مقالات منتشرشده مرکزتحقیقات بیماریهای عفونی و گرمسیری در سال ۲۰۱۷(۱۳۹۶)

1-Abdizadeh, M. F., et al. (2017). "A novel medium-throughput biological assay system for HTLV-1 infectivity and drug discovery." Iranian Journal of Basic Medical Sciences 20(10): 1109-1118.

Objective(s): Here, a reporter cell line containing two reporter vectors were developed, in order to monitor the Human T-Lymphotropic Virus type1(HTLV-1) infectivity and the cell viability simultaneously. Materials and Methods: The reporter cell line was constructed by stably transfected baby hamster's kidney cell line (BHK-21), with the genomes expressing two different reporters in separate plasmids. The first reporter gene is transactivated by the HTLV-1 tax protein, while the second reporter is continuously expressed when introduced into a mammalian cell. In order to show its functionality, the effect of the drug mix on HTLV-1 was assayed by this system and was compared to the results obtained by other methods. Results: HTLV-1 reporter cell line was found to produce high level of luciferase when co-cultured with MT-2 and Hut-102 cells but not with Jurkat cell. Moreover, the combination therapy against HTLV-1 can reduce luciferase expression of the cell when co-cultured with MT-2 and Hut-102 comparable to the ELISA (R=0.932, P-value = 0.002). In addition, the results revealed the superiority of the present system over the molecular methods. Conclusion: The results demonstrated that the biological assay system is a beneficial tool for the medium-throughput anti-HTLV-1 drug screening and inhibitory effect.

2-Ahmadi, M., et al. (2017). "A novel salt-tolerant bacterial consortium for biodegradation of saline and recalcitrant petrochemical wastewater." Journal of Environmental Management 191: 198-208.

Treatment of a saline petrochemical wastewater with BOD5/COD ratio of less than 0.1 was investigated using a consortium consisted of three isolated salt-tolerant bacteria namely, Kocuria turfanesis, Halomonas alkaliphila and Pseudomonas balearica. Selected bacteria were isolated from petrochemical wastewater containing mineral salt mediums of 3% salinity. A lab-scale activated sludge bioreactor was used for startup in batch mode operation and after obtaining the MLSS concentration of about 3000 mg/L, the operation was changed to continuous flow mode to determine the biokinetic coefficients under different organic loading rates of 0.33-1.21 kg CODm(-3) d(-1). The COD removal efficiency of 78.7%-61.5% was observed for treatment of real saline wastewater with a decreasing trend along with increasing the organic loading rate. In addition, results of kinetic investigation demonstrated that the yield(Y), endogenous decay coefficient (K-d), maximum reaction rate (K-max), maximum specific growth rate (mu(max)) and

saturation constant (K-s) were 0.54 mg VSS mg COD-1, 0.014 day(-1), 1.23 day(-1), 0.66 day(-1), and 1315 mg 171, respectively. (C) 2017 Elsevier Ltd. All rights reserved.

3- Amin, M., et al. (2017). "In vitro antimicrobial activities of metabolites from vaginal Lactobacillus strains against Clostridium perfringens isolated from a woman's vagina." Journal of the Chinese Medical Association 80(1): 29-33.

Background: More than 50 different species of bacteria may live in a woman's vagina, with lactobacilli being the predominant microorganism found in healthy adult females. Lactobacilli are relevant as a barrier to infection and arc important in the impairment of colonization by pathogens, owing to competitive adherence to adhesion sites in the vaginal epithelium and their capacity to produce antimicrobial compounds. Methods: The aim of the present study was to demonstrate the inhibitory capability of Lactobacillus metabolites against Clostridium perfringens, an anaerobic Gram-positive bacterium. These bacteria were isolated from vaginal swabs by using culture-dependent approaches, and the bacteriostatic effect of Lactobacillus metabolites, extracted from different isolates, was assessed using a modified E test. Results: Among the 100 vaginal swabs, 59 (59%) samples showed the presence of Lactobacillus strains and only one sample contained C. perfringens. Lactobacillus metabolites demonstrated the significant potency of in vitro activity against C. perfringens, with minimal inhibitory concentration values ranging from 15.6 mu g/mL to 31.2 mu g/mL. Conclusion: This study suggests that women without vaginal Lactobacillus strains may be susceptible to nonindigenous and potentially harmful microorganisms. Copyright (C) 2016, the Chinese Medical Association. Published by Elsevier Taiwan LLC. This is an open access article under the CC BY-NC-ND license.

4- Arshadi, M., et al. (2017). "High prevalence of diverse vancomycin resistance Enterococcus faecium isolates in clinical and environmental sources in ICU wards in southwest of Iran." Microbial Pathogenesis 111: 212-217.

This study aimed at determining the prevalence, antibiotic resistance patterns, and genetic linkage of Vancomycin Resistant Enterococcus faecium (VREfm) from different sources in the southwest of Iran. A total of 51 VREfm isolates were obtained and subjected to antibiotic susceptibility testing, carriage of virulence genes, and pulsed-field gel electrophoresis (PFGE) method. All the VRE isolates exhibited a high level of resistance to teicoplanin, ampicillin, erythromycin, ciprofloxacin, and gentamicin, also carried the vanA gene. A total of 59% and 34% of the VREfm strains harbored esp and hyl genes, respectively. The results from PFGE showed 31 PFGE patterns including 10 common types (CT) and 21 single types

(ST) among the VRE isolates. Furthermore, isolates from different sources in each common type revealed cross transmission between clinical and environmental sources. Overall, the study showed a high prevalence of diverse VRE faecium strains with threatening resistance phenotypes in the environment and clinical sections among different ICU wards of Ahvaz hospitals. (C) 2017 Elsevier Ltd. All rights reserved.

5-Azizolahi, B., et al. (2017). "Cloning and Expression of a Secretory form of Truncated ORF2 (112-607 aa) from Hepatitis E Virus in the pVAX1 Vector." Jundishapur Journal of Microbiology 10(11).

Background: The hepatitis E virus (HEV) accounts for the hepatitis E infection with a high mortality rate in pregnant women. Therefore, the design of the novel and effective vaccines seems essential and the DNA vaccine approach could be useful to achieve this anticipated goal. Objectives: The present study aimed at cloning the lone tPAsp-PADRE-truncated ORF2 (112-607 aa) from HEV into the eukaryotic expression pVAX1 vector and evaluating the expression of this recombinant protein in eukaryotic cells. Methods: The truncated ORF2 gene (112-607 aa) was cloned in the pVAX plasmid, followed by digestion, and confirmed by digestion and sequencing. Then, the recombinant plasmid was transfected into eukaryotic cells to confirm expression. The expressed protein in the cell lysate and supernatant was evaluated by immunofluorescence assay (IFA) andWestern blot assay. Results: The cloning of the tPAsp-PADRE-truncated ORF2 gene (112-607 aa) to the pVAX1 eukaryotic expression path was set by colony PCR, restriction enzymes digestion, and DNA sequencing of the recombinant plasmid. The appearance of the truncated ORF2 protein in the eukaryotic cells was accepted by the Western blot assay, reverse transcriptase polymerase chain reaction (RTPCR) method, and the immunofluorescence assay (IFA). Conclusions: All outcomes of the present research showed that pVAX-tPAsp-PADRE-Truncated ORF2 (112-607 aa) recombinant plasmid was able to express truncated ORF2 from HEV as a potential candidate vaccine.

6-Azizolahi, B., et al. (2017). "Low detection of hepatitis B and occult hepatitis B infection in patients with rheumatic diseases." Egyptian Rheumatologist 39(4): 239-243.

Background: A new form of hepatitis B virus (HBV) infection, occult hepatitis B infection (OBI), has been identified and reported among patients with rheumatic diseases. Aim of the work: To determine the incidence of HBV infection and OBI in patients with rheumatic diseases referred to major hospitals in the city of Ahvaz in Iran. Patients and methods: 136 patients with rheumatic

diseases were included. Serological assays for HBV markers (HBsAg, HBcAb and HBsAb) were performed by enzyme-linked immunosorbent assay. All the sera were tested for HBV DNA using nested PCR and real-time PCR. All samples were negative for antiHCV and anti-HIV antibodies. Results: The mean age of the patients was 43.5 +/- 12.02 years with a F: M 2.24: 1. 2 (1.47%) cases with undifferentiated connective tissue disease tested positive for both HBsAg and HBV DNA. Quantitative HBV real-time PCR was carried out for the 134 negative HBsAg samples and only 1 (0.74%) patient was positive for OBI. The results of sequencing and alignment showed that the detected HBV DNAs belonged to the D genotype, ayw2 subtype. The nucleic acid sequence of OBI case revealed substitution changes in amino acids in the positions of the 171-4 of HBsAg gene. Conclusion: A moderate rate of HBV infection and low detection of OBI is found in patients with rheumatic diseases in southwest Iran. The amino acid substitutions and mutation have been observed at the position of 171-4 in the S gene region of HBV DNA which may affect the detection of HBsAg by commercial immunoassay methods. (C) 2017 Egyptian Society of Rheumatic Diseases. Publishing services provided by Elsevier B. V.

7- Balootaki, P. A., et al. (2017). "Isolation and Detection of Erysipelothrix rhusiopathiae and Its Distribution in Humans and Animals by Phenotypical and Molecular Methods in Ahvaz-Iran in 2015." Iranian Journal of Medical Sciences 42(4): 377-383.

Background: Erysipelothrix rhusiopathiae (E. rhusiopathiae) is generally transmitted into the gastrointestinal tract of animals by the intake of contaminated food or water and causes great economic loss in agriculture worldwide. Some of the Erysipelothrix spp. are the causative agents of erysipeloid, which is an occupational infection in humans. The aim of the present study was to isolate E. rhusiopathiae from animals as well as the hands of the butchers working in Ahvaz, Iran, and to determine their susceptibility to antibiotics. Methods: Totally, 150 samples were taken from slaughterhouse workers, fishermen, and livers and hearts of sheep and calves by the swabbing method. Phenotypical methods and polymerase chain reaction (PCR) were used for the isolation and identification of E. rhusiopathiae. The isolates were tested for their susceptibility to commonly used antimicrobial agents using the disk diffusion protocol described by the Clinical and Laboratory Standards Institute. Results: Out of the 150 samples examined via phenotypical and biochemical tests, 16 samples were positive as putative Erysipelothrix spp. twelve cases out of the 16 putative Erysipelothrix spp. were confirmed by PCR. The tested isolates were highly sensitive to the antibiotics used. The results of the sensitivity and specificity of PCR revealed that the sensitivity and specificity of indirect PCR were higher than those of direct PCR. Conclusion: E. rhusiopathiae is widely distributed on seafood and presents as a commensal pathogen in nature and animals. Infection with this microorganism should be emphasized because it is a rare organism causing severe infections such as infectious endocarditis and polyarthritis following localized infections.

8- Beiromvand, M., et al. (2017). "Comparative Prevalence of Blastocystis in Patients with the Irritable Bowel Syndrome and Healthy Individuals: A Case Control Study." Jundishapur Journal of Microbiology 10(6).

Background: Blastocystis is one of the most common anaerobic protozoa found in the intestinal tract of humans and various animals, with a worldwide distribution. The parasite has been linked to the pathogenesis of the irritable bowel syndrome (IBS), previously. Objectives: The aim of this study was to evaluate the prevalence of Blastocystis in IBS patients compared to healthy individuals. Methods: The collected feces from 152 patients with Gastrointestinal (GI) symptoms, and 130 healthy volunteers from Ahvaz, southwest Iran, were examined using the direct saline smear, Lugol's iodine staining, and inoculated in a Jones' medium for Blastocystis detection. The DNA was extracted from all culture-positive samples, and then the polymerase chain reaction (PCR) was performed by the SSU-rDNA gene. Results: Blastocystis was identified in 18 (6.4%) samples, including two (1.3%) of the IBS patients and 16 (12.3%) of the control group by microscopy. Stool culture was positive in 15 with IBS, one without IBS, and 40 control samples. From these, the expected 600 bp fragments of the SSU-rDNA gene were identified in 15 (27.3%) cases and 40 (72.7%) controls. Subtypes (STs) 1, 2, and 3 were identified from the 54 successfully sequenced samples. Subtype 3 was the most common ST with the frequency of 46.3%, followed by ST2, 37% and ST1, 16.7% in the case and control groups. The highest frequency of Blastocystis STs (27.8%) was identified in the age group of 31-40 years and the lowest was found in the age groups of under 10 years and over 81 years. Conclusions: The findings of the current studyshowedthat Blastocystis wasmorecommonin the control group compared to the IBS patients. Therefore, our findings highlight the contrast between Blastocystis infection and GI disorders. Furthermore, these results support the hypothesis that Blastocystis could be a GI health marker.

9-de Hoog, G. S., et al. (2017). "Toward a Novel Multilocus Phylogenetic Taxonomy for the Dermatophytes." Mycopathologia 182(1-2): 5-31.

Type and reference strains of members of the onygenalean family Arthrodermataceae have been sequenced for rDNA ITS and partial LSU, the ribosomal 60S protein, and fragments of b-tubulin and translation elongation factor 3. The resulting phylogenetic trees showed a large degree of correspondence, and topologies matched those of earlier published phylogenies demonstrating that the phylogenetic representation of dermatophytes and dermatophyte-like fungi has reached an acceptable level of stability. All trees showed Trichophyton to be polyphyletic. In the present paper, Trichophyton is restricted to mainly the derived clade, resulting in classification of nearly all soudanense, and T. verrucosum. In the newly proposed taxonomy, Trichophyton contains 16 species, Epidermophyton one species, Nannizzia 9 species, Microsporum

3 species, Lophophyton 1 species, Arthroderma 21 species and Ctenomyces 1 species, but more detailed studies remain needed to establish species borderlines. Each species now has a single valid name. Two new genera are introduced: Guarromyces and Paraphyton. The number of genera has increased, but species that are relevant to routine diagnostics now belong to smaller groups, which enhances their identification.

10-Fathi, N., et al. (2017). "An in vitro study on Hemiscorpiuslepturus (scorpionida: Hemiscorpiidae) venom cytotoxicity effects on K562 cells." Research Journal of Pharmaceutical Biological and Chemical Sciences 8(2): 45-51.

Objective of this study was to evaluate the capacity of Hemiscorpiuslepturus venom on K562 cell lines which had been derived from human chronic myeloid leukemia (CML). After calculating the concentration of protein venom by Bradford method, the cells were treated with H.lepturus venom using an increasing rate of concentrations during a 24 hour incubation period. Inhibition of CML growth was assessed by MTT assay. IC50 was determined about 14 mu g/ml.

11-Geravandi, S., et al. (2017). "Prevalence of Nosocomial Infection at a Razi teaching Hospital, during 2010-2015." Research Journal of Pharmaceutical Biological and Chemical Sciences 8(1): 542-548.

There is no doubt that Nosocomial Infections (NIs) have adverse impacts on patients and sometimes the health care workers (HCWs). NIs causes an extra cost of health care. The main objective of this study was to evaluate the prevalence of NIs in Razi teaching Hospital, Ahvaz, southwest of Iran, during 2010-2015. The present study was a descriptive and cross-sectional study. This study, conducted on all the patients who were hospitalized with signs and symptoms of infection after 48 hours of hospitalization in Razi teaching Hospital in Ahvaz, Iran, during 2010-20145. Data was taken from Infection Disease Committee (IDC). Sampling was already performed for 6 years during 2010-2015. Data about the patients' site of infection, ward of hospitalization, type of NIs were collected. Raw data of NIs was processed using Excel software. After processing data, outputs were classified into charts and tables in term of Nosocomial infections cases. Based on our result, the highest cases for NIs observed in 2015. We concluded that the incidence of NIs was low (< 2%) in this hospital during 2010-20145. Numbers of NIs were estimated 128, 142, 174, 154, 189 and 207 persons for 2010, 2011, 2012, 2013, 2014 and 2015, respectively. The results of the present study showed that the Most NIs was reported in wards of obstetrics and gynecology (OBGYN). Regarding the etiology of infection, Escherichia coli were the most frequent pathogen. The finding of this study showed that the incidence of NIs was lower than national standard. We also noticed that Number of NIs during six successive years were term of increasing.

12-Geravandi, S., et al. (2017). "Risk of Sharps and Needle Stick Injuries among health care workers in a Teaching Hospital, southwest of Iran." Research Journal of Pharmaceutical Biological and Chemical Sciences 8(1): 912-918.

Needle stick injuries (NSIs) are one of the most important threats for the health care workers (HCWs) in teaching hospitals. Our aim was to estimate the Prevalence of Needle Sticks Injuries (NSIs) among Health Care Workers (HCWs) in a teaching hospital of Ahvaz, southwest of Iran, during 2014. This study was a descriptive incidence one conducted on 600 HCWs at the Razi hospital of Ahvaz, Iran. Data about health care workers, type of NSIs, wards and their activities were collected. Data were summarized, using descriptive statistical methods which were processed with SPSS version 16. Based on the results, nurses were at highest risk of NSIs among other HCW groups. In this hospital, 41 cases of NSIs were found. Based on the findings, recapping needles was found in 36.58%, handling needle on a tray in 21.95%, suturing in 17.07%, passing needle in 12.19%, transit of disposal needle devices in 4.87% and dissembling needle devices in 7.31% of cases. The most NSIs were reported in the wards of general surgery, ICU, emergency, obstetrics and gynecological (OBGYN), orthopedic, operating room, and infectious diseases during 2014. The results indicated that recapping the needles was the most risk factor for NSIs. According to the findings of our study, Number of NSIs among nurses was higher compared to other health care workers The finding of this study showed that training programs related to the prevention of NSIs would be one of the priorities in the Razi teaching hospital.

13- Ghafari, S., et al. (2017). "Prevalence of HIV-1 transmitted drug resistance in recently infected, treatment-naive persons in the Southwest of Iran, 2014-2015." Archives of Virology 162(9): 2737-2745.

The emergence and transmission of drug resistant HIV mutants is a major concern, especially in resource-limited countries with expanding antiretroviral therapy. Studies have recently reported the prevalence of HIV-1 transmitted drug resistance (TDR) mutations in certain Iranian cities; however, no information is currently available about the level of TDR, as well as the nature of the circulating HIV-1 subtypes, in the Southwestern bordering province of Iran, Khuzestan. Herein, we used a WHO-recommended TDR survey method to classify the prevalence of TDR in indigenous people of Khuzestan province. For this purpose, between March 2014 and February 2015, blood samples were collected from 52 newly diagnosed, antiretroviral treatment-na < ve, HIV-1 infected persons aged from 18 to 30 years. TDR mutations were determined by sequencing the protease (PR) and reverse transcriptase (RT) genes and interpreted using the WHO drug resistance mutations surveillance list. HIV-1 subtypes were characterized by sequencing the PR-RT, C2-V5, and p17 regions of the pol, env and gag genes, respectively. Two participants had non-nucleoside reverse transcriptase inhibitor (NNRTI) resistance mutations, specifically K103N in one individual and K101EK/K103KN/G190AG in the other. No nucleoside reverse transcriptase

inhibitor (NRTI) or major protease inhibitor (PI) mutations were identified. HIV-1 subtyping revealed that all participants were infected with HIV-1 CRF35_AD. According to the WHO sequential sampling method, the prevalence of HIV-1 TDR in the sampling area (Khuzestan province) was classified as moderate for NNRTIs and low for NRTIs and PIs. This is the first HIV-1 drug resistance threshold survey in the Khuzestan province of Iran and shows a predominance of NNRTI TDR mutations in this area.

14- Gohar, A. A., et al. (2017). "Expression Patterns of ABC Transporter Genes in Fluconazole-Resistant Candida glabrata." Mycopathologia 182(3-4): 273-284.

Clinical management of fungal diseases is compromised by the emergence of antifungal drug resistance in fungi, which leads to elimination of available drug classes as treatment options. An understanding of antifungal resistance at molecular level is, therefore, essential for the development of strategies to combat the resistance. This study presents the assessment of molecular mechanisms associated with fluconazole resistance in clinical Candida glabrata isolates originated from Iran.

15-Goudarzi, G., et al. (2017). "ASSOCIATION OF PARTICULATE MATERS ATTRIBUTED TO OUTDOOR AIR IN AHVAZ, IRAN DURING COLD -WARM SEASON OF 2017." Fresenius Environmental Bulletin 26(8): 5428-5433.

Microscopic solid or liquid matter suspended in earth's atmosphere is definition atmospheric particulate matter. Particles with diameters that are generally 10 micrometers and smaller (PM10) are one of the main components of indoor and outdoor air quality that can very dangerous for humans. The purpose of this study was to assess the Milo of the outdoor air in in Ahvaz outdoor air at industrial, high traffic and residential areas during the warm and cold seasons of 2017. Data collected was performed by used active sampling system. High volume air samplers and equipped with quartz filters were utilized for sampling in this study. In this study for determine and analyzed the effects of PMic, during warm and cold season was used to Statistical software SPSS version 16. The results show that the average PM10 concentration in cold and warm season were 156 and 139 g/m3, respectively. Result of this study showed the mean of PK10 concentration in cold season was significantly higher than standard. Also, according to results level of PM10 during cold season were higher than the warm season. We can reduce the exposed to PMio in outdoor air by increase environmental monitoring, decreasing PM10 in source and increase knowledge.

16-Haddad, M. H. F., et al. (2017). "Antimalarial evaluation of selected medicinal plant extracts used in Iranian traditional medicine." Iranian Journal of Basic Medical Sciences 20(4): 415-422.

Objective(s): In an attempt to discover new natural active extracts against malaria parasites, the present study evaluated the antiplasmodial properties of selected plants based on Iranian traditional medicine. Materials and Methods: Ten plant species found in Iran were selected and collected based on the available literature about the Iranian traditional medicine. The methanolic extracts of these plants were investigated for in vitro antimalarial properties against chloroquine-sensitive (3D7) and multidrug resistant (K1) strains of Plasmodium falciparum. Their in vivo activity against Plasmodium berghei infection in mice was also determined. Cytotoxicity tests were carried out using the Raji cells line using the MTT assay. The extracts were phytochemically screened for their active constituents. Results: According to the IC50 and selectivity index (SI) values, of the 10 selected plant species, Citrullus colocynthis, Physalis alkekengi, and Solanum nigrum displayed potent in vitro antimalarial activity against both 3D7 and K1 strains with no toxicity (IC50= 2.01-18.67 mu g/ml and SI= 3.55 to 19.25). Comparisons between treated and untreated control mice showed that the mentioned plant species reduced parasitemia by 65.08%, 57.97%, and 60.68%, respectively. The existence of antiplasmodial compounds was detected in these plant extracts. Conclusion: This was the first study to highlight the in vitro and in vivo antiplasmodial effects of C. colocynthis, P. alkekengi, and S. nigrum in Iran. Future studies can use these findings to design further biological tests to identify the active constituents of the mentioned plant species and clarify their mechanism of action.

17-Heidarnejadi, S. M., et al. (2017). "Neonatal Rat; A Suitable Animal Model for Experimental Cryptosporidiosis." Jundishapur Journal of Microbiology 10(7).

Background: Cryptosporidiosis is a major public health problem for neonatal livestock worldwide. Cryptosporidium parvum infects intestinal epithelial cells via contaminated food or drinking water and leads to cryptosporidiosis. Most of the animal model studies on infectivity of C. parvumare conducted on the neonatal mice. Objectives: The current study aimed at evaluating the infectivity of C. parvum in neonatal rat as an animal model. Methods: A dose of 100,000 to 120,000 C. parvum oocysts (Iowa strain, BTF Company, Sydney, Australia) was orally inoculated in a group of 30 neonatal Wistar rats aged 2 days old. Eight days postinfection, jejunum, ileum, cecum, colon, and rectum were removed and contents were homogenized and purified using sucrose gradient method. Results: Our results indicated that 6 to 12 million C. parvum was found per rat Conclusions: Analysis of the study results revealed that the neonatal rat could be used as an alternative animal model to investigate C. parvum.

18- Joolayi, F., et al. (2017). "Comparison of Chlamydia trachomatis infection among infertile and fertile women in Ahvaz, Iran: A case-control study." International Journal of Reproductive Biomedicine 15(11): 713-718.

Background: Chlamydia trachomatis (C. trachomatis) is the main cause of bacterial sexually transmitted infections. In women, this infection can lead to tubal infertility. Objective: In this study we investigated C. trachomatis among infertile and fertile women with both polymerase chain reaction (PCR) and ELISA methods in Ahvaz, Iran. Materials and Methods: This case-control study was conducted at the Infertility Clinic of University Jahad, Ahvaz, Iran from January to August 2017. A total of 225 vaginal swabs and blood samples (100 infertile and 125 fertile women) were collected. Detection of C. trachomatis DNA was performed from vaginal swabs by amplification of MOMP gene. Also, anti C. trachomatis immunoglobulin M (IgM) and immunoglobulin G antibodies in the serum samples were recognized by enzyme-linked immunosorbent assay (ELISA). Results: Results showed that, 6 (6%) infertile and 2 (1.6%) fertile women were positive for IgM (p=0.21). Also, PCR was positive for C. trachomatis infection in 5 infertile (5%) and 2 fertile women (1.6%) (p=0.35). We did not find any seropositive immunoglobulin G in both groups. Conclusion: In this study, no significant difference was found between fertile and infertile groups for C. trachomatis infection. Also, the correlation between IgM and PCR results revealed a relatively strong agreement and seems both PCR and IgM assays are appropriate for the accurate diagnosis of C. trachomatis infections.

19-Khademvatan, S., et al. (2017). "Spatial distribution and epidemiological features of cutaneous leishmaniasis in southwest of Iran." Alexandria Journal of Medicine 53(1): 93-98.

Introduction: Leishmaniasis, as a major health concern exists in 14 out of 22 countries of the Eastern Mediterranean Region (EMR). Therefore, the aim of present investigation was to evaluate the epidemiological features and spatial distribution of cutaneous leishmaniasis (CL) during six consecutive years (2009-2014). Material and methods: In current retrospective cross-sectional study among 2009-2014, simple direct smear was taken from all suspicious CL subjects who referred to health centers affiliated to Ahvaz Jundishapur University of Medical Sciences. For each patient a questionnaire including some demographic details was filled. Eventually data analysis was done by SPSS.16. Results: Trend of CL in the region was unstable. Spatial distribution of CL in central and west cities was higher than in others. During the years, a total of 4137 smear positive individuals were diagnosed. Of these 55.7 A lived in urban and 44.3 A lived in rural districts. Frequency of CL was higher in men (60.1%) than in women (39.9 A). Also based on age range, 11-30 was the most afflicted group (45.7 A). Anatomic location of ulcers was as follows: hands 45.7 A, feet 27.4 A, face 19.1% and other places 7.8%. Conclusions: Regarding high incidence of CL in southwest of Iran, special programs related to vector and reservoir control

should be adopted and implemented. Traffic control of immigrants and travelers from neighboring endemic countries, also can be helpful. (C) 2016 Alexandria University Faculty of Medicine. Production and hosting by Elsevier B.V. This is an open access article under the CC BY-NC-ND license (http://creativecommons.org/licenses/by-nc-nd/4.0/).

20-Khaefi, M., et al. (2017). "Association of Particulate Matter Impact on Prevalence of Chronic Obstructive Pulmonary Disease in Ahvaz, Southwest Iran during 2009-2013." Aerosol and Air Quality Research 17(1): 230-237.

Air pollutants produced in environments have many detrimental impacts on human health. Chronic obstructive pulmonary disease (COPD) is a common worldwide respiratory disease. The aim of this study was to estimate the association between the load of particulate matters and the prevalence of COPD in Ahvaz, southwest of Iran, during 2009-2013. This epidemiological and used-model study was performed in Ahvaz. Particulate matter equal or less than 10 micro meters (PM10) was monitored by Ahvaz Environmental Protection Agency (AEPA). Sampling was performed hourly during the study period in 4 stations. In this study, 175200 (4 x 24 x 365 x 5) samples of air were taken and collected. Sampling and analysis were performed according to EPA guideline. We utilized the relative risk values and baseline incidence measures by the WHO (Middle East) drawn from Health Effects Association of Particulate Matter. Finally, prevalence of COPD attributed to particulate matter exposure was calculated by Air Q model. According to our findings, the prevalence of COPD attributed to particulate matters decreased during 2009-2013 and followed a decreasing trend. Accordingly, the yearly prevalence of COPD during the period 2009-2013 were 121, 111, 94, 102, and 98, and the yearly average PM10 concentrations during the same period were 313.72, 281.98, 288.38, 278.12, and 242.29 mu g m(-3), respectively. Although the average of 5-year study was higher than WHO and NAAQS values, a descending trend for COPD indicates that the level of PM10 was diminished from 2009 to 2013. Therefore mitigating air pollutant particularly PM10 as one of the main hazards could be possibly led to remarkable decrease in the rate of mortality and morbidity particularly COPD attributed to PM10.

21-Khosravi, A. D., et al. (2017). "Identification of Mycobacterium tuberculosis in Clinical Specimens of Patients Suspected of Having Extrapulmonary Tuberculosis by Application of Nested PCR on Five Different Genes." Frontiers in Cellular and Infection Microbiology 7.

Definitive and rapid diagnosis of extrapulmonary tuberculosis (EPTB) is challenging since conventional techniques have limitations due to the paucibacillary nature of the disease. To increase the sensitivity of detection of Mycobacteriurn tuberculosis (MTB) in EPTB specimens, we

performed a nested PCR assay targeting several genes of MTB on EPTB specimens. A total of 100 clinical specimens from suspected cases of EPTB were processed. Standard staining for acid fast bacilli (AFB) was performed as the preliminary screening test. Extracted DNAs from specimens were subjected to Nested PCR technique for the detection of five different MTB target genes of 16110, 1S1081, hsp65kd, mbp64, and mtp40. On performing AFB staining, only 13% of specimens were positive, of which ascites fluid (33.3%), followed by pleural effusion (30.8%) showed the greatest AFB positivity rate. We demonstrated slight improvement in yields in lymph node which comprised the majority of specimens in this study, by employing PCR targeted to 1S6110- and hsp65-genes in comparison to AFB staining. However, the yields in ascites fluid and pleural effusion were not substantially improved by PCR, but those from bone and wound were, as in nested PCR employing either gene, the same positivity rate were obtained for ascites fluid (33.3%), while for pleural effusion specimens only 1S1081 based PCR showed identical positivity rate with AFB stain (30.8%). The results for bone and wound specimens, however, demonstrated an improved yield mainly by employing 1S1081 gene. Here, we report higher detection rate of EPTB in clinical specimens using five different targeted MTB genes. This nested PCR approach facilitates the comparison and the selection of the most frequently detected genes. Of course this study demonstrated the priority of 151081 followed by mtp40 and 156110, among the five tested genes and indicates the effectiveness of any of the three genes in the design of an efficient nested-PCR test that facilitates an early diagnosis of paucibacillary EPTB cases, which are difficult to diagnose with the available standard.

22-Khosravi, A. D., et al. (2017). "Frequency of rrs and rpsL mutations in streptomycin-resistant Mycobacterium tuberculosis isolates from Iranian patients." Journal of Global Antimicrobial Resistance 9: 51-56.

Objectives: Streptomycin (SM) is one of the most effective drugs for the treatment of multidrug-resistant (MDR) tuberculosis. However, resistance to SM is increasingly reported, mainly due to mutations in the rpsL and rrs genes. This study was designed with the aim of determining the nature of SM resistance and the type and frequency of rpsL and rrs mutations among SM-resistant Mycobacterium tuberculosis (MTB) isolates from Iran. Methods: A total of 100 clinical monoresistant and MDR MTB isolates were subjected to drug susceptibility testing (DST) for SM. SM-resistant isolates were genotyped by MIRU-VNTR typing. Fragments of the rpsL and rrs genes were amplified to investigate the most common mutations, with subsequent sequence analysis. Results: By DST, 32 isolates (32%) were identified as SM-resistant, of which 50% (16/ 32) were MDR. By MIRU-VNTR typing, the SM-resistant isolates were classified into 20 different MIRU types and 8 clusters, with Beijing (22%) being the most prevalent genotype. Mutations in the rrs and rpsL genes were identified in 14 (44%) and 10 (31%) of the 32 SM-resistant isolates, respectively. The most common mutations were at rpsL nucleotide 128 (AAG -> AGG, Lys43Arg), found in 7 SM-resistant isolates (22%) and nucleotide 263 (A -> G, Lys88Arg) in

3 SM-resistant isolates (9%). Conclusions: The results suggest an association between rpsL mutation and SM-resistant strains of Beijing genotype. The existence of SM resistance in 25% of isolates without mutation in rrs and rpsL suggests the occurrence of further mechanisms associated with SM resistance in these isolates. (C) 2017 International Society for Chemotherapy of Infection and Cancer. Published by Elsevier Ltd. All rights reserved.

23-Khosravi, A. D., et al. (2017). "Differential Identification of Mycobacterial Species Using High-Resolution Melting Analysis." Frontiers in Microbiology 8.

Infections caused by non-tuberculous mycobacteria (NTM) is increasing wordwide. Due to the difference in treatment of NTM infections and tuberculosis, rapid species identification of mycobacterial clinical isolates is necessary for the effective management of mycobacterial diseases treatment and their control strategy. In this study, a cost-effective technique, real-time PCR coupled with high-resolution melting (HRM) analysis, was developed for the differentiation of Mycobacterial species using a novel rpoBC sequence. A total of 107 mycobacterial isolates (nine references and 98 clinical isolates) were subjected to differentiation using rpoBC locus sequence in a real-time PCR-HRM assay scheme. From 98 Mycobacterium clinical isolates, 88 species (89.7%), were identified at the species level by rpoBC locus sequence analysis as a gold standard method. M. simiae was the most frequently encountered species (41 isolates), followed by M. fortuitum (20 isolates), M. tuberculosis (15 isolates), M. kansassi (10 isolates), M. abscessus group (5 isolates), M. avium (5 isolates), and M. chelonae and M. intracellulare one isolate each. The HRM analysis generated six unique specific groups representing M. tuberculosis complex, M. kansasii, M. simiae, M. fortuitum, M. abscessus-M. chelonae group, and M. avium complex. In conclusion, this study showed that the rpoBC-based real-time PCR followed by HRM analysis could differentiate the majority of mycobacterial species that are commonly encountered in clinical specimens.

24-Khosravi, A. D., et al. (2017). "Distribution of genes encoding resistance to aminoglycoside modifying enzymes in methicillin-resistant &ITStaphylococcus aureus&IT (MRSA) strains." Kaohsiung Journal of Medical Sciences 33(12): 587-593.

Today Methicillin-Resistant Staphylococcus aureus (MRSA) have acquired multiple resistance to a wide range of antibiotics including aminoglycosides. So, this study was aimed to investigate the rate of aminoglycoside resistance and the frequency of aminoglycoside resistance mediated genes of aac(la)-2, aph(3)-IIIa and ant(4')-la among MRSA strains. A total of 467 staphylococci isolates were collected from various clinical samples. S. aureus strains were identified by standard culture and identification criteria and investigating of presence of 16S rRNA

and nuc genes. Cefoxitin disk diffusion, and oxacillin-salt agar screening methods were used to detect the MRSA strains with subsequent molecular identification for the presence of mecA gene. Antibiotic susceptibility of MRSA strains against aminoglycoside antibiotics was evaluated by using agar disk diffusion method. Multiplex PCR for the presence of aac(la)-2, aph(3)-IIIa and ant(4')-la encoding genes for aminoglycosides were performed for MRSA strains. From total staphylococci tested isolates, 262 (56.1%) were identified as S. aureus, of which 161 (61.45%) were detected as MRSA and all comprised mecA gene. The resistance pattern of MRSA strains to aminoglycoside antibiotics were: gentamicin 136 (84.5%); amikacin 125 (77.6%); kanamycin 139 (86.3%); tobramycin 132 (82%); and neomycin 155 (96.3%). The frequency of aac(la)-2, aph(3)-llla, and ant(4')-la genes among MRSA strains, were 64%, 42% and 11.8% respectively. In conclusion, as MRSA strains are of great concern in human infections, the results of present study could provide a useful resource for health sectors for choosing appropriate antibiotics for the effective treatment of infections due to MRSA strains. Copyright (C) 2017, Kaohsiung Medical University. Published by Elsevier Taiwan LLC.

25-Khosravi, A. D., et al. (2017). "The frequency of class1 and 2 integrons in Pseudomonas aeruginosa strains isolated from burn patients in a burn center of Ahvaz, Iran." PLoS ONE 12(8).

Background Pseudomonas aeruginosa is an opportunistic pathogen with the ability to cause severe nosocomial infections and remains a major problem in burn patients. This organism shows a remarkable antimicrobial resistance and is often resistant to multiple antibiotics. Integron genes as mobile genetic elements are playing an important role in the spread of P. aeruginosa antibiotic resistance. This study was aimed to investigate the occurrence of class 1, and 2 integron genes (int1, int2), among P. aeruginosa strains isolated from patients with burn infections. Methods In total 93 clinical isolates of P. aeruginosa were screened. The antimicrobial susceptibilities of 9 common antimicrobial agents were tested against the isolates using disk diffusion method. PCR amplification was performed on extracted DNAs for the detection of int1, and int2 genes using the set of specific primers. Results The majority of P. aeruginosa isolates were from wound infection (69.9%). In disk diffusion method, most isolates showed remarkable resistance to tested antibiotics with highest against gentamicin (94.62%) and ciprofloxacin (93.55%). PCR amplification revealed that 89(95.7%) of P. aeruginosa strains carried int1, but none of them harbored int2 genes. The distribution of int1 gene was highest in blood (100%), followed by wound isolates (95.38%). Conclusions We demonstrated a high antimicrobial resistance among P. aeruginosa isolates in our setting. int1 was prevalent and seems to play an important role in multidrug resistance among the isolates. So, performance of antibiotic surveillance programs is necessary for choosing the appropriate therapy and management of infection control practices.

25-Khosravi, A. D., et al. (2017). "Genetic diversity of multidrug-resistant Mycobacterium tuberculosis strains isolated from tuberculosis patients in Iran using MIRU-VNTR technique." Kaohsiung Journal of Medical Sciences 33(11): 550-557.

Tuberculosis (TB) is considered as one of the most important infectious diseases in the world, and recent rise and spread of multidrug-resistant (MDR) Mycobacterium tuberculosis (MTB) strains, have made the matter worsened. Due to the importance of TB prevalence in Iran, this study was designed to investigate the genetic diversity among MDR strains of MTB by MIRU-VNTR typing scheme. A total of 88 drug resistant M. tuberculosis isolates belong to pulmonary TB cases were collected from several TB reference centers of Iran. Drug susceptibility testing for Isoniazid and Rifampin was performed using the agar proportion method and MDR isolates were underwent genotyping by using 12-locus-based MIRU-VNTR typing. On performing proportion method, 22 isolates were identified as MDR. By typing of MDR isolates using 12-loci MIRU-VNTR technique, high diversity were demonstrated in MDR strains and these were classified into 20 distinct MIRU-VNTR genotypes. MIRU loci 10 and 26 were the most discriminatory loci with 8 and 7 alleles respectively; while MIRU loci 2, 20, 24 and 39 were found to be the least discriminatory with 1-2 alleles each. We noticed a mixed infection in isolate 53, as this isolate comprised simultaneous two alleles in MIRU loci 40, 10, 16 and 39. In conclusion, this result represents MIRU-VNTR typing as a useful tool for studying genetic diversity of MDR-MTB in regional settings, and will help the health sectors to construct a preventive program for MDR-TB. Additionally, it can detect mixed infection which can facilitate management of treatment. Copyright (C) 2017, Kaohsiung Medical University. Published by Elsevier Taiwan LLC. This is an open access article under the CC BY-NC-ND license.

26-Kiasat, N., et al. (2017). "Qualitative and Quantitative Assessment of Airborne Fungal Spores in the Hospitals Environment of Ahvaz City (2016)." Jundishapur Journal of Microbiology 10(10).

Background: Invasive fungal infections acquired in the hospital have progressively emerged as an important cause of life-threatening infection. In particular, airborne fungi in hospitals are considered critical pathogens of hospital-associated infections. Objectives: This study aimed to investigate the airborne fungi of indoor environments of educational hospitals in the city of Ahvaz, Iran. Methods: The air samples were taken from seven wards in five hospitals using Quick Take 30 samplepump. A total of 175 air samples were cultured into Sabouraud dextrose agar and incubated at 25 degrees C for 7 to 10 days. Fungal species were identified by macroscopic and microscopic features. The number of airborne fungi was presented in colony-forming unit per cubic meter (CFU/m(3)). Results: A total of 2906 fungal colonies were isolated. The highest and least numbers of fungi were related to surgical (446 CFU/m(3)) and neonatal

intensive care unit wards (103 CFU/m(3)), respectively. The most frequent fungal species was Cladosporium spp. (35.3%), followed by yeasts (27.3%), Aspergillus spp. (15.1%), Penicillium spp. (12.1%), and other fungal species (10.2%) Conclusions: All wards under study were heavily contaminated with different types of fungi. Thus, it is suggested to monitor the indoor air to prevent possible hospital infections.

27-Makvandi, M., et al. (2017). "A Study on the Virus-Like Particle Formation of Hepatitis E Virus ORF2 and Rotavirus NSP4 Protein in the Eukaryotic and Prokaryotic Expression Systems." Jundishapur Journal of Microbiology 10(12).

Background: Hepatitis E virus (HEV) is able to induce fulminant hepatitis E infection in immunosuppressed individuals. Previous studies showed that the Baculovirus expression system (BES) could be used for developing hepatitis E virus-like particles (VLPs). Objectives: In the present study, the formation of VLPs of the recombinant proteins of HEV truncated open reading frame 2 (ORF2; 112-607) and Rotavirus non-structural protein 4 (NSP4) (OSU-a) were investigated in BES and Escherichia. coli. Methods: To construct VLPs, the truncated ORF2-NSP4 protein was expressed in BES. The expression of protein was confirmed by western blot. This protein was expressed in E. coli. The truncated ORF2-NSP4 gene was subcloned in pET28a, and then transformed into E. coli DH5 alpha. The confirmed colonies were transformed into E. coli BL21. The solubility of protein were checked by SDS-PAGE and western blot analysis. In the final step, to verify the VLP formation in BES and E. coli, the recombinant proteins were stained with 2% uranyl acetate and checked by transmission electron microscopy (TEM). Results: The 75 KDa truncated ORF2-NSP4 protein was successfully expressed in Sf9 cells, assembled, and formed VLP according to TEM results. In the prokaryotic expression system (E. coli), the ORF2-NSP4 gene was successfully subcloned and expressed in BL21 but VLP was not detected in TEM analysis. Conclusions: The truncated ORF2-NSP4 VLP were efficiently expressed in the SF9 cells, as a potential mucosal vaccine against HEV and Rotavirus. In the prokaryotic expression system (E. coli), the ORF2-NSP4 gene was successfully expressed.

28-Moosavian, M., et al. (2017). "Detection of the Legionnaires' Disease Agent in Patients With Respiratory Symptoms by Culture, Detection of Urinary Antigen and Polymerase Chain Reaction of the 16S rRNA Gene in Ahvaz, Iran." Jundishapur Journal of Microbiology 10(4).

Background: Legionnaires' disease (LD) is a common form of severe pneumonia, caused by Legionella spp. Legionella pneumophila is an important agent of severe pneumonia including 15 serogroups, which are all human pathogens. However, L. pneumophila serogroup 1 is the most prevalent agent of LD. Fatality rates among elderly and immunocompromised patients are high

and may occur as a result of infection with this pathogen. Objectives: The aim of this study was to detect the LD agent in clinical samples of patients with respiratory symptoms by culture, urinary antigen and polymerase chain reaction (PCR) of the 16SrRNA gene. Methods: In this study, a total of 200 specimens (including 100 urine and 100 respiratory samples), which were collected from hospitalized patients with respiratory symptoms were examined. The respiratory specimens were inoculated to the buffered charcoalyeast extract and modified Wodowsky and Yee agar media for isolation of the Legionella spp. The 16S rRNA gene in the respiratory specimens was amplified by the PCR method and the urinary antigen of L. pneumophila serogroup 1 was detected by EIA (enzyme immunoassay) test using the Coris Legionella V-test kit. Results: From a total of 200 specimens from patients with respiratory symptoms, 5% of urine specimens and 3% of respiratory specimens were positive for L. pneumophila using the EIA test and PCR of the 16SrRNA gene, respectively. The results of the culture of the respiratory samples showed that 1% of them were positive for Legionella spp. Conclusions: In this study, the LD agent was detected by the rapid EIA test. In addition, the sensitivity of the urinary antigen test using the Coris Legionella V-test kit for detection of L. pneumophila in respiratory specimens was more than those of the PCR and culture methods.

29- Moosavian, M., et al. (2017). "Phenotypic and Genotypic Detection of Extended Spectrum beta-lactamase and Carbapenemases Production Including bla TEM, bla PER and bla NDM-1 Genes Among Acinetobacter baumannii Clinical Isolates." Jundishapur Journal of Microbiology 10(12).

Background: Acinetobacter baumannii has appeared as an important opportunistic pathogen responsible for nosocomial infections. The rising trend of antibiotic resistance amongst A. baumannii isolates has become a global concern. The most prevalent procedure of resistance is beta-lactamase and carbapenemases production with genes on mobile elements. Objectives: The aim of the current research was to assess antibiotic susceptibility schema and the frequency of TEM, PER, and NDM-1 genes among A. baumannii isolates. Methods: One hundred and eighty three specimens from November 2014 to February 2015 were collected from Golestan and Imam Khomeini hospitals in Ahvaz, Iran. Drug susceptibility tests were carried out by Kirby-Bauer method. Extended spectrum-beta-lactamases (ESBLs) production was determined by the combination disk method and carbapenemases production was determined by the modified hodge test (MHT) according to the CLSI recommendations. TEM, PER, and NDM-1 were detected by PCR. Results: Out of 183 Acinetobacter isolates, 151 (82.5 %) were identified as A. baumannii by standard chemical tests. The highest resistance was determined to ciprofloxacin (97.3 %), whereas the higher rate of susceptibility was observed to colistin (98.7%). 1.3% of the A. baumannii isolates were positive for ESBL in combined disc test. Production of carbapenemase was detected in 47.1% of the A. baumannii isolates using MHT. The prevalence of TEM and PER genes was 36.4 % and 25.1 %, respectively. NDM-1 genes were not detected. Conclusions: The

prevalence of carbapenemase positive A. baumannii isolates in the current study makes a serious concern and highlights the need for infection control through antibiotic management protocols and rapid detection of resistant strains.

30- Nashibi, R., et al. (2017). "Epidemiology and Treatment Outcome of Mucormycosis in Khuzestan, Southwest of Iran." Archives of Clinical Infectious Diseases 12(1).

Background: Mucormycosis is an uncommon life-threatening fungal infection. The major risk factors of this infection include uncontrolled diabetes mellitus, prolonged steroid therapy, persistent neutropenia, hematological malignancies, autoimmune disorders, trauma, burns and surgical wounds. Objectives: The current study aimed to determine the epidemiology and treatment outcome of mucormycosis in Khuzestan province, southwest of Iran. Methods: This cross-sectional study was performed during a period of 10 years from April 2004 to March 2014 at Razi hospital in Ahvaz, southwest of Iran, during years 2004 to 2014. Demographic data, laboratory data, clinical features, antifungal treatment, the need for surgical debridement and the outcome were collected. Data were summarized using descriptive statistical methods and analyzed by SPSS version 15 software. Results: The study included 20 patients with a biopsy-proven diagnosis of mucormycosis. Regarding the findings, the mean age was 51.4 +/- 9.7 years. Eighty-five percent of patients had uncontrolled diabetes mellitus. Findings showed that all the cases received amphotericin B, but surgical debridement was performed on 10 patients (50%). Most prevalent season of mucormycosis was winter (40%). Conclusions: Prognosis of patients that underwent surgery and medical therapy was significantly better than medical therapy alone (90% vs. 50% patient's survival).

31-Navayan, A., et al. (2017). "Evaluation of the Mosquito Repellent Activity of Nano-sized Microemulsion of Eucalyptus globulus Essential Oil Against Culicinae." Jundishapur Journal of Natural Pharmaceutical Products 12(4).

Background: The mosquitoes of Culicidae family are serious vectors of several tropical diseases, such as malaria, filariasis, encephalitis, and nuisance. Control of mosquitoes and protection of people from their bites are of the most important ways to prevent transmitted diseases. Although the efficacy of N, N-diethyl-m-toluamide (DEET) is high and generally used as mosquito repellent, yet a number of biting diptera are tolerant to DEET. Furthermore, there are concerns about the safety of DEET and its allergic and toxic effects. Therefore, it is necessary to use other repellents like plant essential oils. Objectives: The aim of this work was to develop a safe repellent with a long-lasting protection based on micro-emulsion of eucalyptus essential oil. Methods: Eucalyptus globulus essential oil was obtained by water distillation in a Clevenger

apparatus. The larvae of Culicidae were collected and adult mosquitoes reared for the repellency test. Preparation of micro-emulsions of Eucalyptus globulus essential oil was made by mixing the specified surfactant (Tween 80 and Span 20) and the appropriate amount of co-surfactant (propylene glycol) under the water titration method. The laboratory method, arm in cage, was used to estimate the time of protection of essential oil micro-emulsion against mosquitoes and DEET used as a standard repellent. Results: Physicochemical properties of formulated micro-emulsions were appropriate and suitable for topical application. Particle size of eucalyptus oil 15% w/w micro-emulsion was lowest. When applying eucalyptus oil micro-emulsion at concentrations of 5, 10, and 15% w/w, time of protection against mosquitoes were 82 +/- 15.8, 135.7 +/- 26.4, and 170.7 +/- 26 minutes, respectively. These times of protection were similar to DEET at same concentrations and significantly more than eucalyptus essential oil. Conclusions: The formulated micro-emulsion of eucalyptus oil at a concentration of 15% w/w has potential repellency to the extent of DEET. It seems that nano-sized microemulsion is stable in terms of thermodynamics and kinetics. In conclusion, preparation of nano-sized microemulsion could delay the volatility of eucalyptus essential oil and volatile oil release from formulations and consequently increase protection time against mosquitoes.

32-Rahdar, M. and T. Kardooni (2017). "Molecular Identification of Sarcocystis spp. in Sheep and Cattle by PCR-RFLP from Southwest of Iran." Jundishapur Journal of Microbiology 10(8).

Background: Sarcocystis species are obligatory intracellular parasites of manyvertebrate hosts. Some pathogen species cause major economic loss and hygienic problems in the animal and human population, respectively. Objectives: The goal of the current study was conducted to identify Sarcocystis species in meat-producer animals and to evaluate the risk of transmission of parasites after consumption of infected meat by humans. Methods: Fifty samples of sheep and cattle muscles were collected from the abattoir. The samples were collected from the heart, tongue, diaphragm, and skeletal muscles. The PCR method was used for amplifying the 18S ribosomal RNA gene for distinguish Sarcocystis species using 2 primers and 3 restricted enzymes including Hinf, Mbo1, and EcoR1. Results: The results showed that all cattle samples were infected by Sarcocystiscruzi (100%) and sheep samples were contaminated by S. tenella (80%) as well as S. capracanis (20%). No human Sarcocystis species were detected. Conclusions: Meat-producer animals are infected by S. cruzi as well as S. tenella and the consumption of infected meat is not important for human sarcocystosis in this area.

33-Rahpeyma, M., et al. (2017). "Expression and characterization of codon-optimized Crimean-Congo hemorrhagic fever virus Gn glycoprotein in insect cells." Archives of Virology 162(7): 1951-1962.

Crimean-Congo hemorrhagic fever virus (CCHFV) is a major cause of tick-borne viral hemorrhagic disease in the world. Despite of its importance as a deadly pathogen, there is currently no licensed vaccine against CCHF disease. The attachment glycoprotein of CCHFV (Gn) is a potentially important target for protective antiviral immune responses. To characterize the expression of recombinant CCHFV Gn in an insect-cell-based system, we developed a gene expression system expressing the full-length coding sequence under a polyhedron promoter in Sf9 cells using recombinant baculovirus. Recombinant Gn was purified by affinity chromatography, and the immunoreactivity of the protein was evaluated using sera from patients with confirmed CCHF infection. Codon-optimized Gn was successfully expressed, and the product had the expected molecular weight for CCHFV Gn glycoprotein of 37 kDa. In time course studies, the optimum expression of Gn occurred between 36 and 48 hours postinfection. The immunoreactivity of the recombinant protein in Western blot assay against human sera was positive and was similar to the results obtained with the anti-V5 tag antibody. Additionally, mice were subjected to subcutaneous injection with recombinant Gn, and the cellular and humoral immune response was monitored. The results showed that recombinant Gn protein was highly immunogenic and could elicit high titers of antigen-specific antibodies. Induction of the inflammatory cytokine interferon-gamma and the regulatory cytokine IL-10 was also detected. In conclusion, a recombinant baculovirus harboring CCHFV Gn was constructed and expressed in Sf9 host cells for the first time, and it was demonstrated that this approach is a suitable expression system for producing immunogenic CCHFV Gn protein without any biosafety concerns.

34- Rezaei-Matehkolaei, A., et al. (2017). "Morpho-Molecular Characterization of Soil Inhabitant Dermatophytes from Ahvaz, Southwest of Iran, a High Occurrence of Microsporum fulvum." Mycopathologia 182(7-8): 691-699.

Occurrence and diversity of dermatophyte mycoflora in 298 soil samples from Ahvaz, Southwest of Iran was investigated by using the hair-baiting technique. The samples were collected during spring (n = 210) and autumn (n = 88) of 2015, and the fungal isolates were identified based on the macro- and micro-morphology of colonies and with further ITS-rDNA RFLP and sequencing. Totally, 60 soil samples (20.1%) were positive for dermatophyte growth whose pH varied from 7.0 to 7.9. The highest (26.6%) and the lowest (14.3%) recovery rates were from the animal resorts and the streets soils samples, respectively. Seasonally, 16.7% of the spring samples and 28.4% of the autumn samples were positive. Based on molecular identification, three species of two genera were identified viz. M. fulvum (n = 57), M. canis (n = 2) and zoophilic Trichophyton interdigitale (n = 1). As a specific goal in the study, differentiation of the species in Microsporum gypseum complex was established by measuring the mean length and width of macroconidia in some strains of M. gypseum, M. fulvum and M. incurvatum. Mean size for macroconidia length and width in three species showed that M. gypseum and M. incurvatum can morphologically be differentiated from M. fulvum but not from each other. M. fulvum was the

most abundant species isolated from the soils of Ahvaz; however, to comprehensively specify the distribution pattern of geophilic dermatophytes in the soils of this city further investigations are needed. Identification based on micro-morphometric is not effective for species distinction in M. gypseum complex, while molecular procedures based on sequencing of certain DNA regions are the most reliable and applicable strategies for this purpose.

35-Sadeghi-Nejad, B., et al. (2017). "Isolation and antifungal activity evaluation of Satureja khuzestanica Jamzad extract against some clinically important dermatophytes." Journal de Mycologie Medicale 27(4): 554-560.

Objective. - Among the fungi, dermatophytes are the major cause of spectrum of superficial mycoses medically known as dermatophytosis (tinea) in human and animal. Treatment of these infections has still remained difficult. The aim of this survey was to evaluate in vitro anti-dermatophytic activity of ethanolic extract (EtOH) from Satureja khuzestanica leaf (SKLE) against some clinically important dermatophyte species from the genera of Trichophyton, Microsporum and Epidermophyton. Minimal inhibition concentration (MIC) of SKLE was tested against 14 dermatophyte strains of 5 species by using agar dilution method. Phytochemical screening of SKLE was carried out by High Performance Thin Layer Chromatography (HPTLC). The results of in vitro anti-dermatophytic activity of SKLE showed with MIC values between 1.250 and 10 mg/mL. MIC90 and MIC50 values were as 0.625-1.250 and 0.156-0.312 mg/mL, respectively. The MFC values of SKLE were in the range of 1.250-2.50 mg/mL and possessed biological activity against dermatophytes. Morever, phytochemical analysis by HPTLC revealed that the ethyl acetate (EtOAc) extracts of SKL contain triterpenes which are known to have biological activity and it seems that this compound be responsible for the anti-dermatophytic activity of this plant. In conclusion, the results of in vitro antifungal susceptibility testing and phytochemical screening revealed that SKLE had both fungistatic and fungicidal activities against dermatophytes and can potentially be helpful as a supplementary or alternative for treatment of dermatophytosis. (C) 2017 Elsevier Masson SAS. All rights reserved.

36-Salehi-Vaziri, M., et al. (2017). "An Outbreak of Crimean-Congo Hemorrhagic Fever in the SouthWest of Iran." Jundishapur Journal of Microbiology 10(1).

Introduction: Crimean-Congo hemorrhagic fever (CCHF) is an acute viral zoonotic disease, which is endemic in vast geographic areas including the Middle East. The causative agent, Crimean-Congo hemorrhagic fever virus (CCHFV), is a Nairovirus, which is mainly transmitted to human from infected hard ticks and viremic livestock. Case Presentation: In April 2016, an outbreak of CCHF occurred in Khuzestan province, Iran, because of slaughtering a tick-infested calf and manipulation of its meat. Discussion: Given that viremic livestock are the main source of

CCHF outbreaks in Iran, limitation of the livestock smuggling and unhealthy slaughtering is of great importance in the prevention of CCHF in endemic regions.

37-Savari, M., et al. (2017). "Plasmid borne Carbapenem-Hydrolyzing Class D beta-Lactamases (CHDLs) and AdeABC efflux pump conferring carbapenem-tigecycline resistance among Acinetobacter baumannii isolates harboring TnAbaRs." Microbial Pathogenesis 104: 310-317.

Here we studied the prevalence and mechanisms of simultaneous resistance to carbapenem and tige-cycline and accumulation of resistance determinants reservoirs in genome of Acinetobacter baumannii (A. baumannii) clinical isolates. Susceptibility of the isolates were measured to 18 antimicrobial agents. Genetic diversity of the microbial population was determined using the International Clonal lineage typing (IC typing), multiple locus VNTR analysis (MLVA) and plasmid profiling methods. To detect the AbaRs, Carbapenem-Hydrolyzing Class D beta-Lactamases (CHDLs) genes, AdeABC efflux pump genes and resistance determinants, PCR was used. Filter mating experiments were used to prove that if carbapenem resistance genes are located on conjugative plasmids or not. Among the A. baumannii clinical isolates, 40.8% were carbapenem-tigecycline resistant and in this population, 46.9% were belonging to IC I, IC II or IC III and 53.1% were IC variants. These isolates had fallen in 40 MLVA types and were harboring plasmids in multiple numbers and sizes. In this study, blaoxA-23-iike was the most prevalent CHDL and conjugation analysis proved that the carbapenem resistance genes are located on conjugative plasmids. All efflux pump genes, except for adeC, were detected in all carbapenem-tigecycline resistant A. baumannii (CTRAb) isolates. Resistance determinants were distributed in both TnAbaRs and R plasmids with a shift toward the R plasmids. Emerging of carbapenem resistant A. baumannii (CRAB) with simultaneous resistance to the last line therapy including tigecycline represent emerging of extensively drug resistance (XDR) and pandrug resistance (PDR) phenotypes that would be a great threat to our public health system. (C) 2017 Elsevier Ltd. All rights reserved.

38-Shahraki, A. H., et al. (2017). "Mycobacterium aquaticum sp nov., a rapidly growing species isolated from haemodialysis water." International Journal of Systematic and Evolutionary Microbiology 67(9): 3279-3282.

The characterization of five Iranian isolates, four from hospital haemodialysis water and one from the sputum of a patient, led to the detection of a novel mycobacterium species. The strains were characterized by mucoid colonies developing in 35 days at temperatures ranging from 25 to 37 degrees C. The biochemical test pattern was unremarkable while the HPLC profile of mycolic acids resembled that of Mycobacterium fortuitum. The sequences of three major

housekeeping genes (16S rRNA, hsp65 and rpoB) were unique and differed from those of any other mycobacterium. Mycobacterium brisbanense, which is the species that shared the highest 16S rRNA gene sequence similarity (99.03 %), was distinct, as shown by the average nucleotide identity and by the genome to genome distance values (91.05 and 43.10 %, respectively). The strains are thus considered to represent a novel species of the genus Mycobacterium, for which the name Mycobacterium aquaticum sp. nov. is proposed. The type strain is RW6(T) (= DSM 104277(T) = CIP111198(T)).

39-Shahraki, A. H., et al. (2017). "Mycobacterium persicum sp nov., a novel species closely related to Mycobacterium kansasii and Mycobacterium gastri." International Journal of Systematic and Evolutionary Microbiology 67(6): 1766-1770.

Four strains isolated in Iran from pulmonary specimens of unrelated patients are proposed as representative of a novel Mycobacterium species. Similarity, at the phenotypic level, with Mycobacterium kansasii is remarkable with the photochromogenic yellow pigmentation of the colonies being the salient feature. They differ, however, genotypically from this species and present unique sequences in 16S rRNA, hsp65 and rpoB genes. The average nucleotide identity and the genome-to-genome distance fully support the status of an independent species. The name proposed for this species is Mycobacterium persicum sp. nov. with AFPC-000227(T) (=DSM 104278(T) = CIP 111197(T)) as the type strain.

40-Sheikh, A. F., et al. (2017). "Pathogen Identification in Suspected Cases of Pyogenic Spondylodiscitis." Frontiers in Cellular and Infection Microbiology 7.

Pyogenic spinal infection continues to represent a worldwide problem. In approximately one-third of patients with pyogenic spondylodiscitis, the infectious agent is never identified. Of the cases that lead to organismal identification, bacteria are more commonly isolated from the spine rather than fungi and parasites. This study applied universal prokaryotic 16S rRNA PCR as a rapid diagnostic tool for the detection of bacterial agents in specimens from patients suspected of pyogenic spondylodiscitis. Gram and Ziehl-Neelsen staining were used as a preliminary screening measure for microbiologic evaluation of patient samples. PCR amplification targeting 16S rRNA gene was performed on DNA extracted from 57 cases including specimens from epidural abscesses, vertebral, and disc biopsies. Positive samples were directly sequenced. MRI findings demonstrated that disc destruction and inflammation were the major imaging features of suspected pyogenic spondylodiscitis cases, as 44 cases showed such features. The most common site of infection was the lumbar spine (66.7%), followed by thoracic spine (19%), the sacroiliac joint (9.5%), and lumbar-thoracic spine (4.8%) regions. A total of 21 samples amplified the 16S

rRNA -PCR product. Sanger sequencing of the PCR products identified the following bacteriological agents: Mycobacterium tuberculosis (n = 9; 42.9%), Staphylococcusaureus (n = 6; 28.5%), Mycobacterium abscessus (n = 5; 23.8%), and Mycobacteriumchelonae (n = 1; 4.8%). 36 samples displayed no visible 1 6S rRNA PCR signal, which suggested that non-bacterial infectious agents (e. g., fungi) or non-infectious processes (e. g., inflammatory, or neoplastic) may be responsible for some of these cases. The L3-L4 site (23.8%) was the most frequent site of infection. Single disc/vertebral infection were observed in 9 patients (42.85%), while 12 patients (57.15%) had 2 infected adjacent vertebrae. Elevated erythrocyte sedimentation rate (ESR) and C-reactive protein (CRP) inflammatory markers were noted in majority of the patients. In conclusion, microbiological methods and MRI findings are vital components for the proper diagnosis of pyogenic spondylodiscitis. Our findings suggest that molecular methods such as clinical application of 16S rRN A PCR and sequencing may be useful as adjunctive diagnostic tools for pyogenic spondylodiscitis. The rapid turnaround time of 16S rRNA PCR and sequencing submission and results can potentially decrease the time to diagnosis and improve the therapeutic management and outcome of these infections. Although S. aureus and M. tuberculosis were the most common causes of pyogenic spinal infections in this study, other infectious agents and non-infectious etiologies should be considered. Based on study results, we advise that antibiotic therapy should be initiated after a definitive etiological diagnosis.

41-Shirani, F., et al. (2017). "Using rats as a research model to investigate the effect of human adenovirus 36 on weight gain." ARYA Atherosclerosis 13(4).

BACKGROUND: Recent evidence has shown a positive correlation between obesity and viral infections with a particular emphasis on the human adenovirus-36 (Ad-36). Ad-36 is the first human virus that may increase adiposity in animals, and it is considered as a possible risk factor for obesity in humans; however, the results were not consistent across all the studies. The present study was conducted to examine the influence of Ad-36 infection on obesity in a rat model. METHODS: Eight-week-old male Wistar rats weighing 170-240 gram (g), were randomly divided into two groups, infection group (48 rats) and a control group (12 rats). The rats in the infection group were infected with human Ad-36. All rats were given free access to a normal chow diet and water. They were weighed weekly. RESULTS: The mean +/- standard deviation (SD) body weights were 229.0 +/- 25.9 g and 232.3 +/- 16.6 g in the infection and control groups, respectively at the time of infection. The mean +/- SD body weight of the infection group (304.0 +/- 39.0 g) was higher than the control group (301.0 +/- 36.5 g) at 12 weeks post-infection (P = 0.82). Although two groups had approximately same food intakes, the mean change in body weight was greater in the infection group than the control group (75.8 +/- 27.9 g vs. 70.8 +/- 24.5 g) but it was not significant (P = 0.57). CONCLUSION: We did not find a statistically significant association between weight gain and Ad-36 infection in the rat model. It seems that longer follow-up duration is needed to develop a significant weight gain in the infected rats. Rats can be used as a good animal model

for further investigations about Ad-36-induced obesity, provided not to rely merely on weight measurements. Evaluating body composition or histopathological assessments are suggested.

42- Shoja, S., et al. (2017). "Dissemination of carbapenem-resistant Acinetobacter baumannii in patients with burn injuries." Journal of the Chinese Medical Association 80(4): 245-252.

Background: Carbapenem-resistant Acinetobacter baumannii has emerged as an important cause of infection in burn patients. This study aimed to characterize the antimicrobial susceptibility pattern, determine the prevalence of oxacillinase and metallo-beta-lactamase (MBL) genes, and type the A. baumannii isolates obtained from burn patients. Methods: During a 1-year period, a total of 40 nonduplicated isolates of A. baumannii were obtained from burn patients who were hospitalized in the Taleghani Burn Hospital in Ahvaz, in the southwest of Iran. Testing for antimicrobial susceptibility was carried out by disk diffusion and E-test. To screen MBL production, a double disk synergy and MBL E-test were performed. The presence of bla(OXA-23-like), bla(OXA-24-like), bla(OXA-51-like) and bla(OXA-58-like), bla(VIM), bla(IMP) and bla(SPM), and bla(NDM) was sought by polymerase chain reaction (PCR). Repetitive extragenic palindromic sequence-based PCR was carried out for determination of isolates clonality. Results: Overall, 92.5% of isolates were carbapenem-resistant. Polymyxin B, colistin, and ampicillin-sulbactam were the most effective agents in vitro, with a susceptibility rate of 100%, 97.5%, and 72.5%, respectively. According to the double disk synergy and E-test, 55.6% and 97.3% of isolates were MBL producers, respectively. Furthermore, 70% of isolates harbored bla(OXA-23-like) and 20% were positive for bla(OXA-24-like). However, no encoding genes were detected for bla(VIM), bla(IMP) and bla(SPM), bla(NDM), and bla(OXA-58-like). Repetitive extragenic palindromic sequence-based PCR revealed that carbapenem-resistant isolates belonged to four clones, including A, B, C, and D; the predominant clones were B and C. Conclusion: The rate of carbapenem resistance was high, and it appeared that bla(OXA-23-like) and bla(OXA-24-like) contributed to the carbapenem resistance of A. baumannii isolates. This result suggests that the two predominant clones of A. baumannii were spread among burn patients. In order to prevent future dissemination of resistant isolates among burn patients, an effective infection control plan is necessary. Copyright (C) 2017. Published by Elsevier Taiwan LLC.

43- Shokoohi, G. R., et al. (2017). "In Vitro Activities of Luliconazole, Lanoconazole, and Efinaconazole Compared with Those of Five Antifungal Drugs against Melanized Fungi and Relatives." Antimicrobial Agents and Chemotherapy *61(11).*

The in vitro activities of novel azoles compared to those of five antifungal drugs against clinical (n = 28) and environmental (n = 102) isolates of black mold and melanized yeast were determined. Luliconazole and lanoconazole had the lowest geometric mean MICs, followed by efinaconazole, against tested isolates compared to the other drugs. Therefore, it appears that these new imidazole and triazole drugs are promising candidates for the treatment of infections due to melanized fungi and their relatives.

44- Soltani, S., et al. (2017). "Evaluation of the Hydatid Cyst Membrane Permeability of Albendazole and Albendazole Sulfoxide-Loaded Solid Lipid Nanoparticles." Jundishapur Journal of Natural Pharmaceutical Products 12(2).

Background: Albendazole (ABZ) and albendazole sulfoxide (ABZSO) have a basic role in the treatment of hydatid cysts. However, their poor solubility and limited intestinal permeability are the main problems in their formulation. Objectives: The preparation and characterization of ABZ and ABZSO-loaded solid lipid nanoparticles (SLNs) to increase the hydatid cyst membrane permeation by loading into SLNs. Materials and Methods: First, ABZ and ABZSO-loaded SLNs were prepared by micro emulsification and high shear homogenization. Physicochemical characterization of the formulations for particle size, polydispersity index, drug entrapment efficiency (EE) and drug loading (DL), zeta potential, particle shape, drug stability, and in vitro drug release studies were evaluated. Next, the permeability of conventional and prepared formulations on hydatid cysts was evaluated by quantifying the drug concentrations in cyst fluid using high-performance liquid chromatography (HPLC). Results: The prepared formulations showed particle sizes < 180 nm, polydispersity index values around 0.08 with narrow size distributions, a high EE of (91%) for ABZ-SLN and (94%) for ABZSO-SLN, and ideal stabilities with regard to their largely negative zeta potentials. The in vitro drug release of free drugs exhibited very fast release in the initial time, but displayed a biphasic pattern for drug-loaded SLNs. Greater permeability was achieved using the SLN preparations. Conclusions: ABZ and ABZSO achieved good physicochemical characterizations, controlled release, higher permeability and efficacy by loading into SLNs, and are promising for the treatment of this disease.

45- Tavalla, M., et al. (2017). "Molecular Study of Cryptosporidium spp. in Dogs from Southwest of Iran." Jundishapur Journal of Microbiology 10(4).

Background: Cryptosporidium is a protozoan parasite that effects rodents, dogs, calves, humans, and cats. Infection with this parasite is known as cryptosporidiosis. Cryptosporidium spp. may induce clinical or subclinical signs in infected hosts. In the life cycle of this parasite infected dogs freely living in urban and rural areas of Khuzestan province are the definitive hosts that should be considered as a real problem in public health for humans. Objectives: This study aimed

at determining the frequency of cryptosporidiosis in dogs in southwest of Iran. Methods: Overall, 350 fresh fecal samples were collected from domestic dogs living in 43 villages, from June 2012 to September 2013. All samples were investigated by Sheather's concentration method and fecal smears were stained with modified Ziehl-Neelsen followed by light microscope examination, and polymerase chain reaction (PCR). Results: The results revealed that frequency of Cryptosporidium infection was 8% and 12.3%, using direct smear and molecular method, respectively. Conclusions: The present findings indicated that domestic dog feces from southwest of Iran may contain zoonotic parasites such as Cryptosporidium spp. and may be a potential risk for humans and other animals, especially when they contaminate the environment. The role of dogs as source of human infection should be investigated by further studies.

46-Tavalla, M., et al. (2017). "Molecular identification of Enterocytozoon bieneusi and Encephalitozoon spp. in immunodeficient patients in Ahvaz, Southwest of Iran." Acta Tropica 172: 107-112.

Microsporidia are often considered as an opportunistic infection in patients with impaired immune systems such as transplant recipients and patients with acquired immune deficiency syndrome (AIDS). Due to the increasing prevalence of parasitic infections and immunodeficiency diseases; the aim of the study is to evaluate molecular identification of Enterocytozoon bieneusi and Encephalitozoon spp. in immunodeficient patients in Ahvaz, southwest of Iran. At first, 310 stool samples were collected from patients with immunodeficiency. The specimens were stained by modified trichrome (weber) and were examined microscopically. The extracted DNA samples were evaluated by multiplex/nested PCR method. The products of multiplex/nested PCR were explored by RFLP method using the restriction enzyme of Mnl1. Of 310, 93 samples were suspected positive for microsporidia by the staining. Also, of 310, 88 samples were positive by the multiplex/nested-PCR test that 62 samples were positive for E. bieneusi as well as 26 were detected as Encephalitozoon species that including 3 E. cuniculi, 19 E. intestinalis and 4 E. hellem. Of 62 E. bieneusi, 45, 16 and 1 were detected as genotype D, M and WL11, respectively. Also, Of 3 E. cuniculi, 1 and 2 cases were identified as genotype I and II, respectively. All E. hellem samples were included genotype 1A. Our findings revealed a relatively high prevalence of microsporidia species in immunodeficient patients. The highest risk of this infection is at individuals with impaired immune systems that it can be life-threatening in people with immune system dysfunction. It is essential that the high-risk people should be receiving the information about the risk of direct contact with infected individuals and animals.

47-Zarean, M., et al. (2017). "Correlation between clinical responses with the drug-susceptibility of parasites in Iranian cutaneous leishmaniasis caused by Leishmania major." Tropical Biomedicine 34(2): 338-345.

Reviews have shown increasing number of Iranian patients with cutaneous leishmaniasis (CL) who are unresponsive to pentavalent antimonial compounds such as meglumine antimoniate (Glucantime, MA). The present investigation aims to determine the correlation between clinical responses (healing, or non-healing) with susceptibility of Leishmania parasites to glucantime. Initially, in vitro susceptibility of Leishmania parasites was carried out on 93 isolates using macrophage models. Identification of these species was also performed by molecular methods including Nested-PCR and PCR-RFLP. The f indicated that total isolated were L. major. A significant association between the clinical outcome and the in vitro effective concentration 50% (EC50) values was observed. Leishmania derived from patients with non-healing lesions had EC50 values at least 3-fold higher than parasites isolated from lesions of healing patients. By molecular methods, patterns for both sensitive and resistant samples demonstrated restriction band which is related to L. major. The obtained findings in the present study demonstrated that MA-resistant L. major field isolates are now frequent in Iran. Such studies help to find strategies for rapidly diagnosing resistance in order to improve the clinical management of CL.

48-Zargaran, M., et al. (2017). "Luliconazole, an alternative antifungal agent against Aspergillus terreus." Journal de Mycologie Medicale 27(3): 351-356.

Aspergillus terreus is the fourth leading cause of invasive and non-invasive aspergillosis and one of the causative agents of morbidity and mortality among immunocompromised and high-risk patients. A. terreus appears to have increased as a cause of opportunistic fungal infections from superficial to serious invasive infections. Although, invasive aspergillosis is often treated empirically with amphotericin B, most A. terreus isolates are resistant both in vivo and in vitro to some antifungal drugs. In this study, we aimed to evaluate antifungals susceptibility profiles of the different strains of A. terreus against amphotericin B, caspofungin, fluconazole, voriconazole, posaconazole and luliconazole. Forty A. terreus strains originating from environmental sources (air and soil) were identified using by macroscopic and microscopic features. Six antifungals including, amphotericin B, caspofungin, fluconazole, voriconazole, posaconazole and luliconazole were applied for susceptibility tests. Our results show that tested isolates had different susceptibility to antifungals. The lowest MICGM related to luliconazole (0.00236 mu g/ml), followed by posaconazole (0.18621 mu g/ml), voriconazole (0.22925 mu g/ml), caspofungin (0.86 mu g/ml), fluconazole (8 mu g/ml) and amphotericin B (11.12 mu g/ml). This study demonstrated that luliconazole had an excellent in vitro activity against all tested isolates of A. terreus, with MICGM 0.00236 mu g/mL than other tested antifungals. As a result, luliconazole could be a possible alternative antifungal for the treatment of aspergillosis due to A. terreus. (C) 2017 Elsevier Masson SAS. All rights reserved.

49- Ahmadi, F., et al. (2017). "Serum mannan-binding lectin in patients with pulmonary tuberculosis: Its lack of a relationship to the disease and response to treatment." Med J Islam Repub Iran 31: 66.

Background: Lectin pathway mediates complement activation, which is activated by many microorganisms. This study aimed at determining the serum levels of mannose-binding lectin (MBL) in patients with pulmonary tuberculosis, assessing its relationship to antiuberculosis treatment response, and comparing them with a control group. Methods: This cross-sectional study was conducted on patients with pulmonary tuberculosis during 2012 and 2013 in South West of Iran. PPD-ST-negative individuals were selected as controls from healthy relatives of patients. Serum MBL levels were measured using ELISA kit (Human MBL HK323, Hycultbiotech Company, Netherlands). All patients were followed- up for response to treatment. We applied Mann-Whitney and Fisher's exact tests and used SPSS Version 17 software for statistical analysis. Results: The study included 62 patients as the case group and 63 noninfected TB patients as the control group. The MBL (ng/mL) in patients with pulmonary tuberculosis (median = 1012) was significantly (p= 0.037) higher than that of the control group (median= 296.2). No significant difference was found in the MBL level (ng/mL) between patients with response to antituberculosis treatment (median= 1012) and patients with treatment failure (median= 798.9) (p= 0.84). Conclusion: MBL may be involved in the pathogenesis of tuberculosis and in the low values that are protective against tuberculosis, and it seems that it has no effect on the antituberculosis treatment response.

50-Alizadeh, M., et al. (2017). "Identification of Candida species isolated from vulvovaginitis using matrix assisted laser desorption ionization-time of flight mass spectrometry." Curr Med Mycol 3(4): 21-25.

Background and Purpose: Vulvovaginal candidiasis (VVC) is a common problem in women. The purpose of this study was to identify Candida isolates by matrix assisted laser desorption ionization-time of flight mass spectrometry (MALDI-TOF MS) from women with vulvovaginitis that were referred to Ghaem Hospital, Mashhad, Iran. Materials and Methods: This study was conducted on 65 clinical samples isolated from women that were referred to Ghaem Hospital. All specimens were identified using phenotyping techniques, such as microscopy and culture on Sabouraud dextrose agar and corn meal agar. In addition, all isolates were processed for MALDI-TOF MS identification. Results: Out of the 65 analyzed isolates, 61 (94%) samples were recognized by MALDI-TOF MS. However, the remaining four isolates (6%) had no reliable identification. According to the results, C. albicans (58.5%) was the most frequently isolated species, followed by C. tropicalis (16.9%), C. glabrata (7.7%), C. parapsilosis (7.7%), and guilliermondii (3.1%). Conclusion: As the findings indicated, MALDI TOF MS was successful in the identification of clinical Candida species. C. albicans was identified as the most common Candida species isolated from

the women with VVC. Moreover, C. tropicalis was the most common species among the non-albicans Candida species.

51-Amin, M., et al. (2017). "Prevalence of class 1 integrons and plasmid-mediated qnr-genes among Enterobacter isolates obtained from hospitalized patients in Ahvaz, Iran." Infez Med 25(4): 351-357.

Quinolones are frequently used classes of antimicrobials in hospitals, crucial for the treatment of infections caused by Gram-negative bacteria. The inappropriate use of quinolones and other antimicrobial agents for the treatment of bacterial infections leads to a significant increase of resistant isolates. The acquisition of antimicrobial resistance may be related to achievement of resistance determinant genes mediated by plasmids, transposons and gene cassettes in integrons. The objective of this cross-sectional study, conducted from December 2015 to July 2016 at two teaching hospitals in Ahvaz, southern Iran, was to screen for the presence of class 1 integrons and quinolone resistance genes in clinical isolates of Enterobacter spp. In all, 152 non-duplicated Enterobacter isolates were collected from clinical specimens and identified as Enterobacter spp. using standard microbiological methods. Antimicrobial susceptibility test was determined using the disc diffusion method according to the CLSI recommendation. Determination of class 1 integrons and PMQR genes was assessed by PCR. Analysis of antibiotic susceptibility tests showed that the highest antibiotic resistance was toward ciprofloxacin (55.3%), while the lowest level was observed against meropenem (34.9%). Moreover, 47.4% (72/152) and 29% (44/152) of isolates were positive for class 1 integron and quinolone resistance genes, respectively. The relative frequencies of antibiotic resistance were significantly higher among class 1 integron-positive isolates. In summary, our results highlight the importance of PMQR genes in the emergence of quinolone-resistant Enterobacter isolates. Moreover, it seems that class 1 integrons have a widespread distribution among Enterobacter isolates and have clinical relevance to multiple-drug-resistant isolates.

52-Badiee, P., et al. (2017). "Antifungal susceptibility testing of Candida species isolated from the immunocompromised patients admitted to ten university hospitals in Iran: comparison of colonizing and infecting isolates." BMC Infect Dis 17(1): 727.

BACKGROUND: Antifungal susceptibility testing is a subject of interest in the field of medical mycology. The aim of the present study were the distributions and antifungal susceptibility patterns of various Candida species isolated from colonized and infected immunocompromised patients admitted to ten university hospitals in Iran. METHODS: In totally, 846 Candida species were isolated from more than 4000 clinical samples and identified by the API

20 C AUX system. Antifungal susceptibility testing was performed by broth microdilution method according to CLSI. RESULTS: The most frequent Candida species isolated from all patients was Candida albicans (510/846). The epidemiological cutoff value and percentage of wild-type species for amphotericin B and fluconazole in Candida albicans, Candida tropicalis, Candida glabrata and Candida krusei were 0.5 mug/ml (95%) and 4 mug/ml (96%); 1 mug/ml (95%) and 8 mug/ml (95%); 0.5 mug/ml (99%) and 19 mug/ml (98%); and 4 mug/ml (95%) and 64 mug/ml (95%), respectively. The MIC90 and epidemiological cutoff values to posaconazole in Candida krusei were 0.5 mug/ml. There were significant differences between infecting and colonizing isolates of Candida tropicalis in MIC 90 values of amphotericin B, and isolates of Candida glabrata in values of amphotericin B, caspofungin, and voriconazole (P < 0.05). CONCLUSIONS: Our findings suggest that the susceptibility patterns of Candida species (colonizing and infecting isolates) in immunocompromised patients are not the same and acquired resistance was seen in some species.

53-Badiee, P., et al. (2017). "Antifungal susceptibility patterns of colonized Candida species isolates from immunocompromised pediatric patients in five university hospitals." Iran J Microbiol 9(6): 363-371.

Background and Objectives: Colonization of Candida species is common in pediatric patients admitted to hematology-oncology wards. The aim of this study was to identify colonized Candida species and their susceptibility patterns in hematologic pediatric patients. Materials and Methods: Samples were collected from mouth, nose, urine and stool of the patients admitted to five university hospitals and cultured on sabouraud dextrose agar. The isolates were identified by API 20 C AUX system and their susceptibility patterns were evaluated by CLSI M27-A3 and S4. Results: From 650 patients, 320 (49.2%) were colonized with 387 Candida species. Candida albicans was the most prevalent isolated species, followed by Candida glabrata, Candida tropicalis, Candida famata, Candida kefyr and Candida kuresi. The epidemiological cut off value (ECV) for all Candida species to amphotericin B was </=0.25 mug except C. krusei (4 mug). The resistance rate to fluconazole in this study in C. albicans was 4.9% with ECV 8 mug/ml, followed by C. tropicalis 8.8% with ECV 0.5 mug/ml. Voriconazole and posaconazole were effective antifungal agents for all Candida isolates. The ECV of C. albicans, Candida parapsilosis, C. tropicalis, C. glabrata and C. krusei for itraconazole were 0.5, 0.25, 0.5, 1 and 2 mug, respectively. The resistant and intermediate rates of Candida species to caspofungin in this study were 2.9%, 5.9%, 18.8%, 47.9%, 0.0% and 16.7% in C. tropicalis, C. glabrata and C. parapsilosis respectively. Conclusion: C. albicans was the most prevalent species in pediatric colonized patients. New azole agents like voriconazole and posaconazole are effective against non-albicans Candida species. Increase in intermediate species is alarming to future emerging resistant species.

54-Beiranvand, M., et al. (2017). "Antimicrobial activity of endophytic bacterial populations isolated from medical plants of Iran." Iran J Microbiol 9(1): 11-18.

BACKGROUND AND OBJECTIVES: Endophytic actinobacteria colonize inside the plant tissues without causing damages to the host plant. Since these microorganisms colonize in the different parts of plants and can stop plant disease, they have been applied as biological agents for controlling human diseases. The aim of this study was molecular identification and measuring the antimicrobial activity of endophytic Actinomycetes isolated from medicinal plants of Iran. MATERIALS AND METHODS: The total of 23 medicinal plant samples were collected, sterilized, and crushed. Small pieces of the crushed samples were then cultured directly on three selective media. Grown colonies were identified by 16S rRNA gene sequencing method. Each isolate was cultured in TSB medium and then antimicrobial compound was extracted using ethyl acetate and tested against the target bacteria. RESULTS: Sixteen out of 23 bacterial isolates (69%) exhibited antimicrobial activity against the selected pathogenic bacteria, such as Bacillus cereus, Staphylococcus aureus, Bacillus subtilis, Klebsiella pneumoniae, Citrobacter freundii, Proteus mirabilis, Shigella flexneri and Escherichia coli. CONCLUSION: Our Study showed a high phylogenetic diversity and the potent antibiotic activity of endophytic bacteria in medicinal plants of Iran.

55-Dastranj, M., et al. (2017). "State of Globe: Biofilm Formation in Staphylococcus aureus Isolates." J Glob Infect Dis 9(3): 91-92.

56-Fallahi, A. A., et al. (2017). "Epidemiological status of dermatophytosis in Guilan, north of Iran." Curr Med Mycol 3(1): 20-24.

Background and Purpose: The epidemiological features of dermatophytoses have been characterized in many geographical locations of Iran, but not in Guilan, North of Iran. This study was carried out to determine the distribution pattern of dermatophytoses and their relevant agents in Guilan, North of Iran, over a period of one year, from April 2010 to April 2011. Materials and Methods: The clinical samples of skin, hair, and nail from 889 outpatients (317 men vs. 572 women) were used for direct microscopy and culture. All the culture-positive samples were then subjected to amplification of the internal transcribed spacer (ITS) of the nuclear rDNA followed by a restriction fragment length polymorphism (RFLP) assay to verify the causative agents. Results: The infection was confirmed in 90 (44.3%) males and 113 (55.7%) females. The most common type of dermatophytoses was tinea cruris (42.9%), followed by tinea pedis (20.2%), tinea corporis (11.3%), tinea unguium (7.4%), tinea faciei (6.9%), tinea manuum (6.4%), and tinea capitis (4.9%). ITS-RFLP based of the identification of isolates, showed that the infections were significantly associated with anthropophilic species, of Trichophyton rubrum (41.9%), Epidermophyton

floccosum (19.7%), T. tonsurans (5.4%), and T.violaceum (2%). Other causative agents were T. interdigitale (22.6%), Microsporum canis (4.9%), T. verrucosum (2.5%), and M. gypseum (1%). Conclusion: The higher prevalence of T. rubrum, as the agent of dermatophytoses, than other species has never been reported from Iran and is of public health concern because of the chronic nature of infections with anthropophilic species. To thoroughly investigate the epidemiological trend of dermatophytoses in Iran, further periodical and molecular-based studies are necessary.

57-Fatahinia, M., et al. (2017). "Mycological aspects of onychomycosis in Khuzestan Province, Iran: A shift from dermatophytes towards yeasts." Curr Med Mycol 3(4): 26-31.

Background and Purpose: Onychomycosis is fungal infection of the nails with an overall increasing incidence, worldwide. The epidemiological aspects of onychomycosis in Khuzestan, Iran, have not been established. In this study, we aimed to evaluate the clinical and mycological status of fungal nail infection in Khuzestan Province, Iran. Materials and Methods: The study population included 433 patients (143 males vs. 290 females). Nail samples underwent primary direct microscopy and culture. The isolated yeasts and dermatophytes were then subjected to additional molecular identification by r-DNA ITS-RFLP. Identification of some non-dermatophytic molds (NDMs) and unknown yeasts was accomplished by ITS and beta-tubulin sequencing. Results: Onychomycosis was confirmed in 154 patients (males: 36.4%; n=56 vs. females: 63.6%; n=98), whose age ranged from 2 to 85 years, with the highest prevalence in the age group of 41-50 years. Infection mostly occurred due to yeasts (57.15%), with Candida albicans as the most frequent (29.35%) species, followed by C. parapsilosis (13.8%) and C. tropicalis (4.5%). Dermatophytes were isolated in 38.35% of the cases; the most common isolates were found to be Trichophyton interdigitale (21.1%), Epidermophyton floccosum (10.5%), T. rubrum (5.25%), and Microsporum canis (1.5%). NDMs were isolated from 4.5% of the cases with Aspergillus spp. as the most common agent. Dermatophytes and NDMs were more frequently seen in toenails, whereas yeasts mostly infected fingernails. Fingernail onychomycosis was significantly more prevalent among females than in males (P<0.05). Conclusion: The study highlights that in Khuzestan province, the causative agents of onychomycosis have shifted from dermatophytes to yeasts.

58-Jalilian, S., et al. (2017). "An in-vitro transcription assay for development of Rotavirus VP7." Iran J Microbiol 9(3): 186-194.

Background and Objectives: Human rotavirus (RV) is responsible for most cases of acute gastroenteritis in infants, worldwide. Today, in vitro transcription (IVT) assay is widely used to develop efficient RNA for the biological experiments such as gene function analysis and reverse

genetics. The aim of this study was to develop optimal full-length transcripts of the VP7 segment, using in vitro transcription assay. Materials and Methods: Special primers were designed in order to synthesize VP7 sequence of sense RNA in the process of IVT using T7 RNA polymerase. RT-PCR was performed using forward and reverse primers, containing T7 promoter sequence and BstUI restriction enzyme site, respectively. In order to synthesize ssRNA VP7, in accordance with the IVT technique, RV4-VP7 fragment was subcloned into PTZ57 R/T plasmid and digested by BstUI enzyme. Results: The sequencing of the VP7 gene showed 99% identity withVP7 gene of rotavirus RV4 strain (Sequence ID: M64666.1). The analysis of purity of DNA fragment and ssRNA VP7 segment revealed that OD ratio of A260/A280 and quantity of nucleic acids were (1.9, 0.036 mug/muL) and (2.02, 0.98 mug/muL), respectively. Conclusion: In the present study, a modified methodology of RNA synthetase was described by IVT assay, using T7RNA polymerase in order to transcribe the full-length transcripts of human VP7-RV4 strain. This method is applicable for reverse genetic approaches, especially for the production of reassortant RV vaccine.

59- Kavarizadeh, F., et al. (2017). "Molecular characterization of Leishmania parasites isolated from sandflies species of a zoonotic cutaneous leishmaniasis in Musiyan south west Iran." J Parasit Dis 41(1): 274-281.

Cutaneous leishmaniasis (CL) is vector borne parasitic disease, considered as public health problem especially in border of Iran and Iraq, Dehloran County (Musian district). The aim of this study was molecular identification of Leishmania parasites in sandfly as vectors of Leishmaniasis. Totally 280 female sandflies were trapped by sticky traps from 7 rural areas of Musiyan in September-November 2012. All sandflies were identified using morphological characters of the head and abdominal terminalia. DNA was extracted from female sandflies and Leishmania was identified using PCR and sequencing. All 280 trapped sandflies were identified as Phelobotumus Papatasi and Leishmania infections were detected in 3.2 % out of 280 female sandflies. All leishmania were identified as L. major and submitted in Gene bank as: LC014642.1, LC014641.1, LC014640.1 and LC014639.1. Frequency of Phlebotomus Papatasi and infection with L. major in studied regions showed that this vector is dominant in these areas.

60- Mehravaran, H., et al. (2017). "Association of Human Cytomegalovirus with Hodgkin's Disease and Non-Hodgkin's lymphomas." Asian Pac J Cancer Prev 18(3): 593-597.

Background and Objective: The human cytomegalovirus (HCMV) can persist lifelong as a latent infection and may result in a series of disorders. Associations with both Hodgkin's disease and non-Hodgkin s lymphomas have been reported. Expression of the unique long (UL)138 gene of HCMV is linked with the viral latency phase while that of the immediate-early (IE)1 gene is

typical of the viral replication phase in patients. This study conducted to determine the prevalence of CMV latent infection in histological tissue samples from patients with Hodgkin's and Non-Hodgkin s lymphomas. Material and Methods: A cross sectional study was carried out with a total of 50 paraffin embedded tissues blocks, including 25 samples for Hodgkin's disease and 25 samples for non-Hodgkin s lymphomas. After RNA extraction and cDNA preparation, detection of IE1 mRNA was conducted by RT-PCR and identification of mRNA UL138 was achieved by nested PCR. Results: Among 25 cases of Non-Hodgkin s lymphoma, 5 (20%) were positive for UL 138 and 1 (4%) for both IE1 and UL 138. Among 25 cases of Hodgkin only 1 (4%) was positive for UL 138 and all were negative for IE1 .Conclusion: A relatively high 20% rate of expression of UL 138 was detected in patients with non-Hodgkin s lymphoma, so that latent CMV infection may play a role in development of the disease.

61-Moosavian, M., et al. (2018). "Typing of staphylococcal cassette chromosome mec encoding methicillin resistance in Staphylococcus aureus isolates in Ahvaz, Iran." New Microbes New Infect 21: 90-94.

Methicillin-resistant Staphylococcus aureus (MRSA) is a major nosocomial pathogen. We sought to determine the frequency of the different types of SCCmec in MRSA isolates by performing a cross-sectional study. A total of 72 S. aureus isolates were collected from Imam Khomeini and Golestan hospitals and analysed for MRSA and SCCmec typing by multiplex PCR. The pattern of antibiotic resistance among S. aureus isolates was determined by disc diffusion analysis. Of the 72 S. aureus isolates, 29 (40.27%) were recognized as MRSA. SCCmec type III was the most common type, with 55.17% (16/29), followed by type II with 27.58% (8/29); type IV with 10.34% (3/29); and type I with 6.89% (2/29). All 29 MRSA isolates were resistant to chloramphenicol and erythromycin. In addition, resistance to cephalothin, gentamicin, clindamycin, ciprofloxacin, tetracycline and rifampicin was seen in 24 (75%), 26 (63.4%), 17 (94.4%), 27 (71.05%), 10 (71.42%) and 13 (68.42%) MRSA isolates, respectively. A decreased sensitivity of MRSA to the antibiotics used was observed, with type III SCCmec being the predominant isolate.

62-Mousavi, E., et al. (2018). "Antiviral effects of Lactobacillus crispatus against HSV-2 in mammalian cell lines." J Chin Med Assoc 81(3): 262-267.

BACKGROUND: Herpes simplex virus type 2 (HSV-2) infectious disease is one of the most common viral sexually transmitted diseases. As regards, vaginal lactobacilli play an important role in protecting host against the urogenital pathogens; here we assessed the potential antiviral activity of Lactobacillus crispatus against HSV-2 infection in vitro. METHODS: Both Vero and HeLa cell lines were treated by L. crispatus before, during and after HSV-2 infection. The pre-incubation

assay was also performed for the evaluating of virus adsorption by L. crispatus. Virus titer reduction in each stage was determined by a plaque reduction assay. RESULTS: L. crispatus significantly decreased the infectivity of the HSV-2 in initial steps on both cell lines; however, no significant inhibition was ascertained during adsorption and multiplication process. The lactobacilli adhere on Vero cells two-fold stronger than HeLa and subsequently protect the Vero cells nearly 2.5 fold higher than HeLa cell against the virion. Co-incubation of HSV-2 with bacterial cells prior to virus inoculation significantly decreased the virus titer. CONCLUSION: L. crispatus appears to inhibit the entry of the virus into cells by trapping HSV-2 particles. In addition, formation of L. crispatus microcolonies in the cell surface could block HSV-2 receptors and prevent viral entry to cells in initial infection steps.

63-Nashibi, R., et al. (2018). "Infection after open heart surgery in Golestan teaching hospital of Ahvaz, Iran." Data Brief 16: 478-482.

The present study surveyed demographic and infection data which were obtained after open heart surgery (OHS) through patient's admission in Golestan teaching hospital, Ahvaz metropolitan city of Iran, taking into account the confirmed location of the infection, microorganism and antibiotic susceptibility. The occurrence of infection among patients during 48 to 72 h after surgery and hospital admission is the definition of Nosocomial infections (NIs) (Salmanzadeh et al., 2015) [1]. All of them after OHS were chosen for this study. In this paper, type of catheter, fever, type of microorganism, antibiotic susceptibility, location of the infection and outcome (live or death) were studied (Juhl et al., 2017; Salsano et al., 2017) [2], [3]. After the completion of the observations and recording patients' medical records, the coded data were fed into EXCELL. Data analysis was performed using SPSS 16.

64-Nikfar, R., et al. (2017). "A Study of prevalence of Shigella species and antimicrobial resistance patterns in paediatric medical center, Ahvaz, Iran." Iran J Microbiol 9(5): 277-283.

Background and Objectives: Shigella infections are one of the major causes of diarrhea worldwide, and especially in developing countries. Antimicrobial resistance has complicated the empirical treatment. The aim of this study was to define the clinical and antibiotic resistance patterns of Shigella gastroenteritis cases. Materials and Methods: Stool samples of patients with diarrhea and fever diagnosed with shigellosis were collected, from June 2013 to May 2014 at Abuzar Hospital, Iran. All samples were cultured for Shigella spp on selective and differential media. Shigella isolates were evaluated for antimicrobial resistance. Results: Among 193 Shigella isolates, S. flexneri (64.8%) was the predominant species followed by S. sonnei (32.6%). The most frequent antibiotic resistance observed, was towards co-trimoxazole (89%), ampicillin (77%) and

ceftriaxone (51%) and the lowest resistance were seen in ciprofloxacin (1.5%), azithromycin (7%). Conclusion: Due to the high resistance to ceftriaxone, this drug is not recommended as an empirical therapy for shigellosis. However, azithromycin should be used as the first-line treatment for paediatric patients, suffering from shigellosis and ciprofloxacin can be used as an alternative.

65-Piranshahi, A. R., et al. (2018). "Genomic analysis of Blastocystis hominis isolates in patients with HIV-positive using locus SSU-rDNA." J Parasit Dis 42(1): 28-33.

Blastocystis hominis (B. hominis) is a protozoan zoonosis which clinical signs of infection with this parasite has been reported to be more severe in patients with weakened immune systems than healthy controls. So, the aim of the study was to evaluate genomic analysis of B. hominis isolates obtained from patients with HIV-positive using locus SSU-rDNA. At first, 268 stool samples were randomly collected from patients with HIV-positive referred to health centers of Khuzestan province, southwest of Iran. Formol-ether and direct smear techniques were used for the detection of parasitic agents. After extracting DNA, the samples were analyzed by the PCR method. Finally, the subtypes were determined by the sequencing and PCR methods. New samples were used for the preparation of positive control sample; they were cultured in coagulant-serum biphasic cultivation media. Of 268 stool samples, 33 (12.3%) cases were detected positive for B. hominis using Formol-Ether technique but 51 (19%) cases were positive using molecular method. The most common isolates were related to the subtype III with 29 positive cases (56.8%), then, genotype I with 11 (21.6%) cases, 6 cases (11.8%) with genotype II, 3 (5.9%) combined cases with genotypes I and III as well as 2 cases (3.9%) with genotype VI. There was a significant difference between two groups of HIV-positive patients (infected with the parasite and/or without the parasite) in the term of the mean of TCD4-positive cells. The results indicated a relatively high prevalence of B. hominis in HIV-positive patients as well as our findings may represent that the number reduction of TCD4-positive cells has an effective role in the increased risk of the parasitic infection in HIV-positive patients.

66-Rostami, S., et al. (2018). "Investigating of four main carbapenem-resistance mechanisms in high-level carbapenem resistant Pseudomonas aeruginosa isolated from burn patients." J Chin Med Assoc 81(2): 127-132.

BACKGROUND: Pseudomonas aeruginosa is an opportunistic pathogen involved in many infections. Carbapenem-resistant P.aeruginosa has emerged as an important cause of infection in different hospitals worldwide. We aimed to determine frequencies of the four main resistance mechanisms [metallo-beta lactamase (MBL) production (blaIMP, blaVIM, blaSPM and blaNDM), overproduction of the MexAB-OprM and MexXY efflux pumps, overproduction of chromosome-

encoded AmpC beta-lactamase, and reduced OprD expression] in high-level carbapenem-resistant P.aeruginosa isolated from patients with burns. METHODS: In a descriptive study, 107 P. aeruginosa isolates were collected from patients with burn injuries and tested for antibiotic susceptibility, by an E-test for carbapenems, an E-test for metallo-beta-lactamase producer isolates, and PCR to detect MBL genes. Furthermore, high-level carbapenem-resistant isolates were tested by real-time PCR for the expression levels of the mexB, mexY, ampC, and oprD genes. RESULTS: Amongst all P. aeruginosa isolates, 78.5%, 46.7%, and 15% were imipenem-, meropenem-, and doripenem-resistant, respectively; 72% of isolates were multidrug-resistant. The blaIMP and blaVIM genes were detected in 17.9% and 1.2% of isolates; respectively. The blaSPM and blaNDM genes were not observed. Among the resistant isolates, mexB overexpression (63.2%) was the most frequent mechanism, followed by mexY overexpression (52.6%), ampC overexpression (36.8%), and reduced oprD expression (21.1%). CONCLUSION: Emerging antimicrobial resistance in burn wound bacterial pathogens is a serious therapeutic challenge for clinicians. In the present study, most of the isolates were MDR. This finding indicated an alarming spread of resistant isolates and suggested that infection control strategies should be considered. Resistance to carbapenems is influenced by several factors, not all of which were evaluated in our study; however, the results showed that production of MBLs and overexpression of the mexB gene were the most frequent mechanisms in carbapenem-resistant isolates.

67-Saki, J., et al. (2017). "Detection and genotyping of Toxoplasma gondii isolated from soil in Ahvaz, southwest of Iran." J Parasit Dis 41(1): 202-205.

To detection and genotype of Toxoplasma gondii isolated from soil in Ahvaz, southwest of Iran. Between August 2011 and May 2012 at different sites located in the area of the Ahvaz city south west Iran. A total of 200 soil samples were taken from different points of the region. Oocysts were recovered using the flotation method. Then, PCR reactions targeting the GRA6 gene were performed for specific T. gondii detection. The positive samples were studied by RFLP (random amplified fragment length polymorphism) using MseI enzymes to confirm the parasite linage. Toxoplasma DNA was found in 18 samples. Among them, 12 samples were successfully genotyped as GRA6 type III and 6 as GRA6 Type II. This is the first investigation detecting and genotyping T. gondii oocyst in environmental soil samples of Ahvaz, South west of Iran. The results of this study indicated that soil contaminated with T. gondii oocysts especially in public park may play a role in the epidemiology of human toxoplasmosis in southwest of Iran.

68-Saki, J., et al. (2017). "Seroprevalence and molecular evaluation of toxoplasmosis in children with cancer in Khuzestan province, Southwest of Iran." J Parasit Dis 41(4): 947-951.

Toxoplasma gondii is an intracellular parasite with global distribution. Toxoplasmosis in individuals with normal immune system is usually asymptomatic, but in immunocompromised patients may lead to death if not cured. In this study, the prevalence rate of acute and chronic toxoplasmosis in children with cancer was investigated using serological and molecular methods. Blood samples were taken from 372 children with cancer in Shafa hospital in Ahvaz, southwest of Iran. Anti-T. gondii IgG and IgM antibodies were investigated by ELISA. The presence of Toxoplasma in the blood samples was evaluated by Nested PCR. Among 372 children with cancer, 155 (41.7%) were positive for anti-T. gondii IgG antibodies and 24 (6.4%) were positive for anti-T. gondii IgM antibodies, as well. In IgG avidity test, 34 (22%) had antibodies indicating acute phase and 121 (78%) had antibodies indicating chronic phase. The Nested PCR results were showed T. gondii parasite in 34 (100%) patients among 34 IgG antibody-positive patients with acute infection, among 16 IgG antibody-positive patients with chronic infection, 10 patients were indicative of T. gondii and 6 patients were not indicative of T. gondii. A total of 50 cases, 44 (88%) were T. gondii-positive and 6 (12%) were T. gondii-negative in Nested PCR. This study showed high prevalence of toxoplasmosis in children with cancer. Results of serological techniques (ELISA and IgG avidity) had a higher overlap with Nested PCR in identifying T. gondii of seropositive patients.

69- Shahani, T., et al. (2017). "Frequency of Epstein Barr Virus Type 1 Among Nasopharyngeal Carcinomas in Iranian Patients." Asian Pac J Cancer Prev 18(2): 327-331.

Background: Around 95% of the world's population are infected with the Epstein-Barr virus (EBV), which can persist latent in B lymphocytes and epithelial cells life-long. EBV has been linked with lymphoid and epithelial cancers and persistence of EBV infection in lymphoid or epithelial cells may result in virus-associated B-cell tumors or nasopharyngeal carcinomas (NPC). This study was conducted to determine the frequency of EBV DNA in nasopharyngeal carcinoma tissue of Iranian patients. Materials and methods: A total of 50 blocks of formalin-fixed paraffin-embedded tissue of NPCs from 38 (76 %) male and 12 (24%) female patients were collected from archives of Ahvaz hospitals. Sections were cut at 5 mum and DNA was extracted for detection of EBV DNA and EBV typing by mested PCR. DNA sequencing was performed to confirm PCR results. The distribution of EBV DNA was compared among WHO histological subtypes of NPC. Results: Some 3 female and 11 (22%) male NPC samples showed positive for EBV DNA type 1, 2/14(22.2%)WHO histological type II and 12/41(29.3%) WHO histological type III. Conclusions: The frequency of EBV DNA among NPCs in Iranian patients was found to be 28%, EBV type I predominating. Both WHO histological type II and III NPC subtypes demonstrated approximately the same detection prevalence.

70-Taghipour, S., et al. (2017). "Luliconazole, a new antifungal against Candida species isolated from different sources." J Mycol Med.

OBJECTIVE: Luliconazole is an inhibitor for sterol 14-alpha-demethylase in fungal cells with a broad-spectrum antifungal activity against dermatophytes, Candida albicans, Malassezia species, dematiaceous and hyaline hyphomycetes. Furthermore, luliconazole has been clinically used for the treatment of pityriasis versicolor, dermatophytosis, onychomycosis, cutaneous and mucocutaneous candidiasis. In the present study, we aimed to evaluate in vitro antifungal activity of luliconazole against several strains of Candida species recovered from different clinical materials. MATERIALS AND METHODS: In the present study, 104 strains of Candida species including, 34 isolates from vaginitis, 23 isolates from AIDS patients with vaginal candidiasis, 24 isolates from neutropenic patients and 24 isolates from tracheal tubes, were examined for susceptibility tests. A serial dilution of luliconazole (4-0.008mug/mL) was tested against different strains of Candida species recovered from different sources. RESULTS: The minimum inhibitory concentration (MIC) range and MIC90 of vaginal isolates (HIV(-)) were 1-0.063 and 1mug/mL. Furthermore, the most of strains (50%) had a MIC of 0.5mug/mL. The MIC ranges were similar (2-0.016mug/mL) for both vaginal (HIV(+)) and neutropenic patients isolates, whereas, MIC90 for them were 0.5 and 1mug/mL, respectively. All tracheal tubes strains were inhibited at the range of 2-0.008mug/mL with MIC90=1mug/mL. Totally, the lowest MIC50 (MIC=0.015mug/mL), MIC90 (MIC=1mug/mL) and MICGM (MIC=0.05mug/mL) are correlated to C. glabrata, a non-albicans species. CONCLUSION: It is concluded that, luliconazole could be an alternative anti-Candida agent, however, in vivo studies must be confirmed usefulness of drug for clinical usage.

71-Zarrin, M., et al. (2017). "In Vitro Nematophagous Activity of Predatory Fungi on Infective Nematodes Larval Stage of Strongyloidae Family." Open Access Maced J Med Sci 5(3): 281-284.

AIM: The main goal of the present research conducted to assess the in vitro activity of the nematophagous fungi Duddingtonia flagrans, Fusarium solani, Verticillium chlamidosporium, and Trichoderma harzianum. MATERIAL AND METHODS: Four isolates of fungi including D. flagrans, F. solani, V. chlamidosporium and T. harzianum were used in this study. Horse faeces were used to provide the larvae stage of Strongyloidae family for the experiments. RESULTS: D. flagrans was the most effective fungus to reduce the population of the larval nematodes. D. flagrans was able to kill 100% of larvae after 14 days of incubation. The significant effect was seen after 7 days of incubation, therefore, the live larvae was decreased to 9, 11, 19 and 25 for D. flagrans, V. chlamidosporium, F. solani and T. harzianum, respectively. CONCLUSION: Our results illustrated that D. flagrans were most successful fungus for reducing the number of Strongylidae family larva stage from horse faeces. Follow D. flagrans, the live larvae was significantly reduced for V. chlamidosporium, F. solani and T. harzianum, respectively.

72-Zarrin, M., et al. (2017). "Rapid Identification of Aspergillus Fumigatus Using Betaeta-Tubulin and RodletA Genes." Open Access Maced J Med Sci 5(7): 848-851.

AIM: The main purpose of the present study was to test the beta-tubulin and rodletA genes for rapid identification of Aspergillus fumigatus. MATERIALS AND METHODS: Fifty-one A. fumigatus strains including environmental, clinical and reference isolates were tested in this research. PCR was carried out based on betatub and rodA partial gene sequences. RESULTS: A 198 bp DNA fragment was obtained using betatub gene. PCR amplification of the rodA gene resulted in a 313 bp band. The betatub and rodA genes PCR products exhibited a 100% homology with the associated sequences in the GenBank. CONCLUSION: In the present study, we used a PCR approach that was able to discriminate A. fumigatus from other related species within the section Fumigati.

73-Alavi, S. M., et al. (2017). "Diagnostic value of serum creatine kinase-BB for acute meningitis in adults." Asian Pacific Journal of Tropical Disease 7(1): 18-20.

74-Gharibi, Z., et al. (2017). "Entamoeba spp. diagnosis in patients with inflammatory diarrhea by staining, copro-antigen ELISA and multiplex PCR methods." Asian Pacific Journal of Tropical Disease 7(10): 601-603.

75- Halvaeezadeh, M. and A. Z. Mahmoudabadi (2017). "Anti-Candida activity of biosurfactant produced by Rhodotorula paludigena." Current Enzyme Inhibition 13(3): 204-209.

76- Jelowdar, A., et al. (2017). "Efficacy of combined albendazol and praziquntel and their loaded solid lipid nanoparticles components in chemoprophylaxis of experimental hydatidosis." Asian Pacific Journal of Tropical Biomedicine 7(6): 549-554.

77- Kazemi, F., et al. (2017). "Prevalence of Toxocara species in park soils of Ahvaz City, southwest of Iran." Asian Pacific Journal of Tropical Disease 7(12): 705-707.

78- Mardani-Kateki, M., et al. (2017). "Molecular detection of Pneumocystis jiroveci in wild rats in Southwest of Iran." Biochemical and Cellular Archives 17(1): 213-217.

79- Mehravaran, H., et al. (2017). "Association of human cytomegalovirus with Hodgkin's disease and non-Hodgkin's lymphomas." Asian Pacific Journal of Cancer Prevention 18(3): 593-597.

80- Mohseni, H., et al. (2017). "Circulating 25-hydroxy vitamin D relative to vitamin D receptor polymorphism after vitamin D3 supplementation in breast cancer women: A randomized, double-blind controlled clinical trial." Asian Pacific Journal of Cancer Prevention 18(7): 1953-1959.

81- Piranshahi, A. R., et al. (2017). "Prevalence of parasitic contamination in fast food salads in Ahvaz, southwest of Iran." Asian Pacific Journal of Tropical Disease 7(12): 724-726.

82-Rahdar, M., et al. (2017). "Immunization against leishmania major using UV-irradiated promastigote in experimental model Balb/c mice." Biochemical and Cellular Archives 17(2): 447-449.

83-Rahdar, M., et al. (2017). "The Treatment and prophylaxis effect of albedazole in animal model with histological evidence." Biochemical and Cellular Archives 17(1): 255-259.

84-Shokoohizadeh, L., et al. (2017). "Molecular characterization of Shigella spp. isolates from a pediatric hospital in Southwestern Iran." Gastroenterology and Hepatology from Bed to Bench 10(4): 319-322.

85- Tavalla, M., et al. (2017). "Molecular identification of Enterocytozoon bieneusi and Encephalitozoon species in pigeons of southwest of Iran." Asian Pacific Journal of Tropical Disease 7(9): 536-538.