Prevalence of Staphylococcus aureus and Staphylococcus saprophyticus in Imam Khomayni Hospital, Ilam, 2011-2012

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Abstract
Background and objective: Staphylococcus aureus is one of the main causes of hospital infections. Staphylococcus saprophyticus is a common agent of urinary tract infections. Hospital acquired infection as an old challenge has high importance in hospital infection control and Staphylococcus spp. play main role among routine pathogens. this study designed to investigate the of Staphylococcus aureus and Staphylococcus saprophyticus among ICU, Men and Children wards.
Materials and methods: Samples collected randomly from ICU, Men and Children wards. Through 203 sampling of wall, floor, bed, pillow and blanket, 75 Staphylococcus spp. isolated. Species recognizes base on culture on Mannitol salt agar and Novobiocin susceptibility determination.
Result: Among 75 positive samples, 62 (82.7%), and 13 isolates were Staphylococcus saprophyticus, Staphylococcus aureus, respectively. 51% of bacteria isolated from ICU, 29% from children ward and 20% from men surgery ward. Staphylococcus saprophyticus comprised 87%, 82% and 73% of isolates pertaining to ICU, pediatric and men surgery wards, in a row.
Conclusion: Our funding indicate there is an inappropriate instrument to deal with infection in hospital specially ICU. Regards to this issue that Staphylococcus spp. as a main pathogen which has potency to form biofilm and show high resistance to extended broad antibiotics therefore it is suggested to prepare proper guideline to cope with bacteria dissemination and resistance emergence in hospital.
Keywords: Staphylococcus saprophyticus, Staphylococcus aureus, ICU, hospital, Ilam

Frequency of Non-tuberculosis Mycobacterium by PCR Restriction Fragment Length Polymorphism Analysis (PRA) Method

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Abstract

Background and objective: Atypical Mycobacterium cause various infections and some of them lead to Tuberculosis-like disease. Treatment of atypical mycobacterium is different from tuberculosis so identification of mycobacterium species is important for better control of tuberculosis. PRA is a more rapid and accurate method in comparison with phenotypic ones. During the present study using 3 restriction enzymes for digestion of 644 bp PCR product of hsp65 gene, identification of 50 mycobacterium isolates were accomplished.

Materials and methods: All of the 50 different atypical mycobacterium isolates from patients referred to the Pasteur Institute of Iran over 89-90 years were tested for PRA. A 644 bp fragment of hsp65 gene was amplified by PCR. Subsequently, PCR products were digested with AvaII, HphI and HpaII enzymes. Digested fragments were compared with standard algorithm and identified with GelcomparII software.

Results: Forty nine of 50 atypical Mycobacteria were identified in to 13 groups including 15 M.fortuitum,12 M.simiae، 6 M.kansasii، 3 M.szulgai, 2 M.triviale ، 2.M.gordonae، 2 M.aichiense، 2 M.gallinarum.1 M.hassiacum،1 M.malmoense،1 M.aurum، 1 M.marinum،1 M.abscessus and one unknown species.

Conclusion: The results showed PRA using AvaII، HphI وHpaII is a simple,fast and accurate for identification of atypical mycobacteral isolates into species or sub species level. Rapid and exact identification of atypical mycobacterium from Mycobacterium tuberculosis is essential for effectiveness of TB surveillance programs.

Keywords: Rapid identification, atypical mycobacterium, PRA

Antibacterial Activity of Melittin Derived from Honey Bee Venom

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Abstract

Background and objective: Bacterial peritonitis is one of the nosocomial infections that is due to direct invasion of bacteria to peritoneal membrane. Resistance to antibiotic is of great significance in this disease and could be led to morbidity and mortality of patients. During the past decade, tracing for natural antimicrobial peptide is more considered. Among them, melittin has been extracted from honey bee venom and its antibacterial activity is being examined. The main goal of this study was isolation of melittin from honey bee venom and evaluation of its antibacterial activity against the agents of bacterial peritonitis.

Materials and methods: Honey bee venom prepared using electrical stimulation and the quality of venom confirmed by SDS-PAGE. Melittin isolated from the venom using a linear gradient of acetonitrile and C18 column by Reverse Phase-High Performance Chromatography (RP-HPLC). Minimal Inhibition and Bactericidal concentration for melittin examined on Escherichia coli, Staphylococcus aureus, and Pseudomonas aeruginosa.

Results: Honey bee venom composed of twenty distinct fraction in which melittin was the major one. Melittin inhibited Escherichia coli, Staphylococcus aureus, and Pseudomonas aeruginosa growth at 0.39, 6.25, and 12.5 µg and was bactericide at 1.56, 25, and >50 µg respectively.

Conclusion: Melittin specifically invade the corresponding bacteria and induce significant inhibitory and bactericidal activity against the main agents of bacterial peritonitis. Complementary studies in animal model would be overcome bacterial drug resistance issue specifically in bacterial peritonitis.

Key words: Honey bee venom, Antimicrobial peptide, Melittin, Peritonitis, HPLC

Inhibitory and Lethal Effects of Aqueous and Ethanolic Extracts of Kelussia odoratissima on Bacillus cereus , Listeria innocua and Escherichia coli "in vitro"

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Abstract

Background and objectives: Karafs Koohi with the scientific name of Kelussia odoratissima and the local name of Keloss belongs to the Apiaceace family, and is a biannual or perennial plant. The present study aims at investigating the antimicrobial effects of the ethanolic and aqueous extracts of Kelussia odoratissima on Bacillus cereus , Listeria innocua and Escherichia coli

Materials and methods: In this study, different concentration levels (20, 40, 60, 80 mg/ml) of ethanolic and aqueous extracts of Kelussia odoratissima leaves were prepared. The antibacterial effect of extracts were investigated using spreading of the extract on medium surface (pour plate) and disk agar diffusion test. Minimum Inhibitory Concentration (MIC) and Minimum Bactericidal Concentration (MBC) were also studied using the dilution method .Statistical analysis was carried out by analysis of variance (ANOVA).

Results: In disk agar diffusion Method all concentrations of ethanolic extract have inhibitory effect against Bacillus cereus and Listeria innocua. Minimum Inhibitory Concentration (MIC) of Kelussia odoratissima leaves of aqueous and ethanolic extracts for Bacillus cereus and Listeria innocua was 16 and 8 mg/ml and for Escherichia coli was 32and 16 mg/ml, respectively . Minimum *Bactericidal* Concentration (MBC) of Kelussia odoratissima leaves of aqueous and ethanolic extracts for Bacillus cereus and Listeria innocua was 32 and 16 mg/ml and for Escherichia coli was 64 and 32mg/ml, respectively. Escherichia coli exhibited the most resistance against aqueous and ethanol extracts of Kelussia odoratissima leaves.

Conclusions: The results showed that the ethanolic extract of Kelussia odoratissima leaves had greater inhibitory effects on the strains studied compared to aqueous extracts in vitro.

Keywords: Kelussia odoratissima, Ethanolic and aqueous extract, Antibacterial effects

Simultaneous Specific Detection of Streptococcus pneumoniae, Haemophilus influenzae and Mycoplasma pneumoniae in Sputum Samples from Patients with Suspected Influenza by Multiplex-PCR

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Abstract

Background and objective: Streptococcus pneumoniae, Haemophilus influenza and Mycoplasma pneumoniae are the most common cause in bacterial pneumonia. Also these agents can cause bacterial superinfection in patients with influenza. Aim of this study was Simultaneous specific detection of Streptococcus pneumoniae, Haemophilus influenza and Mycoplasma pneumoniae in sputum samples from patients with suspected influenza by Multiplex-PCR.

Materials and methods: In this study, 170 sputum samples in patients with suspected influenza with age from 3 months to 70 years, received the Influenza Reference Laboratory – Tehran Medical university were tested by Multiplex PCR. Amplified DNA fragments size was 394 bp for Streptococcus pneumoniae, 199 bp for Haemophilus influenzae and 416 bp for Mycoplasma pneumoniae.

Results: of all 170 samples, 30 samples were positive for Streptococcus pneumoniae and Haemophilus influenza. Of the 30 positive samples, 27 samples (15/8 %) and 3 samples (1/7 %) were positive for S. pneumoniae, Haemophilus influenza respectively.

Conclusion: This study showed that Multiplex-PCR able to diagnosis desired bacteria in short time and so this molecular method can use as complementary technique especially when the results of gram stain, culture or serological test are negative.

Keyword: Detection, Streptococcus pneumoniae, Haemophilus influenza, Mycoplasma pneumoniae, Multiplex-PCR

Seroepidemiology of Hepatitis E in Children in Kashan , 2012

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Abstract

Background and objective: Hepatitis E is a viral disease that is transmitted through contaminated water and foods. This disease is variable e from a simple asymptomatic infection to a fulminant disease. Its mortality is about 1-4% but in pregnant women increases the amount of about 20%.
his study was performed in children in Kashan to determine prevalence of hepatitis E serological positive and relationship by age and sex.

Materials and methods: This cross-sectional study using cluster sampling was conducted on 558 children 1 to 15 years in Kashan and Anti-HEV IgG was evaluated using the ELISA method.

Results: The prevalence of hepatitis E in the study population was 3.7%(21 people). The prevalence of positive cases was significantly correlated with age and number of family members, but was not related to child sex.

Conclusion: The findings suggest that HEV infection is endemic in the region. Thus, the use of appropriate health programs, public health, public education will be effective in controlling the infection.

Key words: Hepatitis E, Seroepidemiology, Children

Antibiotic Resistance Pattern of Mthicillin Resistant Staphylococcus epidermidis Isolated from Clinical Samples in Tehran

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Abstract
Background and objective: Staphylococcus epidermidis, the most frequently isolated species of coagulase-negative staphylococci (CONS), is the leading cause of infections related to implanted medical devices and became a serious problem in antimicrobial chemotherapy. The aim of the study was to detect and analyze the antibiotic resistance pattern among methicillin resistant S. epidermidis isolated from two hospitals in Tehran in 2012-2013.
Materials and methods: Totally 193 isolates of S. epidermidis from clinical samples were collected from two hospitals in Tehran. All isolates were identified at the species level using standard biochemical tests. Susceptibility to eighteen antibiotics was determined using disc diffusion method. MIC of oxacillin and vancomycin in MRSA isolates was also done using Etest according to CLSI recommendation. PCR was used to detect mecA gene.
Results: the frequency of oxacillin resistance was 37.3%. The highest level of resistance was observed to penicillin, erythromycin, ciprofloxacin, clindamycin, kanamycin, tobramycin, amikacin and tetracycline respectively. MIC results showed that 42% of isolates showed high level resistant to oxacillin (MIC≥128 µg/ml). None of the MRSA isolates were resistant to vancomycin, linezolid and synercid. One hundred percent of the isolates contained mecA gene.
Conclusion: This study showed that the prevalence of methicillin resistant S. epidermidis isolates was lower than the other studies in Iran. Synercid, linezolid and vancomycin are the most effective antibiotics against MRSA infections. High resistance of methicillin resistant strains to 1st and second line of antibiotics could be an urgent for public health
Key words: S. epidermidis, methicillin, Etest, vancomycin, mecA, Tehran

Polymorphism Identification of VNTR30 and VNTR36 Loci in Pathogenic Leptospira Serovares in Iran

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Abstract

Background and objective: Leptospirosis, is the zoonotic disease which is characterized as an emerging infectious disease with large documented outbreaks. Epidemiological investigations are needed to distinguish outbreak situations or to trace reservoirs of the organisms. Today MLVA technique is used for segregating and identifying of Leptospira serovares. The method has potential application in furthering the understanding of Leptospiral molecular epidemiology. The propose of this study is rapid identification of pathogenic Leptospira serovares in Iran.

Materials and methods: A total 12 pathogenic Leptospiral serovares and 1 saprophytic serovar that maintained from microbial bank of Razi Vaccine and Serum Research Institute, Karaj, Iran. The Genomic DNA of Leptospira was extracted .PCR was performed with primers for loci VNTR30, VNTR36. The amplified fragments were analyzed by gel electrophoresis . The sizes of the amplified products were estimated by comparison with a 100 -bp ladder.

Results: All loci successfully amplified in all pathogenic leptospira serovars. The saprophytic serovar showed no amplified fragments. The results show VNTR30 has a wide range of polymorphism between Atumnalis, Hardjo St.Hardjo bovis, Pomona St. UT364, Icterohaemorrhagia St. RGA and VNTR36 shows variation between Canicola St. Hondutrecht IV , Hardjo St.Hardjo bovis, Pomona St. UT364

Conclusion: Most of the VNTR patterns were similar in different serovares while showed significant differences with same serovares of South America and Europe. On the other our serovares resemble Southeast Asia serovares because of the same geographical area. Among serovares Canicola St. Hondutrecht IV and Canicola St. Fiocruz LV133 identified by MLVA, PFGE was unable to differentiate them. In conclusion MLVA technique with wide range of polymorphism is known as good marker for identification serovares.

Key world: VNTR, MLVA method, Leptospires

Frequency and Antibiotic Resistance Pattern in Staphylococcus aureus Strains Isolated from Clinical Samples of Tehran's Araad Hospital in 2007-2011

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ABSTRACT

Background and objective: Todays, the resistance to antibiotics among of pathogen bacteria is one of the main concerns of doctors all around the world, with consideration to different reports about Staphylococcus aureus bacteria's sensitivity, this study was done to examine the pattern of sensitivity and antibiotic resistance of Staphylococcus aureus strains collected from clinical samples of patients hospitalized in Tehran's Araad hospital.

Materials and methods: In this descriptive examination, after extracting Staphylococcus aureus derivations from clinical samples (urine, catheter, phlegm, wound, bronchial and blood), their sensitivity was measured using standard Kirby-Bauer test, in contract with following antibiotics Amikacin, Ciprofloxacin, Vancomycin, Imipenem, Sulfametoxazole Trimetoprime, Tetracycline, Oxacillin, Ceftriaxone and Penicillin.

Results: In this study 260 samples of Staphylococcus aureus isolated from clinical specimens in three years. The most sensivity was to Vancomycin and the most resistance was to Penicillin and Oxacillin.

Conclusion: The results of this study are indicating that Staphylococcus aureus strains resistance has increased against Penicillin and Oxacillin; presumably it is due to excessive consumption of these antibiotics. It is obvious that, with regard to increasing consumption of antibiotics and consequently, augmentation of antibacterial resistance, control of this resistance factor is necessary and inevitable, so it is recommended to avoid unnecessary usage of antibiotics.

Key words: Antimicrobial Resistance, Antibiotics, Staphylococcus aureus, Araad hospital.

The Risk of Avian Influenzaand and Salmonellosis Transmission from Pigeon in the Holy Shrine of Fatima Masooma.

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Abstract
Background and objective: Pigeons are potential resources of spreading many zoonotic pathogens such as Salmonella and avian influenza.Therefore the presence of these species of birds which was exposed with human population would result in spreading of Salmonellosis and avian influenza within people. One of the prominent characteristics of religious places is the presence of pigeons, so pilgrims and service providers are highly exposed to these birds and their feces. Pigeons as reservoir of these agents would transmit these diseases to pilgrims and public as a whole.
Materials and methods: In this survey which was conducted in 2009,cloaca swabs and blood samples of 220 pigeons were taken in the holy shrine of Fatima Masooma.Serum samples were examined with haemagglutination inhibition test by using H7, H5 and H9N2 antigens and cloaca swabs were cultivated to detect salmonella spp.
Results: It was founded that none of the serum samples had antibodies titers against H5 and H7 antigens.However in 2 cases (1/8%),1 and 3 titers of antibodies were detected against H9N2. Moreover, none of feces' samples were positive in salmonella culture.
Conclusion: Because these pigeons haven't had any history of influenza vaccination, the low titers of antibodies against this virus could represent infection by wild virus. Although the results of cultivating feces were negative,however because of the presence of Iranian and foreign pilgrims in the holy shrine and the important role of pigeons in maintenance and transmission of these pathogens, health and hygiene controls must be considered for the population of these birds as a reservoir of potential infection.
Keywords:Avian Influenza, Holy Shrineof FatimaMasooma, Pigeon, Salmonella

Escherichia coli O157:H7 Contamination Rates Using Chromogenic Medium in Selected Foods Consumed at some Restaurants in Tehran

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Abstract

Background and objective: Eschirichia coli are considered as a contamination indicator of water and foods to coliform pathogens. Some E. coli serotypes such as E. coli O157:H7 cause serious complications such as hemorrhagic colitis and hemolytic uremia syndrome. The main objective of this study was to the determination of E. coli O157:H7 contamination rates using chromogenic medium in some selected foods consumed at some restaurants in Tehran.

Materials and methods: A total of 96 food samples, including 48 salads and 48 crushed kebabs were randomly collected from four restaurants in Tehran. Using sterile collection equipment, 12 samples from each restaurant were collected two times with two month interval. Standard biochemical and bacteriological methods and chromogenic medium were used for the detection of E. coli and E. coli serotype O157:H7.

Results: The results of this study showed that out of 96 tested samples, contamination to E. coli in 29 samples (30/2%) was confirmed in which 17 samples were contaminated to E. coli O157 however no E. coli O157:H7 strains were detected when all positive E. coli O157 isolates were subjected to serotyping.

Conclusion: The results of this study showed that the hygienic quality of ready-to-use salads and foods consumed in the restaurants under study was not ideal; therefore the implementation of more surveillance and supervision on those restaurants is recommended.

Keywords: Chromogenic medium, E. coli O157:H7, Restaurants