مقالات منتشر شده مرکز تحقیقات بیماریهای عفونی و گرمسیری در سال ۲۰۱۶ (۱۳۹۵)

1-Abastabar, M., et al. (2016). "Genetic and Morphological Diversity of the Genus Penicillium From Mazandaran and Tehran Provinces, Iran." Jundishapur J Microbiol 9(1).

Background: The genus Penicillium contains a large number of ubiquitous environmental taxa, of which some species are clinically important. Identification of Penicillium down to the species level is currently based on polyphasic criteria, including phenotypic features and genetic markers. Biodiversity of the genus Penicillium from Mazandaran and Tehran provinces has not been described. Objectives: The current paper focused on the environmental biodiversity of Penicillium isolates within some areas of Mazandaran and Tehran provinces, based on morphological traits and the molecular data from partial sequence of the beta-tubulin (BT2) gene. Materials and Methods: A total of 400 strains were isolated from the environment and investigated using morphological tests and sequencing of BT2, in order to characterize the spectrum of the Penicillium species. Results: Sequence analysis of BT2 and morphological criteria of 20 strains representative of 10 species showed that Penicillium chrysogenum was the most prevalent species (n = 6), followed by P. polonicum (n = 3), P. glabrum (n = 2), P. palitans (n = 2), P. melanoconidium (n = 2), and other species, including P. expansum, P. canescense, P. griseofulvum, P. italicum, and P. raistrickii with one case each. Conclusions: It was shown that partial beta-tubulin sequence, as a reliable genetic target, supported specific morphological criteria for identification of the Penicillium species. Like other assessments throughout the world, P. chrysogenum remains the most frequent environmental Penicillium species in Mazandaran and Tehran Provinces.

2-Abastabar, M., et al. (2016). "Potent Activities of Novel Imidazoles Lanoconazole and Luliconazole against a Collection of Azole-Resistant and -Susceptible Aspergillus fumigatus Strains." Antimicrob Agents Chemother 60(11): 6916-6919.

A collection of azole-susceptible (n = 141) and azole-resistant (n = 27) Aspergillus fumigatus isolates was tested against seven antifungal drugs, including the new imidazoles lanoconazole and luliconazole. The luliconazole and lanoconazole MIC90 values for the azole-susceptible strains were 0.001 mu g/ml and 0.008 mu g/ml, and those for the azole-resistant strains were 0.016 mu g/ml and 0.032 mu g/ml.

3-Abbasi, S., et al. (2016). "The Prevalence of SEN Virus and Occult Hepatitis B (OBI) Virus Infection Among Blood Donors in Ahvaz City." Jundishapur J Microbiol 9(7).

Background: The SEN virus (SENV) is a prevalent blood borne pathogen that has a worldwide incidence. SENV is comprised of eight genotypes; genotypes Hand Dare frequently associated with the pathogenesis of non-A-E hepatitis and post-transfusion hepatitis in blood donors and hepatitis patients. So far, no SENV pathogenesis has been reported in the liver biopsies of SENV carriers, but the frequency of SENV and its related genotypes requires further molecular epidemiology studies in different regions of the world. Occult hepatitis B infection (OBI) is another global public health problem that is primarily transmitted via blood transfusions. Therefore, the identification of OBI among blood donors is key to preventing the spread of this disease. The relationship between SENV and OBI requires further evaluation. Objectives: The aim of this study was to determine the prevalence of SENV-D and SENV-H in blood donors in Ahvaz city with a particular focus on co-infection with OBI. Patients and Methods: This study had a cross-sectional design and included 184 healthy consecutive blood donors who visited a blood transfusion center in Ahvaz city from October-November 2013. The sera of all blood donors negative for HBsAg, anti-HCV antibody, and anti-HIV antibody were tested for SENV-D and SENV-H using nested polymerase chain reaction (PCR). In addition, tests for HBV DNA (PCR), HBcIgG (ELISA), liver function (aspartate transaminase and alanine transaminase), and alkaline phosphatase were carried out. Results: Liver function tests in the healthy blood donors were within the normal range. The incidence rates of SENV-D and SENV-H in the 184 total blood donors were 10 (5.4%) (95% confidence interval (CI): 2.1% - 9.0%) and 32 (17.4%) cases (95% CI: 12.0% - 23.0%), respectively. SENV-H/D co-infection occurred in 2 (1.1%) patients. The sera of 8/184 (4.3%) were positive for anti-HBc antibody but negative for HBV DNA. Conclusions: Regardless of the presence of nonpathogenic SENV, 44/184 (24%) blood donors tested positive for both SENV-D and SENV-H. Although 4.3% of blood donors were positive for HBcIgG but negative for HBV DNA, the presence of OBI cannot be ruled out unless their liver biopsies show negative for HBV DNA.

4-Ahmadi, E., et al. (2016). "Development of Poly (A)-Tailed Universal Reverse Transcription PCR Method for Sequence-Independent Amplification of Rearranged Rotavirus." Arch Iran Med 19(9): 625-630.

BackgrOund:-Group A Rotaviruses (GARV) are the main viral cause Of acute gastroenteritis, leading to 870,000 deaths annually in the developing world and representing a major health problem. Therefore, diagnosis and treatment of this disease are crucial. Gene rearrangement-within segmented viruses as well as rotavirus is seen throughout chronic rotavirus infeCtion in immunodeficient young children and through serial pasgage of rotavirus in

cell culture at a high multiplicity of infection. Detailed knowledge of rotavirus biology allows design da vaccine against rotavirus by engineered antigens. The aim of this studrwas to develop Poly(A) =Tailed universal Reverse Transcription POlynnerase Chain Reaction (RT-PCR) method and compare the efficacy of this procedure with specific multiplex PCR protocol for detecting normal and rearranged segments. Methods: Virus win propagated on confluent monolayer of MA-104 cells and aNuots of each passage were kept frozen for further RNA genomic profiles analysis by polyacrylamide gel electrophoresis. Purified'Rota virus RNAwas polyadenylated and used for the amplification and detection Of normal and rearranged segments of rotavirus using RT-PCR. Results: The genetation of gene rearrangement through multiple serial passages of rotavirus was shown using MOI 1. The rearranged RNA segments of NSP1 and NSP3 genes with different, migration pattern in PAGE. were detected by poly(A)RT-PQR. Conclution: In the current research, a novel Poly(A)-Tailed UniverSal Reverse Transcription PCR method was introduced for the high throughput amplification and analysis of the informative untranslated regions of the rotavirus genome.

5-Amin, M., et al. (2016). "Detection of Haemophilus influenzae type b, Streptococcus agalactiae, Streptococcus pneumoniae and Neisseria meningitidis in CSF specimens of children suspicious of Meningitis in Ahvaz, Iran." Kaohsiung Journal of Medical Sciences 32(10): 501-506.

Meningitis is a life-threatening infection associated with a high mortality and morbidity worldwide. Neisseria meningitidis, Haemophilus influenzae, and Streptococcus pneumoniae are the most prevalent infectious agents that cause bacterial meningitis (BM). The objective of this study was to determine the frequencies of these three bacteria using bacterial cultures and polymerase chain reaction (PCR). In our cross-sectional study, cerebrospinal fluid (CSF) specimens were obtained from 196 patients who were suspected of having BM and referred to the pediatric ward of Abuzar Hospital (Ahvaz, Iran). The samples were monitored by gram stain, cultures, and the PCR method. The patients' age mean was 23 +/- 0.56 months. The 196 patients comprised 92 (46.9%) boys and 104 (53.06%) girls. Based on bacterial cultures, just three isolates of H. influenzae were detected. However, PCR detected this bacterium in eight patients. Streptococcus pneumoniae was detected in five (2.5%) patients by the amplification of the lytA gene and in one (0.5%) patient by ply. In this study, no N. meningitidis isolate was in the CSF samples, based on the bacterial culture or PCR results. Streptococcus agalactiae was detected only in one patient, based on PCR. In conclusion, in the present study, the PCR method was more sensitive and rapid than culture for detecting the infectious agents in BM. For this reason, this diagnosis method is recommended for BM. Copyright (C) 2016, Kaohsiung Medical University. Published by Elsevier Taiwan LLC.

6-Amirrajab, N., et al. (2016). "In Vitro Activities of Six Antifungal Drugs Against Candida glabrata Isolates: An Emerging Pathogen." Jundishapur J Microbiol 9(5).

Background: Candida glabrata is a pathogenic yeast with several unique biological features and associated with an increased incidence rate of candidiasis. It exhibits a great degree of variation in its pathogenicity and antifungal susceptibility. Objectives: The aim of the present study was to evaluate the in vitro antifungal susceptibilities of the following six antifungal drugs against clinical C. glabrata strains: amphotericin B (AmB), ketoconazole (KTZ), fluconazole (FCZ), itraconazole (ITZ), voriconazole (VCZ), and caspofungin (CASP). Materials and Methods: Forty clinical C. glabrata strains were investigated using DNA sequencing. The in vitro antifungal susceptibility was determined as described in clinical laboratory standard institute (CLSI) documents (M27-A3 and M27-S4). Results: The sequence analysis of the isolate confirmed as C. glabrata and deposited on NCBI GenBank under the accession number no. KT763084-KT763123. The geometric mean MICs against all the tested strains were as follows, in increasing order: CASP (0.17 g/mL), VCZ (0.67 g/mL), AmB (1.1 g/mL), ITZ (1.82 g/mL), KTZ (1.85 g/mL), and FCZ (6.7 g/mL). The resistance rates of the isolates to CASP, FCZ, ITZ, VZ, KTZ, and AmB were 5%, 10%, 72.5%, 37.5%, 47.5%, and 27.5%, respectively. Conclusions: These findings confirm that CASP, compared to the other antifungals, is the potent agent for treating candidiasis caused by C. glabrata. However, the clinical efficacy of these novel antifungals remains to be determined.

7-Amirrajab, N., et al. (2016). "Migratory Birds as a Potential Reservoirs of Cryptococcus Neoformans." International Journal of Environmental Research 10(3): 459-464.

Migratory birds can become long-distance vectors for a wide range of microorganisms. The objective of the present study was to investigate the presence of Cryptococcus neoformansin the cloacae, crop and nasal cavity of migratory birds in order to assess their role as potential reservoirs and/or mechanical vectors of human and animal cryptococcosis. A total of 700 samples (cloacae, crops and nasal secretions) of 300 wild migratory birds (with the permission of the local Department of Environment) were collected and inoculated on Niger seed agar (NSA), incubated for two weeks at 30 degrees C and daily observed for the presence of brown yeast colonies, which is presumptive for C. neoformans. The species identification was confirmed using conventional and molecular methods. Out of 700 samples, 4 samples (0.6%) from cloacae of 2 Anascrecca (2 cases), Anasplatyrhychos (1 case) and Fulicaatra (1 case) were positive for C. neoformans. To the best of our knowledge, due to low isolation rate of C. neoformansfrom cloacae, crops and nasal secretions, transmission from these samples could be as a minimal risk factor for human and animal cryptococcosis, unlike the dry excreta of wild pigeons.

8-Ansari, S., et al. (2016). "A 9-Month-Old Girl from Iran with Extensive Erythematous Plaques Due to Trichophyton simii, a Zoophilic Dermatophyte." Mycopathologia 181(5-6): 451-455.

The incidence of dermatophytosis due to Trichophyton simii is generally considered to be limited to endemic areas, particularly one area of India. However, the high similarity between the morphological features of atypical T. simii isolates and those of other dermatophytes such as Trichophyton interdigitale and Arthroderma benhamiae may lead to misidentification of the cause of dermatophytosis in many instances. We investigated a rare case of tinea corporis in a 9-month-old female with extensive erythematous lesions. Morphological features of the recovered isolate from the culture resulted in the identification of Trichophyton interdigitale. For accurate identification, the internal transcribed spacer regions (ITS1 and ITS2) of the ribosomal DNA (rDNA) gene were sequenced and the isolate was ultimately identified as T. simii. In conclusion, T. simii, which has been formerly known to be restricted to specific endemic regions, appears to be not infrequent in non-endemic areas but instead simply less well-known and consequently underestimated. To determine its actual prevalence of infection, the application of DNA-based molecular methodologies is required.

9-Azaran, A., et al. (2016). "Study on Rotavirus Infection and Its Genotyping in Children Below 5 Years in South West Iran." Iran J Pediatr 26(2).

Background: Human rotaviruses are the most important agents for severe dehydrating diarrhea in children below 5 years old. Rotaviruses (RV) is a serious public health problem in developing and developed countries. Objectives: The aim of this study was to determine the prevalence of rotavirus infection and their genotypes in children younger than 5 years of age with acute diarrhea in Ahvaz, Iran. Materials and Methods: For this study, 200 stool samples from children below 5 years of age with acute diarrhea were collected between October 2011 and March 2012. Initially all stool samples were tested for rotavirus antigen by ELISA, and positive samples were confirmed by RT-PCR targeting the VP6 rotavirus gene. Determination of rotavirus genotypes was carried out by performing RT-PCR for G and P types. Altogether, 15 samples were sequenced. Results: Out of 200 stool samples, 100 (50%) had rotavirus antigen detected by ELISA and 73 (36.5%) were found positive by RT-PCR. Of the rotavirus strains identified, only 63 (86.3%) were positive for both VP7 and VP4 while 10 (13.7%) strains were found nontypeable. Rotavirus infection accounts for 36.5% of gastroenteritis cases in samples from symptomatic children. The most prevalent rotavirus genotypes were G1P [8] (80%) followed by G2P [4] (20%). Conclusions: Our results suggest that group A rotavirus is a major pathogene of acute diarrhea in Ahvaz city. The genotypes circulating are similar with those of other countries.

10-Baghi, N., et al. (2016). "In vitro activity of new azoles luliconazole and lanoconazole compared with ten other antifungal drugs against clinical dermatophyte isolates." Medical Mycology 54(7): 757-763.

In vitro susceptibilities of 100 clinical dermatophyte isolates belonging to five species from Iran toward lanoconazole and luliconazole were compared with ten other antifungal agents including econazole, itraconazole, miconazole, fluconazole, griseofulvin, butenafine, terbinafine, caspofungin, anidulafungin and tolnaftate. MIC and MEC values were analyzed according to CLSI M38-A2 document. The isolates were previously identified to the species level using PCR-RFLP on ITS rDNA region. The range of luliconazole and lanoconazole minimum inhibitory concentrations (MICs) was 0.016-0.032 and 0.063-1 mu g/ml, respectively for dermatophyte species. Luliconazole and lanoconazole revealed potent activity against all dermatophyte isolates. Anidulafungin, caspofungin, and luliconazole showed the best activity with the lowest geometric mean 0.01, 0.016, and 0.018 mu g/ml, respectively, followed by tolnaftate (0.06 mu g/ml), terbinafine (0.07 mu g/ml), itraconazole (0.183 mu g/ml), butenafine (0.188 mu g/ml), econazole (0.20 mu g/ml), lanoconazole (0.24 mu g/ml), griseofulvin (1.28 mu g/ml), miconazole (2.34 mu g/ml) and fluconazole (15.34 mu g/ml). The current study demonstrated luliconazole and lanoconazole displayed excellent activity against all dermatophyte isolates, although the majority of dermatophyte isolates showed low susceptibility to griseofulvin and very low to miconazole, and fluconazole.

11-Bidgani, S., et al. (2016). "Comparison of group B streptococci colonization in vaginal and rectal specimens by culture method and polymerase chain reaction technique." Journal of the Chinese Medical Association 79(3): 141-145.

Background: Streptococcus agalactiae (group B streptococci, GBS) is a colonizing microorganism in pregnant women and without causing symptoms. Colonization of GBS in the rectovaginal region in late of pregnancy is a risk factor for newborn diseases. GBS infection in newborn babies is acquired by the aspiration of infected amniotic fluid or vertical transmission during delivery through the birth canal. The aim of this study was determination of GBS prevalence among vaginal and anorectal specimens at gestation females by polymerase chain reaction (PCR) and culture-based methods. Methods: In this study, 137 rectal and vaginal swabs were separately collected from women with gestational age 35-37 weeks from July 2013 to March 2014 at the teaching hospital of Razi, Ahvaz, Iran. All samples were enrichment in selective culture media Todd-Hewitt broth for 24 hours and recognized by standard culture using blood agar, phenotypic tests, and amplification of the CFB gene. Results: Age range was 16-45 years (mean, 28.34 +/- 0.7 years). Of rectal samples, 42 (30.7%) were positive based on culture method and 57 (41.6%) samples were positive by PCR. Of 137 vaginal samples, 38

(27.7%) were positive by culture and 60 (43.8%) samples were positive by PCR. The chance of colonization with GBS was increased in women with a history of urinary tract infection. Conclusion: The frequency of GBS culture from rectal samples was higher than vaginal samples. However, the detection percentage of GBS using PCR from vaginal samples was higher than rectal samples. By contrast, the culture is a time-consuming method requiring at least 48 hours for GBS fully identification but PCR is a sensitive and rapid technique in detection of GBS, with the result was acquired during 3 hours. Copyright (C) 2015, the Chinese Medical Association. Published by Elsevier Taiwan LLC.

12- Feiz Haddad, M. H., et al. (2016). "Identification of Leishmania Species Isolated from Human Cutaneous Leishmaniasis in Mehran, Western Iran Using Nested PCR." Iran J Parasitol 11(1): 65-72.

Background: The incidence of cutaneous leishmaniasis in the city of Mehran has risen sharply in recent years because the city borders Iraq, which has allowed entrance of different Leishmania strains. These strains have different shapes, periods of disease, and healing of lesions. The present study identified and determined cutaneous leishmaniasis species in this region. Methods: This cross-sectional study was carried out by preparing slides from 92 patients with suspected cutaneous leishmaniasis lesions from Mehran during 2012-2013. Parasite genomic DNA was extracted and CSB2XF and CSB1XR primers were used to amplify the Leishmania minicircle kDNA regions. The parasite species were detected by specific 13Z and LIR primers by applying nested PCR technique. Results: All banding patterns were diagnosed as L. major parasite by comparison of standard models with amplified fragments 560 bp in length from bands. The patients were 56.5% male and 43.5% female. The most frequently-infected age group was the 21-30 years group at a rate of 27.2%. About 56.3% of patients had a single lesion and a significant correlation was observed between age and number of lesions (P > 0.05). Conclusion: The nested PCR technique was shown to be an effective method with high sensitivity and specificity for identification of human Leishmania parasites. Molecular analysis revealed that parasites isolated from Mehran were identified as L. major and the disease was rural in form.

13-Foroutan-Rad, M., et al. (2016). "Toxoplasmosis in Blood Donors: A Systematic Review and Meta-Analysis." Transfusion Medicine Reviews 30(3): 116-122.

Transfusion-transmissible infections include pathogens that may cause severe and debilitating diseases. Toxoplasmosis is a cosmopolitan neglected parasitic infection that can lead to severe complications including death in immune compromised patients or following

infection in utero. Multiple studies have demonstrated the transmission of Toxoplasma gondii by blood transfusion. The objective of this review was to comprehensively assess the seroprevalence rate of Toxoplasma in blood donors from a worldwide perspective. Seven electronic databases (PubMed, Science Direct, Web of Science, Scopus, Cochrane, Ovid, and Google Scholar) were searched using medical subject headings terms. A total of 43 records met the inclusion criteria in which 20,964 donors were tested during the period from January 1980 to June 2015. The overall weighted prevalence of exposure to toxoplasmosis in blood donors was 33% (95% confidence interval [CI], 28%-39%). The seroprevalences of immunoglobulin (Ig)M and both IgG and IgM antibodies were 1.8% (95% CI, 1.1%-2.4%) and 1.1% (95% CI, 0.3%-1.8%), respectively. The highest and the lowest seroprevalences of toxoplasmosis were observed in Africa (46%; 95% CI, 14%-78%) and in Asia (29%; 95% CI, 23%-35%), respectively. Brazil (75%) and Ethiopia (73%) were identified as countries with high seroprevalence. Because positive serology does not imply infectiousness and because seroprevalence is high in some nations, a positive serology test result alone cannot be used as an effective method for donor screening. Future research for methods to prevent transfusion-transmitted toxoplasmosis may derive benefit from studies conducted in areas of high endemicity. (C) 2016 Elsevier Inc. All rights reserved.

14-Gharaghani, M., et al. (2016). "The Frequency, Antifungal Susceptibility and Enzymatic Profiles of Candida Species Isolated from Neutropenic Patients." Jundishapur J Microbiol 9(11).

Background: Neutropenia, as a predisposing factor for invasive candidiasis, is defined as a reduction in neutrophil count to less than 1500/mm(3). It is a common condition in patients with hematological malignancy and cytostatic chemotherapy. Extensive chemotherapy and prophylaxis with antifungals have increased the resistance of Candida isolates to antifungal drugs. Although, Candida albicans is the most common causative agent among neutropenic patients, there is an increasing rate of non-albicans species. Extracellular enzymes activity pattern and antifungal agent sensitivity profiles are two important factors for spreading resistant strains. Objectives: The aim of the present study was to identify the Candida strains isolated from hospitalized neutropenic patients. The patterns of antifungal susceptibility of the causative agents to antifungals and the extracellular enzymes activity of the isolates were also evaluated. Patients and Methods: In the present study, 243 urine and 243 oral swab samples were collected from neutropenic patients and inoculated on CHROMagar Candida. In addition, 100 blood samples were also inoculated in biphasic Brain Heart Infusion medium. Several yeast isolates were isolated from samples and identified by classical and molecular techniques. The profiles of extracellular enzymes and the susceptibility of recovered agents to amphotericin B, fluconazole and caspofungin were also evaluated. Results: A total of 110 yeast strains isolated from urine and oral cavities were identified as C. albicans (51.8%), C. krusei (25.5%), C. glabrata

(6.4%) and other yeasts (16.3%). No yeast species was isolated from blood samples. Our result showed that in 90% of the isolates, the range of secretion of extracellular enzymes was medium (2+) and high (3+), however only a few isolates were negative for this characteristic. All isolates were sensitive to caspofungin and fluconazole, whereas 54.7% of isolates were resistant to amphotericin B. Conclusions: We found a marked increase in the incidence of non-albicans species (48.2%) among neutropenic patients. Only a few strains failed to produce extracellular enzymes. Finally, in addition to fluconazole, caspofungin can be considered as the first line treatment against Candida species among neutropenic patients.

15-Heidarieh, P., et al. (2016). "In Vitro Antimicrobial Susceptibility of Nontuberculous Mycobacteria in Iran." Microbial Drug Resistance 22(2): 172-178.

Many species of nontuberculous mycobacteria (NTM) have long been identified as important causes of human disease, the incidence of which is rising. Several reports have suggested increasing trend of both in vitro and in vivo resistance to available treatment regimes. The aim of this study was to evaluate antibiotic susceptibility of clinically relevant NTM isolates using standard microbroth dilution test. Antimicrobial susceptibility testing was performed following National Committee for Clinical Laboratory Standards methods for NTM isolates, including 85 Mycobacterium fortuitum, 39 Mycobacterium chelonae, and 30 Mycobacterium abscessus subsp. abscessus as rapidly growing mycobacteria and 48 Mycobacterium simiae and 40 Mycobacterium kansasii as slowly growing mycobacteria. All isolates were recovered from various types of clinical samples and identified by multilocus sequence analysis. Trimethoprim-sulfamethoxazole (TMP-SMZ), amikacin, tobramycin, clarithromycin, moxifloxacin, linezolid, and imipenem showed better activity against M. fortuitum rather than meropenem, ciprofloxacin, cefoxitin, and doxycycline. Amikacin was active against 93% of M. abscessus subsp. abscessus. Linezolid, clarithromycin, cefoxitin, ciprofloxacin, imipenem, moxifloxacin, tobramycin, TMP-SMZ, doxycycline, and meropenem showed some activities on M. abscessus subsp. abscessus as well. The majority of M. abscessus subsp. abscessus and M. chelonae strains were multidrug resistant. Among the 40 isolates of M. kansasii, all were susceptible to ethambutol, isoniazid, clarithromycin, moxifloxacin, and linezolid. These isolates were also resistant to doxycycline and 50% were resistant to rifampicin and ciprofloxacin. M. simiae was resistant to clarithromycin, doxycycline, isoniazid, and TMP-SMZ, and the majority of isolates showed high levels of resistance to linezolid, ethambutol, ciprofloxacin, streptomycin, and rifampicin. The majority of M. simiae isolates were multidrug resistant. Our data confirm the need for performing of standard susceptibility testing of any clinically important NTM isolate.

16-Izadpour, F., et al. (2016). "An Investigation of Antibacterial Resistance Patterns Among Acinetobacter baumannii and Pseudomonas aeruginosa Isolates Collected from Intensive Care Units of a University-Affiliated Hospital in Ahvaz, Iran." Jundishapur J Microbiol 9(8).

Background: In recent decades, multidrug-resistant non-fermenting Gram-negative pathogens, particularly Acinetobacter baumannii and Pseudomonas aeruginosa, have been recognized as a major cause of healthcare-associated and nosocomial infections and outbreaks. Objectives: The aim of this study was to determine the prevalence and pattern of antibiotic resistance in A. baumannii and P. aeruginosa isolates collected from intensive care units (ICUs). Methods: One hundred fifty-five clinical isolates, including 80 (51.6%) isolates of A. baumannii and 75 (48.4%) isolates of P. aeruginosa, from hospitalized patients in the ICUs of a teaching hospital in Ahvaz, Iran, were collected from January 1 to December 30, 2013. The organisms were identified with conventional bacteriological methods, and antimicrobial susceptibility testing was performed on all isolates in accordance with clinical laboratory and standards institute (CLSI) guidelines. Results: The maximum resistance rates among A. baumannii isolates were observed for ciprofloxacin and trimethoprim-sulfamethoxazole (96.9% and 95.2%, respectively). For P. aeruginosa isolates, the maximum resistance rates were reported for ceftriaxone and trimethoprim-sulfamethoxazole (97.2% and 92.4%, respectively). Conclusions: The majority of A. baumannii and P. aeruginosa isolates were found to be resistant to commonly recommended antibiotics. Therefore, surveillance of antibiotic consumption and proper antibiotic administration guidelines are essential for preventing major outbreaks in the future.

17-Khademvatan, S., et al. (2016). "Elimination of urogenital schistosomiasis in Iran: past history and the current situation." Parasitology 143(11): 1390-1396.

In recent years, through a national programme for schistosomiasis control, this infection has been eliminated from Iran. The aim of this study was to report the process of significant decrease of urogenital schistosomiasis in southwestern Iran. During national programme surveillance for urogenital schistosomiasis control which was implemented by Centres for Disease Control and Prevention (CDC) of Khuzestan province from 1975 to 2013, more than 1.3 million urine samples were taken from inhabitants of high risk foci. All urine samples were gathered between 10: 00 a.m and 02:00 p.m and, after centrifuging, specimens were tested under optical microscope in order to detect Schistosoma haematobium eggs. Data analysis was performed using SPSS 18 software. In this retrospective study significant reduction was seen in number of infections between 1975 and 2013. During the years 1975-1980, 1981-1990 and 1991-2000 there were 1582, 761 and 79 cases of S. haematobium, respectively. In 2001 only one case was reported from Ahvaz and indeed this was the last case of urogenital schistosomiasis in Khuzestan and of course, in Iran. Prevalence from 1.064% between 1975 and 1980 slumped to

0% in 2012-2013. During several projects for surveillance of urogenital schistosomiasis, selective population chemotherapy, snail control, population education, environmental improvement, etc were carried out throughout the surveillance period. According to elimination of S. haematobium in Khuzestan province, the only endemic region of Iran, control of disease, especially the campaign with intermediate host snails should be continued. Iran can be a successful model for countries suffering from this disease.

18-Khaefi, M., et al. (2016). "AN ASSOCIATION BETWEEN AMBIENT POLLUTANTS AND HOSPITAL ADMITTED RESPIRATORY CASES IN AHVAZ, IRAN." Fresenius Environmental Bulletin 25(10): 3955-3961.

Air pollutants have harmful effects on human health and can intensify rates hospital admissions, asthma attacks, mortality and disease. One of the most reliable and valid approach to assess the health effects of air pollution is statistical modeling. Emissions from anthropogenic sources such as transportation, industries and dust storm are two major concerns of air pollution in Ahvaz. The aim of this study to assess hospital admissions respiratory disease of exposure Particle matter (PM10), Sulfur dioxide (S(O)2), Nitrogen dioxide (NO2), and Ground Level Ozone (GLO) in Ahvaz city (located in south-western Iran), during 2012. Daily concentrations of PM10, SO2, NO2, and GLO were used to evaluate the health effects of human exposure to these pollutants. Raw data processing by Excel software and after the impact of meteorological parameters was converted as input file to the model. Finally, were calculated the hospital admissions respiratory diseases of exposure PM10, SO2, NO2, and GLO in Ahvaz, in 2012. The results showed that the concentration of PM10, SO2, NO2, and GLO were related to Ahvaz with annual average 727, 160, 37 and 211 mu g/m(3) in 2012. Findings showed that cumulative cases of hospital admissions respiratory diseases which attributed to PM10, SO2, NO2, and GLO were 2675, 15, 25 and 58 persons, respectively. The higher percentage of these health point perhaps could be the result of higher average this pollutants or because of sustained high concentration days in Ahvaz. In Ahvaz city environmental concerns, most industries and dust storm phenomena are that required to decrease in source produce Air pollutants. Pollution prevention and control measures that reduce pollutants can very useful for expected to reduce people's exposures to Sulfur dioxide.

19-Khanbabaei, H., et al. (2016). "The interplay between microRNAs and Twist1 transcription factor: a systematic review." Tumor Biology 37(6): 7007-7019.

Twist1 (also known as Twist) is a transcription factor that belongs to the family of basic helix-loop-helix (bHLH) proteins. It functions as a negative regulator of epithelial gene expression and a positive regulator of mesenchymal gene expression, thereby leading to

induction of the epithelial mesenchymal transition (EMT), a process in which epithelial cells acquire the motile and migratory characteristics of mesenchymal cells. In addition to regulating the expression of protein-coding genes, Twist1 regulates the expression of microRNAs (miRNAs), adding a regulatory layer to EMT induction. Interestingly, the mRNA of Twist1 represents a downstream target of miRNAs, indicating an intricate network between miRNAs and Twist1. This network was shown to play multiple roles in cancer cell migration, invasion, and metastasis. The network can induce angiogenesis, protect cells from oncogene-induced apoptosis and senescence, enhance cancer cell resistance to conventional therapies, and increase cancer stem cell (CSC) populations. Recently, miRNAs have attracted considerable attention as potential promising tools in cancer therapies. Thus, this systematic review was conducted to clarify the reciprocal link between Twist1 and miRNAs in order to provide potential candidate miRNAs for diagnostic and therapeutic approaches in cancer treatment.

20-Khosravi, A. D., et al. (2016). "Isolation of Streptococcus pyogenes from children with pharyngitis and emm type analysis." Journal of the Chinese Medical Association 79(5): 276-280.

Background: The group A streptococcus (GAS) M protein, encoded by the emm gene, acts as a major virulence factor. Emm-typing is the GAS gold standard molecular typing and is based on the DNA sequence of the nucleotides of the emm gene. The aim of the present study was to isolate GAS from patients and to detect the emm types of the isolates using emm typing. Methods: A total of 1000 throat samples were collected from patients with pharyngitis referred to Aboozar Children's Hospital in Ahvaz, Iran. We performed antimicrobial susceptibility testing on all isolates using the Kirby-Bauer disk diffusion method. Additionally, amplification of the emm gene was performed using polymerase chain reaction using the standard primers and described protocol. Results: From all throat samples screened, 25 isolates (2.5%) were identified as GAS. Antibiotic susceptibility testing revealed that all the GAS isolates were susceptible to penicillin and erythromycin, but 44% showed resistance to vancomycin. Based on polymerase chain reaction for the emm gene, the obtained emm types were: emm-3, observed in 20 isolates (80%); emm-1 observed in four isolates (16%); and emm-75 observed in one isolate (4%). Conclusion: The result of the present study showed that penicillin and erythromycin are still the most effective antibiotics against the organism. The emm typing revealed that emm type-3 was detected in most of the isolates from patients with purulent pharyngitis. On the basis of the findings of this study, we may conclude that emm typing provides new insights on the genetic diversity of the M proteins, and is of demonstrable value for molecular studies of GAS. Copyright (C) 2016, the Chinese Medical Association. Published by Elsevier Taiwan LLC.

21-Khosravi, A. D., et al. (2016). "Genotyping of multidrug-resistant strains of Pseudomonas aeruginosa isolated from burn and wound infections by ERIC-PCR." Acta Cirurgica Brasileira 31(3): 206-211.

PURPOSE: To determine the genetic diversity of MDR P. aeruginosa strains isolated from burn and wound infections in Ahvaz, Iran, by ERIC-PCR. METHODS: From total 99 strains of P. aeruginosa defined as MDR by using drug susceptibility testing, 66 were subjected to ERIC-PCR analysis, comprises 53 strains isolated from burn infection, and 13 randomly selected strains from wound infection with higher resistance to combinations of more numbers of drugs. RESULTS: Eight clusters (I to VIII), and 50 single clones were generated for tested MDR isolates analyzed by ERIC-PCR. The high heterogeneity was observed among the isolates from burn infections including 16 isolates which were categorized in eight clusters and 37 single clones. The isolates in clusters II, III, VI, VIII showed 100% similarity. CONCLUSIONS: The high level of genotypic heterogeneity in P. aeruginosa strains demonstrated no genetic correlation between them. Extremely high drug resistance in isolates from burn, suggests that efficient control measures and proper antibiotic policy should be observed.

22-Khosravi, A. D., et al. (2016). "Prevalence of Escherichia coli O157:H7 in Children with Bloody Diarrhea Referring to Abuzar Teaching Hospital, Ahvaz, Iran." Journal of Clinical and Diagnostic Research 10(1): DC13-DC15.

Introduction: Escherichia coli O157:H7 are recognized as important aetiological agents of diarrhea in children, particularly in developed countries. Aim: The aim of the study was to determine the rates of detection of E. coli O157: H7strains among children in Ahvaz, Iran. Materials and Methods: From June 2010 to December 2010, 137 diarrheal stool samples of children were collected. E. coli was identified by standard microbiological techniques. O157 or O157: H7 subtypes discerned by serological tests. Results: Of the 137 E. coli isolates, enteropathogens were found in 53 (38.7%) of the patients as follow: Shigella spp. (75.5%), EPEC (enteropathogenic E. coli) (16.9%), Campylobacter spp. (3.8%) and Salmonella spp. (3.8%). None of the isolated E. coli was O157: H7 serotype. Conclusion: This shows that non-O157:H7 E. coli are the major cause of paediatric infections in this region of Iran.

23-Khosravi, A. D. and A. Mohammadian (2016). "Efflux MexAB-Mediated Resistance in Multidrug and Pan-Drug Resistant Strains of Pseudomonas aeruginosa Isolated From Patients With Burn and Wound Infections." Jundishapur Journal of Natural Pharmaceutical Products 11(1).

Background: The emergence of highly drug resistant Pseudomonas aeruginosa in burn wounds is becoming a challenging problem for infection control programs. Today, it has been shown that antibiotic resistance in P. aeruginosa is the result of synergism between membrane permeability and multidrug resistance (MDR) efflux pumps. Objectives: The aim of this study was to investigate MDR and pan-drug resistance (PDR) in P. aeruginosa and detection of the presence of efflux pump MexAB genes by the polymerase chain reaction (PCR) technique. Materials and Methods: One-hundred and fifty R aeruginosa were isolated from burn and wound infections. The isolates were confirmed using conventional culture and biochemical tests. Antibiotic resistance was evaluated using agar disk diffusion and broth micro dilution tests. For detection of efflux pump MexAB genes, the PCR technique with subsequent sequencing was used. Results: In total, 99 strains (66%) were MDR and one strain (0.667%) was PDR as detected by traditional susceptibility tests. The MDR isolates belonged to 53 burn (70.66%) and 46 wound (61.33%) infections. The PDR was only seen in one isolate from a burn strain (1.33%). The PCR technique revealed that all the 99 MDR strains and one PDR strain, contained MexA and MexB genes, representing an exhibitive intrinsic existence of these genes in MDR and PDR of P. aeruginosa. Conclusions: This study represented an increasing rate of MDR P. aeruginosa in burn and wound samples. Efflux MexAB genes were detected in all MDR and PDR strains. The P. aeruinosa strain isolated from burn cases showed higher drug resistance and PDR resistance was only noted in a burn sample.

24-Khosravi, A. D., et al. (2016). "The frequency of genes encoding exotoxin A and exoenzyme S in Pseudomonas aeruginosa strains isolated from burn patients." Burns 42(5): 1116-1120.

Background: Pseudomonas aeruginosa infections have emerged as a major infectious disease threat in recent decades with infection particularly in immunocompromised hosts. P. aeruginosa possesses several virulence factors with involvement in pathogenesis. The aim of this study was to examine the prevalence of virulence genes of toxA and toxS and to analyze their relation to antimicrobial resistance of the isolates. Methods: In total 185 clinical isolates of P. aeruginosa were collected from burn patients. Antimicrobial susceptibility testing was done by disk diffusion method. PCR amplification was performed on extracted DNA from the isolates and the presence of encoding genes for exotoxin A (toxA) and exoenzyme S (toxS) we're investigated by using specific primers. Results: In disk diffusion method, the isolates showed high sensitivity to colistin sulfate (100%) followed by imipenem (41.9%). The most prevalent resistance was seen against ceftazidime (90.5%) and gentamicin (88.5%). Multidrug resistance (MDR) demonstrated in 113 isolates (76.35%). According to PCR amplification, 133 (89.8%) and 127 (85.8%) isolates possessed toxA and toxS genes respectively. The frequencies of genes among MDR strains were 102 (76.6%) for toxA and 98 (77.1%) for toxS. Eighty five MDR isolates possessed both genes (73.9%). The non-MDR strains (23.65%), harbored lower prevalence of simultaneous toxA and

toxS genes (26%) compared to MDR strains. Conclusion: The present study established a higher frequency of MDR among P. aeruginosa isolates from burn patients. It was found that the frequency of both toxA &S genes were significantly higher in MDR strains P. aeruginosa strain's.

25-Khosravi, A. D., et al. (2016). "Prevalence of Non-Tuberculous Mycobacteria in Hospital Waters of Major Cities of Khuzestan Province, Iran." Frontiers in Cellular and Infection Microbiology 6.

Non-tuberculous mycobacteria (NTM) are among the emerging pathogens in immunocompromised individuals including hospitalized patients. So, it is important to consider hospitals water supplies as a source for infection. The aim of this study was to determine the prevalence of NTM in the hospital aquatic systems of Khuzestan, South west of Iran. In total, 258 hospital water samples were collected and examined. After initial sample processing, sediment of each sample were inoculated into two Lowenstein-Jensen medium. The positive cultures were studied with phenotypic tests including growth rate, colony morphology, and pigmentation, with subsequent PCR- restriction enzyme analysis (PRA) and rpoB gene sequence analysis. Mycobacterial strains were isolated from 77 samples (29.8%), comprising 52 (70.1%) rapid growing, and 25 (32.4%) slow growing mycobacteria. Based on the overall results, M. fortuitum (44.1%) was the most common mycobacterial species in hospital water samples, followed by M. gordonae (n = 13, 16.8%) and M. senegalense (n = 5, 7.7%). In conclusion, current study demonstrated the NTM strains as one of the major parts of hospital water supplies with probable potential source for nosocomial infections. This finding also help to shed light on to the dynamics of the distribution and diversity of NTM in the water system of hospitals in the region of study.

26-Makvandi, M. (2016). "Update on occult hepatitis B virus infection." World J Gastroenterol 22(39): 8720-8734.

The event of mutations in the surface antigen gene of hepatitis B virus (HBV) results in undetectable hepatitis B surface antigen with positive/negative anti-hepatitis B core (anti-HBc) antibody status in serum and this phenomenon is named occult hepatitis B infection (OBI). The presence of anti-HBc antibody in serum is an important key for OBI tracking, although about 20% of OBI cases are negative for anti-HBc antibody. The diagnosis of OBI is mainly based on polymerase chain reaction (PCR) and real-time PCR assays. However, real-time PCR is a more reliable method than PCR. OBI is a great issue for the public health problem and a challenge for the clinical entity worldwide. The persistence of OBI may lead to the development of cirrhosis and hepatocellular carcinoma. With regard to OBI complications, the screening of HBV DNA by

the highly sensitive molecular means should be implemented for: (1) patients with a previous history of chronic or acute HBV infection; (2) patients co-infected with hepatitis C virus/human immunodeficiency virus; (3) patients undergoing chemotherapy or anti-CD20 therapy; (4) recipients of organ transplant; (5) blood donors; (6) organ transplant donors; (7) thalassemia and hemophilia patients; (8) health care workers; (9) patients with liver related disease (cryptogenic); (10) hemodialysis patients; (11) patients undergoing lamivudine or interferon therapy; and (12) children in time of HBV vaccination especially in highly endemic areas of HBV. Active HBV vaccination should be implemented for the close relatives of patients who are negative for OBI markers. Thus, the goal of this review is to evaluate the rate of OBI with a focus on status of high risk groups in different regions of the world.

27-Makvandi, M., et al. (2016). "Designing, Construction and Expression of a Recombinant Fusion Protein Comprising the Hepatitis E Virus ORF2 and Rotavirus NSP4 in the Baculovirus Expression System." Jundishapur J Microbiol 9(11).

Background: The hepatitis E virus (HEV) accounts for hepatitis E infection with relatively high mortality rate in pregnant women that can lead to fulminant hepatitis. The baculovirus expression system (BES) has the capability to produce high-level recombinant proteins and could be useful for vaccine designing. Objectives: The aim of this study was designing a recombinant hepatitis E virus ORF2 and Rotavirus NSP4 (ORF2-NSP4) and to evaluating construction these recombinant proteins in the BES. Methods: The truncated ORF2 gene (112-607) and truncated ORF2-NSP4 were subcloned in pFastBac1 plasmid, separately, followed by digestion and confirmed by digestion and sequencing. Then the products were transformed into Escherichia coli DH5 alpha and retransformed in DH10Bac competent cells. Finally the white colonies containing Bacmid DNA subjected to PCR for confirming transformation. Bacmid DNA containing HEV truncated ORF2 and HEV truncated ORF2-NSP4 genes were transfected into SF9 cells using BES. The expressed proteins in the cell lysate were evaluated by SDS-PAGE and determined by the western blot assay. Results: The lengths of the subcloned genes, truncated ORF2 and truncated ORF2-NSP4 were 1500 and 2000bp, respectively. After retransforming in DH10Bac, the size of PCR products were 300 bp in Bacmid DNA without recombination while it was 4300 and 3800 bp in Bacmid truncated ORF2-NSP4 and Bacmid truncated ORF2 PCR products. The analysis of protein expression by SDS-PAGE and immunoblotting revealed the presence of 56 KDa for truncated ORF2 and 74.5 KDa for truncated ORF2-NSP4 proteins. Conclusions: The results of the present study showed that the baculovirus expression system (SF9 cells) was able to express truncated ORF2 and truncated ORF2-NSP4 proteins as a potential candidate vaccine.

28-Mohammadpour, N., et al. (2016). "Design of Indigenous ELISA Using Tachyzoites from the RH Strain of Toxoplasma gondii and Comparison with Commercial Kits in Ahvaz, Southwest of Iran, 2015." Jundishapur J Microbiol 9(10).

Background: Toxoplasma gondii is one of the most common causes of latent infections in humans worldwide. Detecting anti-Toxoplasma antibodies in serum using serological tests is a common method to diagnose toxoplasmosis. Objectives: In the present study, an indigenous ELISA kit was prepared using tachyzoites from the RH strain of T. gondii, and its sensitivity and specificity were compared with those of commercial kits. Methods: To produce antigens, 0.02 mL of locally isolated T. gondii RH strain parasites along with 109 tachyzoites were injected into the peritoneal cavities of 50 laboratory mice (BALB/C). Parasites were collected after 4 days. After filtering and washing, the concentration of protein in sonicated tachyzoites was calculated using the Lowry protein assay. The dilution of antigen, serum and alkaline phosphatase conjugate was assessed in designing an indigenous ELISA method; then ELISA was performed based on these dilutions, and its sensitivity was determined using 200 serum samples. In addition, the specificity of the assay was evaluated using 40 serum samples from patients with tuberculosis, leukemia or hydatid cyst. Results: Indigenous ELISA was used to examine 100 serum samples containing anti-T. gondii IgG, with a sensitivity of 98% (commercial kits: 100%). Another 100 serum samples containing anti-T. gondii IgM were also tested, with a sensitivity of 99% (commercial kits: 100%). When 40 serum samples from patients with leukemia, hydatid cyst or tuberculosis were examined using anti-T. gondii IgG, the specificity was 100%, identical to commercial kits. However, the specificity of a similar test with anti-T. gondii IgM was just 28.6% for serum samples from leukemia patients, 21.4% for hydatid cyst and 16.7% for tuberculosis. Conclusions: We found that purified locally isolated soluble crude antigens of the RH strain of T. gondii from the peritoneal cavity of mice may be one of the most promising antigens for detection of human toxoplasmosis in routine screening.

29-Moosavian, M. and N. Ahmadkhosravy (2016). "Survey of CTX-M Gene Frequency in Extended-Spectrum Beta-Lactamase-Producing Enterobacteriaceae Isolates Using the Combination Disk and PCR Methods in Ahvaz, Iran." Jundishapur J Microbiol 9(11).

Background: A common mechanism of resistance to beta-lactam antibiotics is the production of beta-lactamase by Gram-negative bacteria. Recently, nonderivative extended-spectrum beta-lactamases (ESBLs) from the TEM and SHV enzymes, such as CTX-M, that were related to different geographical regions have been recognized. Objectives: The aim of this study was to determine the frequency of the CTX-M gene in ESBL-producing Enterobacteriaceae isolates in hospitalized patients in the teaching hospitals of Ahvaz, Iran. Methods:

Enterobacteriaceae isolates from clinical specimens (other than stool), such as wounds, blood, urine, trachea, discharge, and abscess, were collected and examined. All the isolates were identified using standard biochemical tests. The combination test was carried out based on CLSI criteria for the phenotypic detection of ESBL-producing isolates. After DNA extraction, the CTX-M and CTX-M-1 genes were amplified using PCR among phenotypically positive ESBL isolates. Results: Among 240 Enterobacteriaceae isolates, Escherichia coli and Enterobacter were the most common isolates with 171 (71.3%) and 65 (27.1%), respectively. The combination test results also showed that 108 (45%) Enterobacteriaceae isolates were phenotypic ESBL producers, but 104 (96%) isolates were positive for the blaCTX-M gene and 99 (92%) were positive for the blaCTX-M-1 gene according to the PCR method. Conclusions: The results of this study phenotypically and genotypically confirmed the high frequency of ESBL-producing strains, such as the CTX-M and CTX-M-1 genes, among Enterobacteriaceae isolates in our region. Therefore, use of antibiotic susceptibility testing for the detection of ESBL isolates prior to the prescription of beta-lactam antibiotics is recommended. This could help prevent the spread of bacteria strains that are resistant to beta-lactam antibiotics.

30-Moradi, A., et al. (2016). "Study of determinants of Adherence to Antiretroviral Treatment among HIV Patients covered by Ahwaz Jundishapur University of Medical Sciences." International Journal of Medical Research & Health Sciences 5(11): 477-484.

Adherence to antiretroviral therapy is essential for achieving durable clinical outcomes in patients with HIV. In addition, suboptimal adherence can accelerate development of drug-resistant HIV and mitigate HAART's role in reducing HIV incidence and transmission. The present research has been conducted to study treatment adherence and determine its effective factors on HIV/AIDS patients with the support of Ahvaz JundiShapur University of Medical Sciences in 2015. This is a cross-sectional study in which 158 HIV/AIDS patients who had been registered in the counseling centers of behavioral diseases of Ahvaz and were receiving antiretroviral treatment. They had been selected by census method. Data were collected using the AACTG (Adult Aids Clinical Trials Group) questionnaire. The collected data was analyzed and interpreted using descriptive statistical tests, chi(2) and step by step regression by spss-16 software. The mean age of patients was 32.8+/-10.36. Among them 20.8% were female, 47.5% were single and 35.6% had a job. Also 33.7% of the respondents had CD4+ cell count less than 350 cells/mu L. and average treatment duration was 9 months at study entry. According to the findings of this study, the degree of adherence was reported as % 63.9. The main reasons for non-adherence were forgetfulness (26%) and side effects (19%). There were no significant differences between highly adherent and less adherent patients with regard to age, gender, education Employment status, Treatment duration, time of diagnosis. Adherence to HAART is a key factor in disease course in persons with HIV/AIDS. Low-level adherence in subjects of the

study indicated that educational and intervention is quite necessary for patients in order to improve their medication self-management.

31-Mortazavi, Y., et al. (2016). "The Evaluation of Nerve Growth Factor Over Expression on Neural Lineage Specific Genes in Human Mesenchymal Stem Cells." Cell J 18(2).

Objective: Treatment and repair of neurodegenerative diseases such as brain tumors, spinal cord injuries, and functional disorders, including Alzheimer's disease, are challenging problems. A common treatment approach for such disorders involves the use of mesenchymal stem cells (MSCs) as an alternative cell source to replace injured cells. However, use of these cells in hosts may potentially cause adverse outcomes such as tumorigenesis and uncontrolled differentiation. In attempt to generate mesenchymal derived neural cells, we have infected MSCs with recombinant lentiviruses that expressed nerve growth factor (NGF) and assessed their neural lineage genes. Materials and Methods: In this experimental study, we cloned the NGF gene sequence into a helper dependent lentiviral vector that contained the green fluorescent protein (GFP) gene. The recombinant vector was amplified in DH5 bacterial cells. Recombinant viruses were generated in the human embryonic kidney 293 (HEK-293) packaging cell line with the helper vectors and analyzed under fluorescent microscopy. Bone marrow mesenchymal cells were infected by recombinant viruses for three days followed by assessment of neural differentiation. We evaluated expression of NGF through measurement of the NGF protein in culture medium by ELISA; neural specific genes were quantified by real-time polymerase chain reaction (PCR). Results: We observed neural morphological changes after three days. Quantitative PCR showed that expressions of NESTIN, glial derived neurotrophic factor (GDNF), glial fibrillary acidic protein (GFAP) and Microtubule-associated protein 2 (MAP2) genes increased following induction of NGF overexpression, whereas expressions of endogenous NGF and brain derived neural growth factor (BDNF) genes reduced. Conclusion: Ectopic expression of NGF can induce neurogenesis in MSCs. Direct injection of MSCs may cause tumorigenesis and an undesirable outcome. Therefore an alternative choice to overcome this obstacle may be the utilization of differentiated neural stem cells.

32-Mousavi, E., et al. (2016). "In vitro adherence of Lactobacillus strains isolated from the vaginas of healthy Iranian women." Journal of the Chinese Medical Association 79(12): 665-671.

Background: The lactobacilli are a part of the bacterial flora of the human vagina. Detection of normal Lactobacillus species in the vaginas of healthy women in different geographical locations, and evaluation of their specific properties, can aid in the selection of the

best species for preventing sexually transmitted diseases in the future. This study was performed to isolate and identify the Lactobacillus species in the vaginas of healthy women and to evaluate the adherence of these lactobacilli to Vero and HeLa cell lines. Methods: The study included 100 women. Bacteria were isolated from healthy women and purified. Phenotypic and biochemical tests were performed to identify the lactobacilli. The Lactobacillus species were detected by molecular methods using polymerase chain reaction amplification of the full length of the 16S rDNA of the isolated bacteria. Several isolates of each species were then selected to study their adherence to Vero and HeLa cell lines. Results: Among the 50 samples taken from healthy women meeting the inclusion criteria, Lactobacillus species were identified in 33 (66%) samples. Of these lactobacilli, 14 isolates were Lactobacillus crispatus, six (18.2%) were Lactobacillus gasseri, nine (27%) were Lactobacillus rhamnosus, and the rest were either Lactobacillus salivarius (6%) or Lactobacillus planta rum (6%). L. rhamnosus showed the greatest adhesion to the cells when compared to the other tested species. All the lactobacilli isolated in this study showed a smaller capacity for cell adherence when compared with control species. Conclusion: L. crispatus, L. rhamnosus, and L. gasseri were the dominant Lactobacillus species in the vaginas of healthy women in Iran. L. rhamnosus attached more readily to the cells than did the other species; therefore, this isolate is a good candidate for further studies on the potential health benefits and application of lactobacilli as probiotics. Copyright (C) 2016, the Chinese Medical Association. Published by Elsevier Taiwan LLC.

33-Naghashpour, M., et al. (2016). "Brain-derived neurotrophic and immunologic factors: beneficial effects of riboflavin on motor disability in murine model of multiple sclerosis." Iranian Journal of Basic Medical Sciences 19(4): 439-448.

Objective(s): In the present study, C57BL/6 female mice (n= 56) were used to explore the neuroprotective effects of riboflavin in motor disability of experimental autoimmune encephalomyelitis (EAE) as a model of multiple sclerosis. Materials and Methods: The animals were assigned into 7 groups: sham-operated 1 (SO1), healthy mice receiving PBS (phosphate buffer saline); sham-operated 2 (SO2), healthy mice receiving PBS and riboflavin; sham treatment 1 (ST1), EAE mice receiving water; sham treatment 2 (ST2), EAE mice receiving sodium acetate buffer; treatment 1 (T1), EAE mice receiving interferon beta-1a (INF beta-1a); treatment 2 (T2), EAE mice receiving riboflavin; treatment 3 (T3), EAE mice receiving INF beta-1a and riboflavin. After EAE induction, scoring was performed based on clinical signs. Upon detecting score 0.5, riboflavin at 10 mg/kg of body weight and/or INF beta-1a at 150 IU/g of body weight administration was started for two weeks. The brain and spinal cord levels of brain-derived neurotrophic factor (BDNF), interleukin-6 (IL-6), and interleukin-17A (IL-17A) were studied using real-time PCR and ELISA methods. Results: BDNF expression and protein levels were increased in the brain and spinal cord of the T3 group compared with the other groups

(P<0.01). IL-6 and IL-17A expressions were increased in the brains of the T3 and T1 groups, respectively, compared to the other groups (P< 0.01). The daily clinical score was reduced significantly by riboflavin in both effector and chronic phases of the disease compared with that of the controls (P< 0.05). Conclusion: Our findings showed that riboflavin is capable of suppressing the neurological disability mediated by BDNF and IL-6.

34-Nashibi, R., et al. (2016). "Is there any difference between antimicrobial resistance patterns of bacteria isolated in admitted patients of tertiary care center in two consecutive years?" International Journal of Pharmaceutical Research and Allied Sciences 5(2): 119-127.

Infection is the most common cause of death following injury and as one of the main causes of morbidity and mortality worldwide. Antibiotics are the first and most effective agents for reducing the mortality in bacterial infections. However, recent years have witnessed a relative dramatic increase in the emergence pathogens that are resistant to antibacterial agents. clinical applications of antibiotics pathogens and the human normal flora have faced a near continuous exposure to these selective agents. As a consequence, multidrug-resistant pathogens evolve which can become virtually untreatable. Although a surveillance system has been established in Iran to monitor antimicrobial resistance, there is a few published data available on antimicrobial resistance patterns. While awareness of antimicrobial resistance patterns, particularly in hospital, is crucial for choosing an appropriate antimicrobial treatment and consequently minimizing the hospitalization period, mortality, and morbidity. This study aims to assess the antimicrobial resistance patterns of predominant pathogens from hospitalized patients in one of the referral university hospitals of Ahvaz, Iran.

35-Pchelin, I. M., et al. (2016). "Reconstruction of phylogenetic relationships in dermatomycete genus Trichophyton Malmsten 1848 based on ribosomal internal transcribed spacer region, partial 28S rRNA and beta-tubulin genes sequences." Mycoses 59(9): 566-575.

Trichophyton spp. are important causative agents of superficial mycoses. The phylogeny of the genus and accurate strain identification, based on the ribosomal ITS region sequencing, are still under development. The present work is aimed at (i) inferring the genus phylogeny from partial ITS, LSU and BT2 sequences (ii) description of ribosomal ITS region polymorphism in 15 strains of Trichophyton interdigitale. We performed DNA sequence-based species identification and phylogenetic analysis on 48 strains belonging to the genus Trichophyton. Phylogenetic relationships were inferred by maximum likelihood and Bayesian methods on concatenated ITS, LSU and BT2 sequences. Ribosomal ITS region polymorphisms were assessed directly on the

alignment. By phylogenetic reconstruction, we reveal major anthropophilic and zoophilic species clusters in the genus Trichophyton. We describe several sequences of the ITS region of T. interdigitale, which do not fit in the traditional polymorphism scheme and propose emendations in this scheme for discrimination between ITS sequence types in T. interdigitale. The new polymorphism scheme will allow inclusion of a wider spectrum of isolates while retaining its explanatory power. This scheme was also found to be partially congruent with NTS typing technique.

36-Pourjabari, K., et al. (2016). "Prevalence, reactivation and genotyping of John Cunningham virus among end-stage renal disease and kidney transplant patients." Future Virology 11(7): 489-496.

Aim: Infection of John Cunningham virus (JCV) usually occurs in early childhood and can lead to progressive multifocal leukoencephalopathy in immunosuppressed individuals. In this study, prevalence, reactivation and genotypes of JCV were evaluated. Materials & methods: Overall, 128 sex-matched individuals, including 64 patients with end-stage renal disease (ESRD) and 64 kidney transplant (KT) patients were evaluated using PCR and reverse transcriptase-PCR. Results: JCV DNA was detected in the urine samples of 17.2% of KT recipients and 1.6% of ESRD patients. Reactivation of JCV was determined in 12.5% of KT patients. All JCV-DNA-positive samples belonged to Af2 genotype (subtype b). Conclusion: Rare excretion of JCV in the ESRD urine samples can be associated with kidney function. JCV shedding and reactivation occur more frequently in the first 2 years following kidney transplantation. The genotype of Af2-b is circulating among the population of Iran.

37-Rasti, M., et al. (2016). "Three cases of mumps virus and enterovirus coinfection in children with enteroviral meningitis." Medicine 95(49).

Several viruses are responsible for aseptic meningitis; however, in the region of Southwest Iran, the role played by each virus is still not very well known. The aim of this study is to determine the relative frequencies of mumps virus, herpes viruses, and enteroviruses, as well as coinfections among them, in patients with aseptic meningitis. In this cross-sectional study, samples of cerebrospinal fluid were collected between December 2012 and December 2013 from patients under 14 years, who were hospitalized in Abuzar Children's Hospital in Ahvaz, Southwest Iran (the only children's hospital in Khuzestan province and Southwest Iran). All 66 cerebrospinal fluid samples and corresponding clinical data were collected from patients with aseptic meningitis by specialists, and with the patients' consent. The DNA and RNA were extracted from these samples and subjected to polymerase chain reaction as well as reverse transcription polymerase chain reaction (RT-PCR) for detection of mumps virus, herpes viruses,

and enteroviruses. Nine of the samples (3 mumps-positive and 6 enterovirus-positive) were sequenced. The mumps virus sequences were investigated for possible mutations in the SH and partial HN regions. Up to 39 patients (59.09%) were found to be positive for enteroviruses, 3 (4.5%) for mumps virus, and 1 (1.5%) for herpes viruses (specifically, the varicella-zoster virus). Two patients (3.03%) had a mumps virus and enterovirus coinfection. Among the 3 detected mumps virus samples, 1 belonged to genotype B, while the others belonged to genotype N. Six sequenced enteroviruses indicated the highest similarity with Echovirus 30. An amino acid substitution at position 51 (N -> T) was detected in the HN region of genotype N mumps virus samples, in comparison to the reference strain.

38-Rezaei-Matehkolaei, A., et al. (2016). "Dermatophytosis due to Microsporum incurvatum: Notification and Identification of a Neglected Pathogenic Species." Mycopathologia 181(1-2): 107-113.

A 4-year-old Iranian boy developed erythematous, itchy and annular lesion on his face. Microscopic examination of the scraped samples with 10 % potassium hydroxide (KOH) revealed fungal septate hyphae and arthroconidia. The etiological agent was found to be Microsporum gypseum in mycological examinations. Amplification and restriction digestion of the internal transcribed spacers (ITS) of rDNA was not helpful for identification, but in ITS sequencing the isolate showed 98 % homology to Microsporum incurvatum strain CBS 172.64. Empirical treatment of the patient with griseofulvin for 4 weeks was successful. Other than our isolate, the ITS1 sequences of 38 strains from related species were retrieved from GenBank and phylogenetic tree using maximum likelihood method was constructed. The case isolate clustered apart from other strains of M. incurvatum. Pairwise comparison of ITS1 showed intraspecies variations of 0-13 nucleotides among M. incurvatum strains and an extensive interspecies variation of 33-80 bp and remarkable interspecies size polymorphism between the three sister species in the M. gypseum complex. The high level of ITS1 intraspecific variation is suitable for species identification rather than phylogeographic analysis of M. gypseum complex.

39- Rezaei-Matehkolaei, A., et al. (2016). "Epidemiological Aspects of Dermatophytosis in Khuzestan, southwestern Iran, an Update." Mycopathologia 181(7-8): 547-553.

Dermatophytosis is among the most common superficial mycoses in Iran. The purpose of this report was to update the clinical and mycological features of human dermatophytosis in the Khuzestan, southwestern Iran. In the framework of a one-year survey, a total of 4120 skin, hair and nail samples obtained from the outpatients with symptoms suggestive of tinea were analyzed by using direct microscopy, culture and molecular identification methods. Strains

isolated from cultures were subjected to amplification of the nuclear rDNA ITS regions in a PCR assay followed by an early established RFLP analysis. For confirmation of species identification, 100 isolates as representatives of all presumable species were subjected to ITS sequencing. Infection was confirmed in 1123 individuals (27.25 %) in the age range of 1-89 years by direct microscopy and/or culture including 603 males versus 520 females. Frequencies of infections were the highest and the lowest in age groups of 21-30 and 11-20 years, respectively. Tinea corporis was the most prevalent clinical manifestation followed by tinea cruris, tinea capitis, tinea manuum, tinea pedis, tinea unguium, tinea faciei and tinea barbae. Trichophyton interdigitale (58.7 %) was the most dominant isolate followed by Epidermophyton floccosum (35.4 %), Microsporum canis (3 %), T. rubrum (1.5 %), T. species of Arthroderma benhamiae (0.5 %), T. tonsurans (0.3 %) and T. violaceum (0.3 %). Other species included M. gypseum, M. fulvum and T. verrucosum (each one 0.1 %). Such a high occurrence of infection with T. interdigitale, which has not been reported from Iran, is due to the use of accurate molecular methods based on new species concept in dermatophytes. The prevalence of dermatophytoses caused by zoophilic species remarkably increased and Trichophyton species of A. benhamiae has emerged as a new agent of dermatophytosis in southwestern Iran, while infections due to anthropophilic species, except E. floccosum, took a decreasing trend.

40-Sadeghi, P., et al. (2016). "Identification of clinical isolates of Acinetobacter baumannii from Iran and study of their heterogeneity." Journal of the Chinese Medical Association 79(7): 382-386.

Background: Acinetobacter baumannii has become one of the most serious causative agents of nosocomial infections due to its significant ability to survive on hospital surfaces. It is mainly an emerging opportunistic pathogen infecting patients in intensive care units. This study was aimed to identify the clinical isolates of A. baumannii and to investigate their heterogeneity using polymerase chain reaction (PCR)-based typing methods. Methods: A total of 197 nonduplicate isolates recovered from a wide range of clinical samples were subjected to conventional cultural and biochemical tests. For those isolates that were preliminary identified as A. baumannii, rpoB-based PCR with subsequent restriction fragment length polymorphism (RFLP) using two restriction enzymes (TagI and HaeIII) was performed to investigate the genetic diversity of the strains and their presumptive relationships with different clinical presentation of the disease caused by this pathogen. Results: In total, 50 isolates (25.4%) were identified as A. baumannii using conventional phenotypic methods with subsequent confirmation by rpoB sequencing. RFLP analysis demonstrated five different restriction enzyme patterns, designated as A-E clusters. Most A. baumannii isolates were categorized under Cluster A (32%). We found no significant relationship between clinical presentation and the clustering of the isolates. Conclusion: This study showed that the rpoB region possesses high discriminatory power to identify the isolates to the species level. This marker showed high interspecies variability that

might be useful for strain typing. The results also suggest the possibility of the existence of a predominant clone of A. baumannii among infected patients in Iran. Copyright (C) 2016, the Chinese Medical Association. Published by Elsevier Taiwan LLC.

41-Saki, J., et al. (2016). "Molecular Characterization of Cryptosporidium spp. in Wild Rodents of Southwestern Iran Using 18s rRNA Gene Nested-PCR-RFLP and Sequencing Techniques." J Trop Med.

Background. Rodents could act as reservoir for Cryptosporidium spp. specially C. parvum, a zoonotic agent responsible for human infections. Since there is no information about Cryptosporidium infection in rodents of Ahvaz city, southwest of Iran, hence, this survey was performed to determine the prevalence and molecular characterization of Cryptosporidium spp. in this region. Materials and Methods. One hundred rodents were trapped from different regions of Ahvaz city. Intestine contents and fecal specimens of rodents were studied using both microscopy examination to identify oocyst and nested-polymerase chain reaction (PCR) technique for 18s rRNA gene detection. Eventually restriction fragment length polymorphism (RFLP) method using SspI and VspI restriction enzymes was carried out to genotype the species and then obtained results were sequenced. Results. Three out of 100 samples were diagnosed as positive and overall prevalence of Cryptosporidium spp. was 3% using both modified Ziehl-Neelsen staining under light microscope and nested-PCR (830 bp) methods. Afterwards, PCR-RFLP was performed on positive samples and C. parvum pattern was identified. Finally PCR-RFLP findings were sequenced and presence of C. parvum was confirmed again. Conclusions. Our study showed rodents could be potential reservoir for C. parvum. So an integrated program for control and combat with them should be adopted and continued.

42-Salmanzadeh, S., et al. (2016). "Knowledge and Attitudes of Acquired Immunodeficiency Syndrome among Nurses Working in Teaching University Hospitals, Southwest Iran." International Journal of Pharmaceutical Research and Allied Sciences 5(2): 194-199.

Human immunodeficiency virus (HIV) is among the only viruses for them it can be said that prevention is the only and the best treatment. The aim of this study was to assess the knowledge and attitude of acquired immunodeficiency syndrome (AIDS) prevention in nurses of a teaching hospital in Ahvaz. In this descriptive cross sectional study, through a two-stage cluster random sampling, 147 nurses working in four teaching hospitals in Ahvaz south west Iran were studied. Data collected by a questionnaire in three sections consisting of demographic information, occupation history, and knowledge / attitudes was analyzed using statistical software SPSS version 20. The mean knowledge and attitude score was 28.25+/-7.04 and

13.4+/-3.79, respectively. Significant relationship between attitude and sex (P < 0.05) and between the knowledge and attitudes were observed (P < 0.01). In the present study the knowledge and attitude of the majority of the subjects was moderate. It is essential to implement educational programs in hospitals, in order to change negative attitudes to positive attitudes.

43-Shahrivar, F. F., et al. (2016). "Comparison of therapeutic effects of L-Thyroxin, apelin and a combination of both on antioxidant enzymes in the heart of PTU-induced hypothyroid rats." Brazilian Archives of Biology and Technology 59.

Atherosclerosis is one of the common disorders among hypothyroidism, which, increased the risk of cardiovascular diseases. Reactive oxygen species are associated with atherosclerosis development. Antioxidant defense systems are the scavenger for free radicals. Apelin is an endogenous ligand for the APJ receptor (apelin receptor) that exists in most tissues, acts as an adiponectin. It has been identified that apelin administration, improve the antioxidant capacity (TAC). Therefore, this study was conducted to assess, therapeutic effects of apelin, T4 (L-Thyroxin) or both on antioxidant capacity in 6-propyl-2-thiouracil (PTU)-induced hypothyroid rats. Forty male Wistar rats were randomly assigned into five groups: C: control group; P group (hypothyroid): PTU (0.05 %) administration for six weeks; P+A, P+T and P+A+T groups: after 4 weeks of PTU administration, animals treated with Apelin (200 mu g/kg/day, ip) T4 (0.02 mu g/g/day, gavage) and apelin+T4; for two weeks respectively accompanied by PTU administration. Aplein administration in P+A group and P+A+T group had beneficial effect to lowering of malondialdehyde (MDA) content as compared to hypothyroid group (8.52+0.64 and 8.53+1 vs. 13.67+1.64 nmol/g tissue, P<0.05) and also had increasing effect on Superoxide dismutase (SOD) and glutathion peroxidase (GPx) activity and the total antioxidant capacity (TAC) content compared to the hypothyroid group. This study showed that apelin was able to improve the oxidant-antioxidant balance in the heart tissue of the hypothyroid rats by elevating of antioxidant enzyme activity.

44-Shahrivar, F. F., et al. (2016). "Exogenous apelin changes alpha and beta myosin heavy chain mRNA expression and improves cardiac function in PTU-induced hypothyroid rats." Gene 595(1): 25-30.

The most important conditions associated with hypothyroidism is the cardiac dysfunction. Apelin is an endogenous ligand, involved in energy storage and metabolism which improves cardiac contractility. This study was done to evaluate the effects of apelin, L-Thyroxin (T4) or a combination of both, on cardiac function and mRNA expression of two contractile

proteins, alpha and beta myosin heavy chain (alpha-MHC and beta-mHC), in 6-propyl-2-thiouracil (PTU)-induced hypothyroid rats. Forty male Wistar rats were randomly assigned into five groups: Ctrl (Control), and 4 hypothyroid groups (H, HA, HT, and HAT). The Hypothyroid (H) group received 0.05% PTU in the drinking water for six weeks; the next 3 groups, along with PTU, received apelin (HA, 200 mu g/kg/day, ip), T4 (HT, 20 mu g/kg/day, gavage), or a combination of both drugs (HAT) for the last 2 weeks (weeks 5 and 6). TSH and T4 were measured using ELISA kit Isolated hearts of animals were perfused in Langendorff apparatus and left ventricular developed pressure, cardiac contractility, heart rate, rate pressure product and perfusion pressure were assessed using PowerLab ADInstruments. In addition alpha-MHC and beta-MHC mRNA expression were evaluated by RT-PCR method in heart tissue. Apelin alone or accompanied by T4 significantly increased cardiac contractility and performance as compared to hypothyroid group. Apelin also significantly increased the alpha-MHC mRNA expression and in the presence of T4 significantly decreased beta-MHC mRNA expression. It seems that apelin alone may improve cardiac function in hypothyroid rats via genomic pathways. (C) 2016 Elsevier B.V. All rights reserved.

45-Sharififard, M., et al. (2016). "Epidemiological Survey of Crimean-Congo Hemorrhagic Fever (CCHF), a Fatal Infectious Disease in Khuzestan Province, Southwest Iran, During 1999-2015." Jundishapur J Microbiol 9(5).

Background: Crimean-Congo hemorrhagic fever (CCHF) is an arboviral zoonotic disease transmitted to humans mainly through the bite of blood-sucking Ixodidae ticks and also via contact with the blood and tissues of infected livestock. Objectives: This study is a retrospective descriptive survey based on data collected from the health center of Khuzestan province, Iran, during 1999 - 2015. Patients and Methods: Patients with symptoms of severe headache, high fever, and bleeding were evaluated. Laboratory tests and serological or molecular assays were used to detect probable and confirmed cases, respectively. The epidemiological parameters of this study were analyzed on the basis of probable cases. Results: A total of 42 patients were diagnosed as probable cases, and 17 of these (42.5%) were confirmed serologically. Two peaks of the disease occurred in Khuzestan province, in 2003 and 2010, with seven cases each of those years, leading to the deaths of five and two patients, respectively. Men and women comprised 57.1% and 42.9% of the patients, respectively. Of all probable cases, 64.3% were from urban areas and 35.7% were from rural areas. The age groups of 10 - 19 and 20 - 29 years, with a frequency of 26.2% in each group, were exposed to the most infections. Farmers and housewives were the highest at-risk occupational groups with a frequency of 28.6% and 26%, respectively. Fever, bleeding, and thrombocytopenia were reported in 95% of the patients, and the case-fatality ratio was calculated to be 28.6% (12 of 42 cases). Conclusions: Continuous training is necessary to improve the knowledge and awareness of the highest-risk groups with regard to the transmission modes, prevention, symptoms, and treatment of this disease.

46-Sharififard, M., et al. (2016). "Biocontrol of the Brown-banded Cockroach, Supella longipalpa F. (Blattaria: Blattellidae), with Entomopathogenic Fungus, Metharhizium anisopliae." J Arthropod Borne Dis 10(3): 337-348.

Background: Considering to the high distribution of cockroaches as urban pests, the efficacy of different formulations of Metarhizium anisopliae strain Iran 437C were assessed against the brown-banded cockroach, Supella longipalpa F. under laboratory and field conditions. Methods: Metarhizium anisopliae isolates were screened with immersing adults of the brown-banded cockroachs in aqueous suspension of 10(8) conidia ml(-1) followed by surface or bait treated with different doses of the most virulent isolate against the nymphs. Then formulations of conidia oil-in-water were examined versus cockroach nymphs using different plant oils and paraffin. Then they were evaluated and compared with aqueous suspension and control group. On a large-scale, the sunflower oil-in-water formulation of conidia was sprayed at houses using a hand sprayer. Results: Metarhizium anisopliae IRAN 437C was the most virulent isolate against the brown-banded cockroach, causing 100% mortality in adults at seven days post-exposure. Inoculated bait with this isolate was not enough pathogenic against the cockroach even at two weeks after treatment. Treated surface with conidia as aqueous suspension or oil-in-water formulation was more effective than the bait formulation against the cockroach caused 39.4-97.2% mortality compared with 2.5% mortality in control group after two days. Spraying the conidia formulated with sunflower oil was an effective formulation causing 76.1% reduction in the cockroach density on the third day post treatment in the houses. Conclusion: The oil-in-water formulation of M. anisopliae IRAN 437C could be recommended as a promising alternative for cockroach control.

47-Sheikh, A. F., et al. (2016). "Detection of Streptococcus pneumoniae and Moraxella catarrhalis in patients with paranasal chronic sinusitis by polymerase chain reaction method." Journal of the Chinese Medical Association 79(8): 440-444.

Background: Sinusitis is a complex involvement of the upper respiratory system by bacteria, viruses, fungi, or other allergens. Streptococcus pneumoniae, Haemophilus influenzae, and Moraxella catarrhalis are the dominant bacterial microorganisms involved in acute sinusitis, whereas in chronic sinusitis, Staphylococcus aureus and some anaerobic bacteria are the prevailing pathogens. Appropriate antibiotic treatment requires sinusitis bacteriology assessment. The aim of this study was to isolate bacteria in clinical samples from patients with chronic sinusitis. Methods: A total of 55 samples were collected from patients with chronic sinusitis undergoing surgery at Imam Khomeini Hospital in Ahvaz, Iran. Samples were cultured in conventional medium, and for each culture, Gram staining, catalase, coagulase, oxidase, and

DNAse tests were performed and isolates were stored for polymerase chain reaction analysis. Results: Twenty-three isolates were obtained from five patients, including S. aureus (23.6%), Rhizomucor (1.8%), and Escherichia (1.8%) by the culture method and M. catarrhalis (3.6%) and S. Pneumoniae (7.2%) by the polymerase chain reaction method. Compared with acute sinusitis, the microbiology of chronic sinusitis remains controversial. Results are affected by many factors, including diversity of molecular and culture methods, sterilization of sampling area, sample transfer to laboratory, use of antibiotics prior to surgery, and nasal polyps. Conclusion: In Iran, the causative agents of chronic sinusitis are similar to those in other countries. Compared with other bacteria, S. aureus was observed more often in asthmatic patients with sinusitis.

48-Shoja, S., et al. (2016). "Characterization of Oxacillinase and Metallo-beta-Lactamas Genes and Molecular Typing of Clinical Isolates of Acinetobacter baumannii in Ahvaz, South-West of Iran." Jundishapur J Microbiol 9(5).

Background: Carbapenem resistant Acinetobacter baumannii is an important nosocomial pathogen associated with a variety of infections. Objectives: The current study aimed to characterize the antimicrobial susceptibility, analyze the prevalence of oxacillinase and metallo-beta-lactamase (MBL) genes and molecular typing of clinical isolates of A. baumannii. Materials and Methods: A total of 124 non-repetitive isolates of A. baumannii were collected from various clinical specimens in two teaching hospitals in Ahvaz, south-west of Iran. Antimicrobial susceptibility test was carried out by disk diffusion method. The minimum inhibitory concentrations (MICs) of imipenem, meropenem, colistin and tigecycline were determined using E-test. To screen for MBL production, double disk synergy (DDs) test and MBL E-test were performed. The presence of bla(OXA-23-like), bla(OXA-24-like), bla(OXA-51-like), bla(OXA-58-like), bla(VIM), bla(IMP) and bla(SPM) genes was assessed by polymerase chain reaction (PCR). To identify clonal relatedness, all isolates were subjected to repetitive sequence-based PCR (rep-PCR) Results: Based on disk diffusion results, the highest rate of resistance was observed in rifampin (96.8%). Colistin and polymyxin-B were the most effective agents in vitro. According to the MIC results, the rate of resistance to imipenem, meropenem, colistin and tigecycline were 78.2%, 73.4%, 0.8% and 0, respectively. Metallo-beta-lactamase production was positive in 42.3% and 79.4% of the isolates by DDs test and E-test, respectively. All isolates (100%) carried bla(OXA-51-like) gene. According to the results of multiplex PCR, bla(OXA-23-like) and bla(OXA-24-like) genes were detected in 85.6% and 6.2% of carbapenem resistant isolates, respectively. No bla(OXA-58-like), bla(VIM), bla(IMP) and bla(SPM) were detected. By rep-PCR, carbapenem resistant isolates were separated into six genotypes (A to F). Genotype A (30.9%) was the most prevalent (P value < 0.001). Genotypes B and C were found in 28.9% and 26.8% of the isolates, respectively. Conclusions: The rate of carbapenem resistant A. baumannii isolates were high in this study. Since, bla(OXA-58-like) or MBL genes were not detected, it seems that resistance to

carbapenems is related to bla(OXA-23-like) and bla(OXA-24-like). Moreover, bla(OXA-23-like) was the most prevalent oxacillinase (OXA) gene. Most of the isolates belonged to one of the four dominant genotypes indicating clonal dissemination in the hospitals under study. In order to control the spread of carbapenem-resistant A. baumannii, infection- control strategies are needed.

49-Yari, A. R., et al. (2016). "Study of ground-level ozone and its health risk assessment in residents in Ahvaz City, Iran during 2013." Toxin Reviews 35(3-4): 201-206.

Ozone is a highly oxidative compound and is one of the important pollutants present in the atmosphere and at ground level. Concentration of ground-level ozone (GLO) pollutant depends on different factors such as the amount of VOC and NOX, heat and location in the atmosphere. Ozone can cause health effects such as problems to breathe deeply and vigorously, inflame and damage the airways, bronchitis, reduced lung function in children and adults, emphysema and increase the frequency of asthma attacks. In this work, we focused on the determination of number of hospital admissions associated with ozone in Ahvaz with population of 1000000, during 2013. In this study, ozone data collections were through Iranian Environmental Protection Agency (Iranian EPA) and Meteorological Organization. Ozone data and meteorological parameters were used in Excel software to prepare input file of AirQ model. After running model, outputs presented in term of hospital admissions of ozone exposure were calculated. According to this study, Havashenasi and Naderi had the lowest and the highest ozone concentrations. Results of this study showed that if ozone concentrations were more than 20g/m(3), approximately 12% hospital admissions were attributed by this pollutant. The results showed that the concentration of ozone was related to Ahvaz with an annual average of 223g/m(3). Ozone concentration in Ahvaz was higher than standard. Mitigation measures in industries and transportation system in Ahvaz metropolitan is recommending to reduce the level of ozone in the ambient air. Changing the fuel process and using upgraded vehicles could be possibly very effective to diminish the impact of this pollutants on citizens.

50-Zarrin, M. and M. Erfaninejad (2016). "Molecular variation analysis of Aspergillus flavus using polymerase chain reaction-restriction fragment length polymorphism of the internal transcribed spacer rDNA region." Exp Ther Med 12(3): 1628-1632.

Aspergillus flavus is the second most common disease-causing species of Aspergillus in humans. The fungus is frequently associated with life-threatening infections in immunocompromised hosts. The primary aim of the present study was to analyze the genetic

variability among different isolates of A. flavus using polymerase chain reaction (PCR)-based restriction fragment length polymorphism (RFLP). A total of 62 A. flavus isolates were tested in the study. Molecular variability was searched for by analysis of the PCR amplification of the internal transcribed spacer (ITS) regions of ribosomal DNA using restriction enzymes. PCR using primers for ITS1 and ITS4 resulted in a product of similar to 600 bp. Amplicons were subjected to digestion with restriction endonucleases EcoRI, HaeIII and TaqI. Digestion of the PCR products using these restriction enzymes produced different patterns of fragments among the isolates, with different sizes and numbers of fragments, revealing genetic variability. In conclusion, ITS-RFLP is a useful molecular tool in screening for nucleotide polymorphisms among A. flavus isolates.

51-Zarrin, M., et al. (2016). "Analysis of the rDNA internal transcribed spacer region of the Fusarium species by polymerase chain reaction-restriction fragment length polymorphism." Biomed Rep 4(4): 471-474.

The Fusarium species are a widely spread phytopathogen identified in an extensive variety of hosts. The Fusarium genus is one of the most heterogeneous fungi and is difficult to classify. Polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP) analysis is a useful method in detection of DNA polymorphism in objective sequences. The aim of the present study was to identify the phylogenetic associations and usefulness of the internal transcribed spacer (ITS) region as a genetic marker within the most clinically important strain of the Fusarium species. A total of 50 strains of Fusarium spp. were used in the study, including environmental, clinical and reference isolates. The primers ITS1 and ITS4 were used in the study. Two restriction enzymes, HaeIII and SmaI, were assessed for the digestion of PCR products. A PCR product of similar to 550-base pairs was generated for each Fusarium species. The digested products with HaeIII and SmaI demonstrated that the bands generated for the medically significant Fusarium species, including F. solani, F. oxysporum, F. verticillidea, F. proliferatum and F. fujikuri, have different restriction enzyme patterns. In conclusion, it appears that the PCR-RFLP method used in the present study produces a sufficient restriction profile for differentiation of the most medically significant Fusarium species.

52-Zarrin, M., et al. (2016). "Development of a polymerase chain reaction-restriction fragment length polymorphism method for identification of the Fusarium genus using the transcription elongation factor-1 alpha gene." Biomed Rep 5(6): 705-708.

Fusarium species are well-known plant pathogens and food contaminants that have also appeared as one of the most important groups of medically significant fungi. The sequences of

the translation elongation factor (TEF)-1 alpha gene have been broadly employed for species detection. A total of 50 strains of Fusarium spp., including environmental, clinical and reference isolates were used for the current study. The primer sets, Fu3f and Fu3r, were used to amplify an similar to 420-bp DNA fragment of the TEF-1 alpha gene. Double digestion with two restriction enzymes, XhoI and SduI was used for discrimination of the Fusarium species in the TEF-1 alpha gene fragment. Double digestion of the TEF-1 alpha gene fragment from five clinically important Fusarium species were clearly differentiated from each other: The F. solani species complex, F. oxysporum species complex, F. verticillioides, F. proliferatum and F. fujikuroi. This method facilitates detection and enables verification of the Fusarium genus; therefore, it may be applied for disease control.