and is characterized by a distinctive, high-pitched, catlike cry in infancy with growth failure, microcephaly, facial abnormalities, and mental retardation throughout life. A 7 years old boy with dysmorphic face, microcephaly, cortical atrophy and global developmental delay was referred for genetic counseling. His parents were unrelated and there was no positive family history. Karyotyping, as the first diagnostic step in a dysmorphic patient with mental retardation, was normal. In order to detect submicroscopic anomalies, array CGH was performed, detected a 14.2 Mb deletion on 5p15.33-p15.2, compatible with partial monosomy of 5p, Cri-du-chat syndrome. Although the majority of deletions arise as new mutations, approximately 12% result from...
unbalanced segregation of translocations or recombination involving a pericentric inversion in one of the parents. Therefore, to find out the probability of such cases and the determination of recurrence risk, the parents' chromosomal evaluation is essential. This case illustrates the usefulness of aCGH as an adjunctive investigative tool for detecting chromosomal imbalances.

**Keywords:** Cri-du-chat syndrome, developmental delay, array CGH, Karyotyping
Roles of miR-126 and its genetic variant in type 2 diabetes

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Background: We aimed to evaluate the expression of miR-126 in plasma of type II diabetic patients in comparison to nondiabetic subjects. Since genomic polymorphism of miR-126, SNP rs4636297 plays a prominent role in the processing of pri-miR-126 to mature microRNA, we also investigated the link between this SNP and miR-126 plasma levels as well as the risk of diabetes.

Materials and Method: Genotyping of the SNP rs4636297 was carried out by PCR-RFLP using HaeII enzyme. The expression of miR-126 was quantified by Real-Time PCR technique and miR-16 was selected as the intrinsic reference gene. Fold change in gene expression was calculated by the Relative Expression Software Tool (REST). Data analysis was performed using exact-like logistic regression and Fisher exact test using the elrm package with the R software.

Results: The results indicated an increased incidence of diabetes and diabetic complications for AG and GG genotypes compared to the reference AA genotype. The mean fold decrease in miR-126 gene expression in diabetic samples relative
to normal samples was 0.653 (95% confidence interval: 0.012 - 18.765). Considering the AA genotype as the reference, the odds ratio of diabetic complications for the GG and AG genotype were 1.2 and 1.43, respectively.

**Conclusion:** Reducing the amount of mature miR-126 in cells containing G allele can reduce the production of VEGF and impairs vascular coherence, angiogenesis and wound healing, leading to diabetic complications. Therefore, it is expected that the reduction of miR-126 in GG and AG genotypes would predispose related persons to diabetic complications.

**Key words:** diabetes mellitus type 2, diabetic complication, polymorphism, miR-126

**IRCT:** IR.TMU.REC.1396.579
Association study between polymorphism of interleukin 12A (rs2243123T/C) and chronic hepatitis B virus infection

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Abstract

Background and purpose: B virus (HBV) infection is highly prevalent and one of the major causes of morbidity and death worldwide. HBV can lead to severe liver diseases such as chronic hepatitis, cirrhosis, and HCC. Interleukin-12 (IL-12), a novel pro-inflammatory cytokine belonging to the IL-12 cytokine family, is mainly produced by activated macrophages and can mediate both innate and adaptive immunity. It was initially recognized as an interferon-γ (IFN-γ)-inducing factor and promotion of Th1-type immune responses, and enhancement of the proliferative response and cytokine production of activated T cells. This cytokine was found to play various roles in chronic inflammation and autoimmune diseases, as well as in numerous infectious diseases. In this study, association of IL12A rs2243123T/C polymorphism with chronic HBV infection has been investigated.

Materials and Methods: Genotypes distribution of IL12A rs2243123 were determined in 100 HBV infected patients suffering from chronic disease and 10 healthy controls using polymerase chain restriction fragment length polymorphism (PCR-RFLP) method (during 2013 to 2015).
**Result:** The frequencies of rs2243123TT, TC and CC genotypes in the patients with chronic infection were 75%, 24% and 1% respectively and in healthy controls were 67%, 26% and 7%. (P value =0.08).

**Conclusion:** No statistically significant difference was detected in IL12A rs2243123 genotypes between patient and control groups. Considering the limited study population included herein, additional studies with larger samples and detailed clinical data are warranted in various ethnic populations.

**Keywords:** Hepatitis B virus, single nucleotide polymorphism, Interleukin-12, chronic infection
PBG-20

Genome instability related male infertility and the paradigm of testing Y-chromosome microdeletion in blood.

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Humans are under constant exposure to natural or man-made sources of ionizing radiation and toxic chemicals that might play a critical role in induction of DNA damage, genome instability and many related diseases such as cancer and infertility. De novo alterations might be the cause of many idiopathic conditions of male infertility. Sperm DNA damage, and chromosomal aneuploidy in male infertility, Y chromosome microdeletions are causally related to spermatogenesis defects and abnormal sperms. Although part of genetic damages are inherited and could be traced in blood leukocytes, but is not possible for those de novo alterations induced in spermatogenesis. The aim of this study was to show DNA damage, chromosomal aneuploidy and Y-chromosome microdeletion in sperms of subfertile males with normal genetic status in their leukocytes. To do this, semen and whole blood samples were obtained from different groups of subfertile and normal men. After karyotype analysis and microdeletion study on blood samples, semen samples from karyotypically normal subfertile and normal individuals were used for DNA fragmentation, chromosome aneuploidy and microdeletion analysis. Alkaline comet assay was used to assess sperm DNA damage and chromosome aneuploidy and microdeletion was assessed using a combined primed in situ labeling and fluorescent in situ hybridization (PRINS-FISH) method. A significantly high percentage of DNA fragmentation was observed in subfertile patients compared to control. Similar observation was observed for sex chromosome aneuploidy and DAZ microdeletion ($p<0.01$). A relatively small interindividual difference was seen in all three assays performed. However a mosaic form of microdeletion was observed in Y bearing sperms. Results clearly indicate that subfertile males experience higher genome instability in spermatogenesis and consequently sperms with higher extent of DNA damage and chromosomal aneuploidy or microdeletions are produced. Occurrence of de novo
genetic alterations in sperms might be due to exposure to environmental chemico-physical genotoxic agents.
An exceptionally long CA-repeat in the core promoter of SCGB2B2 links with the evolution of apes and Old World monkeys

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We have recently reported a genome-scale catalog of human protein-coding genes that contain "exceptionally long" STRs (≥6-repeats) in their core promoter, which may be of selective advantage in this species. At the top of that list, SCGB2B2 (also known as SCGBL), contains one of the longest CA-repeat STRs identified in a human gene core promoter, at 25-repeats.

Genomic DNA from two hundred Iranian unrelated humans from the DNA collection of the Genetics Research Center was selected randomly to analyze the minimum length of the SCGB2B2 core promoter CA-repeats in humans. PCR reactions were carried out in 25 μl volume Extreme length determination was performed using 8% polyacrylamide gel. The shortest, medium-size, and longest alleles of the human SCGB2B2 gene promoter CA-repeat were amplified from genomic DNA by PCR. The fragments generated were then cloned into pGL3 basic luciferase vector using the enzymes Xho1 and HindIII, and transfected into human embryonic kidney-293 (HEK-293) cells.

We report that the SCGB2B2 core promoter CA-repeat reaches exceptional lengths, ranging from 9- to 25-repeats, across Apes (Hominoids) and the Old World monkeys (CA>2-repeats were not detected in any other species). The longest CA-repeats and highest identity in the SCGB2B2 protein sequence were observed between human and bonobo. A trend for increased gene expression activity was observed from the shorter to the longer CA-repeats (p<0.009), and the CA-repeat increased gene expression activity, per se (p<0.02).
We propose that the SCGB2B2 gene core promoter CA-repeat functions as an expression code for the evolution of Apes and the Old World monkeys.

SCGB2B2 Ape Old World monkey Evolution CA-repeat
Study of the association between the MDM2 T309G polymorphism and colorectal cancer

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Background: MDM2 is a key component in the regulation of the tumour suppressor p53 gene. The association between the MDM2 polymorphism and colorectal cancer (CRC) has been investigated in Iranian population.

Methods: The polymorphism, T309G (rs2279744) in the MDM2 gene was determined in patients with CRC (n=120) and in healthy control subjects (n=120) using the polymerase chain reaction-restriction fragment length polymorphism method.

Results: Statistical analysis of the genotypic findings (OR=7.648, CI=3.753-15.59, P<0.001 for TG and OR=7.808, CI=3.457-17.64, P<0.001 for GG) and allelic findings (OR=2.792, CI=1.927-4.045, P<0.001) indicated a significant correlation between SNP309T > G in the MDM2 gene and the incidence of colorectal cancer in the population studied.

Conclusion: The results of this study indicated that there is significant association between MDM2 SNP309 polymorphism in the promoter of MDM2 gene and the incidence of colorectal cancer in Iranian population.

Keywords: Mdm2, SNP309, polymorphism, colorectal cancer
The Use of CRISPR-Cas9 system in human genome editing

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Background: Scientists are researching on many disorders gene therapy. Genome editing is a technic that has defined as the addition/deletion of new gene sequences or change a DNA sequence of human cells. Bacteria has a naturally genome editing system called Clustered Regularly Interspaced Short Palindromic Repeats-Cas9 associated proteins (CRISPR-Cas9) that can possess multiple methods to regulate genes. This system can be used in human genes too.

Methods: The CRISPR system provide sequence-specific adaptive immunity against acquired elements. Many researches shows that CRISPRs are then transcribed and processed, by CRISPR-Cas9 into siRNAs, which form part of a ribonucleoprotein complex that guides the crRNA to the complementary nucleic acid and targets this for degradation. Resistance is acquired following viral infection or plasmid uptake when a short sequence of the foreign genome is added to the CRISPR array. Researchers use this system for DNA repair in human genome by manipulating genome sequences and use of some vectors.

Results: The CRISPR system seems to be the most advantageous method in inactivating or repairing the mutated allele in human genome. It can be used for wide variety of diseases treatment, including cystic fibrosis, hemophilia, and sickle cell disease, also for complex disorders such as cancer, heart disease, mental illness, and HIV infection. In addition the CRISPR-Cas system hold tremendous potential for engineering the human genome.
**Conclusion:** We conclude that the CRISPR-Cas9 system can provide therapeutic applications. CRISPR can be used for both the positive and negative selection of genes that are usually implicated in genome editing.

**Keywords:** Genome editing - CRISPR - Caspase9.
Impact of NQO1 genetic polymorphisms on susceptibility risk of chronic myeloid leukemia and treatment response

Although the clinical and biological aspects are well documented, little is known about individual susceptibility to Chronic Myeloid Leukemia (CML). Polymorphic variants of several genes, diet, environmental exposure to carcinogens and individual immune system’s characteristics are potential factors that increase predisposition to leukemia. NAD(P)H: quinone oxidoreductase 1 (NQO1) C609T and C465T gene polymorphisms have been reported to influence the risk for Chronic Myeloid Leukemia (CML) in many studies. This study aimed to investigate influence of polymorphisms of NQO1 C609T and C465T on susceptibility to chronic myeloid leukemia (CML) in patients on imatinib treatment and to determine whether polymorphisms of these two genes could predict the response to imatinib in Iranian CML patients for the first time. The genotype distribution and allele frequencies of two NQO1 C609T and C465T polymorphisms were determined in 93 CML patients and 93 controls by using of PCR-RFLP. All patients received imatinib and were followed for at least three years. The response to imatinib was evaluated by recording the cytogenetic response according to the European Leukemia Net criteria. No significant difference in genotype frequency was found between controls and patients (P>0.05). The achieving of cytogenetic response was lower in patients with mutant allele than to wild types (P= 0.002; OR=4.51;95% CI, 1.34-12.35). These findings suggest that the risk of resistance to imatinib may be associated with NQO1 polymorphisms.
Keywords: CML, Polymorphism, NQO1, Iranian population
Chromosomal and prognosis analysis in adult *denovo* acute myeloid leukemia

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**Background:** Acute myeloid leukemia is a clonal hematopoietic malignant disease resulting from genetic alterations in normal hematopoietic stem cells. Precise diagnosis and prognosis will be helpful in therapeutic decisions. Identification of chromosomal abnormality can be used for this purpose. The purpose of the present study was to investigate chromosomal alterations and prognosis in adult *denovo* acute myeloid leukemia patients.

**Methods:** The bone marrow aspirate and peripheral blood for karyotyping was performed using GTG bonding method from 58 *denovo* adult AML patients. The demographic, para-clinical and survival data were analyzed using SPSS and Medcalc software.

**Results:** The chromosomal abnormalities were observed in 63% of AML patients. From the cytogenetic point of view, patients were categorized according to the European Leukemia Network standard into three categories with good (21%), intermediate (50%) and poor (29%) prognosis. The median follow-up time for all patients were 10 months. The survival rate of AML patients with good,
intermediate and poor cytogenetic prognosis were 94%, 34% and 31%, respectively.

**Conclusion:** Based on the present results, chromosomal abnormalities are common in the AML patients. Therefore, this genetics alteration might play an important role in the disease pathogenesis. Moreover, the present study provides evidence that distinct cytogenetic features have a strong influence on outcome of AML patients. Totally, our results may be helpful in categorizing of the patients, determining prognosis and improving the patients’ treatment.

**Keywords:** Acute myeloid leukemia, chromosomal, prognosis, survival
PBG-27

Next Generation Sequencing: An Emphasis On Its Application Of Clinical Diagnosis

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Abstract

Background: DNA sequencing had been undoubtedly one of the fundamental exploitations in molecular biology, which has also revolutionized the human medical genetics. The next generation sequencing (NGS) technology, which is generally known as second, third, and fourth generations, encompasses a range of steps including the library preparation, sequencing analysis, visualization, genomic fragmentation, ligation of sequenced segments, and data analysis. Current study, made an attempt to offer a comprehensive description of different
NGS techniques and application of clinical diagnosis by securitizing previous and recently studies.

**Methods:** In this study, Suitable keywords like “Next Generation Sequencing”, “Hereditary genetic disorder”, “Clinical diagnosis”, “molecular diagnosis of” and “Genetic disorders” were used for searching in databases like PubMed, Science Direct, Google scholar and Medline and finally 78 articles were extracted for study out of 385.

**Results:** It is obvious that the development of NGS has allowed the scientists to study the biological systems at the levels that were impossible using previous methods. The major clinical diagnosis applications of NGS include the identification of single nucleotide polymorphisms (SNPs), somatic mutations, haplotype and genetic diversity evaluation, epigenetic studies, transcriptome analysis, meta-genomics, and detection of minimal residual disease (MRD).

**Conclusion:** Taken together, the NGS technology is regarded as a breakthrough in the history of biology in which further advances can remarkably enhance its efficacy leading to better understanding of human disease and developing novel therapeutic strategies. Owing to the increasing interest in this method, we aimed to provide clearer insights into these methodologies, by comprehensive description of different NGS techniques and application of clinical diagnosis.

**Key words:** Next Generation Sequencing, Hereditary genetic disorder, Clinical diagnosis, Genetic disorders
PBG-28

Developing a multiplexed assay for analysis of five InDel markers in Alpha globin gene cluster

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Background

Alpha-thalassemia is one of the most common hemoglobin genetic abnormalities in Iran. Considering the importance of using polymorphic markers in alpha thalassemia genetic studies, this study aimed to design a multiplex PCR for investigation of several InDel markers in alpha globin gene cluster.

Methods

UCSC, dbSNP and Iranome databases were used to select a set of InDels with a higher heterozygosity in the alpha globin gene cluster. Primers for a multiplex PCR were designed using Primer3, GeneRunner and Primer-BLAST. The optimization of multiplex PCR conditions started with performing a single PCR for each pair of primers. After this step, various conditions of the multiplex PCR were examined to find the best conditions for optimal amplification of all investigated markers. Fragment analysis was used to InDel analysis for 11 samples.

Results

A panel of five InDel markers including rs147964160 (-/AAGG), rs3056228 (-/CT/TT), rs146967241 (-/AAC), rs141493810 (-/AAAC) and rs149065572 (-/AAAC)
TTGT) in alpha-globin locus control region were selected. Both heterozygous and homozygous states were identified for all five markers.

**Conclusion**

In this study a multiplex PCR reaction was developed for the simultaneous analysis of five InDel markers. Genotyping of these markers in a large sample group can determine heterozygosity of these InDels. These studies can be helpful for finding new markers for indirect genetic studies in families with alpha thalassemia.

**Keywords:** InDel marker, Multiplex PCR, alpha globin gene cluster
Genetic factors in bladder cancer tumorigenicity

Abstract:
Bladder cancer is the second most common cancer of the genitourinary system and makes up 4% of all malignancies. This type of cancer is 2.7 times more common in men than women. For every 15 people in 100,000 the general population worldwide occur. Carcinogens cause DNA damage in transitional cells and cause the carcinogenic process. That one or more triggers or its metabolites cause changes in cellular DNA, which is caused by abnormal protein. P53 is the most commonly altered gene in human cancer. Invasive bladder tumors that are often associated with P53 mutation and high grade. Other genes such as retinoblastoma gene in bladder cancer cell proliferation is involved in the process. In bladder tumorigenesis amplification of normal gene expression involved in cell growth is also important. For example, the incidence further intensified EFG receptors on cancer cells and tumor invasion is a poor prognostic factor. In 80% of cases of bladder cancer depends on a good analysis of the urine is suspected. Although specific for the diagnosis of bladder cancer, such as urine cytology, intravenous urography, ultrasonography, cystoscopy used. But the secondary detection subject to a fine of urine analysis is prone to the disease.

Keyword’s: bladder cancer, P53 gen, cytology
Evaluation of ACTA2 mutations in patients with early onset myocardial infarction referring to Isfahan health centers.

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Abstract

Introduction: Premature myocardial infarction (MI) is characterized by high reinfarction rates, occurrence of severe heart failure and therefore significant cardiovascular long-term mortality at a young age. Previous studies demonstrated that one of the most important risk factors in younger patients is family history and genetic factors. The present research was launched to assess the association of ACTA2 genetic variations with premature MI.

Materials and Methods: Out of eighty unrelated patients with premature MI referred to chamran heart center, Isfahan, patients with autosomal dominant premature MI were included in the study. Exclusion criterias included hypercholesterolemia, hyperlipidemia, diabetes and smoking. Genomic DNA was extracted from the peripheral whole blood. Eight exons and intron/exon
boundaries of the *ACTA2* gene were amplified and all the amplicons were subject to Sanger sequencing.

**Results:** According to the criterias, 16 patients were included in our research. No mutation was found.

**Conclusion:** It seems that the *ACTA2* mutations contribute insignificantly to the MI pathogenesis in the studied population.

**Keyword:** Premature myocardial infarction, *ACTA2*, Mutation
PBG-31

Design and construction of intelligent toilets system capable of testing and displaying important health parameters (pH, ketones, blood glucose, etc.) detectable by urine, on a touch graphic display (patent number: 90251)

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Background: One of the indicators of the progress of each community is the importance of public health. By utilizing e-technology, individuals are able to enjoy the same access to electronic health services. Other applications are helping to prevention and control of contagious diseases and the guidance of human resources specializing in the treatment and acceleration of the delivery of health services. One Part of the health of any community is related to sanitary toilets.

Methods: The current sanitary toilets, both traditional and foreign, have some disadvantages that they have been underestimated. Sanitary toilets are located in places where there is no suitable temperature and In particular, in toilets where the body is in direct contact with the toilet, there is no way to adjust the toilet temperature to the human body. People occasionally leave the toilet door open, which causes an unpleasant smell in the air. The shortcomings mentioned are solved by using this system. Another significant feature of this system is its laboratory system, by analyzing a few drops of urine, a person can obtain comprehensive and useful information about the amount of predetermined parameters such as PH, ketones, blood glucose, etc., and simultaneously displayed on the system screen.

Results: This simple urinalysis is a key test for the diagnosis of kidney disease, for example Excess fatty acids in the liver are converted to "ketones", including "acetone", which have acidic properties, if ketones in the urine are not detected in
the early stages, and the ketones are accumulated in the blood, resulting in diabetic glucocorticoids.

**Conclusion:** Warm toilet seat with automatic and manual temperature control, automatic closure for opening and closing the door intelligently based on the consumer's distance, setting of parameters by the full-touch graphic display are some of the main features of this medical device.

**Keywords:** Intelligent Toilet, Urinalysis, Touch Graphic Display
Effect of Royal Jelly and silver-nanoparticle on H2O2 and Anxiety-Related Behavior at hippocampus and serum in male Rat

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Background: Silver nanoparticles are small scale substance (<100 nm) used in food technology and medical industry are important in many applications of nanoparticles on human health. The data suggest that nanosilver may produce neurotoxicity by generating free radical-induced oxidative stress and anxiogenic function. The purpose of this study was to investigate the possible protective role of Royal jelly against some detrimental effects of silver nanoparticles on anxiety-like behavioral and oxidative stress at hippocampus and serum in male rat.

Materials and methods: 28 male Wistar rats were divided into four groups of control and three groups of the treatment. The control group received saline and the treatment groups received gavage of silver nanoparticles at doses of 30 mg/kg. Ten days after the last gavage, the performance of hippocampus was evaluated by plus maze (PM) tests then serum and the hippocampal region was dissected and removed and then the expression of H2O2 was evaluated according to kit recipe.

Result: In this study the expression of H2O2 was significantly reduced in the treatment whit royal gelly groups compared to the Ag-NPs group. Addition royal
jelly significantly increased the percentage of open arm entry (OAE) compared Ag-NPs. group and (p<0.05)

**Conclusion:** The data suggest that silver nanoparticles may produce oxidative stress by altering H2O2 expression, in rat brain hippocampus and serum additional causes an anxiogenic respons.

**Keywords:** Silver nanoparticles, Hippocampus, Anxiety, Royal jelly, H2O2
Bacteriophage treatment of *Klebsiella pneumoniae*-mediated lobar pneumonia infection in a mouse model

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**Background and aim:**
Multidrug-resistant (MDR) *Klebsiella pneumoniae* is a common cause of infection in humans especially in immunocompromised patients. In the recent years, the potential of phage therapy as an alternative treatment for these difficult to treat infections, has gained interest. In this study, a lytic bacteriophage isolated from wastewater was used to evaluate its ability for treatment of mice challenged with *K. pneumoniae*.

**Material and methods:**
A specific phage with lytic activity for *K. pneumoniae* isolated and characterized from sewage was evaluated for treatment of mice infected with *K. pneumoniae* in an experimental model of lobar pneumonia. Six groups of 10 BalbC mice were challenged by intranasal inoculation (i.n) with $10^8$ colony forming units (CFU) of *K. pneumoniae* ATCC10033. Groups one and two were simultaneously inoculated with a single dose of intraperitoneal injection of the bacteriophage using $10^{10}$ and $10^9$ plaque forming units (PFU) representing multiplicities of infection (MOI) of 100 and 10, respectively. Groups three and four were treated similar to groups one and two but received the phage 24h post-infection. The fifth group of mice was left untreated and group 6 received bacteriophage alone and was used to evaluate phage toxicity in the eukaryotic host. The mice were euthanized every 24h up to 7 days post-infection followed by enumeration of phage and bacteria in the lung homogenates.
Results:
The results of this study showed that treatment of mice with a single injection of phage simultaneously resulted in over 7 logs decrease of CFU up to 72h after administration with MOI of 100 and 5 logs using MOI of 10. The same trend was observed when phage was administered 24h post-infection. The phage showed no toxicity in the eukaryotic host.

Conclusion:
These results show that the isolated phage may have the potential to be used for treatment of *K. pneumoniae* infections.

Keywords: Bacteriophage therapy, *Klebsiella pneumoniae*, mice lobar pneumonia
PBG-34

Transfection of MDA-MB-231 cell line by pcDNA3.1hygro-shPD-1 construct

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**Background:** Transfection is method of insertion of nucleic acids into cells. Various methods have been applied for transfection. we evaluate two methods including electroporation and reagent mediated transfection, for insertion of pcDNA3.1hygro\(^+\)-shPD-1 plasmid into a eukaryotic cell named MDA-MB-231 cell line (1-3).

**Methods:** We designed soluble human programed cell death proteien-1 (shPD-1) construct which was contained three parts including; secretory signal peptide, PD-1 sequence and Green florescent protein sequences. Two restriction enzyme sites were placed at the beginning and the end of the construct. This construct was cloned at multiple cloning sites of pcDNA3.1hygro plasmid. The pcDNA3.1hygro\(^+\)-shPD-1 plasmid was transfected by polyfect into MDA-MB-231 cell line on two sequential days. On the first day, cell lines were trypsinized and sub-cultured on 12 or 24 well plates. On the second day, transfection reagent containing 0.4µg pcDNA3.1hygro+-shPD-1 plasmid and 2µL polyfect was prepared in 20µL medium. The transfection reagent was added in the cell lines with 80% confluences. In addition, MDA-MB-231 cells were transfected by electroporation using an electrophorator with the following settings: capacitance 960 µF, voltage 220 v. Twenty-four hours after transfection, fluorescence microscopy and flow cytometry method were used to evaluate expression of shPD-1 in transfected cell lines.

**Results:** successive expression of shPD-1 in MDA-MB-231 cell line was confirmed by fluorescent microscopy and flow cytometry methods. The cells
with bright GFP fluorescence with fluorescent microscope and detected cells in FL1 channel of flow cytometry were confirmed plasmid insertion in the cell line. **Conclusion:** High expression of shPD-1 after transfection by polyfект, shows successful method of transfection of pcDNA3.1hygro-shPD-1 for production of recombinant proteins in eukaryotic cells.

**Keywords:** Transfection, Electroporation, MDA-MB-231 cell, Polyfect, pcDNA3.1hygro+ -shPD-1 plasmid.
PBG-35

Electrospun poly-L-lactic acid\textregistered poly vinyl alcohol nanofibers improved insulin producing cells differentiation potential of human adipose derived-mesenchymal stem cells

Seyed Ehsan Enderami

Combination of adipose derived-mesenchymal stem cells (ADSCs) and synthetic materials in term of pancreatic tissue engineering can be considered as a treatment for diabetes. This study was designed to evaluate pancreatic differentiation of human ADSCs as an available cell source with low immunogenicity, on poly-L-lactic acid/poly vinyl alcohol (PLLA/PVA) nanofibers as a 3D scaffold. Mesenchymal stem cells (MSCs) isolated from fresh adipose tissue and characterized for mesenchymal surface markers by flow cytometry. After that ADSCs seeded on PLLA/PVA scaffolds and tread with pancreatic differentiation medium. Immunostaining assay showed that highly efficient differentiation of ADSCs into relatively homogeneous population of insulin producing cells (IPCs). Real-time RT-PCR results indicated that expression of pancreas- specific
transcription factors (Pdx1, Insulin, Glucagon, Ngn3 and Glut2) in PLLA/PVA was significantly higher than tissue culture plates. Additionally, Functional assays showed that concentration of insulin and C-peptide secreted in supernatant in response to various concentrations of glucose in PLLA/PVA scaffold group was significantly higher than 2D culture. Altogether the current results demonstrated that PLLA/PVA scaffold seeded with ADSCs could be a suitable option in pancreatic tissue engineering and can be used to treat diabetes in the future.
PBG-36

Silk nanofibers promotes differentiation of induced pluripotent stem cells into insulin producing cells

Seyed Ehsan Enderami

Abstract

Scaffold with stem cells has a high potential for application in the pancreas tissue engineering. Construction of a nanofibrous scaffold similar to the natural extracellular matrix is one of the methods that can be used to reconstruct the pancreatic tissue. The aim of this study was investigate the insulin producing cells (IPC) differentiation potential of human induced pluripotent stem cells (hiPSCs) while cultured on the silk nanofibrous scaffold, which can simulate pancreatic tissue microenvironment. After silk nanofibers fabrication and characterization, hiPSCs were seeded on the nanofibers and differentiated into the IPCs. Specific pancreatic markers such as insulin and pdx1 were applied for IPC generation evaluation by using of immunocytochemistry and real-time RT-PCR methods. Results acquired via SEM and MTT assay demonstrated that silk nanofibers could support from hiPSCs attachment and proliferation. The expression of pancreatic
genes and protein markers was higher in cultured hiPSCs on silk scaffold in comparison with those cultured on tissue culture plate as well as insulin and C-peptide secretion. According to the results, electrospun silk nanofibers could have used as an appropriate substrate for pancreatic tissue regeneration and showed have a promising potential to use in the treatment of the patients with pancreatic dysfunctions.
Nanobodies: emerging tools for research, diagnostics and therapy

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Background: Since the introduction of heavy-chain antibodies (HcAbs) two decades ago and the explanation of nanobodies, valuable biochemical properties of nanobodies have generated the interest of researchers on their use in diagnosis and therapy of tumor. Various specific nanobodies (VHHs or sdAbs) have been selected from library and detected high affinity with their antigens. The small size of nanobodies (∼15 kDa, 4 nm long and 2.5 nm wide) make it easy for them to penetrate the tissue or get through the blood brain barrier as drugs. Furthermore, nanobodies have been offered in conjugates with other effector domains and in drug delivery systems as targeting for tumors. The nanobodies has the potential to make effective biomedical carriers in the fields of research, diagnostics and therapy. In this review we have explained the important advances in the field of nanobodies. Nevertheless, there are many potentials to further develop and improve nanobody-mediated tumor targeting. In the near future, new targets and their corresponding nanobodies must be identified. Currently, some researchers exploited available nanobodies against tumor-specific receptors for delivering drugs or toxins to tumors, therewith reducing nonspecific toxicity to normal cells and lessening side effects.

Conclusion: In conclusion, nanobodies as targeting carrier appear to be a promising method of tumor targeting therapy and diagnosis.

Keywords: Nanobodies, research, diagnostics, therapy
**PBG-39**

**Preparation of nanoparticles carrying Recombinant protein of type IV pili *pseudomonas aeruginosa* as vaccine candidate.**

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**Background:** *Pseudomonas aeruginosa* is an opportunistic and gram negative pathogen. The infection of *P. aeruginosa* is the most important factor for increasing the patients mortality. Type IV pili (subclasses to type IVa pilus and type IVb pili) are role in adhesion of pathogenic bacteria to their host cells and biofilm formation. Actually, Bacterial attachment is preliminary steps for the establishment of infection in the specific host. The aim of this study is Preparation of nanoparticles carrying Recombinant protein of type IV pili *pseudomonas aeruginosa* as vaccine candidate.

**Materials:** recombinant flp protein (type Ivb) *P. aeruginosa* were produced. Nanoparticles were produced. The size and morphology of the nanoparticles were investigated by DLS.

**Results:** the size and morphology of the nanoparticles were investigated. DSL confirmed size and zeta potential of the nanoparticle.

**Conclusion:** In this study we suggested recombinant subfamily of type IVb protein for production of vaccine and estimated Immune Responses against Nanoparticle carrying of type IVb pilin. Nanoparticle can use for vaccine and drug therapy. Today, the technology that use of nanoparticle vector for offer
recombinant protein are very good for development of immune responses and this technology could be reduce of antigen dose and reduce the toxicity of antigen. this strategy can gradation of competence the recombinant protein.

**Key words:** Pseudomonas aeruginosa, type IV pili, Nanoparticle, recombinant protein, vaccination
Designing and Production nanovaccine for Recombinant protein of type IVb pili _pseudomonas aeruginosa_

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Background: _Pseudomonas aeruginosa_ is an opportunistic pathogen that found in most environments such as water reservoirs and air and soil and hospital environment. The infection of _P. aeruginosa_ is the most important factor for increasing the patients mortality. The pathogenesis of this bacteria infections is multifactorial and includes a complex of virulence factors but Type IV pili (T4P) is essential virulence factor of _P. aeruginosa_. the aim of this study is Production of Nanoparticle carrying Recombinant protein of type IV pili _pseudomonas aeruginosa_ as vaccine candidate.

Material: The review of 30 articles were published between 2000 and 2018 show Bacterial attachment is preliminary steps for the establishment of infection in the specific host. Type IV pili is role in adhesion of pathogenic bacteria to their host cells and biofilm formation. today numerous _P. aeruginosa_ antigens and delivery systems have been investigated as vaccine candidates such as pilA, pilQ and… but there is not any research about Flp( subfamily of type Ivb pili )

Result: This study We have reported on a synthetic peptide vaccine of type IVb protein and estimated Immune Responses against Nanoparticle carrying of type IV pilin. Nanoparticle can use for vaccine and drug therapy.
**Conclusion**: the technology that use of nanoparticle vector for offer recombinant protein are good for development of immune responses and this technology could be reduce of antigene dose and reduce the toxicity of antigene. this strategy can gradation of competence the recombinant protein

**Key words**: *Pseudomonas aeruginosa*, type IV pili, Nanoparticle carrying, recombinant protein, vaccination, Bacterial attachment
Synthesis and Characterisation of Monodisperse Selenium Nanoparticles Stabilised by Polysorbate 80

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Background: Selenium nanoparticles (SeNPs) have recently drawn significant attention due to having variety of applications in medicine. Nevertheless, there are still many constraints in particle preparation and their stabilisation. The aim of this investigation was to synthesise monodisperse SeNPs by a facile reduction method, controlling the size of nanoparticles with polysorbate 80 which is widely used due to biocompatibility of its derivatives.

methods: Stock solutions of 5.7mM Sodium selenite and 56.8 mM Ascorbic acid were prepared. 0.5 ml Ascorbic Acid was added to the 1 ml sodium selenite solution with magnetic stirring. To reduce the size of Se nanoparticles, 10µl polysorbate 80 was added between ascorbic acid addition. The nanoparticles were characterised by dynamic light scattering (DLS), ultraviolet–visible (UV–Vis) absorption spectroscopy and scanning electron microscopy (SEM).

Result: Monodisperse SeNPs were synthesised by a facile reduction method. Ascorbic acid was used as a reduction agent and polysorbate 80 (surfactant) was added to control the size of nanoparticles. The absorption spectra of the Se nanoparticles was observed around 265nm showing formation of the nanoparticles. DLS analysis confirmed the possibility of controlling size of the prepared nanoparticles via addition of the surfactant. The average size of the nanoparticles prepared without addition of the polysorbate 80 was 121 nm which remarkably decreased upon addition of the surfactant, i.e. 43 nm with a narrow size distribution (PDI value of 0.05).

Conclusions: The new synthesis strategy for SeNPs presented here is facile and user-friendly. Furthermore, the particle size can be significantly controlled by
addition of polysorbate 80, yielding well-dispersed selenium nanoparticles. Results of this effort paves the way for having control over the size and monodispersity of selenium nanoparticles which can be considered as a prerequisite for any applications of interest.

**Keywords**: Selenium Nanoparticles, Polysorbate 80, Polydispersity Index
PBG-43
The Frequency and Sensitivity of Some Clinical Candidates Isolated from Patients Against the Nanoparticles of Mango Seed in Several Medical Laboratories of Isfahan

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Background and objective

The increase of using chemical drugs increased the resistance of different pathogenic candidates to the common antibiotic “fluconazole”. The present study aimed to investigate the frequency and sensitivity of some clinical candidates isolated from patients against the nanoparticles of mango seed in several medical laboratories of Isfahan.

Materials and methods

First, 25 clinical isolates were selected from some medical laboratories in Isfahan and transferred to the research laboratory of Islamic Azad University, Falavarjan Branch. Typical laboratory methods were used for detecting the species, including chlamydoconidial production, germ tube production, direct lam, common chromium agar growth medium, and color changes in the colony of yeasts. A cubic and diagonal nanoparticle of about 65 nm was prepared from mango seeds using several physical methods. In order to test the sensitivity of isolates against fluconazole and the nanoparticles of mango seed, the methods of cup plate and serial dilutions in the tube were used. For statistical analysis, ANOVA and SPSS software version 20 were used at P ≤ 0.05 significance level.
Findings

After applying the morphological and biochemical tests among the studied clinical isolates, *Candida albicans* with frequency of 52.38%, *Candida krusei* with frequency of 33.33%, *Candida tropicalis* with frequency of 9.52%, and *Candida glabrata* with the frequency of 4.76%, respectively had the highest and lowest frequencies among 25 isolates. Among the clinical isolates by cap plate method, *Candida krusei* had the most sensitivity to fluconazole and the nanoparticle of mango seed with the zone diameter (32 mm) and *Candida albicans* indicated the highest resistance to the nanoparticle of mango seed with zone diameter (8 mm). In accordance with Macrodilution method (MIC), *Candida krusei* against the nanoparticle of mango seed was obtained equal to 0.008 mg / ml while *Candida albicans* was obtained equal to 0.46 mg / ml.

Discussion and conclusion

Among the studied isolates, 58% isolates were sensitive to fluconazole antibiotic while 42% of the isolates were sensitive to both nanoparticle of mango seed and fluconazole. Therefore, due to fewer side effects of herbal remedies, using the nanoparticles of mango seed after testing on rats under in vitro conditions was recommended instead of the chemical agent of fluconazole because of fewer side effects.

**Keywords:** Anti-candidiasis effects, Fluconazole, Candida sp, Cup plate, Macrodilution, Nanoparticle of mango seed
PBG-44

Future directions for applying Hematopoietic Stem Cell in transfusion Medicine

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Background
Hematopoietic stem cell (HSC) transplantation (HSCT) used to treat a variety of disorders. HSCT reduced risk of graft-versus-host disease (GvHD) and need for post-transplant immunosuppressive drugs. Before HSCT, antigen and allele matching of donor and recipient must be performed.

Future Directions
Nowadays two collection protocols are available: continuous Mononuclear Cell Collection (cMNC) and MNC, which former is more efficient in unrelated donors and donors with low pre-apheresis peripheral HSC count. Risk of adverse events/effects and G-CSF administration are lower in children donors for peripheral blood SC collection; a promising avenue about donor safety that benefit from pediatric donors. GvHD will alleviated by reducing pre-transplantation routine RBC transfusion, simultaneously HSC-organ transplantation, using blood redox state biomarker and suppressing signaling associated chronic GvHD pathogenesis. Pre-transplantation cytomegalovirus-positive patients, higher ferritin and busulphan level experienced a higher risk of poorer outcomes, while higher absolute lymphocyte count and increased albumin level associated with improved outcomes.

The technically demanding, being expensive, no correlation between numbers of storage days at 4 °C and viability after storage during cryopreservation of HSC
may could be improved using non-cryopreserved PBSC. Genetic HSC disorders could be treated with converting haemogenic endothelium into functional HSC via recovering specific transcription factors. Applying genome-editing technologies specially clustered regularly interspaced short palindromic repeat (CRISPR)/Cas9 nuclease may widen the opportunity for introducing precise changes in HSC.

Conclusion
cMNC collection and non-cryopreserved PBSC storage are more efficient and cost-effective methods. GvHD could be improved by controlling routine RBC transfusion and signaling of GvHD pathogenesis. Frequently HSCT could be reduced via applying CRISPR-based system. Simple blood tests better used for assaying occurred risks in patients receiving myeloablative allogeneic HSCT.

**Keywords:** Hematopoietic stem cells; Graft-versus-host disease; Blood Transfusion.

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Background: For the first time, spherical nucleic acids (SANs) were introduced by Chad A. Mirkin and coworkers [1] where single-stranded nucleic acids at high density had been confined around spherical nanoparticles (especially gold nanoparticles). In recent years, AuNP-core SNAs have been promised as versatile platforms for yielding access to the accurate biodiagnostic tools for the detection of biomolecules at analytical sensitivities rivaling and, in some cases, even surpassing PCR and ELISA [2].

Methods: In this study, we report a low-cost and simple but robust and rational strategy to colorimetric detection of HIV-1 nucleic acids based on assembly of AuNP-core SNAs, which has intense red color, via a linker with palindromic tail. Linker hybridization to spherical nucleic acids, induces the assembly of SNAs via self-complementary which leads to agglutination of SNAs followed by a color change from red to very low pink. However, hybridization to the target strand, leads to inhibition of SNA agglutination, eventually, the solution color remains red.

Results: With that in mind, we designed a single-component system according to essence of HIV genome, as the innovative approach for the affordable and accurate detection of HIV-1 RNA based on inhibition agglutination of SNAs, which can rival the nucleic acid amplification techniques (NATs) in sensitivity.

Conclusion: The ease and frugality of synthesis of SNAs without any requirement of expensive equipment can provide a practical guide the development of commercial clinical products which will lead to improve the point-of-care (POC) diagnostic tools for HIV-1.
**Keywords:** AuNPs, Spherical Nucleic Acids, Colorimetric Detection, Viral Nucleic Acids, HIV-1.
Nanoemulsions loaded with *Thymus vulgaris*: A promising agent against fluconazole-resistant *Candida* isolates

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**Background:** Azole antifungals such as fluconazole are often preferred treatment for many *Candida* infections as it is inexpensive, exhibits limited toxicity, and is available for oral administration. However extensive documentations reported the high frequency of fluconazole resistant *Candida* isolates in the clinical setting. For this reason, there is a need for new natural-originated drugs with low side effects and minimum inhibitory concentrations. *Thymus vulgaris* is a species of flowering plant in the mint family lamiaceae, native to southern Europe from the western Mediterranean to southern Italy. *Thymus vulgaris* essential oil is a combination of monoterpenes which act as antioxidative, antimicrobial, antitussive, antispasmodic, and antibacterial agent.

**Methods:** In the present research, the nanoemulsion-loaded Thymus vulgaris were prepared using probe ultrasonication techniques and the efficacy of the optimal formulation on a large number of *Candida* isolate was investigated. In
total, 60 fluconazole resistant and susceptible isolate of *Candida albicans*, *Candida glabrata* and *Candida parapsilosis* were examined. To determine minimum inhibitory concentrations (MIC) for both Thyme oil and nanoemulsion formulation, the clinical and laboratory standards institute document M27-A3 and M27-S4 were used as a guideline. Fluconazole applied along with each test as the reference drug.

**Results:** The nanoemulsion-loaded Thymus vulgaris particles presented a spherical shape with a mean diameter, zeta potential and entrapment efficiency of 126.4 ±15.2 nm, -35.1 ±3.0 mV, and 93.6 ± 3.5%, respectively. The MIC$_{50}$ value for thyme oil was obtained 80 µg/ml against both fluconazole resistant and susceptible strains of *C. albicans*, *C. glabrata*, and 160 µg/ml for *C. parapsilosis*; while both fluconazole resistant and susceptible strains of *C. albicans*, *C. glabrata* and *C. parapsilosis showed MIC$_{50}$ 5 µg/ml and 20 µg/ml, respectively.

**Conclusion:** This study showed the effectiveness of nanoemulsion loaded *Thymus vulgaris* as a delivery system against fluconazole-resistant *Candida* isolates. In conclusion, novel antifungal agents with natural origin might be used as part of therapeutic strategy or alternative treatment of candidiasis in the future.

**Key words:** *Thymus vulgaris*, Nanoemulsion, Fluconazole, *Candida*, Drug delivery
Blood cancer (leukemia) is a prevalent cancer globally which is caused by a variety of genetic abnormalities and environmental factors, such as exposure to chemicals and radiation. Chemotherapy and radiotherapy as the first line of therapy are not the definitive treatment method and cause drug resistance in patients. Nanotechnology, the science of making and using nanoscale structures sizing between 10-100 nm, is a new strategy in the field of medicine, which is called nanomedicine. Nowadays, the applications of nanomedicine are vast, which span from diagnosis to treatment of different diseases, especially cancers. Medical imaging, drug delivery, and gene delivery are some of the most important applications of nanomedicine. Hence, the use of nanoparticles in the treatment of leukemia may be useful based on their drug delivery properties. Iron oxide nanoparticles (IONPs) are magnetic nanoparticles that are easily produced and functionalized and widely used in the field of medicine. They are influential in leukemia chemotherapy treatment and overcoming drug resistance by their application in drug delivery. However, normal tissue injury and interfering with their function might occur when using nanoparticles. This may be caused by IONPs native properties and their targeting of non-specific markers on the surface of cancer cells. Considering the effective role of nanoparticles in the delivery of
chemotherapy drugs and reducing their side effects, it seems that the use of nanoscales will be more commonplace in the future, yet their undesirable effects on normal tissues will be a major challenge to resolve.

**Keywords:** Leukemia, iron oxide nanoparticle, chemotherapy, drug delivery
Different strategies for manipulation of mesenchymal stem cells in vitro to enhance their potentialities

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Background

Mesenchymal stem cells (MSCs) are under intensive investigation for use in cell-based therapies because their differentiation abilities, immunomodulatory effects, and homing properties offer potential for significantly augmenting regenerative capacity of many tissues. Nevertheless, major impediments to their therapeutic application, such as low proliferation and survival rates remain as obstacles to broad clinical use of MSCs. Another major challenge to evolution of MSC-based therapies is functional degradation of these cells as a result of their exposure to oxidative stressors during isolation. For this reason, any strategies that enhance the viability and proliferative capacity of MSCs associated with their therapeutic use are of great value.

Methods

Here, recent strategies used by various researchers to improve MSC allograft function are reviewed, with particular focus on in vitro conditioning of MSCs in preparation for clinical application. Preconditioning with oxidative stress, hypoxia and serum deprivation condition, genetic manipulation, optimization of MSC culture conditions and using of bioreactors are some examples of the methodologies, along with novel strategies such as treatment of MSCs with conditioned medium and MSC-derived microvesicles.
Results

These topic methods are likely to find value as a guide for both research and clinical use of MSC allografts and for improvement of the value that use of these cells brings to health care. Due to alteration of intrinsic signaling pathways of some growth factors, cytokines, and chemokines and the expression levels of their receptors (especially CXCR4), they improve survival, chemotaxis, differentiation, proliferation and migration capacities of MSCs.

Conclusion

Implementation of different strategies including preconditioning, genetic manipulation and improvement of cultivation condition could resist MSCs to harsh stress condition. Knowledge and understanding of these conditions will contribute to the improvement of MSCs-based cell therapy

Keywords: Mesenchymal stem cell, Preconditioning, Conditioned medium, Microenvironment, Bioreactor.
Designing a Mycoplasma Detection Kit

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Background: Mycoplasma contamination is one of the major problems of cell culture and some species including M. arginini, M. fermentans, M. hyorhinis, M. orale, M. hominis and Acholeplasma laidlawii are the most common ones found in cell cultures. Since cell culture is used extensively and Mycoplasmas contamination can have inevitable consequences such as severe cytopathic effects (CPE), Chromosomal aberration and unreliable final results, it is important to trace these bacteria. Of note, various techniques have been developed to detect Mycoplasma contamination but above all PCR is the most appropriate one due to its accuracy and sensitivity. The present study aimed to design a novel kit to detect common Mycoplasma species in cell cultures on the basis of proliferation of common sequence gene by new designed primer sequences.

Methods: According to common genome sequences of six Mycoplasma species, the primer was designed using In-Silico and Blast method with product length of 268 bp. Total DNA was extracted from several cell lines and then PCR was carried out using the designed primer. After electrophoresis, the PCR product of positive sample was separated from electrophoresis gel and sent for genome sequencing for identification of species. The target gene of bacterium was cloned into Ecoli TA vector and then extracted from the plasmid. The copy numbers of bacterium was calculated and sensitivity of the designed method was determined by serial dilution of DNA.
Results: The results showed that the designed kit was able to detect the contamination of mycoplasma specie in cell culture. Additionally, the sensitivity of the kit is considerably high and can detect the 10 bacteria in the infected sample.

Conclusion: Our study suggests that the designed kit is capable of detecting mycoplasma contamination with very high sensitivity and can be used as an appropriate and rapid technique in laboratory diagnostic procedures.

Keywords: Mycoplasma contamination, Cell Culture, Primer, PCR, kit
Bacterial growth control in infectious ulcers with essential oils- An Invivo study
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Control of Acinetobacter growth is very difficult due to its considerable resistance to a wide range of antibiotics. In this research, the herbal treatment of infective wound in rat was studied. In this research, the essential oils of Oregano were prepared by Clevenger. A clinical strain of Acinetobacter baumannii was isolated and detection was confirmed by conventional microbiological methods. Drug susceptibility testing was carried out for antibiotic resistance. Susceptibility to diluted essential oil was accomplished by and Broth microdilution Broth. Invivo study was conducted by 21 Wistar rats were randomly divided into three groups: healthy, control, and control group. All of three groups were shaved after general anesthetic with ketamine and xylazine. A 1-inch wound is injected between two scapulae of the rats. Fresh bacterial culture was inoculated with insulin syringe to the wounds. After 24h, 500 μl of diluted Oregano essential oils were sprayed onto their wounds twice a day, and the healthy control group had the same amount of essential oil in the hair-cut areas between the two scapulae. Results: In the disk diffusion test, zone of inhibition was around 39 mm. The minimum inhibitory concentration (MIC) was 78μcg/ml. Rats in test group in 11 days period of investigation were not shown any wound infection. in control group four rat were dead and the others shown the signs of infection. Conclusion: Oregano diluted essential oil was able to control the wound infection by Acinetobacter in rat.

Key words: Acinetobacter, Oregano, Wound
PBG-52

The peroxidase-mimicking activity and clinical application of a new graphene-based nanostructure

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Background: Nowadays, artificial enzymes are suitable alternatives to natural enzymes due to their high stability, robustness, ease of production, long-term storability and low cost. These nanozymes display enzyme-like activity and have been applied in numerous fields, including biosensing, immunoassay for cancer diagnostics and pollutant removal. Although they are still in the initial stages of research, but are growing fast.

Methods: The peroxidase-like activity of graphene-based nanozyme was determined and its kinetic parameters were measured using TMB (3,3′,5,5′-Tetramethylbenzidine) and H₂O₂ as substrate by monitoring the absorbance changes at 652 nm. The peroxidase-mimicking nanozyme coupled assay with glucose oxidase (GOₓ) to develop a colorimetric method for detection of glucose concentration in serum samples.

Results: The designed graphene-based nanozyme exhibited appropriate peroxidase-like activity toward H₂O₂ and TMB, showing comparable kinetic parameters with HRP. Since H₂O₂ generates during the catalytic reaction of GOₓ, using a coupled assay of GOₓ reaction with nanozyme, H₂O₂ and glucose were successfully detected in the presence of TMB. The linear range for glucose concentration was from 2.5 ×10⁻⁴ to 2 ×10⁻³ M.

Conclusion: A cheap peroxidase-mimicking nanostructure was applied in a simple and sensitive colorimetric method for detection of glucose concentration in
human serum samples. The data were in good accord with the results of clinical laboratory.

**Keywords:** Nanozyme, Peroxidase-mimicking, Glucose detection, Graphene-based nanostructure
Using a novel transition metal dichalcogenid-based nanozyme with peroxidase-like activity for colorimetric sensing of glucose

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Background: Due to their wide biomedical applications, nanozymes have attracted much attention as emerging alternatives for artificial enzymes over the past decade. Compared with natural enzymes, nanozymes are advantageous in several aspects, such as excellent robustness, higher stability, facile and cost-effective large scale production. The application of nanozymes in bio-sensing, bio imaging, therapeutics and environmental remediation have been demonstrated.

Methods: The peroxidase-like activity of TMD-based nanoparticles and the steady state kinetic analysis with H₂O₂ and TMB as substrates was performed by varying the concentrations of TMB at fixed H₂O₂ concentration and vice versa. Nanozyme coupled assay with glucose oxidase (Go₅) developed a sensitive colorimetric assay to detect glucose in serum samples. The absorption was measured at 652 nm.

Results: The steady state kinetic analysis shows that the catalytic process of nanozyme accord with Michaelis-Menten behavior toward both substrates. As a result of glucose sensing in serum samples a typical glucose standard curve was obtained with a linear range from 6 x 10⁻⁴ M to 125 x 10⁻⁵ M. The results resembled those obtained using the conventional enzymatic method.
Conclusion: The novel nanostructure from the family of transition metal dichalcogenides possessed efficient intrinsic peroxidase-like activity and was successfully used for a sensitive glucose sensing of serum samples. The data were in good agreement with the results provided by medical laboratory.

Keywords: Nanozyme, Peroxidase mimetic, Bio-sensing, Transition metal dichalcogenide
PBG-54

Decellularized amniotic membrane extracellular matrix as a promising scaffold for promoting hepatic differentiation of human induced pluripotent stem cells

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Abstract:

Human induced pluripotent stem cells derived hepatocyte-like cells (hiPSCs-HLCs) holds considerable promise for future clinical personalized therapy of liver disease. However, the low engraftment of these cells in damaged liver microenvironment is still an obstacle for potential application. In this study, we explored the effectiveness of decellularized amniotic membrane (dAM) matrices for culturing of iPSCs and promoting their differentiation into HLCs. The DNA quantitative assay and histological evaluation indicated that cellular and nuclear residues were efficiently removed and the AM extracellular matrix component was maintained during decellularization. DAM matrices were developed as three-dimensional scaffolds and hiPSCs were seeded into these scaffolds in defined induction media. In dAM scaffolds, hiPSCs-HLCs gradually took a polygonal...
shape, a typical shape of hepatocytes. HiPSCs-HLCs that were cultured into dAM scaffolds showed a higher level of hepatic markers than those cultured in tissue culture plates. Moreover, the albumin and urea synthesis were significantly higher in dAM scaffolds than those cultured in culture dishes over the same differentiation period. Thus, based on our results, dAM scaffold might have a considerable potential in liver tissue engineering, because it can improve hepatic differentiation of hiPSCs which exhibited higher level of hepatic marker and more stable metabolic functions.

**KEYWORDS:** Liver tissue engineering; Amniotic membrane; decellularized scaffold; human induced pluripotent stem cells; hepatic differentiation
Aromatic cluster improves stability of Chondroitinase ABC I enzyme

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Chondroitinase ABC I (ChABC I) is a bacterial enzyme that can remove chondroitin sulfate glycosaminoglycans from proteoglycans without any deleterious effects in vivo and promotes axonal re-growth and behavior recovery in spinal cord injury. However, the sustained delivery of bioactive ChABC I is a challenge requiring highly invasive methods such as intra-spinal injections, insertion of intrathecal catheters, or implantation of delivery vehicles directly into the tissue. ChABC I is thermally unstable, further complicating its delivery. In other hand, tyrosine has been shown to be more effective in creation of stable clusters and further stabilize of the proteins. Bioinformatics approaches have been used to examine the effect of an extra aromatic cluster at the surface of ChABC I. In this study two amino acids i.e., Asn⁸⁰⁶ and Gln⁸¹⁰ were mutated to tyrosine and to alanine as negative control. In this way, four variants i.e., N806Y/Q810Y, N806A/Q810Y, N806Y/Q810A and N806A/Q810A were created. The results showed that N806Y/Q810Y mutation improved both activity and thermal stability of the enzyme while Ala substitution reduced the enzyme activity and destabilized it. Structural analysis of mutants showed an increase in intrinsic fluorescence intensity and secondary structure content of N806Y/Q810Y mutant when compared to the wild type enzyme indicating a more rigid structure of this variant. Moreover, the N806Y/Q810Y enzyme displayed a remarkable resistance against trypsin degradation with a half-life ($t_{1/2}$) of 45.0min versus 32.5min of wild-type. In conclusion, the data revealed that structural features and activity of ChABC I can be improved by introducing appropriate aromatic clusters at the surface of the enzyme.
KEYWORDS: Chondroitinase ABC I; Aromatic cluster; Enzyme Stability; Spinal Cord Injury.
PBG-56
Advances in nano-delivery systems for doxorubicin to reduce Cardiotoxicity

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Abstract

Doxorubicin (Dox) is the most effective chemotherapeutic drug developed against broad range of cancers such as solid tumours, transplantable leukemias and lymphomas. Conventional Dox-induced cardiotoxicity has limited its use. We fabricated a targeted delivery system for Dox using β-1,3-glucan (Glu) extracted from cell wall of Candida albicans which shown comparatively reduced cardiotoxicity. The entrapment of Dox in biocompatible, biodegradable and safe nano delivery systems can prevent its degradation in circulation minimising its toxicity. To investigate heart damage through treatment, the levels of several indicator enzymes were measured in serum of female Balb/C mice. The levels of the cardiac enzymes (AST, LDH and CKmb) showed that, in the cases of treatment with Glu-Dox significantly reduced in serum (160, 231, and 270 respectively) while the group with Dox alone showed evident abnormalities (370, 900 and 1342 respectively compared to the control (150, 230, and 255 respectively). This novel method is a promising strategy to reduce Cardiotoxicity of Dox.

Key words: Nano-delivery systems, Doxorubicin, Cardiotoxicity.
PBG-57
Computational prediction of linear and discontinuous epitopes in *Echinococcus granulosus* antigen B/1

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**Background:** Antigen B of *E. granulosus* (EgAgB) is an important protein of hydatid cyst fluid that have roles in immunogenicity and preparation of antibodies against CE. As an endemic region for CE, molecular and computational surveys on the mentioned gene and related protein have less done in Iran. This study aimed to use molecular and computational analysis in an important subunit of antigen B (EgAgB/1) of *E. granulosus* in Iran.

**Materials and methods:** Sequences of EgAgB/1 gene were achieved by using specific primers. Three-dimensional structure of the desired amino acid sequence was created by online software to find best discontinuous epitopes. To predict of
desired epitopes, online epitope software prediction including IEDB (http://www.iedb.org/) and SYFPEITHI (www.syfpeithi.de/) was used.

**Results:** According to the results obtained from linear and discontinuous epitopes, the specified residues (a total 3 epitopes) can be considered as a potential candidate for *E. granulosus* vaccines and drug targets.

**Conclusion**

The EgAgB1 as immunogenic protein could be useful for computational investigations. The finding of this study provide the bases for the future investigations on this important protein.

**Keywords:** Computational, *Echinococcus*, Genotype, Antigen B
Background: Toxoplasmosis is a cosmopolitan zoonotic infection, caused by a unicellular protozoan parasite known as Toxoplasma gondii (T. gondii) that belongs to the phylum Apicomplexa. The present investigation was aimed to evaluate the seroprevalence of T. gondii infection in the general population of Abadan city.

Methods: In this cross-sectional study, a total of 496 subjects were participated. Anti-T. gondii IgG and IgM antibodies were tested using commercially available enzyme-linked immunosorbent assay (ELISA). Moreover, a structured questionnaire was completed for each person.

Results: Out of 496 subjects, 188 (37.9%) and 30 (6.05%) samples were seropositive for IgG and IgM, respectively. The more seroprevalence was found during spring season, among female subjects, in rural inhabitants, in persons with the education level of diploma or lower, from the subjects with a history of contact with cat, in individuals who consumed raw/undercooked meat, and amongst who drink unpurified water.
Conclusion: The results showed that inhabitants of tropical areas, may be heavily exposed to *T. gondii*. Increase of knowledge of people about toxoplasmosis, certainly affects in reduction of the infection.

Keywords: *Toxoplasma gondii*, Seroprevalence, ELISA, Abadan, Iran
Investigation of AIDS Epidemiology in southern Kerman province during 2011 to 2018

Ali khajeh Bahrami

Abstract:

Background and Objectives: HIV-immunodeficiency syndrome is one of the most common diseases in many societies. AIDS is still considered one of the deadliest diseases in the world, according to current statistics. Considering the importance of this disease and identifying ways of transmission and prevention based on the epidemiology of disease, this study was conducted with the aim of investigating the epidemiology of AIDS in southern Kerman province from 2011 to 2018.

Materials and methods: This cross-sectional study was conducted. The case of 40 patients with HIV / AIDS in the southern province of Kerman, who were filed at the Jiroft University of Medical Sciences from 2011 to 2018, were randomly selected and evaluated. Data analysis was done using descriptive statistics.

Results: According to the information obtained, the minimum age of HIV infection is 9 years and the highest age is 58 years. Sexually, 26 were male (65%) and 14 women (35%) had a 95% confidence interval. 7 were single (24.1%) and 22 were married (75.9%). Based on the level of care, 23 (59%) were under care, 12 (30.8%) were not cared for, about 3 (7.7%) did not cooperate, and 1 (2.6%) only for duration Three months are under care. According to the obtained statistics, including transmission channels in south of Kerman province, injecting drug use (48.6%), sex (42.9%), blood and products (2.9%), mother-to-child transmission (2.9%) and mother to fetus (2.9%). Injecting drug addiction is the most common way of transmission of HIV, and later it can be referred to sexual transmission.
Conclusion: The results show that injecting drug addiction is the most common way of transmission of HIV in southern Kerman province. By studying the causes of addiction and reducing addiction, it is likely that effective measures have been taken to reduce the incidence of AIDS in the area.

Key words: AIDS _ HIV _ Epidemiology _ South of Kerman province.
Abstract

**Background:** Immunoglobulins (Igs) have a vital role in defending the body against infections and eradicating them. Immunoglobulin G (IgG) is an important defensive tool against the microorganisms. The serum IgG rate changes in numerous diseases including immunodeficiencies and autoimmunity. Hence IgG has great diagnostic significance. Careful assessment of IgG needs elusive diagnostic implements such as anti IgG- specific monoclonal antibodies (MAbs). Immunogenic determinants are valuable for producing very accomplished MAbs. More flexible areas in a molecule are more immunogenic. Immunoinformatic is helpful in fine delineation of immunogenic determinants through characterization of their physiochemical traits including flexibility by computational study. In this study the flexibility of human IgG heavy chains constant domains has been evaluated by immunoinformatic.
Methods: Amino acid sequence and third structure of human IgG was achieved in PDB database. Second IgG construction was identified by Phyre 2 software. IgG heavy chains flexible segments were recognized by IEDB software.

Results: Most flexible areas were situated in 111 – 125, 175-241, 275-311, 321-345 and 375-415 amino acid arrangements of IgG heavy chains as was detected by IEDB software.

Conclusion: Conferring to our data, the amino acid sequences sited in 111 – 125, 175-241, 275-311, 321-345 and 375-415 locations which are positioned in constant domains of human IgG heavy chains, establish the most flexible areas and consequently are very valuable tools for definition of more immunogenic determinants of human IgG to making highly sensitive and specific anti - IgG MAbs.

Key words: Human IgG, computational, flexibility
PBG-62

Bioinformatics Analysis of Toxin Antitoxin Loci in *Pseudomonas aeruginosa*

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Abstract:

**Background:** *Pseudomonas aeruginosa* is responsible for many infections which harbor many antibiotic resistance and virulence genes. Some focused to toxin antitoxin (TA) systems demonstrated a regulon role of these systems in *P. aeruginosa*. Therefore, in an analysis, we tried to evaluate the potent TA loci and suggesting some of them for experimental analysis.

**Methods:** For identification the novel potent TA loci, RASTA (http://genoweb1.irisa.fr/duals/RASTA-Bacteria/) database was subjected. As described by RASTA database, the scores of those TA loci with more than 50% were focused (because their sequences have at least 50% similarity with existed TA loci in the other databases). For this reason and reliable obtained results, *Pseudomonas aeruginosa* B136-33 was selected for evaluation.
Results: After survey in RASTA database, we faced with approximately 355 different potent TA loci, while it seems to be more, but the analysis nicely indicated the abundance of those TA loci in 50-60% scores were dominant. Hence, the possibility of TA loci came down. When we looked to the top of scores, only 0.28% (n = 5) is shining (figure 1). The only TA locus in this score was higB and there was no unknown potent TA loci obtained. Generally, among all predicted TA loci as listed in table 1, higB, parE, cog3609, vap1, hicB and hth-xre as known TA loci allocated 5, 1, 2, 3, 16, and 1 genes, respectively. While, overall, 327 unknown TA loci were predicted.

Conclusion: Despite the distribution of TA loci in all scores, but obtained results of hth-xre and unknown potent TA loci, suggested further analysis in both bioinformatics and experimental studies.

Keywords: Bioinformatics; Pseudomonas aeruginosa; Toxin antitoxin system; hth-xre
Evaluation and Analyses protein E7 Human Papillomavirus (HPV)

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Background: Human papillomaviruses (HPVs) are a group of circular double-stranded DNA viruses, showing severe tropism to mucosal tissues. HPV type 16 and 18, are the primary etiological cause for several epithelial cell malignancies, Cervical cancer is the fourth most common cancer in women globally. Due to the high prevalence and mortality, HPV-associated cancers have remained as a significant health problem in human society, making an urgent need to develop an effective therapeutic vaccine against them. Achieving this goal is primarily dependent on the identification of efficient tumor-associated epitopes, inducing a robust cell-mediated immune response. Previous information has shown that E5, E6, and E7 early proteins are responsible for the induction and maintenance of HPV-associated cancers. Therefore, the prediction of (MHC) class I T cell epitopes of HPV16, 18, 31 and 45 oncoproteins was targeted in this study.

Methods: Bioinformatics methods were funded by the NCBI National Bank and the World Bank for E7 human papillomavirus genome. For this purpose, a two-step plan was designed to identify the most probable CD8+ T cell epitopes. In the first step, MHC-I and II binding, MHC-I processing, MHC-I population coverage and MHC-I immunogenicity prediction analyses, and in the second step, MHC-I
and II protein-peptide docking, epitope conservation, and cross-reactivity with host antigens' analyses were carried out successively by different tools.

**Results:** Finally, we introduced five probable CD8+ T cell epitopes for each oncoprotein of the HPV genotypes (60 epitopes in total), which obtained better scores by an integrated approach.

**Conclusion:** These predicted epitopes are valuable candidates for in vitro or in vivo therapeutic vaccine studies against the HPV-associated cancers. Additionally, this two-step plan that each step includes several analyses to find appropriate epitopes provides a rational basis for peptide-based vaccine development.