IJMS
Vol 37, No 3, Supplement 1, September 2012

First Global Patient Safety Challenge: Promoting Hand Hygiene and Patient Safety Worldwide

Professor Didier Pittet

Infection Control Program and World Health Organization (WHO) Collaborating Centre on Patient Safety, University of Geneva Hospitals and Faculty of Medicine, Geneva, Switzerland
External Lead, First Global Patient Safety Challenge, WHO Patient Safety, WHO Headquarters, Geneva, Switzerland

Healthcare-associated infection is a global problem. It occurs in every healthcare facility in every country and affects hundreds of millions of patients annually worldwide. Hand hygiene has been recognised as the single, most important preventive measure. Since the launch of the WHO First Global Patient Safety Challenge "Clean Care is Safer Care" in 2005, much has been achieved in healthcare settings around the world to improve infection prevention and control, including hand hygiene practices, with the aim to reduce healthcare-associated infections.

The main output of the Challenge, the WHO Guidelines on Hand Hygiene in Health Care, includes a suite of tools to implement the recommended multimodal improvement strategy aimed at improving and sustaining hand hygiene. This model was developed within a clinical setting and further validated to ensure applicability to all healthcare settings worldwide, irrespective of resources available.

As part of the Challenge, over 140 countries have pledged their support to implement actions to reduce healthcare-associated infection, corresponding to 90% coverage of the world population. Forty-three countries/regions have reported the existence of formal hand hygiene campaigns and WHO has formed a WHO Clean Hands Net to facilitate progress in such countries, as well as to share successes and strategies.

In May 2009, WHO Patient Safety launched the SAVE LIVES: Clean Your Hands initiative to encourage healthcare workers to be part of a global movement to improve and sustain hand hygiene. By May 2012, over 15,000 healthcare facilities from 159 countries had registered their commitment to the initiative. The major challenge for the next decade will be to maintain the "snowball" effect and to show a significant impact on infection prevention across the world. To truly protect our patients, it will take leadership, commitment, a range of actions, and time. The efforts of WHO, together with countries and facilities, should help bring true ownership to healthcare workers in relation to microorganism transmission and its prevention and, subsequently, long-term patient safety improvement.

Antimicrobial Stewardship Program for Worldwide Reduction of Antimicrobials Resistance

Professor WingHong Seto

Director, WHO Collaborating Centre for Infection Control, Hospital Authority, Hong Kong
Senior Advisor (Hon.), Infection Control, Hospital Authority Head Office, Hong Kong
Senior Advisor (Hon.), Quality and Safety, Hong Kong West Cluster, Hospital Authority, Hong Kong
Professor (Hon.), the University of Hong Kong

The WHO has stated that "antimicrobial resistance is clearly a global issue". Resistance to first-line drugs for most of the key pathogens causing infections disease ranges from zero to almost 100%. The WHO has identified antimicrobial use as the key driver of resistance. It is thus critically important to control antibiotics abuse which is the very essence of the Antibiotic Stewardship Program (ASP). It should also be appreciated that the ASP should be developed together with an effective Infection Control program and Surveillance activities[1]. This is logical because Infection Control will prevent the spread of resistant bacteria and only with proper surveillance, can evaluation be made on the efficacy of implemented measures.

In an effective ASP, multiple strategies should be incorporated. There is ample room for local innovations although two core strategies are recommended by the Infectious Disease Society of America. The first is prospective audit with intervention feedback. To be successful a guideline must first be promulgated and feedback should be given to any variance from the guideline. In Hong Kong, the feedback is given on the same day of the audit, a scheme known as Immediate Concurrent Feedback (ICF) with the effective reduction of >10% of the expensive antibiotics prescribed. A summary of the various interventions used in Hong Kong will be provided which resulted in a savings of millions of dollars. The program is carried out by Infection Control nurses with the more difficult cases reserved for physicians.

Finally ASP should also be conducted in the outpatient setting. A summary of programs reported by the CDC and one conducted in Hong Kong will be briefly summarized.

Management of Ventilator Associated Pneumoniae caused by Colistin-only Susceptible *Acinetobacter*

Haluk VahabOglu

Professor of Infectious Disease and Clinical Microbiology, Medeniyet University, Istanbul, Turkey

Diagnosis of ventilator associated pneumonia (VAP) is one of the most complicated issues in the ICU. Chest radiography, microbiology and blood gases should be evaluated together. In any case, however, performance of diagnostic criteria is poor and may be misleading. Over diagnosis cause inappropriate use of antibiotics. On the other side, delay in the institution of effective antibiotics cause adverse outcome. This dilemma is further complicated by the emergence of multi drug resistant strains. *Acinetobacter spp* has a tendency to colonize lower respiratory tract among ventilated patients and cause pneumonia. Carbapenems and sulbactam are effective alternatives in the treatment. Carbapenemases, particularly, OXA-type carbapenemases rapidly spread among *Acinetobacter spp*. Carbapenem resistant *Acinetobacter* are mostly susceptible to colistin. Although, once discarded from the market due to its high toxicity, recent studies encourage the use of colistin in the treatment of VAP caused by colistin-only susceptible *Acinetobacter*. However, controversies still exist in various aspects of colistin treatment. This presentation aims to present the available data and discuss controversies in colistin treatment.

Challenges of Infection Control in the Paediatric Setting

WALTER ZINGG, MD

Healthcare-associated infections (HAIs) in children occur at a rate of 6-9 episodes per 1,000 patient-days in the neonatal intensive care unit (NICU) and 1-31 per 1'000 patient-days in the paediatric intensive care unit (PICU). The overall prevalence in the paediatric setting is about 4-7%. HAI-incidence depends largely on age in children. Bloodstream infection is the leading healthcare-associated infection in the NICU while pneumonia is more common with older age. Antibiotic use in Children's hospitals is highly individualized with third-generation cephalosporins being the leading drug class. With emerging infection in the past years, there is a shift towards the use of broader-spectrum antibiotics. Some paediatric settings in the resource limited settings struggle with extraordinary high rates of multidrug-resistant (MDR) Gram-negative organisms while Gram-positive organisms still remain the predominant organisms associated with HAI. As in adults, MDR organisms are selected by broad-spectrum antibiotic use and the transmission includes family visitors, surfaces, and toys. The latter is rather a neglected topic with a remarkable lack of studies. Antibiotic stewardship is recommended also in paediatric hospitals but compliance is rather poor. A number of outbreaks with MDR organisms, and MRSA in particular, have occurred in the past years in NICUs. Auditing compliance with established prevention strategies proved most useful in this context. Extended-spectrum-beta-lactamase-producing Gram-negative organisms and pan-resistant *Acinetobacter baumannii* or *Serratia marcescens* complicate the use of standard antibiotic treatment and are a particular concern in NICUs because of the limitation in antibiotic classes among neonates. Carbapenem resistance among enterobacteria due to KPC or NDM is a threat also for children's hospitals. Carbapenem-resistant organisms are more widely disseminated than generally anticipated and targeted screening at admission is advisable. Infections due to *Candida spp*. are a concern because of emerging resistance. High incidence with *Candida* should raise suspicion of inappropriate antibiotic use and antibiotic stewardship is the most promising intervention.

A number of studies reported effectiveness of multimodal programmes in the prevention of central line-associated bloodstream infection and ventilator-associated pneumonia in the paediatric setting. Similarly to the adult setting, multidisciplinary and multimodal training and education should be established in children's hospitals for quality improvement. The implementation of (complex) procedures must follow the principles of behaviouralchange and implementation research.

Senior physician of the Infection Control Program of the University of Geneva Hospitals. Geneva, Switzerland

Emerging Resistance – a Global Challenge

WALTER ZINGG, MD

Senior physician of the Infection Control Programme of the University of Geneva Hospitals, Geneva, Switzerland

In the past years, emerging resistance among microorganisms has become a concern. Methicillin-resistant *Staphylococcus aureus* was the predominant multi-drug resistant organism (MDRO) in hospital settings of high-income countries, while resource poorer regions struggled with MDR *Acinetobacter baumannii* infections and *Pseudomonas aeruginosa*. However, most recently, carbapenem-resistant *Enterobacteriaceae* have emerged and due to travel activities and medical tourism have become a global concern. Extended-spectrum beta-lactamase *Escherichia Coli* and other *Enterobacteriaceae* have been identified in food industry and poultry in particular. Countries such as the Netherlands who were proud of controlling MDRO in their hospitals face now a problem that may have been caused by abundant antibiotic use upon livestock breeding. MDRO are selected by broad-spectrum antibiotic use and transmission is facilitated by shortcomings of infection prevention measures. Recommendations for antibiotic stewardship take into account such mechanisms and in addition to suggesting "saying no" to antibiotics and encouraging their wise use, also point out the importance of effective infection prevention programmes to reduce MDRO. Pathogens such as vancomycin-resistant *Staphylococcus aureus*, ESBL-containing *Klebsiella spp*., and MDR *Acinetobacter baumannii* have proved to be a particular challenge to control for in hospital settings, once they got installed. Emerging resistance is the story selection pressure and infection control, but also of globalization and the interconnection of animal husbandry and medicine.

Second Section
Oral Presentations

The Prevalence of Genes Encoding Leukocidins in Staphylococcus aureus Strains Resistant and Sensitive to Methicillin Isolated from Burn Patients in Taleghani Hospital, Ahvaz, Iran

Hajar Hoveizavi, Azardokht Khosravi, Zahra Farshadzadeh

Abstract

Background: *Staphylococcus aureus* is the major cause of nosocomial infection. Various strains of *S. aureus* produce two subunit toxins, i.e. LukE/D, and PVL that are associated with increase of skin diseases, fatal pneumonia, and osteomyelitis and their high morbidity and mortality rate. The aim of this study was to determine the prevalence of genes encoding Leukocidins in *S.aureus* strains which are resistant and sensitive to methicillin isolated from burn patients in Taleghani hospital, Ahvaz, Iran.

Methods: In an eleven month study, 203 *staphylococci* isolates were collected from burned patients. The isolates were examined by traditional culture method to detect *S. aureus* strains and the results were confirmed with standard biochemical tests. Then DNA was extracted from bacterial colony by simple boiling method and PCR was used to detect mecA, PVL and LukE/D genes.

Results: Ninety-five (46.8%) out of total tested isolates were identified as *S. aureus*. Based on the results from PCR, 83 strains (87.36%) were mecA positive, so they were resistant to methicillin and the rest were MSSA. The prevalence of PVL and LukE/D genes in MRSA strains were (7.23%) and (66.26%) respectively; and the prevalence was (33.3%) for both genes in MSSA strains.

Conclusion: There was high prevalence of PVL and LukE/D positive MRSA isolates in the evaluated hospital. Since resulting diseases from these bacteria are severe and may even lead to death, the prevention of disease progress is desired by early diagnosis and proper treatment.

Keywords: Bi-component leukocidins, Methicillin-resistant *S. aureus*, Methicillin-sensitive *S. aureus*, infection

Department of Microbiology, School of Medicine, Infectious and Tropical Diseases Research Center, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran

Evaluating Sensitivity of *Pneumococci* to Ceftriaxone by E-Test Method

Ashraf Tavanaee Sani

Department of Infectious Disease, Imam Reza Hospital, Faculty of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran

Abstract

Background: The emergence of penicillin resistant and multidrug-resistant pneumococcal strains has become a global concern. Several reports have demonstrated a correlation between increased MICs of penicillin and increased MICs of cephalosporins and other β-lactam antibiotics. Pneumococcal resistance to penicillin may predict an unfavorable response to other β-lactam antibiotics. In order to assess the pattern of pneumococcal resistance to ceftriaxone, one of the highly used antimicrobial agents in our region, a microbiological survey was performed on pneumococcal strains, during a 2-year period.

Methods: Thirty-five strains of pneumococci isolated from blood samples of 35 different consecutive patients admitted to two educational hospitals in Mashhad, North East of Iran, during a two-year period were included. Minimal inhibitory concentration (MIC) to ceftriaxone was determined using E-test method.

Results: Amongst thirty five clinical isolates evaluated in this study, only one isolate (2.86%) was resistant to ceftriaxone (MIC>1) and remaining 34 isolates (97.14%) were sensitive to this antibiotic. MIC ranged from 0.012 to 6, MIC_{30} and MIC_{90} was 0.07 and 0.5, respectively.

Conclusion: Considering the low rates of ceftriaxone resistance amongst isolated *Pneumococci* in this study, using ceftriaxone alone for treating invasive pneumococcal infections (other than CNS infections) in adult patients is sufficient; However, in case of pediatrics or CNS infections ceftriaxone should be used along with vancomycin. It is apparent that decrease in vancomycin use will result in decreasing rate of resistance in other bacteria sensitive to this antimicrobial agent (such as methicillin-resistant *Staphylococcus aureus*, *Enterococci* etc.)

Keywords: Sensitivity, Pneumococci, ceftriaxone, E-test

Investigation of Nosocomial Infections in Special Wards of Hospitals, Medical Branch of Islamic Azad University in Tehran

Giti Kashi[1], Niloufar Hejazimehr[2]

Abstract

Background: In spite of significant progresses in antimicrobial therapy, nosocomial infections continue to be clinically and epidemiologically important. Nosocomial infections are one of the serious health-clinical problems in advanced and developing countries. The incidence of nosocomial infections among patients hospitalized in advanced and developing countries is reported to be 5-10%, and 25%, respectively. Nowadays, nosocomial infection control is a universal priority. The aim of this study was to assess and compare the prevailing microbial species of nosocomial infections in special wards of Javaheri and Buali hospitals.

Methods: In this descriptive-analytical study 300 samples were collected and cultured from medical equipment in cardiac care unit (CCU), intensive care unit (ICU), neonatal intensive care unit (NICU), and hemodialysis unit (HDU) of Javaheri and Buali university hospitals before applying disinfectants. The samples were cultured on blood agar, eosin methylene blue agar, mac-conkey agar and microbial agents were identified using differential and biochemical tests. All analyses were performed using software SPSS version 16.

Result: In this study 300 samples were collected and cultured from special wards of Javaheri and Buali hospitals before applying disinfectants. According to findings, the microbial growth are as follows: *Bacillus species* (50%), *Escherichia coli* (20%), *Staphylococcus aureus*, (15%), *Fungi species* (10%), and *Kelebsiella* (5%) in special wards of Javaheri hospital. According to the findings, the microbial growth are as follows: Bacillus subtilis (25%), *Staphylococcus aureus* (25%), *Staphylococcus epidermidis* (14%), *CON Staphylococcus* (11%), *Micrococcus* (6%), *Bacillus cereus* (6%), *Coliform bacteria* (3%), *Bacillus licheniformis* (3%), *Aspergillus niger* (3%), *Candida* (2%), *Staphylococcus saprophyticus* (1%), and *Acinetobacter baumannii* (1%) in special wards of Buali hospital.

Conclusion: The findings indicated that the prevailing microbial species of nosocomial infections in Javaheri and Buali hospitals were Bacillus species. The prevailing microbial species of nosocomial infections in ICU and HDU of Buali hospital were *Staphylococcus species* and *Staphylococcus aureus*, respectively.

Keywords: Nosocomial infections, disinfection, special units

[1]Department of Environmental Health, Medical Branch, Islamic Azad University, Tehran, Iran
[2]Department of Environmental Health, Medical Branch, Islamic Azad University, Tehran, Iran

A Survey about Public Attitude toward Antibiotic Use

Amir Zangouei, Amirreza Liaghat, Mehran Anjomrouz, Ehsan Seydali

Abstract

Background: Due to importance of antibiotic usage and its effect on producing microbial resistance which leads to emergence of resistant microbial pathogens and increases their mortality and virulence, in this study we surveyed public attitude toward antibiotics use.

Methods: This is a cross-sectional survey and self-administered questionnaires were used to gather information from policlinics, clinics, and hospitals.

Results: Seventy percent of surveyed people were male and their average age was 29 years. Usage of antibiotics in 15% of them was low, in 25% was mild. Five percent used high amounts of antibiotics. 40% never had arbitrary usage of antibiotics, 55% had a few arbitrary usages of antibiotics and mild arbitrary usage was reported in 5% of them.

Fifteen percent of participants had no idea about consequences of arbitrary usage of antibiotics, 30% knew a little, 45% had medium level of information about it and 10% had adequate amount of knowledge about the consequences.

In 40% of cases doctors didn't prescribe antibiotics and therefore 22% asked about the reason, 11% of them never went back to that doctor, 22% of them persisted on prescribing antibiotics and 45% of them knew the reason of prescription. Sixty five percent bought antibiotics from the pharmacies without a prescription. Thirty percent knew about the phenomenon of drug resistance, among them 34% knew this by their physician and 65% was informed by media. About reducing antibiotic demand, 85% thought that cultural ways and media can be useful while other 15% believed prescribing antibiotics restricted to physician could be the solution.

Conclusion: Regarding antibiotic usage and circumstantial evidence, drugs should not be provided by pharmacies. Moreover, we should inform people about drug resistance by means of culture, media and papers.

Department of Microbiology, Faculty of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran

Keywords: Antibiotic, drug resistance, arbitrary use of antibiotics

Distribution of Exfoliative Toxin A and TSST-1 Genes in Staphylococcus Aureus Isolated from Clinical Specimens

Roohollah Zareikoosha[1], Abbas Ali Imanifooladi[2]

Abstract

Background: *Staphylococcus aureus* is an important pathogen of humans and livestock. Exfoliative toxins and TSST-1 are virulent factors, which can be produced by several strains of *Staphylococcus aureus*. Some of these strains produce one and different type of toxins. Serologically, almost twenty toxin and super-antigen groups have been recognized (such as enterotoxin A -V, ETs A -D and TSST-1).The principal aim of this study is to evaluate abundance of ETA and TSST-1 genes by multiplex PCR from clinical samples.

Methods: One hundred ninety seven strains of *S. aureus* isolated from clinical samples were subjected to Multiplex PCR. The strains then were maintained on tryptic soy agar plates and DNA extraction was performed by means of Genomic DNA Extraction kit method (bioneer Co. Korea). We designed ETA and TSST-1 primers and evaluated them by blast software (ncbi.com).

Results: After the ETA and TST genes were identified and distinguished, Multiplex PCR analysis was carried out and the products were analyzed by agarose gel electrophoresis according to SPSS software and statistics table suspected patient exfoliative toxin A &TSST-1. In this study, ETA and TSST-1 producing strains were relatively highly prevalent in different hospital wards.

Conclusion: Our results demonstrated that ETA and TSST-1 producing strains have over-distributed in all groups of study; which may suggest that presence of ETA and TSST-1 probably have significant relevance to clinical samples. ETA and TSST-1 should be further studied for their molecular mechanisms and super-antigenic properties.

Keywords: Exfoliative toxin A, TSST-1, Distribution, Multiplex PCR

[1]Department of Microbiology, Jahrom Branch, Islamic Azad University, Jahrom, Iran
[2]Applied Microbiology Research Center, Baqiyatallah University of Medical Sciences, Tehran, Iran

Survey of Microbial Contamination in Hospital ICU Ward with ACC, Visual and SA Index

Ghodratolah Karami[1] Mohamad Khazaei[1], Mohamadreza RezaiMonfared[2], Rabani Davarkhah[2], Hamidreza Ghelasi[3]

Abstract

Background: Microbial contamination specific wards in hospital are one of the most important background parameters of hospital infection. Microorganisms transmit from instrument surfaces due to contacts. Determination of contamination sources is the first step in controlling infection. In this study, microbial contamination of ICU ward, Shahid Beheshti hospital, Kashan, Iran was investigated.

Methods: This semi-experimental study was performed in two phases including before and after cleaning program during ten weeks. Assessment of cleaning circumstances was performed with ACC analysis, Gram staining, Catalase, Coagulase, MSA and DNase. Results were reported as clean or dirty. Mc Nemmar nonparametric analysis was used with version 18 of SPSS software.

Results: Visual assessment of instrument surfaces revealed 86% contamination. Based on SA and ACC indicator, 76.5 and 12.75 percent contamination levels were detected, respectively. The dirtiest surface, based on visual assessment, was door handles with 100% observed contamination. According to ACC index, floor, patient bed and waiting chairs were the dirtiest surfaces (85 % contamination) and based on SA index, the dirtiest objects were bedside desks and waiting chairs (22.5 %). Comparing with "the before cleaning" measurement, cell phones and bedside desks showed significant difference (P=0.021); therefore the rate of contamination decreased after cleaning program based on visual index.

Conclusion: The level of surface contamination was high. Lack of appropriate standard protocol for routine daily cleaning program and traditional monitoring criterion leads to current unacceptable situation. Preparation of an integrated national mandatory program for surface cleaning and monitoring may be useful as a solution to this problem.

Keywords: Environmental Health, infection control, daily cleaning program

[1]Department of Environmental Engineering Health, Qom University of Medical Sciences, Qom, Iran
[2]Department of Environmental Engineering Health, Kashan University of Medical Sciences, Kashan, Iran
[3]Department of Biostatistics and Public Health, Kashan University of Medical Sciences, Kashan, Iran

Genetic Characterization of *Staphylococcus aureus* Strains Isolated from Wound Infections in Selected Isfahan, Mashhad and Tehran Hospitals

Seyed Asghar Havaei[1], Amir Azimian[1], Kiarash Ghazvini[2], Hosein Fazeli[1], Siamak Mirab Samiee[3, 4], Masoud Soleimani[5], Mahmood Naderi[6, 7]

[1]Department of Pathobiology, School of Medicine, Isfahan University of Medical Sciences, Isfahan, Iran
[2]Department of microbiology, School of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran
[3]Food and Drug Laboratory Research Center, Ministry of Health and Medical Education, Tehran, Iran
[4]Reference Health Laboratories, Ministry of Health and Medical Education, Tehran, Iran
[5]Department of Hematology, School of Medical Science, Tarbiat Modares University, Tehran, Iran
[6]Department of Medical Biotechnology, School of Medical Sciences, Tarbiat Modares University, Tehran, Iran
[7]Molecular Biology and Genetic Engineering Department, Stem Cell Technology Research Center, Tehran, Iran

Abstract

Background: *Staphylococcus aureus* is one of the major causes of hospital and Community acquired infections. Molecular epidemiologic studies can help specialists to understand the dissemination ways and therefore design the appropriate instructions to decrease the Staphylococcal infections in community and particularly hospital settings. We performed genetic analysis of *Staphylococcus aureus* strains isolated from wound infections.

Methods: Forty isolates of *Staphylococcus aureus* from wound samples were identified by conventional biochemical tests, and then evaluated with agar screening and MIC for oxacillin resistance. Genetic analysis was performed with the evaluation of mecA gene, SCCmec and agr typing with multiplex PCR method.

Results: Twenty four (60%) of the isolates were oxacillin resistance. Genetic analysis was performed: mecA was positive in 26(65%), SCCmec type III was the most common type 11(43%) and agr group I 22 (55%) was the most prevalent group.

Conclusion: Increasing rate of antimicrobial resistance is the major concern in staphylococcal infections. The prevalence of MRSA strains in our study was 65%, which seems higher in comparison with previous reports. Commonly SCCmec types IV and V (Community Acquired) are dominant in MRSA strains isolated from wound infections but in the present study SCCmec type III (Hospital Acquired) was the prevailing type. It is perhaps due to changing epidemiology of staphylococcal infections.

Keywords: *Staphylococcus aureus*, methicillin, resistance, SCCmec type, agr group, wound

Biological Screening and Identification of Penicillin-G Acylase Producing *E. coli* and Optimization of Production Condition

Hadi Azimi[1], Safar Farajnia[2], Hadi Feizi[1]

[1]Department of Microbiology, Islamic Azad University of Zanjan, Zanjan, Iran
[2]Biotechnology Research Center, Tabriz University of Medical Sciences, Tabriz, Iran

Abstract

Background: Penicillin-G acylase (PGA) of *Escherichia coli* is one of the most widely used enzymes in industrial scale. It is used to hydrolyze penicillin-G to 6-aminopenicillanic acid, an essential intermediate in the production of semisynthetic penicillin. Due to high industrial importance of PGA, numerous efforts have been made toward screening of certain strains which overproduce this enzyme. The objective of this study was to screen clinical samples for isolation and identification of *E. coli* strains producing PGA enzyme.

Methods: The *E. coli* bacteria isolated from clinical samples were screened for PGA activity using the bioassay method. This method is based on the use of *Serratia marcescens* which is sensitive to 6-APA, although comparatively resistant to benzylpenicillin. After primary screening, the PGA production in positive isolates was verified by biochemical assay. Finally, the influence of incubation time, temperature, PAA concentration and media pH on PGA synthesis was measured and the optimum condition for process was determined. The PDAB colorimetric method was used for quantitative PGA activity assay.

Results: Among 121 *E. coli* isolates studied, only 3 isolates showed the PGA activity. Particularly one of them had higher activity. For the selected strain, the optimal condition for enzyme production was obtained as 0.1% PAA, media pH of 7-8, incubation time of 48h and incubation temperature of 32°C.

Conclusion: Results of this study showed that biological screening method is a rapid and efficient way to identify PGA producing bacteria.

Keywords: Penicillin acylase, *E. coli*, biological screening, optimization

Important Survey Mutations in Precore and Basal Core Promoter Regions in Chronic *Hepatitis B* Virus Infection

Soad Ghabeshi[1, 2], Zohre Sharifi[1], Seyed Masoud Hosseini[2], Mahmood Mahmoodian Shooshtari[1]

Abstract

Background: Chronic *Hepatitis B* virus (HBV) infection is associated with 50% of hepatocellular carcinoma (HCC) incidence worldwide, and specific viral factors may increase the risk of HCC development. The HBV genome may undergo mutations during the course of chronic infection and accelerate progression of liver disease. A1896G mutation has been found in patients with HBeAg negative chronic *Hepatitis B*. A1762T and G1764A double mutations can reduce HBeAg synthesis by inhibiting the transcription of precore mRNA. This mutation may up-regulate HBV expression and have been found to independent risk factors for HCC. In this review was investigated the importance mutations in precore (PC) and basal core promoter (BCP) in chronic HBV infection.

Methods: The precore and basal core promoter mutations were determined by applying Line Probe Assay technique (INNO-LiPA HBV Precore Kit). After purification of viral DNA from the sample of patients, purified DNA is replicated in two stages with biotinylated primers. After amplification, biotinylated DNA, of gene C promoter and precore region with immobilized and specific oligonucleotide probes as parallel lines on membrane-based strips. Incubation with BCIP/NBT chromogen results in purple/brown precipitate.

Results: The late studies reported rate of mutations in precore and basal core promoter regions was about 56% and 40% respectively, in Iran. Over 80% of these patients were HBeAb positive. Some studies showed that these patients have high viral load.

Conclusion: In this review we have attempted to show important survey PC/BCP mutations in chronic *Hepatitis B* virus infection and correlation of them with HBV DNA levels which may be affected by these mutations.

Keywords: *Hepatitis B* Virus, precore and basal core promoter mutations, HBV DNA

[1]Blood Transfusion Research Center, High Institute for Research and Education in Transfusion Medicine, Tehran, Iran
[2]Department of Microbiology, Faculty of Biological Science, Shahid Beheshti University, Tehran, Iran

Comparison of Disk Diffusion and PCR Method in Determining Methicillin-Resistant *Staphylococcus aureus* (MRSA) Strains Isolated From Patient in Center of Iran

Mohsen Rezazadeh[1,2], Ehsanollah Ghaznavi-Rad[1], Rasoul Yousefi Mashouf [3], Bita bakhshi [4], Hossein sarmadyan[5]

[1]Department of Medical Microbiology, Faculty of Medicine, Arak University of Medical Sciences, Arak, Iran
[2]Student Research Committee, Arak University of Medical Sciences, Arak, Iran
[3]Department of Medical Microbiology, Faculty of Medicine, Hamadan University of Medical Sciences, Hamadan, Iran
[4]Department of Medical Microbiology, Faculty of Medicine, Tarbiat Modares University
[5]Department of Infectious Diseases, Faculty of Medicine, Arak University of Medical Sciences, Arak, Iran

Abstract

Background: Methicillin-resistant *Staphylococcus aureus* strains are the most important agents responsible for nosocomial infections. The conventional antibiotic susceptibility Methods such as disk diffusion are not suitable for detection of these strains due to their hetero-resistancy. Therefore, in this study, disk diffusion and PCR were compared in aspect of their accuracy for determination of methicillin resistant *Staphylococcus aureus* (MRSA) strains isolated from patients in hospital of center of Iran.

Methods: In this experimental study a total of 50 samples from patients over a period of eight months were collected. All isolates previously identified as species members by hospital laboratory were reconfirmed in microbiology laboratory of Medicine Arak University by standard materials and methods. Isolates were confirmed as Methicillin-resistant *Staphylococcus aureus* by oxacillin and cefoxitin susceptibility testing according to the CLSI guidelines. All isolates were also reevaluated for the presence of the SA442 gene by PCR. Finally, using PCR, isolates were tested for the presence of mecA gene. Results were compared so as to determine sensitivity and specificity of each method.

Results: In this study, 45 of 50 (90%) *Staphylococcus aureus* isolates were resistant to oxacillin and cefoxitin using disk diffusion method. However, mecA gene was detected in all 50 strains (100%). Our results showed that the sensitivity and specificity of disk diffusion method in determining MRSA strains were 90% and 97% respectively in comparison to PCR.

Conclusion: In comparison to PCR, oxacillin and cefoxitin disk diffusion is an inexpensive, practical and phenotypical method suitable for screening MRSA. However, due to its relatively high false negative results, it is not appropriate for screening MRSA strains isolated from patients in hospitals of center of Iran.

Keywords: Methicillin-resistant *Staphylococcus aureus*, sa442, susceptibility pattern, CLSI

The Frequency of Antimicrobial Resistance Patterns in Community-Acquired and Nosocomial *Enterobacteriaceae* Isolates in Teaching Hospitals of Hamedan

Seyyed Hamid Hashemi, Farzaneh Esna-ashari, Shahrzad Tavakoli, Mojgan Mamani, Haleh Nazeri, Katrin Badifarzad

Department of Infectious Diseases, Hamedan University of Medical Sciences, Hamedan, Iran

Abstract

Background: The prevalence of antimicrobial resistance among *Enterobacteriaceae* is increasing worldwide. Identification of pathogens and their resistance to antimicrobials is mandatory for successful empiric antibiotic treatment. The aim of this study was to investigate the prevalence of antimicrobial resistance of *Enterobacteriaceae* isolated from hospital-acquired and community-acquired infections.

Methods: In a descriptive-comparative study, during 2010, all clinical isolates of *Enterobacteriaceae* and their antibiograms from laboratories of teaching hospitals were included. Hospital-acquired infections were identified by records from infection-control units. A questionnaire containing information about demographic characteristics, source of specimen, kind of *Enterobacteriaceae* and their antimicrobial resistance was filled for each patient. Data were analysed using SPSS.

Results: A total of 574 samples were collected, out of which the most prevalent pathogens were *Escherichia Coli* and *Klebsiella pneumoniae*. Almost all isolates of *Enterobacteriaceae* were resistant to ampicillin (98.8%), and the least resistance was to piperacillin (3.7%). Also, most isolates were resistant to cefazolin, cefixime, and co-trimoxazole. Among third generation cephalosporins, the highest resistance was observed to ceftriaxone and the least resistance was to ceftizoxime. Out of 19.3% of isolates were resistant to imipenem. The rates of resistance in nosocomial infections were higher than the rates in community-acquired infections.

Conclusion: The prevalence of multidrug resistant *Enterobacteriaceae* is increasing both in community-acquired and hospital-acquired infections. Because of probable increasing resistance to fluoroquinolones and carbapenems, reassessment of resistance of *Enterobacteriaceae* should continue in future years.

Keywords: *Enterobacteriaceae*, antimicrobial resistance, nosocomial infection

The Effect of Ag, Au and Tio_2 Nanoparticles on Gram-Negative Bacilli Capable of Extended-Spectrum β-Lactamase Enzyme Production

Monir Doudi[1], Marziyeh Karami[2]

Abstract

Background: Antimicrobial resistance in hospital pathogens is an important concern. It can cause longer hospitalization costs, mortality and morbidity in hospitalized patients. The aim of this study was to separate and identify gram-negative bacilli capable of ESBLs production and to study the effect of MIC Ag, Au and Tio_2 nanoparticles on Bacterial strains.

Methods: A total of 300 clinical samples in several hospitals of Isfahan city were studied during six mounts in 1390. Two hundred eighty six gram-negative bacilli containing ESBL were separated. The ESBL assay was performed by disk diffusion method. Additionally, ESBLs production was examined by using the standard ESBL disc and DDT (Double Disk approximation Test) procedures. The ESBL producing bacteria were then subjected to increasing concentrations of Ag, Au and Tio_2 nanoparticles (12.5, 25, 50, 100, 200, 400, 500 ppm) with 10nm diameter from Nutrino Company in Tehran.

Results: From the total of 289 patients studied, 200 (%69/9) had the gram-negative bacilli containing ESBL isolated from their urine infection samples. The most prevalent bacteria were identified as *Klebsiella pneumonia*. Their resistance was to antibiotics specifically. All bacteria were sensitive to Ag, Au and Tio2 nanoparticle solutions with density of 100, 200 and 500 ppm, respectively.

Conclusion: The results seemed to indicate a direct correlation between Ag, Au and Tio_2 nanoparticles solution concentration and the diameter of growth zone for ESBL producing bacteria. The nano-silver was the most potent in comparison to Au and Tio_2 nanoparticles.

Keywords: Gram-negative bacilli, ESBLs, Ag, Au, Tio_2 nanoparticles

[1]Department of Microbiology, Falavarjan Branch, Islamic Azad University, Falavarjan, Isfahan, Iran
[2]Young Researchers Club, Falavarjan Branch, Islamic Azad University, Isfahan, Iran

Pulsed-Field Gel Electrophoresis Genotyping of the Most Common Bacterial Isolates from Renal Transplant Recipients

Maryam Keshtvarz[1], Mohammad Reza Pourmand[1], MaliheTalebi[2], Gholamreza Pourmand[3], RaminYaghubi[4], Mojtaba Anvarinejad[5], Samin Zamani[2]

[1]Department of Pathobiology, School of Public Health, Tehran University of Medial Sciences
[2]Department of Microbiology, Faculty of Medicine, Tehran University of Medical Sciences
[3]Urology Research Center, Tehran University of Medial Sciences
[4]Shiraz Transplant Research Center
[5]Professor Alborzi Clinical Microbiology Research Center, Shiraz University of Medical

Abstract

Background: Urinary tract infection (UTI) is one of the most common complications of renal transplantation which has serious consequences. The aim of this study was to assess UTI in renal transplanted patients and use the PFGE method to obtain the genetic pattern of the most common cause of it.

Methods: In this study, bacterial urinary tract infection in renal transplant recipients was determined. One hundred and seventy three patients were assessed. Susceptibility of all the isolates to different antibiotics was determined by agar disk diffusion method. Then genetic pattern of the commonest isolated bacteria was obtained by PFGE and compared with patterns of antibiotic resistance.

Results: UTI was observed in 47 patients and the most prevalent microorganism was *E. coli* 18. Most of the isolated bacteria were susceptible to imipenem and resistant to tetracycline and trimethoprim-sulfamethoxazole. 17 patterns of antibiotic resistancy were recognized among 18 *E. coli* isolated by disk diffusion method and 16 DNA profiles detected by PFGE method.

Conclusion: Our study confirmed that antibiogram is needed to find the most effective antibiotics rather than empirical treatment. With regard to high differentiation power of PFGE method, obtained patterns and high diversity of these profiles no epidemic UPEC was determined in the studied population.

Keywords: Urinary Tract Infections, Renal transplantation, *E. coli*, PFGE

Survey on Antimicrobial Resistance Patterns of Normal Flora Bacteria Isolated From Hands and Nose of Nurses in NICU of Shiraz Teaching Hospitals In 2011

Hadi Sedigh Ebrahim Sarie[1,3], Reza Khashei[1], Mahsan Hosseini Alfatemi[1], Mahbobe Nakhzari Moghadam[1], Mehdi Mostafavi[2]

[1]Department of Bacteriology and Virology, School of Medicine, Shiraz University of Medical Science, Shiraz, Iran
[2]Medicine students, Shiraz University of Medical Science
[3]Student Research Committee, Shiraz University of Medical Sciences, Shiraz, Iran

Abstract

Background: The hand and nose of nurses may serve as reservoirs for bacteria causing infections, particularly those caused by multi-drug resistant strains in hospitals. Most of neonatal intensive care unit (NICU) infections are caused by bacteria from the flora of hands and nose of nurses. With respect to these issues, we explored the role of flora bacteria in the hands and nose of NICU nurses.

Methods: Hands and nose samples were taken from 48 nurses and 16 non-patient-care hospital staffs as controls. Swabs were cultured in appropriate media and incubated in aerobic conditions. After standard diagnosis, antibiogram was performed by the disk-diffusion method for most antibiotics.

Results: From nurses 102 Coagulase Negative *Staphylococci* (CNS), 9 *S. aureus* and 36 other bacteria species and from the Controls 47 CNS, 2 *S. aureus* and 3 other bacteria species were identified. The results demonstrated higher rates of CNS bacteria on the hands of controls and also more prevalence of multiple-resistant bacteria (cefoxitin, erythromycin, tetracycline, ampicillin, Trimethoprim/sulfamethoxazole) were found on the hand nurses.

Conclusion: The lower rate of bacteria on the hands of nurses can be attributed to the use of disinfectants by nurses. These products encourage the development of resistant isolates. Resistance by common disinfectant seems to be ambiguous in their use. Less antibiotic resistance in CNS bacteria isolated from samples of nasal controls than their hands were seen. However, more resistance in bacteria isolated from the nasal nurses, which showed that new carriers to multiple-resistance in the relevant sectors.

Keywords: Antibiotic Resistance, normal Flora, neonatal intensive care unit

Assessment of Ethambutol Point Mutation in Various Subtypes of Mycobacterium Tuberculosis Using PCR-RFLP, Allele Specific PCR and Spoligotyping

Zahra Derakhshani nezhad[1], Parisa Farnia[2], Fatemehmaryam Sheikolslami[3], Mehdi Kazempoor[4], Mohammadreza Masjedi[5], Aliakbar Velayati[6]

[1]Mycobacteriology Research Center, NRITLD, Masih Daneshvari Hospital, Shahid Beheshti University of Medical Sciences, Tehran, Iran
[2]Mycobacteriology Research Center, NRITLD, Masih Daneshvari Hospital, Shahid Beheshti University of Medical Sciences, Tehran, Iran
[3]Mycobacteriology Research Center, NRITLD, Masih Daneshvari Hospital, Shahid Beheshti University of Medical Sciences, Tehran, Iran
[4]Mycobacteriology Research Center, NRITLD, Masih Daneshvari Hospital, Shahid Beheshti University of Medical Sciences, Tehran, Iran
[5]School of Medicine and Researcher of National Research Institute of Tuberculosis and Lung Disease, Shahid Beheshti University of Medical Sciences, Tehran, Iran
[6]School of Medicine and Researcher of National Research Institute of Tuberculosis and Lung Disease, Shahid Beheshti University of Medical Sciences, Tehran, Iran

Abstract

Background: Ethambutol [(s, s) - 2, 2 (ethylenediimino) di-1-butanol] is one of the 4 main first line drugs for the treatment of tuberculosis. The most common mutation associated with this drug usually occurs in embB codon 306. EMB resistance is generally linked to multiple-drug resistance (MDR). The aim of this study was to detect EMB resistance by PCR-RFLP and Allele-Specific PCR assay.

Methods: Sputum specimens were collected from 140 patients attending Masih Daneshvari Hospital. Routine diagnostic tests such as smear microscopy and culture were performed on all samples. Drug susceptibility testing was carried out on 106 culture positive specimens. DNA was extracted and mutation in embB306 gene was assessed using PCR-RFLP ,Allele Specific-PCR and Spoligotyping.

Results: Out of a hundred and six culture positive samples, 36 isolate (33.9%) showed resistance to ethambutol by proportional method. With PCR-RFLP method, 14 (25%) and with Allele Specific PCR method, 13 (27.6%) resistance samples were detected. The sensitivity and specificity of ethambutol in the first method were 30.3% and 94.2% and in the second method were 31.4% and 97.1%, respectively. Spoligotyping could identify *Mycobacterium tuberculosis* strains into following subfamilies; Beijing (10; 9.4%), Bovis (2; 1.8%), CAS (24; 22.6%), EAI (1; 0.9%), Haarlem (27; 25.4%), LAM (5; 4.7%), Manu (5; 4.7%), T (27; 25.4%) and U (2; 1.8%). The high frequency of mutation in embB gene was belonged to Haarlem, CAS and T subfamilies.

Conclusion: Based on our results, those strains with no mutation detected by exposed molecular Methods could be results of other mechanisms of resistance investigated.

Keywords: PCR-RFLP, allele Specific-PCR, spoligotyping, ethambutol, embB306

Studying the Effectiveness of Two Common Fluoroquinolones on Mycobacterial Strains Isolated From Patients

Abdonaser Rafi, Seyed Reza Moadab

Research center for TB and pulmonary diseases, Faculty of Medicine, Tabriz university of Medical Sciences, Tabriz, Iran

Abstract

Background: Investigation and study of second-line drugs effects on mycobacterial strains has been of great importance due to prevalence of drug resistance especially multi-drug resistance (MDR) in *Mycobacterium tuberculosis* (MTB) strains in recent years. The objective of this research was to determine drug sensitivity of *Mycobacterium tuberculosis* and *mycobacteria* other than tubercle bacilli (MOTT) strains to two common second-line anti-mycobacterial fluoroquinolones, ofloxacin (OFL) and ciprofloxacin (CIP).

Methods: In this study, the in-vitro activities of two drugs of OFL and CIP, considering the effects of first-line drugs (isoniazid, rifampin, streptomycin and ethambutol) were studied on 100 mycobacterial strains containing 90 MTB and 10 MOTT strains isolated from patients admitted to research center for TB and pulmonary diseases in Tabriz, Iran, by proportion method of drug susceptibility on Lowenstein-Jensen (LJ) medium.

Results: Out of ninety MTB strains, 50 strains that were sensitive to the first line drugs were diagnosed as susceptible to OFL and CIP. Of other forty strains which were resistant to the first line drugs, only one strain was resistant to OFL and 2 strains were found to be resistant to CIP. Of 10 MOTT strains, 4 strains were resistant to OFL and 3 strains were found to be resistant to CIP.

Conclusion: The findings of this investigation revealed that OFL and CIP could be effectively used against MTB and MOTT.

Keywords: MTB, MOTT, drug resistance, fluoroquinolones

Prevalence of Transmitted HIV Drug Resistance in Iran between 2010 and 2011

Fatemeh Jahanbakhsh[1,2], Junko Hattori[3], Masakazu Matsuda[3], Shiro Ibl[3], Seyed-Hamid R Monavari[1], Arash Memarnejadian[4],Mohammad R Aghasadeghi[4], Ehsan Mostafavi[6], Minoo Mohraz[5], Hossein Keivani[1], Wataru Sugiura[3*], Kayhan Azadmanesh[2]

[1]Department of Virology, Tehran University of Medical Science, Tehran, Iran
[2]Department of Virology, Institute Pasture of Iran, Tehran, Iran
[3]Clinical Research Center, Nagoya Medical center, Nagoya, Japan
[4]Department of Hepatitis and AIDS, Institute Pasture of Iran, Tehran, Iran
[5]Iranian Research Center for HIV/AIDS, Tehran, Iran
[6]Department of Epidemiology, Pasteur Institute of Iran, Tehran, Iran

Abstract

Background: Drug-resistant (DR) HIV emerges during antiretroviral treatment (ART), creates concern about widespread transmission of DR-HIV as ART in resource-limited countries. The aim of this study was to determine predominant HIV-1 subtypes and prevalence of DR mutations among antiretroviral-naïve patients in Iran. To monitor transmission of DR-HIV, a threshold surveillance based on the WHO guidelines was implemented in Iran.

Methods: For this DR-HIV threshold surveillance study, blood samples were collected from 50 antiretroviral-naïve HIV-1-infected patients. Antiretroviral-resistant mutations were determined by sequencing HIV-1 protease, reverse transcriptase and integrase regions. The HIV-1 subtype was determined by sequencing p17 and C2-V5 regions of gag and env genes respectively.

Results: Phylogenetic analysis of sequenced regions revealed 45 (95.7%) out of 47 samples, successfully obtained, were CRF35_AD. The remaining two cases were subtype B (2.1%) and subtype CRF01-AE (2.1%). Consistent results were also obtained from Env and Gag sequences. Regarding prevalence of transmitted DR viruses, two cases were found to harbor reverse transcriptase-inhibitor-resistant mutations (4.3%). In addition, thirteen minor protease-inhibitor-resistant mutations listed in the International AIDS Society-USA panel of drug resistance mutations were found; although they were not in the WHO list for surveillance of transmitted mutations. No DR mutations were detected in the integrase region.

Conclusion: Our study clarified that CRF35_AD is the major subtype among HIV-1-infected patients in Iran. According to the WHO categorization method of HIVDR threshold survey, the prevalence of transmitted drug resistant HIV in Iran was estimated as moderate (5-15%).

Keywords: Transmitted HIV drug resistance, molecular epidemiology, Iran, CRF35_AD, threshold survey, WHO

Molecular Analysis of Isolated Toxigenic *Clostridium difficile* Strains from Patients with Nosocomial Diarrhea

Mohammad HosseinSalari[1], Noorkhoda Sadeghifard[2], Mohammadreza Ghasemi[1], Davoud Khatibi[3], Farzaneh Amin Harati[1], Sedigheh Ghorchian[1]

Abstract

Background: *Clostridium difficile* is an identified cause of antibiotic-associated diarrhea, antibiotic-associated colitis, pseudomembranous colitis and nosocomial diarrhea. The aim of this survey was to determine molecular characteristics of isolated toxigenic *Clostridium difficile* from patients with nosocomial diarrhea in Tehran University of Medical Sciences (TUMS) hospitals.

Methods: In this study a total of 1822 stool samples from patients with nosocomial diarrhea, hospitalized in Emam Khomeini and Shariati hospital and Children medical center were collected. Samples were cultured and incubated on a selective cycloserine cefoxitin fructose agar medium (CCFA) in an anaerobic condition, at 37°C for 2 days. Isolated *C. difficile* were characterized by conventional biochemical tests. Bacterial cytotoxicity was assayed on tissue culture. In addition, all strains were typed by PCR-ribotyping method.

Results: Among the total Samples124 toxigenic *C. difficile* (6.8%) were isolated. Results of statistical analysis showed no significant difference between the PCR- ribotyping pattern of toxigenic *C. difficile* isolates and sex and age group of patients ($P>0.05$). A total of 28 different ribotypes were detected only among the clinical isolates. The predominant ribotypes from the clinical isolates were ribotypes 13, 14, and 15, which were accounted for 35.6% of all isolates. Ribotypes 13-17 were five distinct clones that were circulating in all three hospitals.

Conclusion: Findings of this study showed that isolates associated with *Clostridium difficile* nosocomial diarrhea have different PCR- ribotyping patterns. Further studies for evaluating PCR-typing are suggested.

Keywords: Molecular analysis, toxigenic *Clostridium difficile*, nosocomial diarrhea

[1]School of Public Health, Tehran University of Medical Sciences, Tehran, Iran
[2]Faculty of Medicin, Ilam University of Medical Sciences, Ilam, Iran
[3]Yazd (Zarch) Payame Noor University, Yazd, Iran

Antibiotic Resistance and Genotypic Characterization of MDR *Enterococcus faecium* Isolates from Clinical and Hospital Environmental Samples by PFGE in Tehran, Iran

Leili Shokoohizadeh[1], Mohammad Reza Zali[2], Ashraf Mohabati Mobarez[1], Masoud Alebouyeh[2], Reza Ranjbar[3], Zeinab Ahmadi[3]

[1]Bacteriology dept, Medical faculty, Tarbiat Modares University, Tehran, Iran
[2]Research Center for Gastroenterology and Liver Diseases, Shahid Beheshti University of Medical Sciences, Tehran, Iran
[3]Molecular Biology Research Center, Baqiyatallah University of Medical Sciences of Tehran, Iran

Abstract

Background: Multi-Drug-Resistant (MDR) *Enterococcus faecium* strains increase dramatically in hospital settings throughout the world. Understanding the exact modes of nosocomial transmission of these strains is important. The aim of this study was to determine the prevalence, patterns of antibiotic resistance, and genetic linkages between the clinical and environmental strains of *E. faecium* isolated in different hospitals of Tehran, Iran.

Methods: During September 2010 to August 2011, the clinical and environmental samples were obtained from different hospitals. All the *E. faecium* isolates were identified according to standard biochemical and molecular identification Methods. Resistance patterns for 11 antibiotics and MIC value for vancomycin were determined and presences of Van A and Van B genes among vancomycin resistant *E. faecium* (VRE) isolates were investigated. Genetic linkages of the isolates were tracked by pulsed-field gel electrophoresis (PFGE).

Results: Out of 70 identified E. faecium isolates, 84.28 % and 15.71 % belonged to clinical and environmental samples, respectively. MDR phenotype was detected in 96.6% and 54.5% of them, in the same order. Thirty five *E. faecium* isolates were resistant to vancomycin with an MIC_{50} of 128 mg/L resistant to teicoplanin, ampicillin, gentamicin, ciprofloxacine, tetracycline and erythromycin was the most frequent antibiotic resistance pattern Analysis of PFGE data showed 17 diverse clonal types with four shared pulsotypes. Most of related pulsotypes belonged to the same hospitals.

Conclusion: Emergence of VR *E. faecium* strains with the same clonal types is an alarm in hospitals of Tehran, Iran, because of their high risk MDR phenotypes.

Keywords: E. faecium, multi-drug resistance, PFGE, hospital

Anti-Fungal Susceptibility Pattern of Yeast Colonization from Onco-Hematological Patients in Shiraz by E-test Method

Zahra Jafarpour[1], Parisa Badiee[1], Soheila Zareifar[2], Pedram Haddadi[2], Hadis Jafarian[1]

Abstract

Background: Fungal infections are a major cause of morbidity and mortality in patients with onco-hematological diseases. Despite antifungal therapy, it is usually fatal due to delay in diagnosis. Practically, all antifungal therapies are empirical. This study aimed to evaluate the incidence of fungal colonization in such patients over a period of twelve months and alternatively, to determine susceptibility patterns of yeast colonization by E-test.

Methods: In total, 779 onco-hematological patients were enrolled. The mean age was 5.6 year (ranged from 3months to18 years), mean neutrophil count was 4100 and male/female ratio was 406/373. ALL was the most common underlying disease (45.7%). Briefly, 1125 clinical samples including urine and swabs from different sites (oral, rectum and nose) were cultured. Susceptibility testing of anti-fungal drugs was done by E-test method.

Results: As revealed a hundred sixty nine cultures (15.02%) were positive and 45.4% of the patients exhibited one or more sites of colonization. The yeasts were mainly isolated by *Candida spp*, consisting sequentially *Candida albicans* (59.2%), *Candida kruzei* (6.57%), *Candida glabrata* (5.26%), *Candida tropicalis* (3.94%), and other species of *Candida* (25.03%). The most resistant following antifungal drugs were Itraconazole (73%) and Fluconazole (37.8%), while caspofungin was the most effective agent.

Conclusion: Colonization of *Candida* has been shown to precede invasive fungal infections in many instances especially in onco-hematological patients. Early detection and identification of fungal infection is essential. Therefore, studying *Candida* colonization and analysis of anti-fungal susceptibility patterns is necessary for appropriate and timely management of life threatening fungal infections.

Keywords: *Candida* colonization, onco-hematological patients, E-test

[1]Professor Alborzi Clinical Microbiology Research Center, Shiraz University of Medical Sciences, Shiraz, Iran
[2]Department of Pediatrics, Hematology Research Center, Shiraz University, Shiraz, Iran

Rigid Report for an Antimicrobial Resistance Surveillance Study among Six ICUs in Tehran, Iran

Somayeh Jahani Sherafat, Maryam Razaghi, Sima Seyed Javadi, Elahe Tajeddin, Marjan Rashidan, Masoud Alebouyeh, Ehsan Nazemalhosseini Mojarad, Mohammad Reza Zali

Gastroenterology and Liver Diseases Research center, Shahid Beheshti University of Medical Sciences, Tehran, Iran

Abstract

Background: Nosocomial infections constitute an important health problem in hospitalized patients especially in developing countries. Present study aimed to analyze Intensive Care Units (ICUs) of six different hospitals to determine prevalence of nosocomial infections and to detect responsible bacteria and their resistance profiles.

Methods: This study was performed in six ICUs in Tehran, Iran. Clinical samples were obtained from patients with nosocomial infections. All of bacterial isolates were identified according to standard biochemical identification schema. Diagnosis of infections was based on modified CDC criteria. Resistancy profiles of the identified bacteria were assessed by means of vast numbers of conventional anti-microbes, recommended by NNIS system.

Results: *Acinetobacter spp*. as the most common isolated organism showed 95.5% resistance to imipenem. All the *S. aureus* isolates were resistant to oxacillin (methicillin-resistant *S. aureus*, MRSA). Twelve (24.5%) of the *Enterococcus spp*. isolates were resistant to vancomycin (VRE). Isolates of *P. aeruginosa* were resistant to cefepime, imipenem and ciprofloxacin with prevalences of 48.1%, 44.4 % and 29.6% respectively. Linezolid and vancomycin were proposed as the most effective drugs in 15 tested antibiotics against these bacteria. Among the isolated bacteria 68.15% showed MDR phenotype. Pneumonia was the most frequent infection among these ICUs.

Conclusion: Dominancy of MRSA, VRE, 3th generation cephalosporin-resistant *Enterobacteriaceae* and imipenem or ciprofloxacin-resistant *P. aeruginosa* and *A. baumannii* among the studied ICUs are of great concern. For these reasons designing programs for controlling the emergence of new resistant organisms and eradication of hyper resistant clonal isolates seems necessary.

Keywords: Nosocomial infections, *Acinetobacter*, MDR

Frequency of Vancomycin-Resistant MRSAs Isolated from Nasal Carriage among Hospitalized Patients of Imam Reza Hospital, Kermanshah, 2011

Parviz Mohajeri[1], Ramin Abiri[1], Amir-Houshang Alvandi[1], Mansour Rezaei[2], Omar Ghaderi[3]

[1] Department of Microbiology, Faculty of Medicine, Kermanshah University of Medical Sciences, Kermanshah, Iran
[2]Department of Biological Statistics, Faculty of Medicine, Kermanshah University of Medical Sciences, Kermanshah, Iran
[3]Student Research Committee, Kermanshah University of Medical Sciences, Kermanshah, Iran

Abstract

Background: *Staphylococcus aureus* is known as a potential pathogen that can cause various infections. *Staphylococcus aureus* resistancy to vancomycin is also a major cause of nosocomial infections and community acquired with multiple resistant to a wide range of antibiotics such as beta lactams, aminoglycosides, tetracyclines, fluoroquinolone and macrolides. Today, various genotypic and phenotypic Methods to detect VRSA are presented.

Methods: Eighty five MRSA isolated from nasal patients hospitalized in Imam Reza Hospital was studied with micro-dilution tests, E-test and PCR against vancomycin.

Results: None of the isolates were completely resistant to vancomycin, but 39 isolates (45.9%) were diagnosed as hVRSA strains. Minimum and maximum MICs with micro-dilution Methods and E-test were 0.125 and 4, respectively. Also population analysis method was used to identify strains with heterogeneous resistance to vancomycin.

Conclusion: Although VISA and VRSA strains were not found in this study and this one promising results in treating clinical infections caused by *Staphylococcus aureus* in our society, but on the other hand, frequency of hVISA was remarkable. This alarm may be dealing with more resistant isolates (VISA and VRSA) in the near future in our country.

Keywords: *Staphylococcus aureus*, vancomycin, MIC, PCR

Molecular Epidemiology of *Human Respiratory Syncytial Virus* in Iran

Ebrahim Faghihloo, Maryam Naseri, Jila Yavarian and Talat Mokhtari-Azad

Department of Virology, Faculty of Public Health, Tehran University of Medical Sciences, Tehran, Iran

Abstract

Background: *Human respiratory syncytial virus* is the most important viral agent responsible for acute lower respiratory tract diseases in infants and young children worldwide. There are limited data of HRSV genotypes from developing countries. The aim of this study was to investigate HRSV genotypes in years 1386, 1388, 1389 and 1390 in Iran.

Methods: In this study, RT-PCR for second hyper variable region of the HRSV G glycoprotein was performed on 347 throat swabs collected from children less than 5 years of age with acute respiratory symptoms.

Results: Of three hundred forty seven throat swabs collected from children with acute respiratory symptoms, 84 (24.2 ٪) were positive for HRSV. Phylogenetic analysis revealed that HRSV-positive samples clustered in genotypes GA2 (56), GA1 (19) and GA5 (1) of subgroup A and genotype BA (8) of subgroup B.

Conclusion: Our results revealed that HRSV prevalence in Iran is similar to that found in studies in both developing and industrialized countries; 21 ٪in Austria, 28٪ in Brazil, 27/08٪ in India and 25/46٪ in Jordan. These results showed that subgroup A strains were more prevalent than subgroup B viruses, and GA2 genotype was the predominant genotype in years 1386, 1389 and 1390 and GA1 was predominant genotype in 1388.

Keywords: HRSV, molecular epidemiology, genotype

HTLV-1 Epidemiology in Torbat Heydarie, Khorasan Razavi

Majid Hasanzadeh, Hosain Rajabzadeh, Sara Rajabzadeh

Torbat Heydarie University of Medical Sciences, Faculty of Medicine, Torbat Heydarie, Iran

Abstract

Background: HTLV-1 infection is endemic in northeast of Iran. Using ELISA method, it was shown that prevalence of HTLV-1 infection is high in general population of Torbat Heydarie, an old city in this area. This study was designed to assess HTLV-1 epidemiology using confirmatory western-blot (WB) test, also evaluating risk factors in positive cases.

Methods: All patient samples referred to the Jihad Daneshgahi laboratory in Torbat Heydarie evaluation center of HTLV-1 were tested with WB for ELISA positive cases. A questionnaire about risk factors of infection was completed for all cases. Data was analyzed by SPSS 13.0.

Results: HTLV infection was positive in 7.3% (35/482) of participants according to the results of ELISA and WB test. Relation between age, family size and number of children, monthly income and HTLV infection was significant. However, gender, birthplace, race and marital status were not significantly related to the infection.

Conclusion: HTLV-1 infection is highly endemic in Neyshabor with a prevalence rate of much higher than what was assumed before. Thus, it is necessary to have effective strategies for managing the situation.

The Prevalence of Community Acquired Methicillin-Resistant *Staphylococcus aureus* among Children Hospitalized for Invasive Staphylococcal Infections in Mashhad, Iran

Reza Karami, Mohammad Saeed Sasan[1], Nahid Donyadide[2], Mahboobeh Naderi Nasab, Toktam Mohammadpour

Pediatric Infectious Disease, Department of Pediatrics, Mashhad University of Medical Sciences, Mashhad, Iran

Abstract

Background: Diseases due to community acquired methicillin resistant *Staphylococcus aureus* (CA-MRSA) are increasingly frequent worldwide.

The aim of this study was to determine the frequency of methicillin-resistance among CA-isolates of *S. aureus* in children admitted in pediatric ward of Imam Reza and Ghaem hospitals.

Methods: This was a retrospective study accomplished by collection of all positive cultures of *S. aureus* from sterile sites of body (blood, joint, bone and lymph node aspiration). Antibiogram was done with disk diffusion method. Differentiation between community and nosocomial acquired *S. aureus* was done with reference to the files of patients according to the criteria of Kaplan's study.

Results: From March 2006 up to March 2007, we collected forty four samples of *S. aureus* from sterile sites of body of which 16 samples were community acquired and 15 nosocomial. Thirteen samples were omitted because of insufficient data for detection of community acquired or nosocomial origin of the organisms. Ten out of sixteen (62.5%) CA-SA and thirteen out of fifteen nosocomial isolates were resistant to methicillin. CA-MRSA showed high frequency of resistance to non-β-lactam antibiotics (70% for erythromycin, 50% for co-trimoxazole and gentamicin and 40% to ciprofloxacin).

We performed D-test, with closure of clindamycin and erythromycin disks, for half of the CA-MRSA samples which were resistant to erythromycin and none of them showed inducible resistance to clindamycin.

Conclusion: Most (62.50%) of community-acquired *Staphylococcus aureus* isolates in children hospitalized in pediatric ward of Imam Reza Hospital were resistant to methicillin. According to this study we recommend that in any invasive disease suspected to be caused by *S. aureus* (sepsis, endocarditis, septic arthritis, osteomyelitis and pneumonia with empyema) primary treatment should be with medicines like vancomycin, linezolid, daptomycin and clindamycin with or without cloxacillin.

Keywords: *S. aureus*, methicillin resistance, community acquired, children

Detection of Mutations in inhA-15 C to T in Clinical Isolates of *Mycobacterium Tuberculosis* Resistant to Isoniazid by MAS-PCR and Sequencing Methods

Roya Abkar[1], Mohamad Reza Zolfaghari[1], Mana Shojapoor [2], Azam Ahmady[3], Mohamad Arjomandzadegan[3]

[1]Department of Microbiology, Qom Branch, Islamic Azad University, Qom, Iran
[2]Research Center of Molecular Medicine, Arak University of Medical Sciences, Arak, Iran
[3]Tuberculosis and Pediatric Infectious Diseases Research Center, Arak University of Medical Sciences, Arak, Iran

Abstract

Background: Isoniazid is the first-line TB drug treatment. Resistance to Isoniazid has created many problems in the treatment of tuberculosis. Mutations that cause resistance to isoniazid (INH) are mainly occurred in codon 315 of katG gene and mabA-inhA regulatory region (-15). In this study, the need to detect mutations in mabA-inhA promoter for routine works of rapid detection of isoniazid resistance was examined.

Methods: From ninety eight clinical strains of *Mycobacterium tuberculosis* in the Tuberculosis Research Center, Arak, 48 strains were examined for mutations in the inhA-15 regulatory region with MAS-PCR and sequencing molecular Methods. Specific primers were used for MAS-PCR that could represent mutant form by creating a 248bp band in all samples and a 174bp band in the mutant strains. The results were compared with sequencing.

Result: Of forty eight strains, thirteen strains (27%) were susceptible and thirty five strains (73%) were resistant to isoniazid. From thirty five isoniazid resistant strains, 5 isolate (14.3%) and from 13 susceptible strains, one strain (7.7 %) had a mutation in the inhA-15. Results of Sequencing showed full compliance with the MAS-PCR results.

Conclusion: The MAS-PCR is a simple and suitable method for rapid detection of isoniazid resistance in clinical strains of *Mycobacterium tuberculosis* in inhA-15 region. Based on the results and the literature review, it is concluded that this test is valuable for determining isoniazid resistance mutations, although it does not provide any information leading to detection of mutation sink at G315.

Keywords: *Mycobacterium tuberculosis*, Drug resistant, Isoniazid, inhA-15

Characterization of Extended-Spectrum Beta-Lactamase-Producing *Escherichia Coli* and *Klebsiella Pneumoniae*

Shahnaz Armin, Azadeh Kiomarci, Fatemeh Fallah, Hossein Rahbar

Pediatric Infections Research Center, Shahid Beheshti University of Medical Sciences, Tehran, Iran

Abstract

Background: Extended spectrum B-lactamase (ESBL)-producing organisms pose unique challenges to clinical microbiologists and clinicians. Although ESBL is a global problem, specific enzymes and genotypes can be different in geographic regions. Knowledge of local resistance patterns is an important issue for clinicians. The aim of this study was to describe phenotypic and genotypic characteristics and antibiotic sensitivity of ESBLs in a pediatric hospital in Iran.

Methods: One-hundred and eighty six extended-spectrum beta-lactamase (ESBL) producer *E. coli* and *Klebsiella pneumoniae* strains isolated from hospitalized children were analyzed for their antibiograms, presence of AmpC genes and their genetic patterns.

Results: A total of 186 isolates of ESBL producer *E. coli* (82.8%) and *K. Pneumonia* (17.2%) were obtained from urine (62.4%), blood (16.1%) and stool (21.5%) samples. Rates of blaTEM, blaCTX-M, blaSHV and blaPER genes in isolates were 154 (82.8%), 147 (79%), 55 (29.6%) and 22 (11.8%), respectively. Imipenem and meropenem were the most effective antibiotics. Rates of resistance to other antibiotics were as follows: cotrimoxazole (83.9%), ciprofloxacin (47.3%), amikacin (36.6%) and gentamicin (33.9%).

Conclusion: In our hospital, the most frequent gene was blaTEM**.** According to the antibiotic resistance results, carbapenems are the best choice in treating conditions caused by ESBL producing organisms.

Keywords: Beta-Lactamase, *Escherichia Coli*, *Klebsiella pneumoniae*

Evaluation of Hand Washing among Nurses and its Role in Prevention of Nosocomial Infections in ICU

Alireza Ghahramani, Roya Rezaei, Irandokht Allahyari

Ardebil Social Security Organization and University of Medical Sciences, Ardabil, Iran

Abstract

Background: Nosocomial infections are considered as infections that occur 48 to 72 hours after admission. Intensive cares have the highest prevalence of nosocomial infection. Previous studies have shown the importance of hand washing to prevent infection in hospitalized patients in ICU. The purpose of this study was to evaluate hand washing in the ICU nurses of Ardebil hospitals.

Methods: This study is a descriptive study and the study population included all nurses (70 persons) working in intensive care units of Ardebil hospitals. The Data collection tool was self-made questionnaire demographic information, assess knowledge and performance check list. Questionnaire validity confirmed by content validity, reliability of knowledge by test-retest and performance simultaneous observation by two observers. Data correlation coefficient test and descriptive statistics were analyzed by ANOVA in SPSS software.

Results: The majority of subjects (44/3 %) had moderate knowledge. Hand washing in 10% of poor performance, 41/4% average performance and48/6% had a good performance. There was not statistically significant relationship between age, work experience and retraining hour and nurse's knowledge and practice.

Conclusion: Considering the important role of nurses in hospital infection control, continuous training and assessment of their activities is recommended to prevent infection.

Keywords: Knowledge, handwashing, nursing staff, nosocomial infection

Detection of Legionella Pneumophila by PCR and Urinary Antigen in Patients with Neutropenic Fever

Nastaran Farzi[1], Leili Chamani-Tabriz[2,3], Farzaneh Hosseini[1]

[1]Department of Microbiology, Islamic Azad University North Tehran branch, Tehran, Iran
[2]Reproductive Biotechnology Research Center, Avicenna Research Institute (ACECR), Tehran, Iran
[3]Infection Diseases and Tropical Medicine Research Center, Shahid Beheshti University of Medical Sciences, Tehran, Iran

Abstract

Background: *Legionella pneumophila* is a thin, aerobic, pleomorphic, flagellated, Gram-negative bacterium which belongs to the genus Legionella and is the causative agent of legionellosis or Legionnaires' disease. Legionellosis occurs both sporadically as well as outbreaks and is mainly found in immune-compromised individuals, including neutropenic patients. The main goal of this present study was to find out the presence of *L. pneumophila* in patients with neutropenic fever.

Methods: In this study, serum and urine specimens were obtained from 80 patients with confirmed neutropenic fever disease. For detecting *L. pneumophila* antigen in all urine samples sandwich ELISA was used. In addition, *L. pneumophila*'sMIP gene was detected in both urine and serum samples by PCR method.

Results: PCR assays were based on the mip gene (mocrophage infectivity potentiator). The samples were collected from neutropenic patients with fever. Among urine samples 36.25% were tested as positive in MIP PCR. In comparison, polymerase chain reaction was estimated to be 7.5% in samples serum. Moreover, 6.25% of 80 urine specimens from patients with neutropenic fever were positive using enzyme immunoassay (EIA) kit.

Conclusion: Our findings revealed that *L. pneumophila* may play an important role among the respiratory pathogens in patients with suppressed immunity. Our results also have shown that urinary antigen detection and serum and urine PCR are valuable tests in the acute phase of disease.

Keywords: *Legionella pneumophila*, Neutropenic, Polymerase Chain Reaction, Enzyme Immunoassay, Bacterial Infections

Application of Pulsed Field Gel Electrophoresis to Study Genetic Diversity of *Mycobacterium Tuberculosis* Isolated from Tuberculosis Patients in Khuzestan Province, Iran

Azardokht Khosravi[1,2], Shideh Vatani[1], Mohammad Mehdi Feizabadi[3], Effat Abasi Montazeri[1], and Abbas Jolodar[4]

[1]Department of Microbiology, School of Medicine, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran
[2]Infectious and Tropical Diseases Research Center, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran
[3]Department of Microbiology, School of Medicine, Tehran University of Medical Sciences, Tehran, Iran
[4]School of Veterinary Medicine, Shahid Chamran University, Ahvaz, Iran

Abstract

Background: *Mycobacterium tuberculosis* (MTB) genotyping can effectively improve TB control program by controlling the disease transmission.Pulsed field gel electrophoresis (PFGE) is a particular powerful tool for determination of clonal identity of bacteria providing information for understanding and controlling the spread of disease.
The aim of present study was to investigate the genetic diversity of MTB strains in Khuzestan province by PFGE technique.

Methods: In total 80 MTB positive cultures were obtained from tuberculosis patients. For PFGE agarose plugs were prepared and after a cell lysis step, they were digested by restriction enzymes of DraI and XbaI according to the standard protocol. Plugs containing digested DNA were then loaded on agarose gels and run using contour-clamped homogenous electric fields.The products were stainedwith ethidium bromide and observed using a gel documentation apparatus.

Results: Fifty and thirty eight distinct DNA banding patterns were obtained by digestion of DNA with DraI and XbaI restriction enzymes respectively. Patterns comprised 17 different clusters with cluster 1 as the major with 6 strains content. Digestion with DraI yielded 15-20 DNA fragments in size of 50-485 kb, while digestion by XbaI produced DNA fragments with smaller size of 50-242 kb. DNA binding patterns could determine some of the epidemiological criteria of tested MTB strains.

Conclusion: PFGE as a robust and reproducible protocol is a useful tool for molecular epidemiology investigation of MTB. However, for higher discrimination of clusters, the application of complementary techniques may be required.

Keywords: *Mycobacterium tuberculosis*, tuberculosis, PFGE, genotyping

Molecular Characterization of Clindamycin Constitutive and Inducible Resistant *Staphylococcus aureus* Strains Isolated from Noses of Carriers

Alireza Japoni-Nejad[1,2], Mohsen Rezazade[1,2], Hamid Kazemian[2], Nasim Fardmousavi[2], Ehsanollah Ghaznavi-Rad[2]

Abstract

Background: Increasing *Staphylococcus aureus* infections and changes in antimicrobial resistance patterns have led to renewed interest in the use of lincosamide– streptogramin B (MLSB) antibiotics for treatment. In Iran no study has ever focused on molecular epidemiology of community-acquired *Staphylococcus aureus* isolate. The aim of this study was to determine the molecular typing and prevalence of the macrolides-lincosamides-streptogramins B (MLSB) resistance in community associated *S. aureus* isolated from healthy students at Arak University of Medical Sciences.

Methods: Five hundred sixty eight healthy students were subjected to this study. All samples were examined by *S. aureus* specific isolation procedures. D-test was performed to determine various phenotypes as well as spa typing done for molecular typing of these strains.

Results: Of the total five hundred sixty eight, eighty four samples had community acquired *Staphylococcus aureus* in which six (7%) were Methicllicin-resistant *Staphylococcus aureus* (CA-MRSA) and seventy eight (93%) were Methicillin-sensitive *Staphylococcus aureus* (CA-MSSA). Of the eighty four *S. aureus* strains, eight (9.5%) showed constitutive resistance with spa type t660, t701, t304, t5598, t012, t3204, t084 and t1944. Two strains (2.5%) demonstrated inducible resistance with spa type, t9024 and t077 and two strains (2.5%) was D-test negative with spa type t084 and t1149. Seventy two (85.5%) strains illustrated susceptible Phenotype. Among CA-MRSA isolates, two strains had constitutive resistance and four remaining CA-MRSAs had susceptible phenotypes.

Conclusion: The results of this study indicated that in community associated *S. aureus* strains constitutive MLSB resistance rate is higher than the rate of inducible resistance. Presence of inducible resistance to clindamycin in CA-MRSA strains demonstrates that D-test should be performed to detect this type of resistance. Among all isolates with inducible and constitutive resistance, D zone negative strains had a different molecular typing.

Keywords: *Staphylococcus aureus*, D-test, inducible clindamycin resistance, spa type

[1]Student research committee, Arak University of medical sciences, Arak-Iran
[2]Department of Medical Microbiology, Faculty of Medicine, Arak University of Medical Sciences

Evaluation of Semi-Nested PCR Method for Diagnosis of Mucorales in Blood and Tissue Specimens from Patients with Suspected Invasive Fungal Infections

Amir Arastefar, Parisa Badiee, Hadis Jafarian

Professor Alborzi Clinical Microbiology Research Center, Shiraz University of Medical Science, Shiraz, Iran

Abstract

Background: There is no serological method for detection of mucormycosis, and the routine Methods including direct microscopy and culture of tissues, which need invasive Methods for processing the tissue sample. The aim of this study was to evaluate direct microscopic examination and comparison with culture, and PCR for the diagnosis of Mucorales in blood and tissue specimens.

Methods: Thirty one patients with suspected invasive fungal infection (IFI) were subjected to collection of blood and tissue specimens. In this study, direct smear was considered as gold standard, and blood and tissue cultures and PCR were compared.PCR test was performed on extracted DNA of blood and tissue specimens, and respective primers targeted 18S rDNA of Mucorales, in a semi nested method.

Results: Of thirty one patients, seven were positive by direct smear, six by PCR, and five by culturing tissue specimens, with their etiologic agents *Mucor* and *Rhizopus*. However, culturing and PCR results for all blood specimens were negative. The specificity, sensitivity, positive and negative predictive value for culture and PCR of tissue samples were 100%, 70%, 100%, 92%, and 96%, 86%, 86%, and 96%, respectively.

Conclusion: PCR is more sensitive than tissue or blood culture Methods. Unfortunately, there is no alternative method for the examination of patients by direct smear, which is an invasive method. Molecular Methods could be helpful in such cases.

Keywords: Invasive Fungal Infection, Mucorales, Semi-Nested PCR, 18S rDNA

Prevalence and Risk Factors of *Clostridium Difficile* Infection in Iranian Hospitalized Patients

Mehdi Azami, Shohreh Farshad, Gholamreza Pouladfar, Mazyar Ziyaeyan, Abdolvahab Alborzi, Maneli Aminshahidi

Professor Alborzi Clinical Microbiology Research Center, School of Medicine, Shiraz University of Medical Sciences, Shiraz, Iran

Abstract

Background: *Clostridium difficile* is a frequently identified cause of nosocomial gastrointestinal diseases. It has been proved to be a causative agent in antibiotic-associated diarrhea, antibiotic-associated colitis, and pseudomembranous colitis. This study was aimed to determine the prevalence and risk factors of *C. difficile*-associated diarrhea (CDAD) in hospitalized patients with nosocomial diarrhea in Shiraz, Iran.

Methods: In this study a total of one hundred twenty two stool samples from patients with nosocomial antibiotic-associated diarrhea that were admitted in to the ICUs (41), surgery (16) and organ transplantation wards (65) during November to June 2012 were collected in Nemazee hospital, Shiraz, Iran. All stool samples were cultured on a selective Cycloserine Cefoxitin Fructose Agar (CCFA) medium. Grown isolates were then analyzed by cytotoxicity assay and enzyme immune assay (EIA) for detection and conformation of toxins.

Results: The mean ± SD of age groups was 49.4 ± 13.8 and 75 (61.5%) patients were male. Nine (7.4%) cases of nosocomial diarrhea were diagnosed as CDAD which means all isolates were toxigenic. Five out of sixty five organ transplanted patients and four out of forty one hospitalized patients in ICU wards had developed CDAD. Neither of samples obtained from surgery ward were infected with C. difficile. Ceftazidime and ampicillin-sulbactam were the most common antimicrobial drugs used. Multivariate analysis showed that use of diapers, antibiotics and immunosuppressive therapies were significantly associated with CDAD development ($p<0.05$).

Conclusion: Hospital transmission of *C. difficile* has commonly occurred supporting infection-appropriate measures directed toward the reduction of CDAD.

Keywords: *Clostridium difficile*, antibiotic associated diarrhea, nosocomial diarrhea

Detection of Extended Spectrum β- Lactamases of VEB and PER Genes in Clinical Isolates of *Pseudomonas Aeruginosa*

Zahra Karimitabar, Mohammad Yousef Alikhani

Abstract

Background: *Pseudomonas Aeruginosa* is a leading cause of nosocomial infections, including pneumonia, urinary tract infections, and bacteremia. *P. aeruginosa* is responsible for 10–15 % of nosocomial infections worldwide. Infections can be particularly severe in patients with impaired immune systems, neutropenic or cancer patients, for instance. Resistance of *Pseudomonas Aeruginosa* strains to the broad-spectrum cephalosporins may be mediated by extended-spectrum b-lactamases (ESBLs). The aim of this study was to determine *P. aeruginosa* antibacterial resistance patterns to the most available antibiotics and to investigate the prevalence of ESBLs producing strains by means of PER-1 and VEB genes.

Methods: A total of 106 clinical isolates of *P. aeruginosa* were studied. The isolates were collected from two university hospitals in Hamadan, Iran, during seven months. The susceptibility of *P. aeruginosa* isolates to 12antimicrobial agents was determined by disc diffusion method and was interpreted according to the CLSI recommendations. ESBL producing strains had been detected by combined disk test and the presence of PER-1 and VEB genes was demonstrated by PCR.

Results: Antibiotic resistance rates against broad-spectrum cephalosporins and monobactames were as follows: cefepime 97%, cefotaxime 92.5% ceftazidime 51%, and aztreonam 27%. Ciprofloxacin (91.5%), imipenem (84.9%) and meropenem (82.07%) were the most effective anti-*Pseudomonas* agents. The results revealed that ninety four (88.7%) isolates were multidrug-resistant and sixty (58.25%) were ESBL positive. Sixteen (26.6%), nine (15%) and three (5%) strains among sixty ESBL-producing strains were positive for blaPER-1, blaVEB and blaPER-1 / blaVEB respectively.

Conclusion: This study highlighted the need to establish antimicrobial resistance surveillance networks for *P. aeruginosa* to determine the appropriate empirical treatment regimen. Bacterial strains resistant to most classes of antibiotics will continue to emerge unless inappropriate uses of drugs decreases and continuous education about infection control maintains. High prevalence of multidrug resistance and production of ESBLs in *P. aeruginosa* isolates obtained from patients confirmed that protocols considering these issues should be more attended in hospitals.

Department of Microbiology, School of Medicine, Hamadan University of Medical Sciences

Keywords: *Pseudomonas aeroginosa*, Antibiotics Resistance, Multidrug resistance, ESBL

Evaluation of EBV Load in Kidney Transplant Patients before and Four Months after Operation

Ali Dehghani Nazhvani[2], Gita Rezvani[1], Mojtaba Habibagahi[2], Neda Pazhoohi[2], Razieh Sedaghat[2], Fatemeh Karimi[2], Elham Ansari[2]

[1]School of Dentistry, Shahed University of Medical Sciences, Tehran, Iran
[2]School of Dentistry, Shiraz University of Medical Sciences, Shiraz, Iran

Abstract

Background: In order to prevent transplant rejection, we have to suppress immune system which will increase the risk of EBV-infected cells proliferation and related diseases. Thus by evaluating and comparing EBV content in transplant receivers' saliva before and after operation, we were looking for a non-aggressive method to measure the amount of EBV and possibility of emergence of related diseases.

Methods: Twenty four hours prior to transplant operation, 2 ml of saliva from thirty nine kidney receivers was collected by using needle-less syringes in Nemazee hospital, Shiraz.

Second samples were taken three to seven months (on average four months) after operation and were kept at -70˚c. Thirty nine pairs of collected samples were evaluated and statistically analyzed by Real time PCR method for detection of viral particles.

Results: EBV Load increased in thirty two samples after transplant and there was a significant difference between the EBV levels of samples taken before and after operation.

However, there was no significant relation between EBV content before and after operation and sex, age and frequency of dialysis before operation.

Conclusion: The amount of EBV increased after receiving transplant. Therefore it is suggested to evaluate patients considering any oral lesions related to EBV. Hence EBV Load measurement in the saliva of these patients might be helpful using Quantitative Real Time PCR.

Keywords: Kidney transplant, quantitative Real Time PCR, saliva sample, *Epstein Bar Virus*

Evaluation of In Vitro Efficacies of Some Current Disinfectants against *Hepatitis B* Virusin Iran

Fatemeh Mazhari[1], Kiarash Ghazvini[2], Akram Aalami[3]

[1]Pediatric Department, School of Dentistry, Mashhad University of Medical Sciences, Mashhad, Iran
[2]Department of Microbiology, Ghaem Hospital, Mashhad University of Medical Sciences, Mashhad, Iran
[3]Dentist, Mashhad, Iran

Abstract

Background: The aim of this study was to assess effect of some current disinfectants in Iran against *Hepatitis B*.

Methods: HBV-infected plasma, which had been exposed to disinfectant agents for certain period set by factory, were added to HepG2 cell culture environment. After 16 hours, the cell culture environment was emptied. It was then rinsed by PBS for several times. Then a new cell culture environment was added to the flask. After an hour virus titer was assessed. On the second day sodium Butyrate was added to the cell culture. On the third day virus titer was assessed and compared with the previous one. The increased titer indicated that the virus was alive while the reduction of titer proved elimination of the virus.

Results: Glutaraldehyde 2% and Hypochlorite 0.01% (fifteen minutes) were able to eliminate the virus in dilution of 10^6. In addition, Deconex Solarsept (one minute), Micro10 2% (fifteen minutes), Medical Percidin 2% (three minutes) and Percidin513 (ten minutes) were able to eliminate the virus in dilution of 10^3 ,while Sanosil 6% (twenty minutes) and Mikrozid (one minute) could do the same in dilution of 10^2. Big Spray was not able to eliminate the virus in neither of dilutions, though.

Conclusion: Glutaraldehyde 2%, Hypochlorite0.01%, Micro10, Deconex Solarsept, Medical Percidin and finally Percidin513 can be used as effective antiviral agents in dentistry but Big Spray and Sanosil and Mikrozid are not effective on *Hepatitis B*.

Keywords: Disinfectants, *Hepatitis B virus*, in vitro

Streptococcus Pneumonia Serotypes Distribution and thirteen-Valent Vaccine Coverage in Nasopharyngeal Samples of Children in Daycare Centers

Mohamad Hadi Amirian[1], Saied Amel Jamehdar[2], Mohamad Hasan Aelami[1], Maryam Jafariani[1], Kiarash Ghazvini[2], Mahmoud Bagheri[2], Hosein Nomani[2], Elnaz Harifi Mood[2], Ali Khorsand Vakilzadeh[3]

[1]Department of Pediatrics, Imam Reza Hospital, Faculty of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran
[2]Microbiology and Virology Research Center, Avicenna Research Institute, Mashhad University of Medical Sciences, Mashhad, Iran
[3]Imam Reza Hospital, Faculty of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran

Abstract

Background: *Streptococcus pneumonia* is a major cause of diseases ranging from noninvasive such as acute otitis media, predominant among young children, to severe invasive infections such as respiratory tract infections, bacteremia and meningitis. This pathogen is also an important causing agent of up to one million deaths per year among children less than five years of age, mostly in developing countries.

Introduction of the pneumococcal conjugated vaccines resulted in a dramatic decline in invasive diseases caused by this pathogen and a significant decline in non-vaccinated population due to a pronounced herd effect. However, accurate serotyping is essential to monitor the changes in the sero-epidemiology of *S. pneumonia*. The purpose of our study was to recognize our common society serotypes to determine efficacy of thirteen-vallent pneumococcal vaccines in Iranian children.

Methods: We have studied three hundred children younger than five years of age and seventy five *S. pneumonia* isolates from adults. Samples were taken from tonsils and tonsillar crypts of children. Samples were cultured on Blood agar medium. Bacterial DNA was extracted and then PCR reaction was done by serotype specific primers on positive samples.

Results: From three hundred children under five years of age in kindergarten, 19% were pneumococcal carriers in their nasopharynx. The most common serotypes were 19F (52.4%), 23F (36.8%), 1 (24.6%), 6A/B (22.8%) and 3(17.5%). Coverage of thirteen-valent and seven-valent vaccines was 91% and 79%, respectively. For invasive samples the most common serotypes were 23F (56.4%), 19A (27.3%), 14(20%), 6A/B (9.1%), 9V and 19 F (7.3%). Thirteen- and seven-valent vaccines coverage was 81% and 73%.

Conclusion: Regarding the high coverage of thirteen-valent vaccine and its different coverage zone from seven-valent vaccine, it is concluded that vaccination with thirteen-valent vaccine is more efficient in Iranian children.

Keywords: *Streptococcus pneumonia*, serotype, thirteen-valent vaccine

Development of a Taq Man Real-Time PCR Assay for Quantification of HTLV-1 Provirus

aied Amel Jamehdar[1], Houshang Rafatpanah[2], Mohammad Derakhshan[1], Mehdi Parian[3], Hosein Nomani[1], Nayereh Khosravi[4]

[1]Microbiology and Virology Research Center, Avicenna Research Institute, Mashhad University of Medical Sciences, Mashhad, Iran
[2]Inflammation and Inflammatory Diseases Research Center, School of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran
[3]Biotechnology Research Center, Pasteur Institute of Iran, Tehran, Iran
[4]Department of Health Promotions and Development, Deputy of Health, Mashhad University of Medical Sciences, Mashhad, Iran

Abstract

Background: *Human T-lymphotropic virus* type I (HTLV-I) is associated etiologically with adult T-cell leukemia and HAM/TSP. HTLV-I infection is endemic in southern Japan, tropical areas of Africa, Melanesia, Latin America and Khorasan Province of Iran. HTLV-I viral load could play a key role in the pathogenesis of HAM/TSP. Also recently the relationship between the proviral load and the pathogenesis of HAM/TSP has been clearly established. In the present study a Real time-PCR assay was developed to quantify HTLV-I DNA using a Taq Man probe.

Methods: Real-time PCR assay using Taq Man probe on the basis of tax region was performed with Rotor Gene system. In this assay, an external standard curve was established with ten fold serial dilutions of a plasmid carrying HTLV-I tax region. A broad linear range 1-10^6 copy of plasmid was observed in this assay. Reproducibility of intra- and inter-assays was assessed. We also measured proviral load in whole blood samples of twenty HTLV-I seropositive patients

Results: The results demonstrated that this technique has a good reproducibility and detects one copy of HTLV-I in reaction. Linearity of this approach was conserved over a wide range of HTLV-I copy numbers. Parallel analysis of 20 HTLV-I positive samples ranged from 2.5×10 to 3.1×10^4 copies.

Conclusion: The sensitivity, good reproducibility and high dynamic range allow determination of a broad range of HTLV-I proviral load in clinical subjects. This assay will facilitate the study of the relationship between proviral load and pathogenesis.

Keywords: HTLV-1, Real Time PCR, Quantification, Taq Man probe

Molecular Identification and Detection of Virulence Genes among *Pseudomonas aeruginosa* Isolated from Wound and Burn Infections

Zeynab Sharafi [1], Aslani Mohamad Mehdi[2], Nikbin Vajihe Sadat[2] and Shahcheraghi Freshteh[2]

Abstract

Background: *Pseudomonas aeruginosa* is the most important gram-negative bacterium cause of nosocomial infection. This pathogen possesses a variety of virulence factors that may contribute to its pathogenicity.

Methods: A total of one hundred fifty *P. aeruginosa* isolates (one hundred burns, fifty wound isolates) were obtained from patients during 1999-2006 of Imam-Khomeini, Tohid and Motahari hospitals in Tehran. Initially the isolates were identified as *P. aeruginosa* by biochemical tests and to confirm the identity of them by using PCR method for oprI, oprL and toxA genes. Chromosomal DNA of the isolates was extracted by Phenol-Chloroform method and used for PCR of oprI, oprL, toxA, lasB, exoS and nan1 genes. Seventy four isolates were selected randomly among genetic groups to investigate clonal diversity of the isolates by using ribotyping. Ribotyping was performed by using SmaI restriction enzyme.

Results: Among one hundred fifty *P. aeruginosa* isolates all carried oprI, oprL and lasB genes; ninety eight (65.3%) of the isolates, one hundred forty two (94.7%) of the isolates and ninteen (12.66%) were positive for exoS, toxA and nan1 genes respectively. The presence of nan1 gene in wound isolates (30%) was significantly higher ($P<0.05$) than in burn isolates (4%). According to the presence of these six genes, the isolates were divided into six genetic groups (I-VI). Eight distinct ribotype patterns (A-H) obtained. Most of isolates (89.19%) belonged to clone A and B. There was no correlation between genetic groups and ribotype patterns.

Conclusion: Our results indicate that PCR method based on amplification of oprI and oprL possesses reliable sensitivity and based on amplification of toxA gene possesses reliable specificity to detect *P. aeruginosa* from clinical samples. 100% prevalence of lasB gene isolates suggests this gene is critical for survival of *P. aeruginosa* in nature. The high prevalence of exoS gene in isolates suggests invasive phenotype of wound and burn isolates. The high prevalence of nan1 gene in wound isolates suggests a possible role of this gene in this infections.The heterogenicity of virulence genes of *P. aeruginosa* isolates suggests that they are associated with different levels of intrinsic virulence and pathogenicity. This may have different consequences on the outcome of wound and burn infections. Persistence of clonal strains in these hospitals for many years indicates that is necessary to focus on reinforcement of measures for infection control.

Keywords: *Pseudomonas aeruginosa*, wound and burn infections, virulence factors

[1]Shahid Beheshti university of Medical Science, School of Pharmacy, Tehran
[2]Department of Microbiology, Pasteur Institute of Iran, Tehran

Seasonal Distribution of Levels of *Aspergillus spp*. Conidia in Indoor and Outdoor Environments at a Hospital

Nedasadat Hosseini[1], Mansour Bayat[2], Shahla Roudbarmohammadi[3]

Abstract

Background: Airborne transmission is a critical way of infection for many opportunist pathogens in outdoor and indoor environments, including hospitals. Unfortunately, there is a paucity of information on the normal air load of *Aspergillus* spores and their seasonal changes. The aim of this study was to determine the types and relative frequencies of both indoor and outdoor airborne fungi especially *Aspergillus* conidia levels in a hospital during different seasons.

Methods: We gathered our samples from indoor and outdoor areas of twenty departments of Hashemi Nezhad hospital. Every point was tested in four seasons. All species were cultured on potato dextrose agar plates and incubated at 35˚c for 5 days. Czapeck agar plates were used as a culture medium for *Aspergillus species*. The fungi identified and counted microscopically and macroscopically. Statistical analyses were performed using SPSS 19 software package.

Results: A total of 2176 Samples were obtained including 1360 Indoor samples and 816 outdoor samples. 13 different genera were isolated from hospital environment, with predominance of *Aspergillus spp*. *Aspergillus fumigatus* was the most prevalent isolated fungus, followed by *Aspergillus flavus*. Both the indoor and outdoor populations were on their largest number in fall and summer and their smallest number in spring. The autumn collection yielded more isolates than that of other seasons.

Conclusion: We found a relatively high number of airborne fungi in different departments of hospital and expressive levels of *Aspergillus spp*. Microbiological and environmental monitoring should be conducted, especially in particular areas which include immune-compromised patients who are more vulnerable to environmental pathogens exposure.

Keywords: *Aspergillus*, conidia levels, outdoor and indoor environments, hospital

[1]Graduated of cell and molecular biology, Faculty of basic sciences, science and research branch, Islamic Azad University, Tehran, Iran
[2]Asisstant professor of Medical and veterinary mycology, Faculty of veterinary specialized sciences, science and research branch, Islamic Azad University, Tehran, Iran
[3]Assistant professor of medical mycology, Faculty of medical sciences, Tarbiat Modarres University, Tehran, Iran

Prevalence of Acute and Latent HHV-6 Infection in Pancreas Transplant Patients

Sara Kadkhodaei[1],Ramin Yaghoubi[2], Bita Geramizadeh [2], Saman Nikeghbalian[3], Ali Malekhosseini[3]

Abstract

Background: *Human herpes virus 6* (HHV-6) as an opportunistic viral pathogen has etiologic role in clinical outcomes of pancreas transplant patients treated with high doses of immunosuppressive drugs. In this study prevalence of acute and latent HHV-6 infection was evaluated in pancreas transplant patients for the first time in Iran.

Methods: In a cross sectional study one hundred and twenty two EDTA-treated blood samples were collected from fifty pancreas transplant patients in different times during post-transplantation period between years 2007 to 2011. Plasma and buffy coats were extracted from collected blood samples. Molecular prevalence of HHV-6 infection was studied by an in house nested–qualitative PCR protocol. Also risk factors related to post pancreas transplant outcomes with or without HHV-6 infection were analyzed statistically by SPSS software.

Results: The prevalence of HHV-6 infection in plasma samples collected in different times during post pancreas transplantation period was as follows: four of forty nine (8.0%) in the first week, five of thirty four (14.7%) in the second week and two of eighteen (11.7%) in the third week of post-transplantation period. The prevalence of HHV-6 infection in buffy coat samples collected in different times during post pancreas transplantation period was as follows: seven of fifty (14.0%) in the first week, two of thirty three (6.1%) in the second week and one of eighteen (5.6%) in the third week post transplantation. Significant correlations were found between indices including sex, age, rejection and the type of pancreas transplantation with HHV-6 infection in both plasma and buffy coat samples of transplanted patients.

Conclusion: High prevalence of HHV-6 infection simultaneously detected in plasma and buffy coat samples of the pancreas transplant patients confirms the important effect of HHV-6 infection in post transplantation outcomes. Though, the subject requires further complementary studies.

Keywords: *Human herpes virus-6*, pancreas transplantation, active infection, latent infection

[1]Islamic Azad University, Jahrom Branch, Jahrom, Iran
[2]Shiraz Transplant Research Center, Nemazee Hospital, Shiraz University of Medical Sciences, Shiraz, Iran
[3]Shiraz Transplant Center, Nemazee Hospital, Shiraz University of Medical Sciences, Shiraz, Iran

Seroprevalence of *Epstein-Barr Virus* in healthy children and adolescents in Shiraz, southern Iran

Gholamreza Pouladfar, Mazyar Rahimi, Mazyar Ziyaeyan, Sadaf Asaei, Mahsa Moeini, Marzieh Hoseini

Abstract

Background: There is little information about the epidemiology of the prevalence and age distribution of *Epstein-Barr virus* (EBV) infection in southern Iran. The aim was to carry out a population-based seroprevalence survey of EBV and to determine some socioeconomic factors affecting its prevalence in children and adolescents in Shiraz.

Methods: The 1151 healthy children and adolescents (52% female) between 6 months and 17 years old were enrolled. Sampling was stratified by age (five age groups) and clustered by geography (9 districts of Shiraz). Anti-viral capsid antigen immunoglobulin G was detected by Enzyme-linked immunosorbent assay method. The socioeconomic factors were assessed by questionnaire.

Result: The seroprevalence was 19.3, 42.3, 50.5, 70.7 and 84 per cent in children at the age range of 1/2-2, 3-5, 6-10, 11-13 and 14-17 years, respectively. The seroprevalence rates were 66.7 and 20 per cent in children of illiterate mothers and mothers with academic education, respectively (< 0.001), but the difference was not significant in children over 5 years. (>0.05). The mean family sizes in seropositive and seronegative groups were 4.58 (± 1.32) and 3.95 (± 1.06), respectively (<0.001). The prevalence varied significantly among the districts of Shiraz (<0.001).

Conclusion: The seroprevalence of EBV infection in children living in Shiraz is less than that in many reported ones from developing countries and higher than that reported in most developed countries. It showed that some risk factors play different roles in various age groups.

Professor Alborzi Clinical Microbiology Research Center, Shiraz University of Medical Sciences, Shiraz, Iran

Keywords: *Epstein-Barr virus*. Seroepidemiology, risk factor, children, Shiraz

Comparison of Sero-Prevalence of HCV Antibodies in Highly Suspected Patients to Viral RNA Load by Immune-Chromatography and Real Time PCR Assay Respectively in Nemazee Hospital, Shiraz, Iran

Mahsa Moeini, Mazyar Ziyaeyan, Nasrin Aliabadi, Marzieh Jamalidoust

Abstract

Background: *Hepatitis C* is an infectious disease affecting primarily the liver, caused by the *Hepatitis C virus* (HCV); most cases of HCV infections become chronic and could be asymptomatic. Detection of HCV antibodies (Ab) is the first step in diagnosis of *Hepatitis C*; Immuno-chromatographic tests are usually used to screen suspected patients. This study was conducted to demonstrate the presence of HCV antibodies in suspected individuals in comparison with HCV RNA detection.

Methods: 257 EDTA treated samples were collected from suspected individuals from different socioeconomic groups, including; drug abusers, thalassemic and hemophiliac patients, immune-compromised patients such as bone marrow transplant, liver and kidney recipients and HIV positive and hemodialysis patients. After separation of plasma from whole blood, immune-chromatographic test (Abone Biopharm (Hangzhou) Co, ltd China as affiliate of Inverness Medical USA) was performed to detect HCV Ab. Furthermore, Real-Time PCR assay was carried out on extracted plasma to detect and quantify HCV RNA.

Results: Out of 257 patients, ranging from 1 to 73 years of age (mean 37.77±12.36 years) 202 were males (78.6%) and 55 (21.4%) were females. 165 (64.2%) individuals were HCV Ab positive, whereas 115 (44.7%) blood samples were HCV Real-Time PCR positive. 106 (92.17%) of those who had antibodies against HCV were HCV RNA positive in which 9(7.82 %) of HCV RNA positive patients were negative for having antibodies against HCV. There was a significant change in the prevalence of HCV Ab between two age groups indicated as I (Under 40 YO) and II (upper 40 YO) ($P \leq 0.05$).

Conclusion: Evaluation of anti HCV antibodies and subsequently detection of HCV RNA in the affected patients' plasmas are essential for early diagnosis of hepatitis infection and the initiation of respective treatment. In our study 7.82% of HCV antibody negative patients had detectable HCV nucleic acid in their plasma, which means they could have either occult infection, especially included hemodialysis patients or early acute infection with HCV. These cases should be considered carefully in the diagnosis of HCV infected patients.

Professor Alborzi Clinical Microbiology Research Center, Shiraz University of Medical Sciences, Shiraz, Iran

Keywords: *Hepatitis C*, Real Time PCR, HCV Antibodies

Effect of Oxidative Stress of Hydrogen Peroxide on Growth and Surface Hydrophobicity of Nosocomial Bacteria

Farnaz Valizadeh[1], Rouha Kasra-Kermanshahi[2]

Abstract

Background: Hydrogen peroxide is used as a disinfectant agent against microorganisms and toxicity of this agent is attributed to transition of metal ions, resulting in production of active oxygen species. *E. coli*, *S. aureus*, *E. faecalis*, *K. Pneumoniae* are pathogen nosocomial bacteria which cause diseases. The common virulence factors include surface hydrophobicity which can lead bacteria adhere to the surfaces such as polymer of surgical instruments. Since the bacteria resistance to antibacterial agents of nosocomial infections is increasing, the aim of this study was to determine the effect of H2O2 oxidative stress on growth and also the virulence factor (hydrophobicity) on nosocomial bacteria.

Methods: *E. coli* , *S. aureus*, *E. faecalis*, *K. pneumoniae*, were originally isolated from patients (Alzahra Hospital, Isfahan).Standard bacteria PTCC1394,PTCC 1431,PTCC 1237,PTCC1290 were also prepared. The cells (5×10^8CFU/ml) were sedimented and samples were suspended in ½ sub-MIC concentration of H_2O_2 after certain times, survived bacteria were determined by colony count method. For hydrophobicity analysis, half-Log population bacteria were centrifuged. The sediment was exposured to ½ sub-MIC concentration of H_2O_2. Bacterial suspension was mixed with 0.3 mL of p-xylene and vortexed. After separating aqua and organic phase hydrophobicity coefficient was calculated by applying the formula.

Results: Results of this study indicate that $H_2O_2$is an effective bactericidal on nosocomial bacteria and standard strains ($P<0.001$).0.9 , 2, 3.15, 2.4 Log reduction were seen for *S. aureus*, *E. coli, E. faecalis*, *K. pneumoniae* pathogen strains after exposure for one hundred and twenty minutes. Chi-square analyzes have showed significantly different mean between population reduction of pathogen and standard strains of GP ($p<0.001$). Chi-square analyzes also have showed significantly different mean between population reduction GN and GP bacteria ($P<0.001$). Duncan analysis have showed significant different mean of reduction hydrophobicity coefficient after exposure to H_2O_2 ($P<0.05$).

Conclusion: The present study showed that oxidative stress caused by exposure to H_2O_2 can reduce nosocomial bacteria but isolated bacteria were survived after eighty minutes of exposure to this agent. It represents the resistance of nosocomial bacteria to antibacterial agents. In this investigation, we observed that oxidative stress in resistant nosocomial bacteria could significantly influence the virulence factors of the bacterium. Surface hydrophobicity of bacteria decreased after exposure to H_2O_2. This in turn may influence the pathogenesis of bacterial infections.

Keywords: Nosocomial bacteria, Oxidative stress, Surface hydrophobicity

[1]Department of Biology, Faculty of Science, University of Isfahan, Isfahan, Iran
[2]Department of Microbiology, Faculty of Science, University of Alzahra, Isfahan, Iran

Isolation of *Cryptococcus* from Environment and Patients and Molecular Identification with PCR Sequencing

Hoda Kashani, Mohamad Javad Najafzadeh, Somaye Dolatabadi, Ali Naseri, Abdolmajid Fata

Abstract

Background: Cryptococcosis is an opportunistic fungal infection caused by *Cryptococcus neoformans* or *Cryptococcus gattii*. Both of the species occur saprobically in nature and the infection is acquired by inhalation of their air-borne yeast cells or basidiospores. Old excreta of pigeons or other avian species is known to be the commonest environmental reservoir of *C. neoformans*. Although the species has been reported from many environmental sources such as soil, bat guano, raw vegetables, and decayed wood in tree trunk hollows, etc. It is potentially fatal unless diagnosed and treated at an early stage with appropriate antifungal Therapy. In this study we are evaluating the rate of contamination of the excreta of pigeons and Eucalyptus leaves with this yeast.

Methods: Thirty four samples collected from different zones of Mashhad, Zahedan and Ramsar. Five grams of each sample is suspended in 50ml saline solution with chloramphenicol and gentamycin, mixed and left it to settle down in room temperature. After thirty minutes, 100 µl of supernatant were streaked on Sabouraud's dextrose agar medium including chloramphenicol and gentamycin. Plates are incubated at 30 °C and 37°C for a month, with weekly observation. Suspected colonies were selected for PCR and Sequencing. DNA extraction, PCR amplification and Sequencing of Internal Transcribed Spacer (ITS) regions were performed as described previously by Najafzadeh et al 2009. Partial sequences of the rDNA ITS were compared with Genebank.

Results: Out of thirty four collected samples, yeast-like colonies were isolated and identified as *Rhodotorula spp.* (29.4%), *Candida glabrata* (17.6%), *Trichosporon spp.* (17.6%), *Aureobasidium pullulance* (17.6%) (From Eucalyptus leaves), *Cryptococcos neoformans Var. grubii* (5.88%), *Candida albicans* (2.94%), *Debaryomyces hansenii* (2.94%), *Clavispora lusitaniae* (2.94%) and *Schwanniomyces polymorphus* (2.94%). Out of six CSF samples suspected to Cryptococosis in Ghaem hospital, Mashhad, none of them were positive in direct examination with Indian ink and culture.

Conclusion: The results of this study demonstrate that presence of *Cryptococcus* in excreta of pigeons is less than *Rhodotorula* and *Candida glabrata*.

Department of Parasitology and Mycology, Ghaem Hospital, School of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran

Keywords: *Cryptococcus*, Pigeon excreta, Eucalyptus

The Prevalence of Constitutive Resistance to Clindamycin in 2595 *Staphylococcus aureus* and *Coagulase-Negative Staphylococci* Isolated from Blood Cultures in Shiraz Hospitals, 2001-2011

Mona Zarafshanian, Gholam Reza Pouladfar, Fatemeh Norouzi, Mojtaba Anvarinejad, Bahman Pourabbas, Aziz Japoni, Mehdi Kalani, Mohammad Ali Dehyadegari and Nooredin Rafaatpour

Professor Alborzi Clinical Microbiology Research Center, Shiraz University of Medical Sciences, Shiraz, Iran

Abstract

Background: *Staphylococcus aureus* and *Coagulase-negative Staphylococci* (CoNS) isolated from patients with nosocomial infections is frequently resistant to multiple antimicrobial agents. Expression of macrolide, lincosamide (clindamycin), and streptogramin (MLS) resistance, most commonly result from acquisition of erythromycin resistance methylase (erm) gene, may be constitutive or inducible. Constitutive resistance to clindamycin can be readily detected by standard susceptibility Methods. The aim was to determine prevalence of constitutive resistance to clindamycin among CoNS and *S. aureus* isolated from blood cultures in Shiraz during the two periods Jan 2001- Dec 2006 and Jan 2010- Dec 2011.

Methods: All CoNS and *S. aureus* isolated from blood samples by BACTEC system in Professor Alborzi Clinical Microbiology Research Center were evaluated to detect the susceptibility to clindamycin and erythromycin by standard susceptibility Methods. These samples were obtained from different wards of hospitals in Shiraz during the two above mentioned periods.

Results: During two periods, 2595 positive cultures were identified: 921 within 2001-2006 and 1683 from 2010 to 2011. The susceptibility to clindamycin in *S. aureus* and CoNS was dropped significantly in these periods: 2001- 2006, 80% and 62% and 2010-2011, 54% and 34%, respectively. The susceptibility to erythromycin in *S. aureus* and CoNS was dropped significantly in these periods: 2004- 2006, 31% and 68% and 2010-2011, 15% and 47%, respectively.

Conclusion: The constitutive resistance to macrolide, lincosamide (clindamycin), and streptogramin (MLS) antibiotics was increased rapidly and consistently over times in Shiraz. Inducible resistance to MLS antibiotics remained to be determined.

Keywords: Antibiotic resistance, clindamycin, erythromycin, *coagulase-negative Staphylococci*, *Staphylococcus aureus*

Dissemination of Metallo-B-Lactamase Producing *Pseudomonas Aeruginosa* in Shiraz, Iran

Mohammad Motamedifar, Mahnaz Sarhangi, Jamal Sarvari, Reza Khashei

Abstract

Background: Metallo-β-lactamase (MBL) producing *Pseudomonas aeruginosa* is responsible for many important nosocomial outbreaks including pneumonia and septicemia. Various studies have reported the increasing spread of *P. aeruginosa* producing MBL enzymes resulted in increasing resistance to multiple antibiotics including carbapenems, cephalosporins and penicillins. The objective of this study was to explore the dissemination of MBL producing *P. aeruginosa* in Shiraz, Iran, based on the standard phenotypic and genotypic Methods.

Methods: During a six months period, from October 2011 to March 2012, 240 *P. aeruginosa* isolates, collected from four teaching hospitals in Shiraz, southwest of Iran, were examined. The isolates were mainly taken from wound, urine, and sputum. Minimum inhibitory concentration (MIC) ≥4 µg/ml to imipenem was determined with Micro-dilution Broth. Identification of *P. aeruginosa* carrying MBL was detected by double disk synergy test (DDST) and polymerase chain reaction (PCR) test using specific primers for bla_{IMP1}, bla_{VIM2}, bla_{SIM1}, bla_{SPM1}. All performed laboratory procedures were according to Clinical and Laboratory Standards Institute (CLSI) recommendations.

Results: From two hundred and forty *P. aeruginosa* isolates, eighty two (34.2%) isolates were imipenem resistant. From these imipenem resistant isolates, nineteen (23.3%) MBL producing *P. aeruginosa* isolates were detected via DDST. A specific PCR test confirmed the occurrence of eighteen (22%) *P. aeruginosa* producing bla_{IMP1} and bla_{VIM2}.

Conclusion: Detected MBL genes were reported in a few studies in Iran including ours. The spread of detected MBLs producing *P. aeruginosa* were unprecedented in the region either due to lack of independent related research or the novel incidence of these genes. This detection must be noted by responsible clinical and health care agents.

Keywords: *Pseudomonas Aeruginosa*, metallo-β-lactamase, Shiraz, Iran

Department of Medical Bacteriology and Virology, Faculty of Medicine, Shiraz HIV/AIDS Research Center (SHARC), Shiraz University of Medical Sciences, Shiraz, Iran

Prevalence of Gentamicin Resistance Genes Aada (1) and Aadb (1) in *Acinetobacter Baumannii* Isolates from Patients of Tabriz City

Safar farajnia[1], Katayun aliakbarzade[2], Ashraf Karimi Nik[2], Amir Peymani[3], Nasrilah Sohrabi[4],Shiva Ahdi Khosroshahi[1]

[1]Biotechnology Research Center, Tabriz University of Medical Sciences, Tabriz, Iran
[2] Department of Microbiology, Science and Research branch, Islamic Azad University of Kerman, Kerman, Iran
[3]Department of Microbiology, Qazvin University of Medical Sciences, Qazvin, Iran
[4] Department of Microbiology, Kermanshah University of Medical Sciences, Kermanshah, Iran

Abstract

Background: *Acinetobacter baumannii* is one of the major causes of nosocomial infections that is resistant to most of available antibiotics and plays an important role in mortality of hospitalized patients. Aminoglycosides are among drugs of choice for treatment of *Acinetobacter* infections; however, the resistance to aminoglycosides has been increased in recent years in these bacteria. The present study investigated the prevalence of genes encoding aminoglycoside modifying enzymes (AME) type aadA (1) and aadB (1) in *Acinetobacter baumannii* strains isolated from patients in Tabriz city.

Methods: In this study a total of 103 *Acinetobacter* isolates were collected from Imam Reza hospital in Tabriz University of medical sciences. Antimicrobial susceptibility patterns of isolates to different antibiotics including gentamicin and amikacin evaluated by disc diffusion method. Strains resistant to aminoglycosides were screened for AME types of aadA (1) and aadB (1) by PCR method.

Results: Antimicrobial susceptibility analysis showed that the highest resistance was to beta-lactam antibiotics including cephalosporins whereas the highest sensitivity was observed to colistin, polymyxin, imipenem and meropenem. The PCR results showed that among one hundred and three *A. baumannii* isolates, twenty four (23.30 %) isolates were positive for aadA(1) and seventeen (17.5%) for aadB (1) resistant genes.

Conclusion: The results of this study indicated that genes encoding for aminoglycoside modifying enzymes are prevalent in the *A. baumannii* strains in the study region which highlighted the necessity of considering preventive measures to control dissemination of resistance genes.

Keywords: *Acinetobacter baumannii*, aminoglycoside resistance genes, aadA(1), aadB(1)

Molecular Typing of *Clostridium difficile* Isolated from Hospitalized Patients by PCR Ribotyping

Mehdi Goudarzi[1, 2], Mohammad Mehdi Aslani[3], Hossein Goudarzi[2], Masoud Alebouyeh[3], Masoumeh Azimi Rad[3] Mohammad Reza Zali[3]

[1]Research Center for Gastroenterology and liver Diseases, Shahid Beheshti university of Medical Sciences, Tehran, Iran
[2]Shahid Beheshti University of Medical Sciences, Tehran, Iran
[3]Department of Microbiology Pasteur Institute, Tehran, Iran

Abstract

Background: *Clostridium difficile* infection (CDI) is a major growing problem in hospitals and its high prevalence has been reported in recent years. Many different Methods have been described for *C. difficile* epidemiological studies. PCR ribotyping has recently been proposed as an effective method for molecular typing of *C. difficile* isolates

Methods: During a twelve month study, seventeen *C. difficile* isolates were collected from 108 patients with CDI. All samples were treated with alcohol and yeast extract broth and treated samples were cultured on a selective cycloserine cefoxitin fructose agar (CCFA) supplemented with 5% sheep blood by streak culture method and incubated in anaerobic conditions, at 37 °C for five days. Cdd-3, tcdA and tcdB genes were identified using PCR assay. PCR ribotyping was performed on *C. difficile* isolates obtained from hospitalized patients.

Results: Out of one hundred and eight stool samples, seventeen (15.7%) were *C. difficile***.** The prevalence of A^+B^+, A^+ B^- and A^- B^+ strains were twelve (70.59%), one (5.9%) and four (23.9%) respectively. Analysis of PCR ribotyping analysis of seventeen isolates showed that all of them had different ribotype patterns.

Conclusion: PCR ribotyping of isolates showed that all isolates were different in various wards of hospital and infection may be community acquired or endogenous.

Keywords: *Clostridium difficile*, Toxin, ribotype, *Clostridium difficile* infection (CDI)

Molecular Epidemiology of *Acinetobacter baumannii* Strains That Isolated from Tehran's Hospitals by PFGE

Reza Mirnejad[2], Neda Farahani[1], Zeinab Ahmadi[2], Dr Noor Amirmozafari[3], Faramarz Masjedian[4]

[1]Department of Biology Science and Research Branch, Islamic Azad University, Tehran, Iran
[2]Molecular Biology Research Center, Baqiyatallah (A.S.) University of Medical Sciences, Tehran, Iran
[3]Department of Microbiology, School of Medicine, Tehran University of Medical Sciences, Tehran, Iran
[4]Department of Medical Bacteriology, Tehran University of Medical Sciences, Tehran, Iran

Abstract

Background: The aim of this study was to determine genotypes of *Acinetobacter baumannii* that is isolated from patients in three large hospitals in Tehran by PFGE method.

Methods: This study was performed on seventy isolates of *Acinetobacter* which were isolated from patients hospitalized in Baghiatallah, Rasoole Akram and Milad hospitals in Tehran. After determining the species of isolates using cultural and biochemical Methods, the susceptibility tests were carried out on fifty isolates of *A. baumannii* using disk diffusion method. Isolates were then examined by PFGE using Apa1 restriction enzyme. Finally, the results of PFGE were analyzed.

Results: The results showed that *A. baumannii* strains isolated from hospitals in Tehran had seven different genetic patterns that two of these patterns were sporadic. Also genotyping patterns were different in every hospital. There were different patterns of genetic resistance to common antibiotics.

Conclusion: Using PFGE, although diversity was observed among strains of *A. baumannii* in Tehran, no epidemic strains were found among them.

Keywords: PFGE, *Acinetobacter baumannii*, genotyping

Mycological Microscopic and Culture Examination of Four Hundred Bronchoalveolar Lavage (BAL) Samples

Hossein Zarrinfar[1],Hossein Mirhendi[2], Abdolmajid Fata[1],Parivash Kordbacheh[2], Sassan Saber[3],Ommolbanin Paknejhad[3],Mohsen Geramishoar[2],K Makimura[4]

[1]Department of Medical Parasitology and Mycology, Faculty of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran
[2]Department of Medical Parasitology and Mycology, School of Public Health, Tehran University of Medical Sciences, Tehran, Iran
[3]Department of Internal medicine, Tehran University of Medical Sciences, Tehran, Iran
[4]Teikyo University, Institute of Medical Mycology, Tokyo, Japan

Abstract

Background: The frequency of invasive opportunistic mycoses has increased significantly over the past decades especially in immune-compromised patients. Invasive aspergillosis (IA) has become a major cause of morbidity and mortality among these patients. As bronchoalveolar lavage (BAL) fluid samples are generally useful specimens in the diagnosis of invasive pulmonary aspergillosis (IPA), this study was designed to evaluate the incidence of fungal elements in at-risk patients by direct microscopy and culture of BAL samples.

Methods: In a 16-month period, four hundred BAL samples were obtained from several groups of different patients with pulmonary and respiratory disorders and examined by using both direct microscopy with %20 of potassium hydroxide (KOH) and then culture on Sabouraud glucose (4%) and Brain Heart Infusion agar (BHI).

Results: Of four hundred samples, sixteen (4%) were positive by direct examination with branching septate hyphae and forty six (11.5%) were positive cultures. Twenty five (54%) *Aspergillus flavus*, six (13%) *A. fumigatus*, 5 (10.9%) *A. niger*, 1 (2.2%) *A. terreus*, 3 (6.5%) *Penicillium spp.* and six (13%) mixed *A. flavus*/*A. niger*. *A. flavus* was the most common cause of *Aspergillus* infection or colonization. Bone marrow transplant (BMT) recipients were the most susceptible group to fungal infection and/or colonization.

Conclusion: Among *Aspergillus species*, *A. flavus* was the most common isolate in both infections and colonization in Iran. More studies and diagnostic Methods are needed to clarify the epidemiological aspect of aspergillosis in Iran.

Keywords: *Aspergillus*, Bronchoalveolar lavage, Fungus, Iran

Protective Activity of Anti-Exotoxin A Antibodies against *Pseudomonas Aeruginosa* Infections

Lida Eftikharvash[1], Safar Farajnia[2], Shahin Najar Peerayeh[3], Asghar Tanomand[4], Leila Rahbarnia[5]

Abstract

Background: *Pseudomonas Aeruginosa* has many antibiotic resistance factors. Antibiotics have failed in treatment of *P. aeruginosa* infections. Regarding high resistance, immune-prophylaxis and immunotherapy might be effective in controlling and treating *P. aeruginosa* infections. In this research, protection properties of recombinant exotoxin A (Domains I, II) against *Pseudomonas Aeruginosa* infections were evaluated in mice.

Methods: After preparation and purification of exotoxin A (domains I, II) by recombinant method, lipopolysaccharide (LPS) contamination was quantified by limulus amoebocyte lysate assay .The exotoxin A (domains I, II) was sterilized by millipore filtration. Finally, the product's concentrations were assessed by Bradford method. Mice were immunized subcutaneously on day 0, 21, 42 with extoxin A (domains I, II) and PBS. Antibody production was evaluated by ELISA method. The immunized and control group were exposed to an approximate 2X LD50 (7×10^7 CFU) of clinical strains of mucoid *P. aeruginosa.*

Results: Vaccination with exotoxin A (domains I, II) produced significant amount of specific IgG antibodies. No significant concentration of IgG antibodies were detected in the negative control group which was injected with PBS alone. Also mice immunizedwith Exotoxin A (domains I, II) showed significant protection against intra-peritoneal challenge with approximate 7×10^7 CFU (2X LD50) clinical strains of mucoid *P. aeruginosa*.

Conclusion: Results of this study suggested that recombinant ExotoxinA (domains I, II) is a highly immunogenic protein which can be used as a *Candida*te vaccine in other studies.

Keywords: *Pseudomonas Aeruginosa*, Exotoxin A, Vaccine, vaccine *Candida*te

[1]Islamic Azad University, MaraghehBranch, Tabriz, Iran
[2]Biotechnology Research Center, Tabriz University of Medical Sciences, Tabriz, Iran
[3]Associate Professor, Department of Bacteriology Faculty of Medical sciences, Tarbiat Modares University, Tehran, Iran
[4]Deptartment of Bacteriology Faculty of Medical sciences, Tarbiat Modares University, Tehran, Iran
[5]Biotechnology Research Center, Tabriz University of Medical Sciences, Tabriz, Iran

Trends in Resistance to Third-Generation of Cephalosporins and Fluoroquinolones in *Enterobacteriaceae* Isolated From Blood Cultures in Shiraz Hospitals, 2001 to 2011

Amin Abbasian, Gholam Reza Pouladfar, Mona Zarafshanian, Norouzi, Anvarinejad, Bahman Pourabbas, Aziz Japoni, Mehdi Kalani

Professor Alborzi Clinical Microbiology Research Center, Shiraz University of Medical Sciences, Shiraz, Iran

Abstract

Background: *Enterobacteriaceae* has become one of the most important causes of nosocomial and community acquired infections. The aim of this study was to evaluate the trends of resistance to cephalosporines and fluoroquinolones in *Enterobacteriaceae* isolated from blood cultures in Shiraz during the two periods from 2001 to 2006 and from 2010 to 2011.

Methods: The *Enterobacteriaceae* isolated from blood samples by BACTEC system in Professor Alborzi Clinical Microbiology Research Center were evaluated. Bacterial identification was done conventionally within 2001-2006 and by API system within 2010-2011.

Results: Of the 5214 isolates, 803 (15%) *Enterobacteriaceae* strains were identified: 303 within 2001-2004 (14% from 2115 isolates) and 500 within 2010-2011 (16% from 3099 isolates). The most common *Enterobacteriaceae* were *Escherichia Coli* (358 isolates, 46%), *Enterobacter spp*. (150 isolates, 19%), *Klebsiella spp*. (123 isolates, 15%), and *Serratia spp*. (82 isolates, 10%). The most *Serratia spp*. isolates (79%) were identified within the second period. Within the two periods 2001-2006 and 2010-2011, resistance to ciprofloxacin increased for *E. coli* (22% vs. 53%, respectively), for *Enterobacter spp*. (13%-21%, respectively) and *Serratia spp*. (9%-24%, respectively), but for *Klebsiella spp*. infections the resistance decreased (27%-13%, respectively). Within the two periods, the susceptibility rate to ceftriaxone remained low for *E. coli* (30%-37%, respectively), for *Klebsiella spp*. (48%-46%, respectively), but increased for *Enterobacter spp*. (30%-59%, respectively) and *Serratia spp*. (25%-37%, respectively).

Conclusion: High resistance to the third-generation cephalosporins and increasing rate to fluoroquinolones were detected in Shiraz Hospitals. In addition to the effect of antibiotic pressure which could change susceptibility patterns over time, identification Methods are also influential in this respect.

Keywords: Antibiotic resistance, Bacteremia, *Enterobacteriaceae*

Comparison of a Novel One-Step Real-Time PCR with Viral Isolation and Direct Fluorescent Antibody Staining for the Detection of Influenza A in Nasopharyngeal Specimens

Mohammad Amin Behzadi, Mazyar Ziyaeyan, Abdolvahab Alborzi

Professor Alborzi Clinical Microbiology Research Center, Shiraz University of Medical Sciences, Nemazee Hospital, Shiraz, Iran

Abstract

Background: The infection caused by *Influenza A virus* is a common contagious respiratory disease in both humans and animals. In this study, a novel designed Real-Time PCR assay with high analytical sensitivity (10 copies of viral RNA/reaction) and specificity was compared with viral isolation and direct fluorescent antibody staining (DFA) for the detection of *Influenza type A viruses* in clinical specimens. The aim of this study was to evaluate the clinical specificity and sensitivity of this one-step Real-Time PCR assay.

Methods: A total of sixty four nasopharyngeal swabs from patients with influenza like illness (ILI) and forty one samples without the ILI symptoms were collected during October 2011to January 2012 in Nemazee hospital, Shiraz, Iran. 200 µl of every sample was transported to MDCK cell culture for virus isolation and incubated for a week to observe the specific cytopathic effect (CPE) of *Influenza A* viruses. DFA was performed on the harvested medium of every culture using commercial kit (Dakocytomation, UK). Moreover, viral RNA was extracted from the specimens and Real-Time assay was done for detection of influenza type A viruses using primer sets and probe base on matrix gene.

Results: The specific *Influenza A* CPE was observed in 6/64 ILI group; however it was not seen in non-ILI one. The results of DFA staining revealed the same results. In addition, the results of our novel one-step Real-Time PCR assay were similar to the results of viral isolation and DFA staining.

Conclusion: It can be concluded that due to short diagnosis time and high clinical and analytical sensitivity and specificity of this novel one-step real time PCR assay, it is recommended that this test is applied for detection of *Influenza type A* both in clinical and experimental specimens. However, more clinical specimens should be evaluated by this method.

Keywords: *Influenza A virus*, Real-time RT-PCR, Viral isolation, Direct fluorescent antibody, Matrix

National Nosocomial Infection Surveillance Report in Iran during 21 Mars 2011 to 20 Mars 2012

Hossein Masoumi asl[1], Zahra Pezeshki[2]

Abstract

Background: Nosocomial infection (NI) affects hundreds of millions of patients worldwide each year that lead to more serious illnesses, prolonged hospitalization, and induce long-term disabilities. In 2007, a national surveillance system was established in Iran for NI based on National Nosocomial Infection Surveillance (NNIS) system definition.

Methods: In this cross sectional study four main groups of NI including urinary tract (UTI), pulmonary (PNEU), surgical site (SSI) and blood stream (BSI) infections was investigated in 377 hospitals from 21th March 2011 to 20th March 2012. Data was gathered through surveillance system that reported to center for communicable disease and analyzed in Iranian Nosocomial Infection Surveillance (INIS) software.

Results: During the study period, a total of 31420 cases have been registered. The NI rate was 0.61%. UTI 32.4%, PNEU 31.2%, SSI 19.2%, and BSI 17.2%. The mortality rate was 15%. High prevalence rates were in transplantation (10.8%), burn (8.6%), ICU (6.6%) and NICU (2.5%) wards.13% of infected patients were under 15 years of age. Invasive measures that have been done for cases were venous (22%), urinary (19%) catheter and then suction, tracheal tube, ventilator and surgery subsequently. 71.4% of diagnosis were laboratory based. *E. coli* (17%), *Acinetobacter* (13%), *Klebsiella* (12%) and *Pseudomonas aeruginosa*(12%) were the most prevalent causative agents in NI cases.

Conclusion: The results showed that it is feasible to collect data from a large number of hospitals that assist interventions and, but because of data under- reporting, it is necessary to encourage and change attitude of authorities and health worker by holding more justification and educational sessions.

Keywords: Surveillance, nosocomial infection, Iran

[1]Nosocomial Infection Program Manager, Center for Communicable Disease Control, Ministry of Health, Tehran, Iran
[2]Senior expert in disease control, Center for Communicable Disease Control, Ministry of Health, Tehran, Iran

High rate of Fluoroquinolone Resistance in *Salmonella spp*. Isolated from Blood Culture in Shiraz, Southern Iran

Gholam Reza Pouladfar[1], Bahman Pourabbas[1], Firoozeh Foroozand[2], Mojtaba Anvarinejad[1], Mona Zarafshanian[1], Noreddin Rafatpour[1]

Abstract

Background: Fluoroquinolones are recommended as first line therapy for children and adults infected with *Salmonella* Typhi and Paratyphi. Fluoroquinolone-resistant strains cause growing concern in developing countries. The aim was to evaluate the trend of Fluoroquinolone resistance in *Salmonella* strains isolated from patients with suspected typhoid fever from hospitals and outpatient clinics in Shiraz within two periods, covering 2001 to 2008 and 2010 to 2011.

Methods: Samples were obtained from outpatients and different wards of hospitals in Shiraz during the above-mentioned two periods. All *Salmonella spp*. were isolated from the blood samples by BACTEC system in Professor Alborzi Clinical Microbiology Research Center with API method.

Results: Of the forty eight isolates, thirty five were identified within 2001-2008 and fourteen strains within 2010-2011. All organisms were sensitive to imipenem. The susceptibility to ciprofloxacin and ceftriaxone decreased from 94% (33/35) and 91% (20/22) within 2001-2008 to 64% (9/14) and 63% (7/11) within 2010-2011, respectively.

Conclusion: The recommendation to use fluoroquinolones as first line therapy for enteric fever irrespective of sensitivity patterns and without a thorough analysis and assessment of quality of evidence could have profound public health implications in southern Iran, particularly in children.

Keywords: Fluoroquinolones, *Salmonella*, Antibiotic resistance

[1]Professor Alborzi Clinical Microbiology Research Center, Shiraz University of Medical Sciences, Shiraz, Iran
[2]Fasa University of Medical Sciences, Fasa, Iran

Evaluation of Nosocomial Infection and Antibiotic Use in Pediatric Ward, Imam Reza Hospital, Mashhad, Iran

Abdolkarim Hamedi[1], Mohammad Hadi Amirian[2]

Abstract

Background: Nosocomial infection is one of the most problematic health challenges in the world since it has induced morbidity and mortality. Nosocomial infection is common in pediatric department and more related to urinary, pulmonary and wound site infections. One of the most important factors in nosocomial infections is antibiotic empirical therapy. The objective of this study was to determine prevalence of microorganisms causing nosocomial infections and pattern of their antibiotic resistance. Then we could present practical strategy about this problem.

Methods: In one year (1.5 2009-1.5.2010) all patients who admitted in pediatric department of Imam Reza Hospital, Mashhad, Iran were under observation by next three weeks after discharge from hospital and whom suspected to nosocomial infections were followed up by complete data in the questionnaire sheet.

Results: Among 1421 patients admitted in pediatric department, Imam Reza Hospital, Mashhad Iran during May 2009 to May 2010, 59% were males, mostly aged 2 to 24 months and the risk of nosocomial infection was 1.12%. The most common positive culture sites were blood and intubation tube. *Pseudomonas* was the most common cultured organism isolated from the site of infection.

Conclusion: Nosocomial infection is a serious fact and we should diagnose it and also attend to resolve it. If nosocomial infection is suspected, we should prescribe broad spectrum antibiotics as soon as possible.

Keywords: Nosocomial infection, Antibiotic use, Pediatric department

[1]Associate professor and pediatric Infectious man, Mashhad University of medical sciences, Imam Reza Hospital, Mashhad, Iran
[2]Departmentof Pediatrics, Imam Reza Hospital, Mashhad University of medical science, Mashhad, Iran

Association of Interleukin-18 Gene Variants with Susceptibility to Visceral Leishmaniasis in Iranian Population

Maral Choopanizadeh[1*], Manoochehr Rasouli[1], Mehdi kalani[1], Sadaf Asaei[1], Ali Moravej[2]

Abstract

Background: Host resistance to Leishmania infection is mediated by cellular immune responses leading to macrophage activation and parasite killing. Interleukin-18 (IL-18), known as interferon-γ (IFN-γ) inducing factor, stimulates IFN-γ production by T cells. According to the important role of IL-18 in the defense against visceral leishmaniasis (VL) and the known effect of IL18 gene polymorphisms on its production, the aim of this study was to investigate the probable relationship between IL-18 gene polymorphisms and the susceptibility to VL.

Methods: The study groups included one hundred and eighteen pediatric patients who suffered from VL and one hundred and fifty six non-relative healthy people from the same endemic area as the patients. IL-18 gene polymorphisms at positions-656 G/T, -137 G/C and +105A/C (codon 35/3) were analyzed by polymerase chain reaction-restricted fragment length polymorphism (PCR-RFLP).

Results: The result showed that the frequency of T allele at position -656 was significantly higher in the control group compared with patients (P=0.047). Regarding the IL-18 genotypes, there was no significant difference between the patients and controls. Although the distribution of ATG single haplotype and AGG/ATG double haplotype were significantly more frequent in the control group (P=0.043) than the patients (P=0.044), respectively, the two P values couldn't tolerate Bonferroni correction. Furthermore, a strong linkage disequilibrium was observed among the -656, -137 and +105 single nucleotide polymorphisms of IL18 gene (all Ps<0.001).

Conclusion: In conclusion, this study suggests that inheritance of T allele at position -656 may be considered as a genetic factor for resistance to VL.

Keywords: Interleukin-18, Genetic polymorphisms, Visceral leishmaniasis, Iran

[1]Department of Immunology, Professor Alborzi Clinical Microbiology Research Center, Shiraz University of Medical Sciences, Shiraz, Iran
[2]Department of Immunology, Fasa University of Medical Sciences, Fasa, Iran

Interleukin-8 But Not Interlukin-6 Gene Polymorphisms Confers Resistance to Brucellosis in Iranian Population

Sadaf Asaei[1], Manoochehr Rasouli[1], Ali Moravej[2]

Abstract

Background: Increased levels of interleukin-8 (IL-8) and interlukin-6 (IL-6) in acute human Brucellosis have been reported. Previous studies showed that production of IL-6 and IL-8 cytokines is associated with polymorphisms of their genes. According to the important role of these two cytokines in outcome of *Brucella* infection and role of polymorphisms in cytokine production, in the present study we attempted to clarify the probable association between IL-6 (-174 C/G) and IL-8 (-251 A/T) gene polymorphisms and susceptibility/resistance to Brucellosis.

Methods: The patient group included one hundred and ninety six patients suffered from *Brucella* infection and the control group consisted of eighty two healthy men from the same geographical area as the patients. IL-8 (-251 A/C) gene polymorphism was analyzed by PCR-RFLP as well as IL-6 (-174 C/G) gene polymorphisms was analyzed using Allele Specific PCR.

Results: The frequency of -251 IL-8 AA genotype was significantly lower in control group compared to patient group (P=0.0098), while the frequencies of other genotypes (AT and TT) and alleles A and T were not significantly different among the participants. In addition, no association was found between the IL-6 (-174 C/G) polymorphism and Brucellosis.

Conclusion: In conclusion, this study indicated that the IL-8 -251 AA genotype may be considered as a genetic susceptibility factor for Brucellosis.

Keywords: Interleukin-8, Interlukin-6, gene polymorphisms, Brucellosis

[1]Department of Immunology, Professor Alborzi Clinical Microbiology Research Center, Shiraz University of Medical Sciences, Shiraz, Iran
[2]Department of Immunology, Fasa University of Medical Sciences, Fasa, Iran

A Comparative View of Infection-Control Nurses and Head Nurses in Their Concept of Hand Hygiene Infrastructure at Different Wards of Imam Reza Hospital, Mashhad, Iran

Irandokht Mostafavi, Atousa Ariafar, Nasrin Khosravi, Hamidreza Naderi, Fereshteh Sheybani, Mohammad Hasan Aelami

Service of prevention and infection control, Imam Reza hospital, Mashhad, Iran

Abstract

Background: Health care associated infections are a major problem for patient safety and its prevention must be a first priority for any health care setting and institution to provide safer patient care. Hand hygiene is a simple and effective measure to reduce the rates of these infections. WHO provided guidelines for hand hygiene in health care settings. For implementation of these guidelines, we need ward structure survey.

Methods: We used a questionnaire including parameters for ward-structure survey on the basis of WHO guidelines in different wards of Imam Reza hospital, Mashhad, Iran during the first three months of 2012. Infection-control nurses and head nurses filled the forms ward by ward personally. Then the differences between two groups were analyzed by statistical measures.

Methods of data collection:

In this study for each ward, two questionnaires and one check list were used:

A. The first questionnaire included ward, services, city, country, department (Medical - Surgical - ICU - EMS - Obstetric - Pediatric - Rehabilitation - outpatient, etc.) and position the person who filled out the questionnaire (experts from the two groups that were supervisors and infection control nurses)

B. The second questionnaire included questions related to hand washing requirements completed by the two groups (supervisors and infection control nurses) answered each question by yes (coded 1), no (coded 2), never (coded 0), rarely (coded 1), alternate (coded 2), always (coded 3). The total point for each person was the sum of question point she/he answered.

C. The check list included information about different Hospital wards' hand washing Requirements

The Cronbach's alpha method was used to determine hand washing questionnaire validity with emphasis on the questions' content.

Results: There were statistically significant differences between two groups for following questions: Are disposable towels available at all sinks, is an alcohol-based hand rub available, are wall dispensers placed at the point of care, does each health-care worker have easy access to hand rub bottles, are hand rub dispensers replaced when empty, are posters illustrating hand rub technique displayed close to the dispensers and in multiple areas of the ward.

Head nurses had positive view on hand hygiene requirements at wards in relation to infection control nurses.

Conclusion: We should consider the differences between views of infection-control nurses and head nurses when we survey ward-structure for hand hygiene.

Keywords: Hand hygiene, infrastructure survey, wards, Iran

Infection Control Status in Hospitals of Qazvin Province in 2009-2010

Msoud Sharifi[1], Zahra Rajabi[2], Farzad RajabiYekta [3]

Abstract

Background: In order to control and prevent hospital-associated infections, members responsible for management need to understand the importance of infection control programs. An accurate comprehension of the tools was enabled to healthcare workers to implement infection control programs effectively in order to protect themselves and patients from the transmission of infections. The aim of this study was to determine the infection control status in hospitals located in Qazvin province in 2010

Methods: The target hospitals were selected. Data was collected through direct observation of documents and interview with infection control nurse during the last trimester of 2009 and first trimester of 2010.

Results: Thirteen hospitals including five educational (38.5%), four governmental- non-educational (30.8%) and four private hospitals (30.8%) were observed. There were 875(54.1%), 446 (18.3%) and 296 (27.5%) beds in the three hospital groups, respectively. The average period of service for infection-control nurses and doctors were 3.6, 1.1, 1.8 and 6.5, 1.5 and 2.3 years in the three groups of hospitals, respectively. The average of the establishment precedence of infection control committee to the infection control team was 1.39, 1.41 and 1.48 years. Structures of the teams were suitable in 0, 2, 2 and the structure of the committee was suitable in 0, 4 and 2 hospitals. The diagnosis and report process of nosocomial infections were correct in 0, 2 and 1 hospitals. Antiseptic usage in high risk wards and hand washing solution usage were correct in 3, 3, 3 and 4, 3 and 3 hospital groups, respectively. Microbial surveillance results in wards were correct in 0, 2 and 1 hospitals.

Conclusion: In all the hospitals, the infection control committee was established before the infection control team. The management of infection control committee was not right in any of the hospitals. So, the output was not valid, too. There was no actual infection control doctor in any of the hospitals.

Keywords: Infection control team, Infection control committee, Educational hospital, Governmental hospital, Qazvin

[1]Councilor of the President of Qazvin University of Medical Sciences in hospital-associated Infection's control
[2]Director of hospitals affairs, Deputy of Treatment, Qazvin University of Medical Sciences, Qazvin, Iran
[3]Director of the office of nursing, Deputy of Treatment, Qazvin University of Medical Sciences, Qazvin, Iran

Comparison of BACTEC Blood Culture with Conventional Blood Culture Method for Detection of Nosocomial Blood Stream Infection in Imam Reza Hospital, During 2011 and 2012

Kiarash Ghazvini[1,2], Masoud Yosefi[2], Saeid Amel Jamehdar[1,2], Mohammad Hasan Aelami[3], Maryam Kamaladini[2], Leila Ataei[2]

[1]Microbiology and Virology Research Center, Avicenna Research Institute, Mashhad University of Medical Sciences, Mashhad, Iran
[2]Department of Microbiology, Imam Reza Hospital, Faculty of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran
[3]Department of Pediatrics, Imam Reza Hospital, Faculty of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran

Abstract

Background: Nosocomial bloodstream infection is an increasingly common cause of mortality and morbidity in hospitals. Different Methods are invented for their detection. This study was performed to compare BACTEC blood culture with conventional blood culture method for detection of nosocomial blood stream infection in Imam Reza hospital during 2011 and 2012.

Methods: The results of blood culture by conventional method during 9 month period were compared with the results of automated blood culture method (BACTEC) in similar 9 months period in Imam Reza University Hospital. The results were analyzed with SPSS software.

Results: The automated blood culture method (BACTEC) has been shown to be superior to the conventional blood culture method for the detection of nosocomial blood stream infection. The BACTEC blood culture allowed detection of more episodes of bacteremia than did the conventional blood culture method ($P < 0.05$). The time for diagnosis is much shorter in BACTEC blood culture method ($P < 0.001$).

Conclusion: We conclude that the automated blood culture method (BACTEC) is an alternative for conventional blood culture method in detection of episodes of infection and has the added benefit of sooner detection.

Effects of Water/Soap and Alcohol on Eliminating Nosocomial Microorganisms

Zahra Mazloum[2], Azadeh Ebrahimzadeh[1], Mahsa Mousavi[3], Majid Zareh[4]

[1]Assistant professor of infectious Disease, Birjand University of Medical Sciences, Birjand, Iran
[2]Assistant professor of Endocrinology Research Center, Mashhad University of Medical Sciences, Mashhad, Iran
[3]Assistant professor of Internal Medicine, Bojnord University of Medical Sciences, Bojnord, Iran
[4]Assistant professor of microbiology, Birjand University of Medical Sciences, Birjand, Iran

Abstract

Background: Nosocomial infections develop after 48 hours of hospitalization or within 30 days of discharge. More than 1.4 million people and 5% of hospitalized patients suffer from nosocomial infections and 2000 people die from these infections every year. One of the most important ways of transmission is contaminated hands of the personnel that can be eliminated by washing hands with water and soap or antimicrobial agents.

The main aim of this study was to examine the effects of water/soap and alcohol on eradication of staff's hand pathogens.

Methods: We took samples from the palms of one hundred personnel while performing nursing care activities, then asked them to wash their hands with water and soap or alcohol 10% for twenty seconds. Then, the sampling was repeated and the results were analyzed.

Results: Washing hands with either water and soap or alcohol eliminated the number of pathogens of the personnel hands (P=0.001). Alcohol was shown to be more effective than water and soap (P<0.002).

The most common microbes were *S. epidermidis*, *Klebsiella pneumonia* and *E. coli*. The most contaminated wards were ICU (100%) and surgery (87.5%).

Conclusion: Alcohol is more effective than water and soap on eradication of staff's hand microorganisms.

Keywords: Hand washing, nosocomial organism, alcohol, water with soap

Quantification of *Epstein-Barr virus* Load by Real-Time PCR in Patients at Risk Post-Transplant Lympho-Proliferative Disorders

Marzieh Jamalidoust[1, 2], Mazyar Ziyaeyan[1], Nasrin Aliabadi[1], Sadaf Asaee[1], Mahsa Moeini[1]

[1]Professor Alborzi Clinical Microbiology Research Center, Shiraz University of Medical Sciences, Shiraz, Iran
[2]Department of Virology, Faculty of Medical Sciences, Tarbiat Modares University, Tehran, Iran

Abstract

Background: *Epstein-Barr virus* (EBV) DNA measurement is being incorporated into routine medical practice to help diagnose, monitor, and predict post-transplant lympho-proliferative disorders (PTLDs) in immune-compromised graft recipients that occurred in 1-10% of these cases. PTLD is often fatal if not recognized and treated promptly.To this purpose, monitoring of EBV DNA load in bone marrow stem cell and kidney transplanted patients sera is considered to be a useful test.

Methods: EBV viral loads were monitored in forty nine (male/female: 33/16) and twenty four (male/female: 13/11) patients undergoing kidney and bone marrow transplant recipients respectively by quantitative Real-Time PCR assay. Serial DNA samples extracted from the plasma of these patients were analyzed.

Results: Plasma EBV DNA was positive in 7/49 (14.2%) kidney recipient patients and in 6/24 (25%) bone marrow transplant recipients. The patients considered to be at high risk for progressive EBV associated diseases, defined as an EBV load >1000 copies per milliliter of plasma were detected in 5/49 kidney recipient patients and 4/24 bone marrow transplant recipients. Median copy numbers were1500 and 2000 for kidney and bone marrow transplant recipients, respectively.

Conclusion: We suggest that quantification of cell-free EBV DNA in patients after BMT or solid-organ transplantation is a sensitive and specific marker for ongoing PTLD. As EBV Real-Time PCR with cell-free specimens is easy to perform, it might be useful for monitoring of patients at risk of developing PTLD after solid-organ transplantation or BMT.

Cytomegalovirus DNA Load in the Plasma from Liver and Kidney Transplant Recipients

Mazyar Ziyaeyan, Nasrin Aliabadi

Professor Alborzi Clinical Microbiology Research Center, Shiraz University of Medical Sciences, Shiraz, Iran

Abstract

Background: *Cytomegalovirus* (CMV) infection and disease are important complications following solid organ transplantation. Sensitive and specific evaluations for the early detection of CMV infection are required to monitor the patients. Also these evaluations are essential for timely application of antiviral therapy. The aim of this study was to monitor CMV active infection using quantitative Real-Time PCR in patient's kidney or undergoing liver transplant.

Methods: The present study included two hundred eighty nine Liver and one hundred and ninety two Kidney transplant patients who had received transplant between November 2009andJulay 2012. Blood samples were collected weekly during the early post-transplant period. In patients with risk factors or clinical suspicion of CMV infection, samples were also collected out of the period. Quantitative PCR was performed on plasma samples using a standard CMV PCR kit.

Results: The specimens consisted of eight hundred sixty EDTA-blood samples from four hundred eighty one patients Liver transplant recipients and one hundred ninety two kidney recipients were included in this study. CMV were detected in 60/289 Liver transplant recipient patients and 46/192kidney transplant recipients. CMV-DNA levels were calculated in the test sample by comparing CMV signal to quantify standard signal for each sample. The linear range of the method was 10^2 –10^6 copies/ml plasma.

Conclusion: The quantitative Real-Time PCR assay is a sensitive and rapid method for the diagnosis of CMV disease in solid organ transplant patients. This assay may be useful for the diagnosis of CMV disease in clinical situations in which CMV is suspected but the diagnosis is difficult to confirm. Also we suggest that Real-time plasma PCR guided preemptive therapy would increase the total number of solid organ recipients treated for CMV infection.

Keywords: *Cytomegalovirus*, Kidney, Liver, Transplantation

Herpes Simplex Virus DNA Detection by Real-Time PCR in Cerebrospinal Fluid of Suspected Patients

Nasrin Aliabadi, Mazyar Ziyaeyan

Professor Alborzi Clinical Microbiology Research Center, Shiraz University of Medical Sciences, Shiraz, Iran

Abstract

Background: *Herpes simplex virus* meningo-encephalitis is an acute infection accompanied by significant morbidity and mortality which can occur in children and adults. PCR has become the gold standard for diagnosis of HSV infection in central nervous system. Our objective was to use real-time PCR assay that reliably and accurately detects HSV in Cerebrospinal fluid (CSF).

Methods: We examined four hundred and thirty three CSF samples obtained from Professor Alborzi Clinical Microbiology Research Center, Nemazee Hospital, Shiraz between January 2009 and July 2012. CSF samples from four hundred and thirty three patients having typical symptoms of HSV CNS infection collected in sterile containers were transported immediately to the laboratory for processing. The samples were extracted by a standard spin column extraction method and analyzed by real-time PCR targeting common region of HSV1 and HSV2.

Results: Off our hundred and thirty three samples tested by real-time PCR, virus was detected in thirty two patients (7%). Sixteen PCR positive patients were male and fourteen were female.

Conclusion: Real-time PCR provides a fast and specific diagnosis. It was also considered as an early, rapid and sensitive diagnostic test and improves specific diagnosis of CNS herpetic infection and allows timely effective treatment leading to better outcomes.

Keywords: CNS infection, PCR, *Herpes Simplex Viru*

Rapid Identification of Pathogenic *Exophiala Species* by Specific Padlock Probes

Mohammad Javad Najafzadeh[1, 2], Saradeghi Keisari[2], GSde Hoog[2]

[1]Department of Parasitology and Mycology, and Cancer Molecular Pathology Research Center, Ghaem Hospital, School of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran
[2]CBS–KNAW Fungal Biodiversity Centre, Utrecht, Netherlands

Abstract

Background: Fungal infections have increased significantly over the last decades. Rapid and specific identification of fungal pathogens is important for appropriate treatment with antifungal agents. Conventional Methods for fungal identification rely on morphological and physiological tests and need several days or weeks and are frequently unspecific. Molecular identification mostly implies sequencing, which is relatively expensive and time-consuming. In this study we used a method based on ligase-mediated nucleotide discrimination with padlock probe technology, and signal amplification by rolling circle amplification (RCA) for Identification of pathogenic *Exophiala species*.

Methods: For the selection of padlock probes, sequences of ITS regions of more than 200 Exophiala strains from the CBS (Centraalbureau voor Schimmelcultures, Utrecht, The Netherlands) were aligned and adjusted manually using BIONUMERICS v. 4.61 to identify informative nucleotide polymorphisms. Four padlock probes targeting the ITS regions of four *Exophiala species* (*E. dermatitidis*, *E. oligosperma*, *E. spinifera*, and *E. jeanselmei*) were designed and were ordered from Invitrogen Inc.

Results: The assay proved to successfully amplify DNA of the target fungi at the level of species; while no cross reactivity was observed. The amplification product was visualized on a 1% agarose gel to verify the specificity of probe-template binding.

Conclusion: This technique proved to be suitable for the identification of four *Exophiala species*. The simplicity, sensitivity, robustness and low costs make it an attractive technique for the reliable identification pathogenic fungi.

Keywords: Padlock probe, *Exophiala*, Identification

Antimicrobial Activity of Novel Drug Delivery Systems Containing Vancomycin and Rifampin on *Staphylococcus epidermidis* Biofilm

Bibi Sedighe Fazly Bazzaz[1], Bijan Malaekeh-Nikouei[2], Bahman Khameneh Bagheri[3]

[1]Biotechnology Research Centre and School of Pharmacy, Mashhad University of Medical Sciences, Mashhad, Iran
[2]Nanotechnology Centre and School of Pharmacy, Mashhad University of Medical Sciences, Mashhad, Iran
[3]School of Pharmacy, Mashhad University of Medical Sciences, Mashhad, Iran

Abstract

Background: *Staphylococcus epidermidis* (SE) biofilms are developed when adherent microorganisms accumulate on medical devices. Many approaches are being pursued in order to eradicate biofilm such as combination therapy. Combination of rifampin and vancomycin show better activity against SE biofilm. Combination therapy is type of conventional treatment suffers from some limitations such as delayed penetration. Liposomes, as novel drug delivery systems, were used to enhance drug penetration. The aim of the present study was to examine the ability of different liposomal formulations loaded with vancomycin or/and rifampin to remove SE biofilm.

Methods: Cationic liposomal formulations loaded with vancomycin or/and rifampin were prepared and characterized, by zeta potential and size distribution, to investigate their effect on SE biofilm producer (DSMZ3270).To investigate antibacterial activity, the individual well of a 96-well microtiter plate was filled with diluted culture and incubated overnight at 37 °C. After incubation, biofilm was attached to the bottom of wells. Formulations were added to each well and their ability on eradication of bacterial biofilm was assessed through optical density (OD).

Results: The zeta potential (mV) of liposomal rifampin, liposomal vancomycin and liposomal combination was 36.87±2.53, 37.60±1.34 and 23.33±2.16, while the mean sizes of these liposomal formulations (nm) were 142.03±4.36, 131.98±1.64 and 140.60±7.50, respectively. OD results showed liposomal rifampin was the most effective formula among other antibiotic liposomal formulations and there was not any synergistic effect between rifampin and vancomycin.

Conclusion: This study highlights the advantages of liposome as a novel drug delivery system for biofilm eradication.

Keywords: Bacterial biofilm, Liposome, *Staphylococcus epidermidis*

HTLV 1(*Human T Lymphocyte Virus Type 1*) In Pregnancy and Breast Feeding

Abdolkarim Hamedi[1], Abdolali Kharazmi[2], Farideh Akhlaghi[3]

Abstract

Background: *Human lymph tropic T-cell virus* is a retrovirus as HIV that produces immune deficiency. Human T-cell leukemia virus type 1(HTLV1) is endemic in the Caribbean, Japan, South America and Iran. Both types of HTLV can be transmitted through breast feeding, sexual contact and blood transfusion. Rate of vertical transmission from mother to child are (2-3) 2.7% in formula fed infants, 5% with three months breast feeding and up to 20 % with prolonged breast feeding and vertically acquired HTLV1 leads to adult T-cell leukemia/lymphoma2-5% of infected infants. The aim of this study was to response this question: Do you need to request HTLV1 antibody in pregnant women? This positive AB had no problem and no preventive in pregnant women for fetus. Antenatal screening for HTLV1 in pregnant mothers should not be recommend unless in high risk mothers who live in endemic areas. So we should not screen this AB routinely in pregnancy.

Methods: Fallow up and effects of HTLV1 positive AB. in pregnant women referred to infectious clinic.

Results: Of 60 pregnant women that need infectious counseling, 45 cases had TORCHS study AB. Fourteen cases (23%) had HTLV1 positive AB. Two mothers in repeated test were negative. Of twelve cases eight mothers had delivery with cesarean for positive HTLV1 AB. Only five infants were breast fed and had no problem until eighteen months of age (HTLV1 AB is negative).

Conclusion: Our results show that we should not screen HTLV1AB in pregnant women routinely. If history of contact with disease (myelopathy, plegia) was in family of pregnant women then we should evaluate HTLV1AB in mother. In the case of this positive AB, there are no harms and no preventions for both mother and fetus/newborn.

Keywords: HTLV1, Pregnancy, Antibody

[1]Department of pediatric Infectious man, Mashhad University of Medical Sciences, Imam Reza Hospital, Mashhad, Iran
[2]professor of Pediatrician, Mashhad University of Medical Sciences, Ghaem Hospital, Mashhad Iran
[3]Associate Professor of Obstetrics and Gynecology Department, Imam Reza Hospital, Mashhad University of medical Science, Mashhad, Iran

Infective Endocarditis in Intravenous Drug Abusers in Mashhad, North-Eastern of Iran

Aliasghar Moeinipour, Mohammad Abbasi Tashnisi, Zohreh Bonakdaran, Ahmad Amouzeshi, Zahra Nasserifar, Golamreza Gorgiji

Abstract

Background: Infective endocarditis (IE) is one of the most severe complications in intravenous drug abusers (IVDA). Infective endocarditis usually involves tricuspid valve. *Staphylococcus aureus* is the most common etiologic agent, and it has a relatively good prognosis. Currently between 40% and 90% of IVDA with Infective endocarditis are HIV infected, and the HIV epidemic has caused a decrease in the incidence of this disease, probably due to changes in drug administration habits undertaken by addicts in order to avoid HIV transmission. Few data exist on infective endocarditis in intravenous drug abuse (IVDA) patients. In particular, clinical features, site of involvement and bacteriologic findings are controversial.

Methods: This descriptive and cross-sectional study was conducted of all patients (intravenous drug abusers patients) admitted in Department of Cardio-surgery, Imam Reza Hospital, Mashhad, IRAN. In 1389-1391 was studied. The clinical and microbiological characteristics of IE in a series of 9 IVDA patients were retrospectively assessed. The entire information system software SPSS 15 were investigated and analyzed.

Results: All our patients were male and the average age was 26.7years. Fifty percent of them were married and 50% were single. All of them were unemployed. Their economic status was lower than normal. All of them were IV addicted to crystal material. Although tricuspid valve involvement was in all IVDA cases, but in one patient, both tricuspid and mitral valve were involved. In addition, *Staphylococcus aureus* (33.3%), *K. pneumonia* (11.1%), *E. coli* (11.1%) and *Acinetobacter* (11.1%) were emerging pathogens in IVDA cases. The rate of pulmonary emboli was 22.2%. The clinical presentations were fever and shivering (100%), chest pain (44.4), myalgia (22.2), anorexia (22.2) and hemostasia (22.2). Fifty five percent had HCV+ and 11.1% of patients were HIV+ and HBV+ respectively. Types of procedure were TVR by biologic valve (77.7%), mechanical valve (22.2%) and repair (22.2%), respectively. Five patients (55%) were readmitted by IE. Preoperative mortality was zero.

Conclusion: Despite the fact that all organisms can cause Infective endocarditis, this study had shown that *Staphylococcus aureus* is the most common etiologic agent and our patients had a good prognosis. Tricuspid valve involvement was in all IVDA cases. The most clinical presentations were fever and shivering. The prevalence of HCV in Infective endocarditis and IVDA was rather than 50% and readmission in our patients was 55% that represented in our IVDA patients had bad hygiene and need to be educated and have socio-economic support.

Department of Cardiac Surgery, Imam Reza hospital, Mashhad University of Medical Sciences, Mashhad, Iran

Keywords: Microorganism, infective endocarditis, intravenous drug abusers patients

Third Section
Poster Presentations
First Day

Waste Management in Mashhad Hospitals

Rozita Davoodi, Golnaz Sabouri, Haleh Ghooshkhanei, Shaghayegh Rahmani, Azadeh Soltanifar, Tayebeh Hoseini, Maryam Zare Hosseini, Mahbobe Asadi

Research Center for Patient Safety and Health Quality, Mashhad University of Medical Sciences, Mashhad, Iran

Abstract

Background: One of the first steps to improve medical waste management is awareness of the quantity of medical waste and monitoring medical waste management. The aim of this study was to determine the present status of waste generation and the process of waste management in hospitals.

Methods: This cross sectional study was performed in 10 hospitals supervised by Mashhad University of Medical Sciences in 2011-12. Standard check list was prepared according to Ministry of Health instructions for waste and completed by two trained environmental health experts. Data were analyzed with SPSS version 16.

Results: The total waste generated in Mashhad hospitals was 7630 kg/day which was comprised of 62.28% of general medical waste, 35.13% infectious waste and 2.59 % sharp waste. The mean generation rate for total waste, general waste, infectious waste and sharp waste, respectively, were 2.58, 1.68, 0.94, 0.07 kg/bed/day. Mean scores of the different steps of waste management process regards to Ministry of Health instructions were as follows: waste segregation 63.89%, waste storage 66.54%, and waste transportation 75.6 % and waste treatment 62.86%.

Conclusion: High rate of infectious waste shows the need for establishing executive rules and standards for medical waste management, increasing staff knowledge and education, careful and constant monitoring of waste management in order to maintain and increase community and environmental safety.

Keywords: Hospital, medical waste, waste management

Genetic Analysis of *Staphylococcus aureus* Strains Isolated from Patients Admitted to Alzahra Hospital in Isfahan

Seyed Asghar Havaei, Mojtaba Shahin, Sharareh Moghim, Amir Azimian, Nafiseh Sadat Hosseini

Microbiology Department, Isfahan University of Medical Sciences, Isfahan, Iran

Abstract

Background: *Staphylococcus aureus* is a major human pathogen associated with a wide range of community and hospital acquired infections. Therefore studying its origin and resistance is of utmost importance for determining an appropriate treatment pattern. The aim of this study was to detect methicillin-resistance gene by PCR and demonstrate its typing using SCC mec and agr Methods.

Methods: A total of one hundred clinical samples were collected from patients admitted to different wards of Esfahan's Alzahra hospital. MIC to methicillin was determined using disc diffusion method. Thereafter the samples containing mecA gene were subjected to SCC mec and agr typing. All samples were ultimately tested for antibiotic resistance using disc diffusion method.

Results: Frequency of mecA gene in *S. aureus* strains was found to be 28% using PCR (Genotypic method). Resistance to oxacillin was determined 24% by agar dilution method (phenotypic method). Results by SCC mec typing revealed that the majority of strains were type IV and the minority were type I whereas agr typing showed type I to be predominant with the minority belonging to type III.

Conclusion: The resistance of *S. aureus* strains to antibiotics is increasing. In addition, SCC mec type IV isolates, being CA-MRSA themselves, are continuing to spread in communities. It should be noted that *S. aureus* strains in different regions have different agr patterns.

Keywords: *Staphylococcus aureus*, methicillin, mecA, SCC mec, agr

Assessment of Consideration toward Hand Hygiene in Shariati Hospital of Isfahan in 1389

Fateme Kafami Ladani[1], Setare Korang Beheshti[2], Vahid Ghanbari[3]

Abstract

Background: Nosocomial infection is one of the most important healthcare problems. Hand hygiene is the basic step to reduce infections. It is a simple step though; the weakness of its acceptance among healthcare supervision is trouble-making worldwide. Present study was aimed to determine consideration toward hand hygiene in Shariati hospital of Isfahan.

Methods: This study is a descriptive-sectional one which has been done on all unites of Shariati hospital of Isfahan (except operation room and intensive care unit). Data were collected through one questionnaire and checklist. The condition of sections and consideration toward hand hygiene were classified in to three levels of good, medium and weak. The collected information was analyzed by using SPSS 11 software and descriptive-analytical statistical tests.

Results: Results showed that hand hygiene in the majority of study units (63%) is in good level. Also the average of scores for washing hands was evaluated to be in medium level (44/87).

Conclusion: In order to reduce nosocomial infections to control epidemics and outbursts of illnesses, it is important to improve the quality of hand hygiene in healthcare systems which indeed require systematic alteration in attention to patients and also changing the personal adherence to hand hygiene.

Keywords: Nosocomial infections, hand hygiene, hand washing

[1]Clinical Nurse Specialist at Intensive Care Unit, Shariati hospital, Shariati Street, Isfahan, Iran
[2]Shariati hospital, Shariati Street, Isfahan, Iran
[3]School of Nursing and Midwifery, Ilam University of Medical Sciences, Ilam, Iran

Contamination of Computer Keyboards Located in Various Wards of Vali-E-Asr University Hospital to Common Nosocomial Pathogens in Birjand

Mohammad Hasan Namaei[1], Sima Surgi[2], Hoda Khoshbakht [2], Nahid Askari[3], Seyed Alireza Javadinia[4]

Abstract

Background: The aim of this study was to evaluate bacterial and *Candida*l contamination of computer keyboards located in various wards of Vali-e-Asr university Hospital, Birjand, Iran.

Methods: In this study all computer keyboards in various wards of Vali-e-Asr hospital were sampled (n=24). The samples were sent to Microbiology Research Laboratory, Birjand University of Medical Sciences. Samples were cultured on Blood agar, Manitol Salt agar and Eosin Methylene Blue media. The isolated bacteria were identified based on their colony morphology and biochemical characteristics.

Results: A total of twenty six samples from twenty four different computer keyboards of sixteen different wards were obtained. Two keyboards of Infectious disease ward and Neurology ward were routinely disinfected at the end of every shift. All samples (100%) showed contamination to different bacteria. The computer keyboard located in Internal Medicine ward (women division) was the most contaminated keyboard. Thirteen different bacterial *spp.* were isolated from keyboards of different computers. Species belong to *Enterobacteriaceae* family (61.5%) were the most common contaminating bacteria followed by Bacillus *spp.* (30.7%)

Conclusion: Based on the results all the sampled keyboards were contaminated to at least one bacterial *spp.* Therefore, it is necessary to pay more attention to disinfection of computer keyboards in hospitals.

Keywords: Nosocomial Infection, Computer Keyboard, Nursing Station

[1]Infectious diseases research center, Birjand University of Medical Sciences, Birjand, Iran
[2]Student Research Committee, Birjand University of Medical Sciences, Birjand, Iran
[3]Microbiology Research Laboratory, Birjand University of Medical Sciences, Birjand, Iran
[4]Student Research Committee; Birjand University of Medical Sciences, Birjand, Iran

Frequency of Pathogenic Bacteria Isolated From Tracheal Secretion of Hospitalized Patients in ICU and Determine Antibiotic Resistance

Elham Jamali-langroudi, Hadi Peyman, Javaher Khajavi-khan, Monireh Yaghoubi, Nourkhoda Sadeghifard

ICU Ward, Emam Khomeini hospital, Ilam University of Medical Sciences, Ilam, Iran

Abstract

Background: Ventilator associated pneumonia (VAP) is one of the most frequent infections in ICU. The current study aimed to determine frequency of pathogenic bacteria isolated from tracheal secretion of hospitalized patients and determine antibiotic resistance in ICU ward of Imam Khomeini hospital in Ilam, 2010-2011.

Methods: In a prospective cross-sectional study, two hundred and thirty nine tracheal secretion samples of ICU patients were assessed. Data was collected from health records using a checklist and was analyzed by SPSS software version 16.

Results: Overall, from two hundred and thirty nine samples studied, eighty nine sample cultures (38.4%) were positive. Most of samples (83.2%) were male and the most prevalent isolated bacteria were *Enterobacteriaceae* (59.3%), *Pseudomonas* (26.4%) and *Staphylococcus* (14.3%). *Enterobacteriaceae*, *Pseudomonas* and *Staphylococcus* were resistant more to cefotaxime, carbenicillin and ceftriaxone respectively.

Conclusion: *Enterobacteriaceae* family members were the most prevalent bacteria isolated of VAP that had high resistance to third generation of cephalosporins. Isolation of bacterial pathogens from the tracheal secretion in order to start immediate and suitable treatment for VAP is necessary.

Keywords: Drug resistant, Ventilator associated pneumonia, ICU, Ilam

The Incidence of Cross Infections in Imam Reza Hospital in Mashhad from 2009-2011

Aida Javanbakht, Mahboubeh Naderinasab, Emran Askari, Irandokht Mostafavi, Negar Moghaddas, Ladan Danesh

Department of Microbiology, Imam Reza Hospital, Mashhad University of Medical Sciences, Mashhad, Iran

Abstract

Background: Cross infections are considered a major public health problem worldwide. It is estimated that 1.4 million patients suffer from cross infections at any given time. They are associated with delay in recovery, increased mortality, morbidity and length of stay in hospital. The purpose of this study was to report the incidence of cross infections in our teaching hospital from 2009-2011.

Methods: In this descriptive cross-sectional study, patients from June 2009 to February 2011 admitted to seventeen wards of Imam Reza Hospital in Mashhad were studied for cross infections. Patient's age, sex, site of infection, ward of hospitalization and type of microbial infections were collected and analyzed by SPSS 16.0.

Results: In 76766 patients, 941 cross infections were identified in 720 patients (50.2% female, 49.8% male with the mean age of 43.2±24.3 years). The overall incidence of cross infections was 0.94%. The highest frequency of cross infections was in burn ward (37%, n=322). The most isolated bacteria in our hospital were *Acinetobacter* (25.5%), *Staphylococcus aureus* (18.4%) and *Pseudomonas Aeruginosa* (17.4%). Also *Staphylococcus epidermidis* had the least prevalence (0.6%). The most frequent types of infection were: surgical site (44.5%), urinary tract (22.7%) and blood stream (16.9%).

Conclusion: Results of the present study showed that the incidence of cross infections was low in our hospital. Improved infection control techniques and sufficient numbers of nurses may reduce the prevalence of it especial in our burn ward.

Keywords: Cross infections, *Acinetobacter, Staphylococcus aureus*, *Pseudomonas Aeruginosa*

Effect of Oral and Dental Care in the Incidence Rate of Ventilator-Associated Pneumonia (VAP) in Intensive Care Unit (ICU)

HedayatolahLalegani[1], Ali Esmaeli Safar[2], Mohamad Rahimi[3], Mehrdad Karimi[4]

Abstract

Background: Ventilator-associated pneumonia (VAP) is the most frequent nosocomial infection among intensive care unit (ICU) patients. The present study was aimed to determine the effect of oral and dental care on the incidence rate of ventilator-associated pneumonia in Intensive Care Unit.

Methods: In this study, patients with more than 18 years of age who were admitted to intensive care unit that received mechanical ventilation for more than 48 hours were considered as sample population. Afterwards, they were randomly assigned to intervention and control groups. Patients whose mouth tracts were not suctioned and brushed or not exposed to antiseptic solutions went through intervention.

Patients in the intervention group were suctioned once every 6 hours. Furthermore, their oral tract was cleansed every 4 hours and brushed twice a day. Among control group patients, only routine dentalcare and oral care were performed.

Results: There were no significant differences between both groups regarding age, sex, and severity of illness (P=0/06). The incidence rate of ventilator-associated pneumonia was 8.6% in the intervention group before intervention. However, it decreased to 6.1% after intervention. In addition, the duration of mechanical ventilation and the length of stay in the ICU were significantly decreased in the intervention group.

Conclusion: Our findings suggest that the use of dental and oral care can significantly reduce frequency of ventilator-associated pneumonia and health care expenses.

Keywords: Dental and oral care, ventilator-associated pneumonia, Intensive Care Unit

[1]Education Center of Kashani hospital, Shahrekord University of Medical Sciences, Shahrekord, Iran
[2]Nursing Center of Kashani Hospital, Shahrekord University of Medical Sciences, Shahrekord, Iran
[3]Education Development Center, Shahrekord University of Medical Sciences, Shahrekord, Iran
[4]Associate Professor and surgery, Shahrekord University of Medical Sciences, Shahrekord, Iran

Efficacy of Barij Antimicrobial Gel and Chemical Hand Rub Gel (0.1% Triclosan) In Controlling Microorganisms of Hand

Mohaddese Mahboubi[1, 2], Nastran Kazempour[1], Hossein Akbari[3]

Abstract

Background: The efficacy of Barij antimicrobial gel with natural ingredients and chemical gel including 0.1% of triclosan were evaluated to reduce the risk of infections. Barij antimicrobial gel was developed by synergistic effects of *Pelargonium graveolens*, *Citrus aurantifolia* and *Eucalyptus globolus* essential oils for reducing the incidence of skin flora.

Methods: The evaluation was performed according to the PrEN 12504 suspension test using *Escherichia Coli*, *Enterobacter aerugenes*, *Salmonella typhimurium*, *Listeria monocytogenes*, *Pseudomonas Aeruginosa*, *Shigella dysentriae*, *Staphylococcus aureus*, *Candida albicans* and *Aspergillus niger*. Cotton swab test was used for evaluating the natural and chemical efficacies on skin flora of sixty three healthy volunteers. No cuts or abrasions and other skin disorders were present on the palm of their hands.

Results: The results of in vitro study exhibited that Barij antimicrobial gel has been removed 99.9% of different microorganisms at 15 s as chemical gel. Barij antimicrobial gel and chemical gel has been reduced *Staphylococcus aureus* (69.6%, 50%), *S. epidermidis* (51.4%, 54.5%), *S. saprophyticus* (78.9%, 75%), *Micrococcus roseus* (100%, 100%), *Aspergillus niger* (83.3%, 100%) and *A. parasiticus* (50%, 100%) on the hand of volunteers.

Conclusion: The antimicrobial activity of Barij antimicrobial gel was higher than chemical gel on skin flora and this difference was not meaningful (P>0.05).

Keywords: Barij antimicrobial gel, triclosan, *Staphylococcus aureus*, Essential oil

[1]Department of Microbiology, Research Center of Barij Essence, Kashan, Iran
[2]Microbiology Group, Medicinal Plants Research Center of Jundi Shapour, Kashan, Iran
[3]Department of Health and Biostatistics, University of Kashan Medical Sciences, Kashan, Iran

Prevalence of Needle Sticks Injuries among Interns, Nursery and Midwifery Students, Nurses and Midwifes in Azad University Hospital

Hossein Mokhtari, Fatemeh Habibi, Arefeh Aboveisani, Toktam Yaghubi, Sepideh Haj Mohammadi

Infectious diseases specialist, Assistant professor of infectious diseases, Islamic Azad University of Mashhad Branch, Mashhad, Iran

Abstract

Background: Prevalence of needle sticks injuries (NSI).

Methods: In a descriptive study, Interns, nursery and midwifery students with history of one year of clinical work, nurses and midwifery were asked with a questionnaire.

This questionnaire has questions of NSI in the past twelve months and also sex and educational fields.

Results: This questionnaire is completed by three hundred and seventy people

1- NSIs in interns were 9 from 50. (18%)
2- NSIs in nursery students were 48 from 138. (34.8%)
3- NSIs in midwifery students were 9 from 58. (15.5%)
4- NSIs in nurses were 63 from 114. (55.3%)
5- NSIs in midwiferies were from 12. (41.7%)
6- NISs in females were 106 from 299. (35-4%) and in males

Conclusion: NSI prevalence in nurses and midwifes was obviously more than students that is related to student's less clinical work. NSI in nursery students were more than interns and midwifery students that showed low standard health care due to low education in this group. So the prevention of NSI is the most important point and suitable medical equipment should be provided. Also health care educations should be increased and special centers treat and follow up these health care groups.

Keywords: Needle sticks injury, Intern, Health care worker

Identification of Bacterial Cause of Ventilator-Associated Pneumonia from the Patients Who Have Been Hospitalized in the Intensive Care Unit of Shahid Rejaei Hospital, Tonekabon

Hoda Ghaffary[*1], Masood ghane[2], Majid Pouya[3], Reza golijani moghadam[2], maryam shafipour[1],mozhgan pourjafari[1]

Abstract

Background: Ventilator-Associated Pneumonia is the most prevalent cause of mortality in ICU patients. Risk of infection is three to ten times more than the patients who have been hospitalized in other wards. The objective of this study was to identify the bacterial cause of Ventilator-Associated pneumonia in patients who have been hospitalized in the ICU of the Shahid Rejaei hospital of Tonekabon.

Methods: In this research which has been carried out one year (2010-2011), among thirty five patients hospitalized in ICU who had used the mechanical ventilation, after the drawing out of the Nedator from the patient's lung, the tube was cut by the sterile scissor and transferred into the brain-heart infusion broth and incubated for 48 hours under 37˚C. Following the incubation period samples was transferred to the blood agar and DNA extraction was carried out using the phenol-chloroform's technique through the appearance of the grown colonies. In order to reproduce the DNA, PCR test was performed using the 16s rRNA universal primers. The PCR product was sequenced in order to identify the isolated bacteria.

Results: Out of thirty sample collections, forty six strains of bacterial isolates eleven had belonged to *Staphylococcus aureus*, two to Corynebacterium, two to *Staphylococcus homonis*, one to *Staphylococcus epidemitis*, one to *Staphylococcus lungodensis* and one to *Staphylococcus intermedius* species and from gram negative bacteria, seven to *Pseudomonas aeruginosa*, six to *Klebsiella pneumonia*, five to *Acenitobacter bumannii*, three to *Enterococcus fecalis*, two to *Alcaligenes fecalis*, two to *Enterobacter cloace*, one to *Enterobacter aeruginosa*, *E. coli* and one to *Shigella flexeneri* observed.

Conclusion: The results obtained from the current research showed that *Staphylococcus aureus* and *Pseudomonas Aeruginosa* are from the most prevalent bacteria of the Ventilator Associated pneumonia. Identification and survey rate of the frequency of the bacterial cause of the nosocomial pneumonia in order to determine the therapeutic strategy in initial confrontation and infection control is regarded to as a necessity.

Keywords: Pneumonia, ICU, ventilator, prevalence

[1]Master of science, microbiology Group, Islamic Azad University, Tonekabon Branch, Tonekabon, Iran
[2]Assistance professor, microbiology Group, Islamic Azad University, Tonekabon Branch, Tonekabon, Iran
[3]Assistance professor, Medicine Group, Islamic Azad University, Tonekabon Branch, Tonekabon, Iran

Evaluation of Nosocomial Infections in Hashemi Nejad Hospital of Mashhad, Associating Four Consecutive Years from 1387 to 1390

Mahnaz Ghazanfari, Hassan porhekmat, Masoumeh Heydari

Hashemi Nejad Hospital, Faculty of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran

Abstract

Background: Nosocomial infections have always been one of the major problems of healthcare system that increases patient's hospitalization. Increased risk of mortality caused by these infections is increasing the cost of hospitalization. This study was to determine factors of nosocomial infections associated in four consecutive years.

Methods: This was a Retrospective-descriptive study which was done during four years in Hashemi-Nejad Hospital. Data collection was carried out based on clinical symptoms from nosocomial infections surveillance system cultivation patterns. The Excel and NNIS forms have been analyzed.

Results: Nosocomial infection in 1387 (96Pneu-, SSI-48, UTI-5, BSI-0) to the 22715 patients hospitalized in the year 1388 (85Pneu-, SSI-48, UTI-4, BSI-5) per 22 850 patient admitted in 1389 Pneu-89), SSI-31, UTI-6, BSI-7) per 22 300 patients hospitalized in the year 1390, 98 Pneu-,22 - SSI, UTI-9, BSI-2 22 750 per patient

Conclusions: Increasing awareness of staff in relation to compliance with all conditions and proffered solutions might be helpful. Communication standard was proposed in order to reduce nosocomial infections in health care and decrease costs.

Keywords: Hospital infections, Hashemi-Nejad hospital

Bacterial Infections of German Cockroaches (*Blattella germanica*) Collected from Hospitals of Hamedan District

Jalil Nejati[1], Amir Keyhani[1], Atefeh Bostanbakhsh[2]

Abstract

Background: Cockroaches are considered as a health problem because they freely move in infected sources and different wards of hospitals. Due to high frequency of German roaches in Hamedan hospitals, this study was aimed to identify the bacterial infection transmitted by their surface and their digestive system.

Methods: In this descriptive-analytic study, two hundred and twenty *Blattella germanica* were collected from fourteen wards of five hospitals. After anesthesia of insects and species identification, all of them were used to isolate bacteria from cuticle and alimentary tract. In this study E.M.B,T.S.I, DNAase, B.A, SF,SS, ONPG, MR, SIM, Manitol salt agar, Lysin, Simmon citrate and Urea were used as bacterial culture method.

Results: Twenty bacteria species isolated from cockroaches' surfaces and twenty one from digestive organ. *Escherichia Coli* were the most predominant bacteria isolated from external surfaces (25.7 %) as well as alimentary tract (29.3%). The frequency of bacteria isolated from the cockroaches' external surface was not significantly different from that of digestive organ except for *Shigella dysentery* ($P<0.001$), *Pseudomonas aeruginosa* ($P<0.001$) and *Klebsiella oxytoca* ($P= 0 .013$)

Conclusion: Since cockroaches can carry pathogenic bacteria, so their existence in hospitals could be a serious public health problem. It is suggested to compile programs in order to control cockroaches especially in the hospitals.

Keywords: *Blattella germanica*, Bacteria, Hospital

[1]Tehran University of Medical Sciences, Tehran, Iran
[2]Hamedan University of Medical Sciences, Hamedan, Iran

The Role of *Chlamydia pneumonia* Infection in Coronary Atherosclerosis

Mohammad Hadi Sadeghian[1], Seyed Abbas Tabatabaee Yazdi[2], Hossein Ayatollahi[3], Mohammad Reza Keramati[4], Kiarash ghazvini[5], Ali Reza Rezai[1], Nasrin Heidari[6], Maryam Sheikhi[7]

[1]Department of Hematology and Blood Bank, Cancer Molecular Pathology Research Center, Ghaem Medical Center, Faculty of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran
[2]Department of Pathology, Mashhad University of Medical Sciences, Mashhad, Iran
[3]Department of Hematology and Blood Bank, Endoscopic and Minimally Invasive Surgery Research Center, Faculty of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran
[4]Neonatal Research Center, Faculty of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran
[5]Department of Microbiology, Mashhad University of Medical Sciences, Mashhad, Iran
[6]Mashhad University of Medical Sciences, Mashhad, Iran
[7]Departmant of Endoscopic and Minimally Invasive Surgery Research Center, Faculty of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran

Abstract

Background: Coronary artery disease is one of the most important causes of death in the world and atherosclerosis is the most important cause of coronary artery disease. It is implicated that atherosclerosis may be triggered by an infectious agent which most likely is *Chlamydia pneumonia*; however, the role of *Chlamydophila pneumonia* in the pathogenesis of coronary atherosclerosis is still controversial. This study was performed to evaluate whether there is a significant relation between coronary artery with and without atherosclerotic plaque for detection of *Chlamydia pneumonia* Deoxy Nucleotide Acid (DNA) by Polymerase chain reaction (PCR) method.

Methods: This case-control study carried out on Formalin-fixed paraffin- embedded (FFPE) tissue biopsy specimens of coronary arteries that had obtained from thirty patients with coronary atherosclerosis and 30 subjects without atherosclerosis. Several tissue sections were prepared from each FFPE specimens; DNA was extracted by salting out method. *Chlamydia pneumonia* DNA was amplified by PCR assay and its products were analyzed by electrophoresis.

Results: The age range in the patients group was from 18 to 50 years and the male to female ratio was 5:1. One of the thirty coronary tissue samples had positive PCR for DNA of *Chlamydia pneumonia* (3.3%) and all of the control samples were negative. Fisher's Exact Test showed no significant difference for detection of *C. pneumonia* DNA between case and control group.

Conclusions: This study showed that *Chlamydia pneumonia* infection is not associated with coronary artery atherosclerosis.

Keywords: *Chlamydia pneumonia*, Atherosclerosis, coronary artery

Rapid Identification of *Atypical Mycobacterium Spp.* from *Mycobacterium Tuberculosis* by PCR-RFLP Analysis of Hsp65 Gene

Azadeh Nahavandi Araghi, Mahnaz Saifi, Esmail Zabar Zadeh, Ahmad Reza Bahremand, Ali karimi, Mahrouz Dezfoulian, Elham Safar Pour

Tuberculosis and pulmonary Research Department, Karaj Azad University and Tehran Pasteur Institute, Karaj, Iran

Abstract

Background: *Atypical Mycobacterium* is Saprophyte pathogens cause various infections. Some of them lead to Tuberculosis-like disease which makes it difficult to distinguish them from *Mycobacterium tuberculosis*. Conventional Methods for identification of *Mycobacterium* are time consuming. Treatment of atypical *Mycobacterium* is difficult because not only are resistant to a wide range of antibiotics, but often difficult to differentiate them from *Mycobacterium tuberculosis*. It is considered one of the important reasons for treatment failure. PCR-RFLP (PRA) method where it is a method for detecting genotyping is more accurate than phenotyping method.

Methods: Samples of positive cultures of *Mycobacterium* from patients referred to the Pastor over 91 years were tested using biochemical diagnostic tests. Strain identification Methods were performed simultaneously by PCR-RFLP. A 644bp region of Heat Shock Protein 65 (Hsp65) was amplified by PCR. Subsequently, PCR products were digested with Ava II enzyme.

Results: with the PRA patterns of the total100 samples positive culture in91,33 cases(33%) of *atypical Mycobacterium* were identified using standard algorithms were classified in 8 groups.

Conclusion: The results showed PCR-RFLP (PRA) using the enzyme Ava II is a simple, fast and accurate for the general grouping of *atypical Mycobacterium* isolates from TB and with reducing time to diagnosis of atypical strains from *Mycobacterium tuberculosis* can be effective in the treatment of Mycobacterial infections.

Keywords: Rapid identification, *Mycobacterium tuberculosis, atypical mycobacterium*

The pattern of Antimicrobial Use in Imam Reza Hospital: a Retrospective Study from 2010 to 2011

Javad Rashid, Nasrin Khosravi, Hamidreza Naderi, Irandokht Mostafavi, Fereshte Sheybani, Shahram Taherzadeh

Abstract

Background: Overuse of antibiotics increases antimicrobial resistance and the number of medicines that are no longer effective against infectious disease.

Methods: This study was conducted to evaluate the antibiotic prescribing pattern in Imam Reza University Hospital, Mashhad, Iran during a 2-years period between 2010 and 2011.

Results: According to the hospital patient registration system, 83634 and 87260 patients were hospitalized during 2010 and 2011 years, respectively. During these periods of time (2010 and 2011), 27.67% and 27.04% of hospitalized patients received antibiotic treatment when just 40.52% and 42.52% of whom had microbial culture results, respectively. There were no significant differences between the antibiotic drugs mostly prescribed during these two periods. The antibiotic drugs most frequently used were as follows: clindamycin (18.10%), ceftriaxone (14.95%), vancomycin (13.5%) and imipenem (12.67%).

Conclusion: According to the results of this study, it seemed that antibiotic prescribing in our center is mostly a symptom-based practice and the empirical antibiotic regimens are not escalated according to the microbiological data. We concluded that the current practice of antimicrobial prescribing in our center may need to be reviewed.

Nosocomial Infection Control, Imam Reza Hospital, Faculty of Medicine, Mashhad University of Medical Sciences, , Mashhad, Iran

Keywords: Antibiotic - culture - imipenem

Report of 3 Months Positive Blood Culture of Children in Hematology-Oncology Ward of Doctor Sheikh Children Hospital

Ali Ghasemi, Abdollah Banihashem, Zahra Badiee, Hamid Farhangi, Mohammadreza Mosaddegh Hesari

Pediatrics Hematology, Doctor Sheikh Hospital, Mashhad University of Medical Sciences, Mashhad, Iran

Abstract

Background: Many chemotherapy regimes are associated with myeloid suppression. In cancer patients, neutropenia is the most important risk factor for infectious complications are related to depth and duration of neutropenia.

Methods: This is a prospective study and evaluates the positive blood culture in admitted children with malignancy. We reviewed positive BC in 323 patients with 2400 admission days.

Results: Twenty-one patients had positive BC (8 ALL, 7 AML, 4 solid tumors, 2 other diagnosis). In positive BC %80 (17 patients) had neutropenia and %70 (12) had sever neutropenia. Duration of neutropenia was more than 7 days in %60 (10) of patients. The pathogens in our patients were *S.* epidermidis, %19(4) *Enterobacter*, %14(3) *Candida*, %9.5 (2) *pneumococcus*, %9.5 (2) *Pseudomonas*, 1 *Enterococcus*, *1 S. aureus*, and 1 *E. coli*. All of positive BC for *S. epidermidis*, *S. aureus* and *Pneumococcus* were sensitive to vancomycin and gram negative pathogens were sensitive to Amikacin.

Conclusion: The most important risk factor for positive BC is severe and prolonged neutropenia in children with malignancy. Appropriate antibiotic for *Staphylococcal* infection and gram negative pathogens was vancomycin and amikacin respectively.

Keywords: Children, malignancy, neutropenia, blood culture

Seroprevalence of *Brucella Canis* among Patients with Active Brucellosis

Manoochehr Rasouli[1], Mohammad Amin Behzadi[1], Mehdi Kalani[1], Asghar Mogheiseh[2]

Abstract

Background: *Brucella canis* infection is a zoonotic disease caused by a rough or mucoid, small, Gram-negative intracellular bacterium that can affect all breeds of dog and rarely human. The infection is endemic in the South and Central America; but it is sporadic in Europe and Asia. The current study was conducted to reveal the seroprevalence of *B. canis* among patients with active Brucellosis in Fars province, southern Iran.

Methods: Serum samples were taken from 68 patients with active Brucellosis including 57 male and 11 female from different areas of Fars province, Iran. The samples were examined with a commercial rapid *B. canis* Ab test kit (Anigen, Animal Genetics, Inc., Korea) base on chromatographic immunoassay. The sensitivity and specificity of the kits vs blood culture were 93% and 100%, respectively.

Results: *B. canis* antibodies were detected in 1/68 (1.47%) of patients. The history of this male individual showed that he had a chronic Brucellosis, which did not treat with routine antibiotic therapies. In addition, he was a shepherd and had close contact with animals especially dogs and this may be a predisposing factor for the transmission of disease to him.

Conclusion: Limited studies showed the existence of *B. canis* infection in companion dogs in Iran; however there is no report of the infection in human and this is the first report of human *B. canis* in Iran. Considering our results, detection of *B. canis* in chronic Brucellosis patients is notable. Due to the increase in close contact of human and companion dogs in recent years, more studies are essential to demonstrate the prevalence of the disease in Iran.

Keywords: *Brucella canis*, Seroprevalence, Human, Iran

[1]Professor Alborzi Clinical Microbiology Research Center, Shiraz University of Medical Sciences, Nemazee Hospital, Shiraz, Iran
[2]Department of Clinical Sciences, School of Veterinary Medicine, Shiraz University, Shiraz, Iran

Genome Phylogenetic Analysis of *A*/H1N1/ pdm09 *Influenza Virus* Isolated from Shiraz, Southern Iran

Mohammad Amin Behzadi, Mazyar Ziyaeyan, Abdolvahab Alborzi

Abstract

Background: A novel *influenza A virus, subtype H1N1* Which caused the first influenza pandemic of the 21st century, emerged in April 2009 and since then continues to circulate globally. In this study, we report the isolation and genome phylogenetic analysis of A/H1N1/pdm09 *Influenza Virus* from Shiraz, southern Iran.

Methods: The partial genome of the matrix protein of the A/H1N1/pdm09 *Influenza Virus* isolated from nasopharyngeal specimens during 2011 influenza season was amplified with specific primer sets and cloned in to the pTZ57R/T vector. The recombinant plasmid was sequenced by an ABI 3730 automated DNA sequencer (Applied Biosystems, USA) using the M13 universal primers. The sequence of the amplified segment was compared with reference sequences published in GenBank followed by topology analysis of the resulting phylogenetic tree using Laser gene sequence analysis software package (DNAStar, Madison, WI, USA).

Results: The data indicated that the prevalent A/H1N1/pdm09 *Influenza Virus* isolated from Shiraz had close relationship with other isolates from all around the world, although the small number of various nucleotides existed.

Conclusion: It can be concluded that the nucleotide differences in this viral genome segment may lead to the existence and prevalence of new isolates in southern Iran, although, complete sequencing of the viral genome is needed. Moreover, for rapid diagnosis of possible future pandemics, isolation and genetic monitoring of *Influenza Virus*es is strongly recommended.

Professor Alborzi Clinical Microbiology Research Center, Shiraz University of Medical Sciences, Namazi Hospital, Shiraz, Iran

Keywords: *Influenza A virus, H1N1pdm09*, Genome phylogenetic analysis, Matrix

Molecular Detection of Herpetic Ocular Infection; A Real-Time PCR Base Study

Roya Feyznezhad, Mazyar Ziyaeyan

Professor Alborzi Clinical Microbiology Research Center, Shiraz University of Medical Sciences, Nemazee Hospital, Shiraz, Iran

Abstract

Background: Herpetic ocular infection caused by *Herpes simplex virus* (HSV) is the major cause of corneal blindness in developed countries. However, in recent years the infection becomes more prevalent in developing countries and causing more blindness. Ocular herpes presents either as a primary infection, or more typically, as a recurrent disease following reactivation of the latent virus. The aim of the present investigation is to explore the usefulness of assessing eye herpetic lesion by Real-Time PCR in corneal scrapings and swab specimens.

Methods: Corneal scrapings or swab samples were obtained from 227 patients consecutively during the period from January 2009 through July 2012 in viral transport media. Viral DNA was extracted using commercial kits according to the manufacturer's instructions. The highly conserved region of HSV1 and HSV2 DNA polymerase was amplified using a TaqMan Real-Time PCR assay.

Results: The samples came from 189 adults and 38 children (129 males and 98 females; median age: 50.7 and range: 1-99 years). HSV DNA was detected in 67/227 (29.5%) corneal scrapings and swab samples submitted for analysis by Real-Time PCR. As revealed, 70.5% of the clinical samples tested were negative for HSV DNA by PCR.

Conclusions: *Herpes simplex virus* types 1 and 2 (HSV-1 and HSV-2) DNA has been found in the corneas of suspected patients with ocular lesions. The presented data in this study reveal that TaqMan Real-Time PCR testing of corneal scrapings and ocular swab samples, as a rapid and persuaded method, can be a first-line diagnostic procedure that is useful as a supplement to history and clinical examination.

Keywords: *Herpes Simplex Virus*, Keratitis, Ocular infection, Real-Time PCR

Incident HIV Infection among *Hepatitis C* Virus Infected patients in South of Iran

Marzye Jamalidoust[1, 2], Mazyar Ziyaeyan[1]

[1]Professor Alborzi Clinical Microbiology Research Center, Shiraz University of Medical Sciences, Shiraz, Iran
[2]Virology Department, Faculty of Medical Science, Tarbiat Modares University, Tehran, Iran

Abstract

Background: Because of shared modes of transmission, patients with *Hepatitis C* virus (HCV) infection are often co-infected with other types of hepatitis viruses and/or HIV. In this study, the prevalence of HIV positive patient and characteristics of HCV in this group have been described.

Methods: Two hundred and eighty three HCV infected patients that have been referred to our laboratory for first time was studied after their HCV infections were confirmed by western blotting test (Trusty one step rapid test-Artron Bioresearch Inc. -Canada). HIV prevalence, HCV RNA level, and HCV genotype were determined.

Results: The weighted overall estimate of HIV prevalence was 16.51% (36 cases), with significant variability depending on risk factors. Among HCV/HIV co-infected patients, 100% were "at risk". Genotype 1 was found in 80% of infected patients. Median HCV RNA level was $3.82 \times 10_6$ IU/mL.

Conclusion: We identified incidence of HIV infection among HCV-infected men involved in HCV therapeutic trials in the Iran. The question of whether rates of HIV infection are truly increasing among HCV-infected patients or whether the perception of increasing incidence is attributable to enhanced ascertainment warrants further investigation.

Rapid Detection of *Herpes Simplex Virus* (HSV) Infection in Mucosal and Cutaneous Ulcers of the Suspected Patients Referred to Nemazee Hospital, Shiraz, Iran by Real-Time PCR

Mazyar Ziyaeyan, Mandana Namayandeh

Professor Alborzi Clinical Microbiology Research Center, Shiraz University of Medical Sciences, Shiraz, Iran

Abstract

Background: The speed and sensitivity of real-time polymerase chain reaction (PCR) have made it a popular method for the detection of microbiological agents in both research and clinical specimens. For the detection and quantification of *Herpes Simplex* virus (HSV) in clinical specimens, real-time PCR has proven to be faster, more sensitive and safer than earlier Methods which included isolation of the virus in cell culture followed by immunofluorescence microscopy. The aim of this study was to detect the HSV DNA in skin samples of the suspected patients by Real-Time PCR

Methods: The study population consisted of 169 male and 148 female patients (n=317). Specimens were collected from various anatomical sites including 100face or lips, 65 oral cavities, 50 genital, 45fingers, and 57 other body parts. Cotton swabs were sent to the laboratory in buffered saline or viral transport medium. DNA was extracted using a viral DNA Isolation Kit according to the manufacturer's instructions. Real-Time PCR was performed on the purified DNA using a standard HSV PCR kit.

Results: The majority (52.05%) of the samples were from face, lips and oral cavity. All the genital lesions samples were taken by gynecologists. HSV DNA was detected in 33.5 of 100 patients with face or lip ulcers (33.5%), 26 of 65 patients with oral mucosa lesions (40%), 45 of 50 patients with genital involvement (90%), 40 of 45 patients with whitlow ulcers (88.8%), and in 14.2 of 57 patients with other body parts ulcers (25%).

Conclusions: Taking into account the high sensitivity, reproducibility and specificity, the Real-Time PCR assay can be used for the rapid detection of HSV DNA from skin origin clinical samples, especially in difficult clinical cases.

Keywords: *Herpes Simplex* Virus, rapid detection, PCR, skin infection

HCV Genotypes 2 and 4 Detection and Its Prevalence by Real-Time PCR in Shiraz

Sadaf Assaei, Mazyar Ziyaeyan

Professor Alborzi Clinical Microbiology Research Center, Shiraz University of Medical Sciences

Abstract

Background: *Hepatitis C* infection is the most common cause of end-stage liver disease in many countries recently. HCV is classified into seven genotypes. HCV Genotype 4 has been identified as the principle genotype amongst infected individuals from the Middle East, north and central Africa although there is a low frequency of detection in populations outside these areas. This study was conducted to determine the rate of genotypes 2 and 4 infection in Shiraz, Southern Iran

Methods: During 2010 to 2012, HCV genotyping was performed on sera of 574 HCV RNA positive patients by a TaqMan real-Time PCR with four specific probes that can detect HCV genotypes 1-4. The study consisted of 501 males (87%) and 73females (7.86%). The age range was 13-79 years with the mean of 34.3 and SD=12.01.

Results: Of the 574 patients examined, only 5 patients were detected with HCV genotype 4 infections, one of whom was living and working in Arabic countries of Persian Gulf residents. One of the patients is positive for HCV Genotype 2 and he was living and working in Arabic countries too.

Conclusion: Genotypes 2 and 4 HCV infections are rare in HCV chronic infected patients in our region. Rare cases that are recognized might have been introduced from the neighboring countries.

Keywords: HCV genotype 2, HCV genotype 4, Middle East

Hepatitis B Virus Occult Infection Detection in Hemodialysis Patients Fasa, Southern Iran

Mahsa Moeini, Mazyar Ziyaeyan

Professor Alborzi Clinical Microbiology Research Center, Shiraz University of Medical Sciences, Shiraz, Iran

Abstract

Background: Occult *Hepatitis B* virus (HBV) infection is defined as the presence of HBV DNA and the absence of detectable *Hepatitis B* surface antigen (HBs Ag) in patients' sera. The aim of this study was to investigate the HBV occult infection and viral load in hemodialysis patients by quantitative Real-Time PCR

Methods: Totally 55 patients in Fasa, main center of hemodialysis, were evaluated using a Real-Time PCR to detect and analysis the quantity of HBV DNA serum. A commercial ELISA kit was used to detect serum HBs antigen in the patients. Also, water wash samples collected from 18 hemodialysis units were investigated for HBV DNA by the PCR.

Results: all the patients were sero-negative for HBs Ag. HBV occult infection was detected in only 4/55 subjects (8%) by PCR, in whom the serum HBV DNA levels were $< 5\times10^3$ copies per mL Low level HBV DNA was detected in three hemodialysis instruments.

Conclusion: The related data indicated that occult HBV infection is frequent in hemodialysis patients and they can contaminate the hemodialysis units during usage, therefore, more attention should be paid to this matter.

Keywords: Hemodialysis patients, *Hepatitis B*, occult infection, Viral load

KPC- Producer Gram Negative Bacteria among Burned Infants in Motahari Hospital, Iran: First Report from Iran

Leila Azimi[1], Abdolaziz Rastegar Lari[1]*, Reza Alaghehbandan[1], Masoud Mohammadpoor, Mohammad Rahbar[2]

[1]Antimicrobial Resistance Research Center, Tehran University of Medical Sciences, Tehran, Iran
[2]Department of Microbiology, Iranian Reference Health laboratory. Ministry of Health and Medical Education, Tehran, Iran

Abstract

Background: To the best of our knowledge, this is the first report of *Klebsiella*, *Acinetobacter* and *Pseudomonas*-producing *Klebsiella pneumonia* Carbapenemase (KPC) among burn infants in Iran. The objective of this study was to determine the phenotypic detection of these KPC among isolated *Pseudomonas Aeruginosa*, *Acinetobacter baumannii* and *Klebsiella spp.*

Methods: A cross-sectional study was performed (February to September 2011) at a tertiary burn hospital in Tehran, Iran. Sixty four strains were isolated from 20 patients. Strain and genus of isolates were confirmed, antibiotic susceptibility testing was implemented and KPC determined by Modified Hodge Test.

Results: Fifteen of 36 strains (6 *Pseudomonas Aeruginosa*, 6 *Acinetobacter baumannii* and 3 *Klebsiella pneumonia*) were resistant to imipenem. Ten strains of 36 gram negative isolates were resistant to all tested antibiotics except for colistin. Thirteen of 15 resistant imipenem strains were confirmed as KPC-producer bacteria that isolated from 9 patients. Six of 36 isolated strains were Extended-spectrum β-lactamase (ESBL)-producing bacteria, of which 4 strains were both KPC and ESBL.

Conclusions: High percentage of Multi drug Resistant (MDR) strains in our center with positive KPC has created a major challenge in terms of mortality and morbidity. Findings of this study highlight the importance of implementation of an effective infection control strategy to prevent and decrease the prevalence of KPC-producing organisms.

Keywords: *Pseudomonas*, *Acinetobacter*, *Klebsiella*, KPC, infant

Cryptosporidium Infection in Children who Have Relationship with Pets

Masoumeh Rostami[1], Fatemeh Soghra Maghsoodloorad, Farideh Tohidi, Heshmatollah Taherkhani

Department of Parasitology and Mycology, School of Medicine, Golestan University of Medical Sciences, Gorgan, Iran

Abstract

Background: *Cryptosporidium* is an important cause of diarrheal disease worldwide and, as several recent waterborne outbreaks have shown, poses a significant threat to public health in Iran. We identified the *Cryptosporidium spp*. in 56 positive children stool samples by direct wet smear method and Sheather's sugar flotation and stained with Modified Z.N.

Methods: The study was conducted in 7-12 year-old primary schoolchildren. Participants provided fecal samples and answered a questionnaire about their demographics and hygiene habits. The samples were examined by two Methods including direct wet smear method and Sheather's sugar flotation and stained with Modified Z.N. in the Parasitology laboratory of the Golestan University of Medical Sciences.

Results: Totally 800 stool specimens were collected from children averagely aged 9.5 years. Overall 56 children (6.9%) were infected by *Cryptosporidium* oocyst. There was significant association(p-value < 0.5) between positive *Cryptosporidium* with clinical symptoms (%٦١)and non-clinical symptoms (%٣٩). 20 children (35.7%) were in contact with domestic animals such as cows and sheep. 19 children (33.9%) were in contact with dogs or cats. also16 children (28.5%) had no contact with any animal.

Conclusion: This work shows that the prevalence of intestinal parasitism is quite high among primary school students in Gorgan city and suggests an imperative for the implementation of control measures.

Keywords: Pets, *Cryptosporidium*, children

Evaluation of Bacteremia in Children Admitted in Pediatric Intensive Care Unit after Surgery

Mohammad Hasan Aelami, Gholamreza khademi, Mojtaba Lotfi, Mohammadreza Mosadegh

Department of Pediatrics, Mashhad University of Medical Science, Mashhad, Iran

Abstract

Background: Nosocomial infections are the most important causes of mortality and morbidity in Pediatric Intensive Care Unit (PICU). The objective of this study was to determine nosocomial infection in children admitted in PICU after surgery. In follow up the patients not admitted again up to two months.

Methods: This is a Cross-sectional study that conducted in PICU of Doctor Sheikh hospital in Mashhad University of Medical Science at Jan-Jun 2012. Our statistical society was 143 patients that admitted in PICU and 50 children were post-surgery patients and were evaluated in this study and all patients had a major surgery (Diaphragmatic hernia and gastrointestinal surgeries). We cultured blood at admission and discharge and compared them. All patients received antibiotics during surgery or up to 72 hours.

Results: Age range was between 1 day and 3 months. Mean admission time in PICU was 4 -12 days. In 50 repeated blood cultures of patients, 2 cases were bacteremia with *Klebsiella* Pneumonia.

Conclusion: From repeated blood culture in infantile post-surgery we find acquired nosocomial infection is low in PICU.

Keywords: Pediatric Intensive Care Unit, Blood culture, Nosocomial infection

Brucella Epididimo-Orchitis in Pediatric Ages Group

Mohammad Esmaeili

Pediatric Nephrologist, Doctor Sheikh Pediatric Hospital, School of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran

Abstract

Background: Brucellosis is a common disease in endemic areas, although epididimo-orchitis is uncommon. In endemic areas, all of the patients with epididimo-orchitis must be worked up for Brucellosis**.**

Methods: A series of twenty one patients in pediatric ages group (3-16 y) presented with epididymo-orchitis between October 1993 - 2003

Results: In 8 cases Brucellosis were diagnosed and in others (13 cases) non spescific bacterial epididimo-orchitis. *Brucella*r group were compared with nonspecific group. The former ones were older, without lower urinary tract symptoms, lesser grade of tenderness and inflammatory sings. There were fever, leukocytosis and increased RBC sedimentation rate only in a few cases.

Conclusion In endemic areas all of the patients with epididimo-orchitis must be worked up for Brucellosis. The distinction between *Brucella*r and nonspecific epididimo-orchitis is essential since the treatments are entirely different.

Keywords: Pediatric ages, Brucellosis, epididimo-orchitis-children

Nasal colonization Rate of Community and Hospital Acquired Methicillin Resistant *Staphylococcus aureus* in Hospitalized Children at Kerman Afzalipour Hospital

Hosseininasab A[1], Farokhnia M[2], Sinaei R[3], Moeinaldini R[4]

Abstract

Background: Prevalence of community and hospital acquired methicillin-resistant *Staphylococcus aureus* (MRSA) infection is increasing. The primary reservoir is the anterior nares; nasal carriage is a risk factor for infection in a variety of populations. Infection due to hospital-acquired colonization is different from community acquired in clinical manifestations and antibiotics susceptibility. In this study, we investigate nasal colonization rate, and antimicrobial susceptibility of community and hospital acquired *Staphylococcus aureus* nasal colonization at childhood.

Methods: This cross-sectional study was conducted in children admitted at Kerman Afzalipour hospital during June to November 2011. Sample was taken from nostrils of 180 patients in the beginning and after 48 hr of admission for *Staphylococcus aureus* nasal colonization and antibiotics susceptibility test.

Results: Of 180 samples at the beginning of hospitalization, 22 (12.2%) had *Staphylococcus aureus* nasal colonization, from these 18/1% were methicillin- resistant (2.2% of total population). Methicillin-resistant *Staphylococcus aurous* colonized children had significantly greater mean age than non -colonized of them ($p< 0.001$). After 48hr, 22 (12.2%) were colonized with *Staphylococcus aurous*, from these11 (50%) were hospital acquired methicillin-resistant. All methicillin-resistant *Staphylococcus aurous* isolates were sensitive to vancomycin. The rate of résistance to the other current in use antibiotics was more common in hospital acquired *Staphylococcus aureus*.

Conclusion: Community acquired methicillin-resistant *Staphylococcus* aurous is sensitive to many anti-*Staphylococcus* agents in our region. MRSA colonization in admitted patients can occur. Empirical antibiotics recommendation in nosocomial infection should be on the base of periodic culture and antibiotics susceptibility test.

Keywords: Nasal colonization, methicillin-resistant *Staphylococcus aurous*, Children

[1]Tropical and Infectious Diseases Research Center, Kerman university of Medical Sciences, Kerman, Iran.
[2]Department of Pediatrics. Kerman University of Medical Sciences, Kerman, Iran.
[3]Department of Microbiology, Afzalipour Hospital, Kerman University of Medical Sciences, Kerman, Iran.

Contamination of Anesthetic Machine and Instruments with Common Method of Disinfection in Operation Room, Babol; 2011 – 2012

Asgharpour F, Mortazavi Y, Shahande Z, Nazerpour R

Abstract

Background: Nowadays, medical equipment is daily used for different patients in hospital. Contamination can be transmitted by anesthetic equipment from on patient to another. The objective of this study was to determine the rate of contamination of anesthetic machine and instruments after using Deconex 53 pulse as a disinfection solution.

Methods: In this descriptive and analytical study, 192 samples of two parts of anesthetic machine and face mask, laryngoscopic, suction, laryngeal mask air way (LMA) and fibrotic bronchoscope were taken in 6 operation rooms of Shahid Beheshti hospital in Babol.

Sampling was taken from the parts of anesthetic machine and instruments before and after washing with Deconex 53 plus. Data was analyzed by chi-square test.

Results: Ninety six samples were taken before washing, 69.8% of them were contaminated. After washing with Deconex 53 plus, 31/3% of samples were contaminated.

Conclusion: According to the results, there was bacterial contamination in anesthetic machine at the stage before and after washing with Deconex 53 plus. Disinfection with using disinfectant solution with substandard concentration was not effective in decreasing of contamination.

Babol University of Medical Sciences, Paramedical, Babol, Iran

Keywords: Anesthetic machine, instruments, Disinfectant, contamination, Deconex 53 plus

Hospital-Acquired Bacterial Pneumonia (HABP) in ICU

Dehghan F. Zolghadri N, Shafii A, Bostan F

Khalij Fars hospital, Bandarabbas, Iran

Abstract

Background: Pneumonia is the most common hospital-acquired infection in ICU, causes high morbidity and mortality in patients. The aim of the study was to determine the hospital-acquired bacterial pneumonia incidence and isolate the bacterial agent of it in ICU patients.

Methods: This cross-sectional study was performed on 214 patients(148 male and 66 female) admitted in the ICU in Khalij Fars hospital of bandarabbas in 2011.Identification of HABP was based on developing clinical signs 48h or more after admission, new chest X-Ray infiltrates and positive culture from endotracheal secretions. SPSS software was used for analysis.

Result: In this study 16 cases of HABP were identified. Overall incidence of HABP in this ward was 7.5%. The most prevalent organism was *Klebsiella pneumonia* (50 %).Other isolated bacteria were *Staphylococcus aureus* (18.7 %), *Acinetobacter spp* (12.5 %), *E. coli*(12.5 %) and *Pseudomonas aeruginosa* (6.3 %).

Conclusion: These findings showed ICU of Khalij Fars hospital had relatively high rate of HABP, therefore, there is need to plan strategies for prevention of HABP.

Keywords: Bacteria, hospital-acquired pneumonia, ICU

Hand Carriage of Methicillin Resistant *Staphylococcus aureus* (MRSA) in Staff of Pediatric Unit of Buali Sina, Sari, 2011-2012

Mohammad Ahanjan, Sara Abdullahi

Mazandaran University of medical sciences, sari, Mazandaran, Iran

Abstract

Background: *Staphylococcus aureus* is one of the most prevalent pathogens in nosocomial infections.

Methods: We designed this cross-sectional study for evaluation of methicillin resistance in *S. aureus* strains that have been harboring in the hands of Booali hospital personnel in Sari, Iran. Samples were obtained by sterile cotton-wool swab moistened with normal saline. They were rotated on palms of both hands. Seventy Samples of personnel immediately cultured on manitol salt agar. Suspected colonies confirmed by biochemical Methods. Methicillin resistance of isolated strains was carried out by agar dilution according to the recommendations of Clinical and Laboratory Standards Institute.

Results: Twenty two percent out of 70 samples were hand carriers of *S. aureus*; 5% of the carriers were methicillin resistant *S. aureus* and all vancomycin sensitive.

Conclusion: There was high prevalence rate of *S. aureus* carriage in hands of Booali hospital personnel, so it is necessary to have plan for decreasing *S. aureus* carriage.

Keywords: MRSA, hand carriage, Mazandaran

Effect of Personal Hygienic and Socioeconomic Factors on the Spreading of *Parvovirus B19* among Pregnant Women Population in East Azarbaijan Area

Shanley Abdolzadeh, Behrouz Naghili. Abolfazl Pourhassan, Leili Aghebati, Adel Mesry, Meharngiz Rajaii

Rabe Rashidi University, Immunology and Infectious and Tropical Diseases andGynecology Research Centers. Tabriz University of Medical Sciences, Tabriz, Iran

Abstract

Background: Human *Parvovirus B19* is a single-stranded, non-enveloped DNA virus and a member of the family Parvoviridae. Up to 50% of women are non-immune and susceptible to *Parvovirus B19* causes a number of clinical illnesses including erythema infection (fifth disease), hydrops fetalis, transient aplastic crisis, arthropathy and congenital aplasia.

Methods: In this cross- sectional study, totally 253 pregnant women were evaluated .They attended for prenatal care in health service centers related to Alzahra Gynecology center of Tabriz University of Medical Sciences from April 2011 to May 2012.They referred 76(%45), 69(35%), 3(%28) cases in first, second, third trimesters respectively. For diagnosis of acute form of *Parvovirus B19* infection, *Parvovirus* specific IgM antibody was assayed. We used ELISA technique and analyzed findings based on age, occupation , season, number of children in household by statistical software SPSS version 15.0 (SPSS Inc, Chicago, USA). P values $\leq$ 0.05 were considered significant.

Results: Totally 253 pregnant women were studied in five age groups (ranged by 4yr intervals19-38) yr. We have found 110(43.47%) (G+M+, G-M+) cases which could be classified as recent or acute infection cases. We have found a direct relation between personal hygienic factors such as washing of hands and socioeconomic factors such as occupation, annual income rate.

Conclusion: The virus is spread via aerosol droplets through the respiratory route. It was transmitted by hand-to-mouth, hand-to- hand contact, blood or blood products and nosocomial infection. It can spread transplacentally to the fetus during active maternal infection. Therefore it must be focused to personal hygienic and socioeconomic factors.

Survey on Circumstances of Hospital Medical Instruments Hygienic Surfaces and Its Impact on Hospital Infectious Control by ICNA and ACC Method

Ghodratolah Karami[1], Mohamad Khazaee[2], Abedin Saghafipoor[2]

Abstract

Background: Hospital infections have been increased in previous decades. In the United States, It was reported that 1.7 million hospital cases and 99000 deaths occurred annually. The surfaces of medical instruments such as blood pressure cuff, stethoscope and dialysis machine can accelerate infection transfer. In this research, hygienic quality of instrument surfaces was investigated in Shahid Beheshti hospital in Qom city.

Methods: This semi-experimental study was performed during 10 weeks in two stages before and after intervention. The intervention was cleaning program which was done with hospital tenants. It was performed two times a week by ICNA and ACC Methods. Results were reported as clean and dirty. Statistical analysis was done with SPSS 18.

Results: Based on ICNA method, 122 objects (61%) and 79 objects (39.5%) were dirty before and after intervention respectively. While, based on ACC method, 152 objects (76%) and 139 objects (69.5%) were dirty before and after intervention respectively. Cleaning intervention had significant impact on increasing hygienic quality according to both ICNA ($P=0.00$) and ACC Methods ($P<0.001$).

Conclusion: Cleaning program can decrease contaminations on medical instrument surfaces effectively. Monitoring of surfaces with ICNA and ACC Methods, as a routine program, is being useful for increasing hygienic quality.

[1]Department of Environmental Engineering Health, Qom University of Medical sciences, Qom, Iran
[2]Department of Public Health, Qom University of Medical sciences, Qom, Iran

Keywords: Environmental health, Hospital infection, Cleaning, ICU

Prevalence of Gram-Negative Bacilli Carriers in Nasopharynx of Healthy Children Aged 10-12 Years in Tabriz, Iran

Hadi Joula[1], Seyyed Reza Moaddab[2], Abdolnaser Rafi[2], Seyyed Morteza Haghgu[1], Seyyed Abasalt Hashemi[1], Javid Sabur[1], Abdolrasul Safaeian[3]

[1]Student Research Committee, Faculty of Paramedicine, Tabriz University of Medical Sciences, Tabriz, Iran
[2]Laboratory Sciences Department, Faculty of Paramedicine, Tabriz University of Medical Sciences, Tabriz, Iran
[3]Epidemiology and Vital statistics Department, Faculty of Health and Nutrition, Tabriz University of Medical Sciences, Tabriz, Iran

Abstract

Background: Colonization of *Gram-negative bacilli* in nasopharynx of healthy people is not prevalent. However, researches show that existence of some conditions such as living in industrial and urban areas, lack of sufficient function of immune system, provides colonization of these bacteria. As regards presence of these microorganisms in favorable conditions can cause pneumonia and its side effects, so the objective of this study is evaluating the prevalence of gram-negative bacilli in nasopharynx of healthy children in collective places as schools.

Methods: This cross-sectional study was performed among 224 healthy students aged from 10 to 12 years using cluster sampling method. Samples were taken from nasopharynx and cultured on the Mc Conkey agar. Afterward the bacteria colonies identified using standard differential Methods. At last, statistical analysis of data was performed by SPSS software.

Results: Of the total of 224 specimens from nasopharynx including 90 specimens taken from males and 134 from females, Gram-negative bacilli were isolated from 15 specimens (6.69%) (12 specimens of females and 3 of males).

Conclusion: The results of our study showed that there was low rate of gram-negative carriers among healthy children (6.69%). More studies about the spread of gram-negative bacilli in collective places such as schools seem necessary.

Keywords: *Gram-negative bacilli*, nasopharynx, pneumonia

Prevalence of Healthy Carriers of *Streptococcus pyogenes* among 400 Children Aged 10-12 Years in Tabriz, Iran

Hadi Joula[1], Seyyed Reza Moaddab[2], Abdolnaser Rafi[2], Seyyed Morteza Haghgu[1], Seyyed Abasalt Hashemi[1], Javid Sabur[1], Abdolrasul Safaeian[3]

[1]Student Research Committee, Faculty of Paramedicine, Tabriz University of Medical Sciences, Tabriz, Iran
[2]Laboratory Sciences Department, Faculty of Paramedicine, Tabriz University of Medical Sciences, Tabriz, Iran
[3]Epidemiology and Vital statistics Department, Faculty of Health and Nutrition, Tabriz University of Medical Sciences,Tabriz, Iran

Abstract

Background: Pharyngitis is a contagious and prevalent disease. *Streptococcus pyogenes* is one of its agents and can cause some diseases such as rheumatic fever and acute glomerulonephritis. The objective of this study was to evaluate the prevalence of healthy carriers of *Streptococcus pyogenes* among 400 children aged 10-12 years in Tabriz, Iran and to determine antibiotic susceptibility of isolated microorganisms.

Methods: This cross-sectional study was performed among 407 healthy students aged 10 to 12 years using cluster sampling method. Specimens were taken from nasopharynx and cultured on blood agar mediums. After identification of isolated strains by standard Methods, antibiotic susceptibility test was done by disk diffusion method. Statistical analysis of data was performed by SPSS software.

Result: Of 407 specimens taken from nasopharynx of these children, 208 specimens were from males and 199 from females. Four specimens (2 specimens of males and 2 of females) were positive for *Streptococcus pyogenes*. The isolates had high rate of susceptibility to erythromycin, vancomycin and clindamycin.

Conclusion: The results of this study showed the low rate of *Streptococcus pyogenes* carriers among students. After Penicillin, Erythromycin still can be used as an effective antibiotic against *Streptococcus pyogenes*.

Keywords: *Streptococcus pyogenes*, nasopharynx, healthy carriers, pharyngitis

Frequency of Extended Spectrum Beta-Lactamase (ESBL) In *Pseudomonas Aeruginosa* Isolates from Nosocomial Infections in Shiraz

Alimadad Nazari Alam, Dr. Abdollah Bazargani, Mohammad Motamedifar, Jamal sarvari, Hossein Khoshkharam

Abstract

Background: ESBL production in *Pseudomonas Aeruginosa* is a major problem in pseudomonad infection treatment. The aim of this study was to determine the frequency of ESBL in *Pseudomonas Aeruginosa* clinical isolates by phenotypic Methods CDT.

Methods: *Pseudomonas Aeruginosa* isolated from specimens of in-patients in teaching hospitals affiliated to Shiraz University of medical sciences were collected and their identity was confirmed by traditional tests during November 2011 to July 2012. For detecting ESBL producing bacteria, all *Pseudomonas Aeruginosa* isolates that were resistant to Cefotaxime and/or Ceftazidime were examined for resistant to combined disks of Ceftazidime + Clavulanic acid and/or Cefotaxime + Clavulanic acid.

Results: Of 146 *Pseudomonas Aeruginosa* isolates, 143 (98%) of the isolates were resistant to Cefotaxime and/or Ceftazidime to and 20 (14%) of them were diagnosed as ESBL producing bacteria.

Conclusion: High frequency of *Pseudomonas Aeruginosa* clinical isolates resistant to third generation Cephalosporins with a notable portion of ESBL producing bacteria in this study indicates to have a proper program in antibiotic prescription in our hospitals.

Bacteriology and Virology department, Medical School, Shiraz University of Medical Sciences, Shiraz, Iran

Keywords: *Pseudomonas Aeruginosa*, antibiotic resistant, ESBL, Shiraz

A Survey on Prevalence Rate of *Rotavirus* Acute Gastroenteritis in Hospitalized Children Less Than 7 Years Old of Yasuj City in 2010-2011

Pouya Khodadadi[1], Mohammad Kargar[2], AbdolAli Moshfea[3], Hossein Ansari[4]

Abstract

Background: Worldwide, rotaviruses are identifying as a major cause of acute gastroenteritis and childhood mortality in infants and young children. The study was designed to investigate *Rotavirus* disease burden and clinical symptoms among children <7years old who were hospitalized for acute diarrhea in Imam Sajjad hospital Yasuj, Iran from 2010 to 2011.

Methods: This cross sectional - descriptive study was done on 184 stool specimens of patients with diarrhea. All samples were routinely screened for the presence of VP6 group A Rotavirus antigen by enzyme immunoassay (EIA). Data were statistically analyzed by SPSS version 16, chi-square, and Fisher's exact tests.

Results: Rotavirus was detected in 52 hospitalized patients by EIA, representing 28.26% of total specimens. The stool samples of the *Rotavirus* episodes, high prevalence of them occurred during the first 2 years of life, with the peak prevalence of severe rotavirus disease occurring in cold seasons. Diarrhea and vomiting observed in all children and convulsion had not seen in any cases. Fever was present in 23/91%. There were no significant relationship between virus outbreak and clinical symptoms. There was also a significant difference between the seasonal distribution and virus detection (p=0/001). Highest incidence of this virus is in autumn (48/08%) and lowest is in spring (5/77%).

Conclusion: Regarding to high prevalence of *Rotavirus* infection, continual surveillance is necessity to provide useful data for formulating effective vaccines and also avoids the high cost of clinical care.

Keywords: *Rotavirus*, Gastroenteritis, EIA, Yasuj

[1]Department of Microbiology, Jahrom Branch, Islamic Azad University, Jahrom, Iran.
[3]Departement of Parasitology, Faculty of Medicine, Yasuj University of Medical Sciences, Yasuj, Iran.
[4]Department of Biology, Yasuj University Payam noor, Yasuj, Iran

Evaluation of Nosocomial Infections and Related Factors in Hospital of Ayatollah Mousavi, Zanjan, 2010

Fatemeh Ghorbani, Azar Avazeh, Freydoon Eskandari, Fatemeh Mohammadi

Zanjan University of Medical Sciences, Zanjan, Iran

Abstract

Background: The progress of science to identify new drugs, widespread use of drugs, use of vascular catheters, urinary catheters and brain shunt and the use of mechanical ventilation, despite helping to save the patient, may cause problems such as hospital infections. Widespread uses of antibiotics that are often empirically used to cover the most common microbes responsible for nosocomial infection lead to colonization with resistant gram-negative microbes. Nosocomial infections are major problems in hospital environments and causes increased morbidity and mortality.

Methods: This was a descriptive cross sectional study over one-year period at Mousavi Hospital. Nosocomial infections were diagnosed on the basis of CDC criteria. Data were collected by questionnaires which contained demographic information of the patients and information related to signs of nosocomial infections. Data were analyzed by SPSS and chi-square test. $P<0.05$ was considered significant.

Results: Of 34814 patients hospitalized at the Hospital of Mousavi in 2010, 206 patients had nosocomial infections. They were 63/5% male and 35/4% female. Highest incidence of these infections was in ICU (54/8%). The most common nosocomial infections were pneumonia (42/7%), surgical wound infections and burns (31%), urinary tract infection (16%), eye infections (5/3%) and blood infections (4/8%). The most common microorganisms were *Pseudomonas* (23/7%) and *Klebsiella* (23/7%).The results showed that there were a significant relationship between age and unit hospitalized and incident of nosocomial infection.($P<0.05$)

Conclusion: Early recognition and diagnosis of nosocomial infections and antibiotic resistance, as well as proper use of antibiotics is the most important principles in every hospital and especially in the intensive care units.

Keywords: Nosocomial infections, Zanjan, Iran

Microbial Contamination Level Assessment of Peripheral Venous Catheter in Hospitalized Patients in 22 Bahman and Aria Hospitals in 2007

Hossien Mokhtari, Marzieh Maleki, Mehdi Masoumian, Nafiseh Khosravi, Sara Rastegari

Islamic Azad University of Mashhad Branch, Mashhad, Iran

Abstract

Background: The aim of this study was to assess microbial contamination level of peripheral venous catheters in hospitalized patients in 22 Bahman and Aria hospitals in 2007.

Methods: Eighty patients that were not received antibiotics had been selected accidentally. After 72 hours of peripheral catheters in site, catheters were removed from the vessels and cultured on blood agar and EMB plate. Then antibiotic sensitivity of positive cultures was done.

Results: The results of cultures were positive in 14(17.5%) and negative in 66(82.5%) of peripheral catheters. The most common bacteria was coagulase negative *Staphylococci* and sensitivity had been 78% to amikacin, gentamycin 71.5%, ciprofloxacin 57%, imipenem 57%, vancomycin 50%, oxacillin 29%, kanamycin 29% and cefixime 29%.

Conclusion: The most common organism cultured from peripheral catheters was coagulase negative *Staphylococcus*. *Staphylococcus epidermidis* is the most common organism of skin normal flora that because of its cellular and molecular features can produce microbial colonies in catheters.

Keywords: Peripheral venous catheter- culture – anti biogram, Iran

Prevalence Determination of Nasal Carriers of Golden *Staphylococcus* and Its Microbial Resistance to Methicillin in Official Practitioner and Therapeutic Personnel in 22 Bahman Hospital, in 2005

Hossien Mokhtari, Marzieh Maleki, Behieh Zarif Zakerian,Reza Sahabi, Fatemeh Habibi, Marzieh Gazerani

Islamic Azad University of Mashhad Branch, Mashhad, Iran

Abstract

Background: The aim of this study was to determine the prevalence of nasal carriers of *Staphylococci* and it's resistance to methicillin in official practitioner and therapeutic personnel in 22 Bahman hospital in 2005. The presence of *Staphylococci* in the anterior nares of the patients especially MRSA is a risk factor for developing extensive and deadly infections due to this bacterium. Hospital personnel have been considered as possible carriers of this organism.

Methods: Samples were obtained using a cotton swab from anterior nares of personnel and placed in manitol-salt-agar environment. Antibiotic sensitivity of positive cultures of golden *Staphylococci* was identified by diffusion disk method. Data had been analyzed with chi-square test.

Results: Among 84 samples, 20 samples (23.8%) had been nasal carriers of golden *Staphylococci*. There were 7 persons (20%) in official practitioners and 13 persons (26.5%) in therapeutic personnel that were not significant statistically. (P = 0.48). All golden *Staphylococci* were resistance to methicillin.

Conclusion: Our results showed that there were significant numbers of carriers of golden *Staphylococci* resistant to methicillin in anterior nares of personnel. It emphasizes the necessity of infection control policies in the hospital to eliminate this organism from hospital environment.

Keywords: Golden *Staphylococci*, nasal carriers, resistance to methicillin

Evaluation of Antibacterial Efficiency of Hygienic Hand Rub "Dermasept"

Maede nakhaee, Mastureh Momen Heravi, Samira Rashidian, Akram Baghani, Kiarash Ghazvini

Abstract

Background: Hands play a major role in the transmission of infection in the community. Considering the importance of hand hygiene in controlling of infections, use of alcohol based hand rubs is strongly recommended because of being fast and not harmful for the skin despite high levels of disinfection's activity. The purpose of this study is the evaluation of a hygienic hand rub Dermasept in comparing with the reference hand rub (propanol 60%).

Methods: According to the national standard of Iran with number 8512, 12 healthy volunteers were chosen. Their hands were contaminated with the nonpathogenic bacteria *E. coli* k12 suspension, and their fingertips were placed in TSB medium before and after use Dermasept and reference hand rub. Then serial dilutions were cultured on the TSA medium, and the number of microorganisms was estimated as the decimal logarithm. Base on Wilcoxon test, Dermasept's performance was determined via comparison of decrease coefficients of Dermasept and reference hand rub.

Results: Based on Wilcoxon test, the ensemble of the decrease coefficients logarithm of the reference and Dermasept were 3.5111 and 3.7903,respectively, and at the difference between the decreases coefficient logarithm Dermasept and reference hand rub, total rating of negative equaled 55 and positive was 23 also p-value = 0.1167 was calculated.

Conclusion: With regard to the total sum of negative ratings was higher than positive ratings, it seems that efficiency of Dermasept is better, but according to the p-value (0.1167) at a meaningful level of 0.05, there weren't significant differences between the coefficient reduction of Dermasept and reference, thus its performance is similar to propanol. Finally, use of Dermasept solution is recommended for hand hygiene due to simple and fast application, no need for water and acceptable antibacterial activity.

Microbiology and Virology Research center, Avicenna Research Institute, Mashhad University of Medical Sciences, Mashhad, Iran

Keywords: Dermasept, hand hygiene, hand rub, antibacterial effect

Evaluation of Efficacy of Typical Disinfectants on *Staphylococcus aureus* and *Pseudomonas Aeruginosa* Isolated from Surface of Shahid Sadughi Accidents Burns Hospital in City of Yazd

Hengameh Zandi[1], Mehdi Mokhtari[2], Fatemeh Sahlabadi[2], Tahereh Jasemizad[2], Akram Montazeri[3]

[1]Department of Microbiology, Shahid Sadoughi University of Medical Sciences, Yazd, Iran
[2]Environmental Health Department, Faculty of Public Health, Yazd University of Medical Sciences, Yazd, Iran
[3]Shahid Sadughi accidents burns hospital, Shahid Sadoughi University of Medical Sciences, Yazd, Iran

Abstract

Background: *Staphylococcus aureus* and *Pseudomonas Aeruginosa* are important pathogens in burn wounds. The aim of this study was to evaluate the efficacy of Deconex 50 AF, Descoscid, Epimax SC and Silvosept on *Staphylococcus aureus* and *Pseudomonas Aeruginosa* isolated from surface of Shahid Sadughi accidents burns hospital in city of Yazd.

Methods: We used simple random sampling in this study. Two hundred forty samples were collected from 30 different surfaces of 4 different parts of the hospital. For every disinfectant we collected 30 samples before and 30 samples after disinfection. The samples were transferred to the Microbiology laboratory of Shahid Sadoughi University Medical Sciences, cultured on blood and EMB agar. Colonies that were suspected to *Staphylococcus aureus* and *Pseudomonas Aeruginosa* were identified by biochemical tests and their colony was determined. Data were analyzed using T-test.

Results: The contaminant average of *Staphylococcus aureus* at 4 parts of burn unit of hospital before disinfecting by Deconex 50 AF, Descoscid, Epimax SC and Silvosept was 48.07, 11.58, 30990.98 and 17.8 respectively and after disinfecting was 1.03, 0.25, 0.61 and 2.74 respectively. Also for *Pseudomonas Aeruginosa* before disinfecting was 15, 0, 18569.23 and 18.65 respectively and after disinfecting was 9.12, 0, 0.77 and 1.83 respectively.

Conclusion: The results showed that these disinfectants, have shown a significant difference ($p<0.05$) in decreasing of *Staphylococcus aureus* but for *Pseudomonas Aeruginosa*, only Epimax SC and Silvosept showed a significant difference. The most effective disinfectant on both bacteria was Epimax SC.

Molecular Epidemiology of HIV-1 Infection in Iran: Genomic Evidence of CRF35_AD Predominance and CRF01_AE Infection among Individuals Associated with Injection Drug Use

Fatemeh Jahanbakhsh,[1] Shiro Ibe,[2] Junko Hattori,[2] Seyed Hamid Reza Monavari,[1] Masakazu Matsuda,[2] Masami Maejima,[2] Yasumasa Iwatani,[2,3] Arash Memarnejadian[4], Kayhan Azadmanesh[5], Wataru Sugiura[2,3], Hossein Keyvani[1]

[1]Department of Virology, Tehran University of Medical Sciences, Tehran, Iran
[2]Clinical Research Center, National Hospital Organization Nagoya Medical Center, Nagoya, Japan
[3]Department of AIDS Research, Nagoya University Graduate School of Medicine, Nagoya, Japan
[4]Department of Hepatitis and AIDS, Pasteur Institute of Iran, Tehran, Iran
[5]Department of Virology, Pasteur Institute of Iran, Tehran, Iran

Abstract

Background: To understand the molecular epidemiology of HIV-1 infection in Iran, we conducted the first study to analyze the genome sequence of Iranian HIV-1 isolates.

Methods: For this cross-sectional study, we enrolled 10 HIV-1infected individuals associated with injection drug use from Tehran, Shiraz, and Kermanshah.

Results: Near full-length genome sequences obtained from their plasma samples were used for phylogenetic tree and similarity plotting analyses. Among 10 isolates, nine were clearly identified as CRF35-AD and the remaining one as CRF01-AE. Interestingly, five of our Iranian CRF35-AD isolates made two significant clusters with 10 Afghan CRF35-AD isolates in a phylogenetic tree, indicating tight epidemiological connections among injection drug users in Iran and Afghanistan. In contrast, our CRF01-AE isolate had no significant genetic relationship with any other CRF01-AE isolates worldwide, even from Afghanistan.

Conclusion: This study provides the first genomic evidence of HIV-1 CRF35-AD predominance and CRF01-AE infection among individuals associated with injection drug use in Iran.

Keywords: Molecular epidemiology of HIV-1, Iran, CRF35_AD, CRF01_AE, Full-length genome sequences

Prevalence of aac (3)-IIa Gene among Clinical Isolates of Uro pathogenic *Escherichia Coli* in Delfan City, Lorestan

Somaye Mommeni Mofrad[1], Gholamreza Goudarzi[2], Pegah Shakib[2], Jamileh Nowroozi [3]

Abstract

Background: Uro pathogenic *Escherichia Coli* are the predominant causative organisms of urinary tract infections (UTIs). Aminoglycosides are the spectrum of clinically useful antibiotics with bactericidal activity against this bacterium. The most common mechanism for resistance to these antibiotics mediated through aminoglycoside-Modifying Enzymes (AMEs). The most common of these enzymes are aminoglycoside Acetyl transferases (AACs). The epidemiology of dominant type of these enzymes, AAC (3)-II, varies from region to region. The aim of this study was to determine antimicrobial susceptibility pattern with a focus on aminoglycosides and the prevalence of aac (3)-IIa gene among clinical isolates of Uro pathogenic *Escherichia Coli* obtained from Delfan city, Lorestan.

Methods: A total of 100 Uro pathogenic *Escherichia Coli* isolates were collected from Boali hospital in Delfan city, Lorestan. Antibiotic susceptibility pattern of strains were determined using disk diffusion method according to CLSI guidelines. Prevalence of aac (3)-IIa gene was determined by using PCR method and relationship between resistance phenotypes to aminoglycosides and presence of aac (3)-IIa gene evaluated.

Results: Isolates exhibited maximal resistance to ampicillin (85%), whereas none showing resistance to imipenem. Resistance rate toward aminoglycoside agents as follows: gentamicin (39%), kanamycin (26%) neomycin (30%), amikacin (1%).Sixty percent of the isolates demonstrated resistance to at least one of the aminoglycosides tested. Forty–four percent of the tested isolates harbored the aac (3)-IIa gene, in which maximal rate of gene presence detected in strains with gentamicin resistant phenotype (92.3%).

Conclusion: Our study revealed that challenge to ensure the continued use of routine antimicrobial agents will require to regional and periodic surveillance on the resistance prevalence at several levels.

Keywords: *Escherichia Coli*, Aminoglycoside Modify Enzymes, aac (3)-IIa, Delfan Lorestan

[1]Department of Biology (Microbiology), Faculty of Science, Olum tahqiqat, Islamic Azad University-Tehran Branch, Iran
[2]Microbiology Department, Faculty of Medicine, Lorestan University of Medical Sciences
[3]Department of Biology (Microbiology), Faculty of Science, Olum tahqiqat, Islamic Azad University-Tehran Branch, Iran

Isolation of Enterotoxigenic *Escherichia coli* (ETEC) Harboring CS3 in Children with Diarrhea

Masoome-Sadat Alerasool, Seyed Latif Mousavi, Shahram Nazarian, Samane Bagheri

Department of Biology, Shahed University, Tehran, Iran

Abstract

Background: Every year more than one million children under the age of five die of diarrhea. The death rate is much higher under unconventional circumstances such as calamities and wars, which threaten human life and health greatly. Enterotoxigenic *Escherichia Coli* (ETEC) is the most common bacterial cause of diarrhoea in the world, annually affecting up to 400,000,000 children living in developing countries. Colonization factors (CFs) mediate attachment of ETEC to the intestinal mucosa and induce protective immunity against ETEC diarrhea. These antigens have been classified into several groups based on their distinct antigenicity. CFA/II is among the most prevalent factors in human ETEC isolates and composed of CS1, CS2 and CS3. CS3 is the mostly stated serotype protein in CFA/II family which is expressed alone and/or together with CS1 and CS2. Detection of strains harboring CS3 by means of polymerase chain reaction (PCR) is the aim of this study.

Methods: Stool samples were collected from children reporting severe diarrhea. *E. coli* isolates were identified by different biochemical tests such as lactose fermentation, Indole production, Methyl-Red and Voges-Proskauer (MR-VP) test and etc. Bacterial genome applied as PCR template using specific primers.

Results: According to screening results, 17 samples out of 40 identified as *E. coli* and PCR results showed 2 $CS3^{+}$ strains among them.

Conclusion: PCR assay is a simple and sensitive diagnostic tool for CFs identification. Recognition of CFs type and frequency is the basis of vaccine development against children diarrhea.

Keywords: Children diarrhea, Enterotoxigenic *Escherichia Coli*, Colonization factors, PCR

Screening of *Higginsia spp.* for Isolation of Antibiotic Producing Symbiosis Bacteria

Meysam Amirkhani[1], Nima Bahador[1], Zahir Heshmatipour[2]

Abstract

Background: Sponges are the oldest group of multicellular animals. Nowadays, sponges interested for their intracellular microbes because of natural products such as, antibiotics and anti tumore compounds. The major purpose of this study was collection of Higginsia sp. from Persian Gulf and evaluation of antimicrobial metabolite produced by isolated microbes.

Methods: The genus of *Higginsia spp.* was collected from Persian Gulf and transported to the laboratory. Afterward, the extracted cells were serially diluted and poured on Marine agar 2216, MacConkey agar, Vibrio agar and Nutrient agar. The plates were incubated for 24- 72 hrs at30ºC. Then single colonies transferred to Luria bertani and Tripticase soy broth for evaluation of antimicrobial metabolites. After 24, 48 and 72 hrs the supernatant (10,000 rpm, 15 min) were evaluated for antimicrobial properties. In addition bacteria after 14 days in shaking condition (150 rpm) at 30ºC were evaluated and the experiment was repeated.

Results: Out of nine isolated colonies, only one bacterial colony had antimicrobial property, which belongs to the genus *Plesiomonas*. In addition after 14 days the bacterium produced antimicrobial metabolite which could be introduced it as an antibiotic.

Conclusion: Although nowadays antibiotic resistant microorganisms are developing, isolation of bacteria with capability to produce antimicrobial metabolite from sponges could helps remedy.

Keywords: Antimicrobial metabolites, *Higginsia spp.*, *Plesiomonas*

[1]Department of Microbiology, Science and Research Branch, Islamic Azad University, Fars, Iran
[2]Department of Microbiology, Islamic Azad University of Tonekabon Branch, Tonekabon, Iran

Prevalence of Extended-Spectrum B-Lactamase-Producing *Klebsiella Pnemoniae* Isolated from Clinical Specimens of Out-Patients and Hospitalized Patients of Imam Reza Hospital

Nafise Izadi[1], Zahra Meshkat[2], Mahboobe Naderi Nasab[1], Elnaz Harifi[1]

[1]Microbiology and Virology Research Center, Mashhad University of Medical Sciences, Mashhad, Iran.
[2]Women's Health Research Center, Mashhad University of Medical Sciences, Mashhad, Iran

Abstract

Background: Extended-spectrum B-lactamases (ESBLs) are cephalosporinase that confer resistance to a wide variety of cephalosporins and are serious therapeutic problem. This study was designed to determine the prevalence of ESBL-producing *Klebsiella pneumonia* (*K. pneumonia*) isolated from clinical samples.

Methods: One hundred and twenty seven isolates *K. Pneumonia* were included in this study. The samples were collected at Imam Reza Hospital from May 2011 to July 2012. ESBL production was determined by the double disk diffusion (DDs) test according to the CLSI guidelines.

Results: A total of 127 patients with *K. pneumonia* infection were 29 out-patients and 99 hospitalized patients. Among 127 *K. pneumonia* infected patients, the most common specimen was urine samples (n=26 in out-patients, n=36 in hospitalized patients, totally 48.8%) followed by wound samples (n=3 in out-patients, n=20 in hospitalized patients, totally 18%), blood samples (n=18 in hospitalized, 14%). The prevalence of ESBL producing *K. Pneumonia* was estimated 43% (n=55).

Conclusions: Our results showed that *K. pneumonia* is a common pathogen of community-acquired and nosocomial infection and high prevalence of ESBL among *K. Pneumonia* isolates were observed.

Keywords: Extended-spectrum B-lactamases, *Klebsiella pneumonia*, cephalosporin

Comparison of Effect of Carvacrol on *Staphylococcus aureus* and *Yersinia Enterocolitica* with Current Antibiotics for Cure of Those In vitro

Noroozi Somaye[1], Asmar Mehdi[2], Amir Mozafari Nor،[3] Rafatjo Anahita[4], Tavafi Hadis[5], Akbari Sheida[6]

Abstract

Background: In today medical world the antibiotics resistance has become concerns of many of countries. One of the taken decisions is to supersede new compounds with natural sources by the synthetic antibiotics. Essential oil of Satureja contains about 90% carvacrol in the flowering stage and before flowering stage. According to the carvacrol existing ، and antimicrobial effects of phenolic compounds such as, thymol and carvacrol, antimicrobial effects of Satureja Khuaistanica was investigated on *Y. entrolitica*, *S. aureus* bacteria. The major aim of this investigation was comparison of the effect of carvacrol existing in the essential oil Satureja Khouaistanica that is available in the Satureja leaves with 18 antibiotics on the *Staphylococcus aureus* and *Yersinia Enterocolitica* that use for cure of those in vitro .

Methods: To investigate the antibacterial properties of carvacrol existing in the essential oil of Satureja Khouaistanica, has been used Disk Diffusion method and dilution in the micro plate .then was determined diameter of inhibition zone for *Y. entrolitica*, *S. aureus* bacteria respectively 16، 30 mm .Result of the minimum inhibitory concentration (MIC)showed for *Y. entrolitica*, *S. aureus* bacteria respectively 0/78 ،0/19µg/mlwhile their minimum bactericidal concentration(MBC) indicated for *Y. entrolitica*, *S. aureus* bacteria respectively 1/56،0/39µg/ml. the diameter of inhibition zone for 18 antibiotics used in the clinical cure ranged between 2 to 15mm for *Y. entrolitica* bacteria and *S. aureus* bacteria.

Results: According to the results, considerably carvacrol existing in the essential oil of Satureja Khuaistanica indicated antibacterial activity on mentioned bacteria.

Conclusion: The results showed that, these carvacrol existing in the essential oil of Satureja Khouaistanica possess antimicrobial effects, considerably, thus, it seems to be suitable alternative to use of synthetic antibiotics that is due to resistance in bacteria.

Keywords: Carvacrol, essential oil of Satureja Khouaistanica, *Y. entrolitica*, *S. aureus*

[1] Department of Microbiology, Islamic Azad University, Lahijan Branch, Iran
[2] Islamic Azad University, Lahijan Branch, Iran
[3] Islamic Azad University, Lahijan Branch, Iran
[4]Department of Microbiology, Islamic Azad University, Lahijan Branch, Iran
[5] Department of biology, Faculty of Science, Malayer University, Iran
[6]Department of Microbiology, Islamic Azad University, Lahijan Branch, Iran

The Incidence and Risk Factors for Ventilator Associated Pneumonia among Hospitalized Patients in Intensive Care Units at Mousavi Hospital, Zanjan, Iran (2011-2012)

Hassan Poormoshtagh[1], Fateme Ghorbani[2], Freydoon Eskandari [2],Fateme Mohammadi[3]

Abstract

Background: Ventilator Associated pneumonia (VAP) occurs forty eight hours or later after initiation of mechanical ventilation. VAP is the most common nosocomial infection in intensive care unit. Therefore, it is necessary to determine the rate, characteristics, risk factors and outcome of VAP in ICU patients.

Methods: A prospective cohort study was conducted at the Mousavi Hospital over a period of one year on all patients who were admitted to ICU and required mechanical ventilation for more than forty eight hours. Diagnosis of VAP was made according to the definition of nosocomial pneumonias by CDC. Risk factors for developing VAP such as duration of mechanical ventilation, sex, age, cause of hospitalization, length of hospital stay and drugs were studied. Data were analyzed by SPSS and chi-square test. $P<0.05$ was considered significant

Results: Mean age of the study population was 53/8 with SD = 21/8 respectively. Seventy -six patients in the intensive care unit developed ventilator associated pneumonia. Trauma with 53/5% of cases (sixty nine patients) was the most frequent cause of hospitalization of patients. The most common microorganisms responsible for ventilator associated pneumonia were *Klebsiella* (38/2%) and Enterobacter (21/1%). Mean duration of hospitalization were 32/6 days. The results showed that there were a significant relationship between age and duration of hospitalization and also cause of hospitalization and incident of nosocomial infection. ($P<0.05$)

Conclusion: VAP occurred at significant rate among mechanically ventilated ICU patients. Regarding the results of this study, for prevention of nosocomial infections, activities and programs requires. Proper use of medical interventions, to limit transmission of microorganisms through handwashing, especially by medical personnel is necessary.

Keywords: Ventilator associated pneumonia, intensive care unit, risk factors

[1]Department of Pediatric Infectious diseases, Zanjan University of Medical Sciences, Zanjan, Iran
[2]Zanjan University of Medical Sciences, Zanjan, Iran
[3]Ayatollah Mousavi Hospital, Zanjan University of Medical Sciences, Zanjan, Iran

Frequency of Torque Teno Midi Virus/Small *Anellovirus* (TTMDV/SAV) in the Sera of Healthy Individuals in Lorestan Province, Iran by Nested-PCR

Maryam Fatholahi, Majid Bouzari

Department of Biology, Faculty of Sciences, University of Isfahan, Isfahan, Iran

Abstract

Background: In 2005, two genotypes of a new circular single stranded DNA virus were identified in the sera of patients with acute viral infectious syndrome for the first time, and finally named as TTMDV/SAV. The prevalence of 20%, 8.6% and 34.5% are reported in blood of healthy individuals in France, Italy and Republic of Korea and also High prevalence of TTMDV/SAV viremia were reported in *Hepatitis C* (45.4%), cervicitis (48.1%), Vasculitis disorders in children (50%) and acute respiratory disease (76%). The geographical distribution of the virus is not well defined. Because of this virus is widespread in healthy individuals has not been determined; the aim of this study was to detect the frequency of (TTMDV/SAV) in the sera of healthy individualsin Lorestan Province.

Methods: Eight hundred serum samples of healthy individuals were collected from pathobiology laboratories in Khorram abad city. Then the sera were subjected to DNA extraction (phenol/chlorophorm/isoamilalchohol). Then Nested-PCR was performed using SMAs/SMAr primers for detection of TTMDV/SAV.

Results: Out of 108 cases, 16 cases were positive for TTMDV/SAV. Totally 14% of cases were positive for presence of genomic DNA of TTMDV/SAV.

Conclusion: This low frequency in healthy individuals and the high frequency of the virus in patients is possible etiologic role for the inducer virus.

Keywords: TTMDV/SAV, healthy individuals, PCR

Elucidating the Origins of Nosocomial Infections with *Staphylococcus aureus* by Both Biotyping and DNA Fingerprinting Methods

Sima Sadat Seyedjavadi, Masoud Alebouyeh, Mohammad Emaneini, Ehsan Nazemalhosseini Mojarad, Mohammad-Reza Zali

Gastroenterology and liver Diseases Research Center, Shahid Beheshti university of Medical Sciences, Tehran, Iran

Abstract

Background: *Staphylococcus aureus* is among the most important causes of hospital-acquired infections worldwide. Detection of sources of these infections can improve management of the infectious disease in hospitals. The maintools used by researchers to reach this goal are moleculartyping methods. In this study, four molecular typing and two biotyping methods were used for detection of main sources of the infection in an ICU in Iran.

Methods: Between August 2011 and March 2012, one hundred and eight *S. aureus* isolates were obtained from clinical, environmental and staffs' samples of an ICU in Tehran, Iran. The isolates were confirmed by standard bacteriological methods. Testing for susceptibility to 14 antibiotics and their oxacillin MIC was performed using a standard disk-diffusion and agar dilution method according to the CLSI guidelines. Each *S. aureus* isolate was examined for existence of a total of seven drug resistance encoding genes (aac (6')-Ie- aph (2'), aph (3')-III, ant (4')-I, aac(6')-Ie, ant9, blaz, mecA). All the isolates were also typed for their spa type, intI1 gene and plasmid profiles.

Results: Results of this study ascertained role of ICU environment andstaff as origins of nosocomial infections in26.6% of the cases. Interestingly, 19% of the isolates failed to be typed correctly by spa typing method. Among the methods under consideration genotyping and integron typing showed the most consistent results. 83% of the typing strains were considered as high-risk strains with high MIC and MDR genotype that this shows the importance of molecular surveillance studies.

Conclusion: These data support the opinion that *S. aureus* are significant nosocomial pathogens in intensive care units and that resistant clone may be transmitted between patients, environment and staffs. Molecular epidemiological tools are helpful for understanding transmission patterns and sources of infection, and are useful for measuring outcomes of intervention strategies implemented to reduce nosocomial *S. aureus*.

Keywords: *Staphylococcus aureus*, Moleculartyping, MIC, Genotyping, Biotyping

Probiotication of Wheat Sprouts Extract by *Lactobacillus acidophilus* and *Bifidobacterium animalis*

Fatemeh noparast[1], Negin Noori[2], Nahid Vousoghi[1], Hassan Hamedi[2], Ali Malekshahi Moghadam[1]

Abstract

Background: Wheat sprout as a type of whole grain is rich in vitamins especially vitamin A, E and B and Also, it is rich in fiber that helps to maintain intestinal flora. The aim of this study was to investigate the possible prebiotic effect of wheat sprout extract on enhancing the survival of *Lactobacillus acidophilus* and Bifidobacteriu animalis in culture media.

Methods: Lyophilized strains of *Lactobacillus acidophilus* LA-5 and *Bifidobacterium animalis* subsp. Lactis were purchased from Chr. Hansen Company (Horsholm, Denmark). Then lyophilized extract of wheat sprout were prepared. The media (MRS broth) with different concentrations of WSE (0, 0.25, 0.5, 0.75, and 1 %) were prepared and inoculated with 1×10^6 CFU/ ml of activated *L. acidophilus* LA-5 and *B. animalis* BB12. The experimental media were incubated at 37ºC for 48 h. The enumeration of *L. acidophilus* LA-5 and *B. animalis* BB12 was carried out on MRS and MRS-C (0.05 % L-cysteine) agar (Merck, Darmstadt, Germany) at different incubation times (0, 12, 24 and 48 hours) aerobically and anaerobically respectively.

Results: Adding various concentrations of WSE increased the survival of bacteria and these effects were significant for both *L. acidophilus* and *B. animalis* ($P<0.05$). The bacterial growth also had a significant relationship with the increase in WSE ($P<0.05$) although this increase in *B. animalis* was more than *L. acidophilus*. A, 4 log increase in bacterial count compared with the control group was observed in 1 % WSE concentration after 24 h incubation.

Conclusion: The utilization of wheat sprout and probiotic could be an interesting approach for the area of functional foods.

Keywords: Prebiotic, wheat sprout extract, probiotic, *Lactobacillus acidophilus*, *Bifidobacterium animalis*

[1]Faculty of Veterinary Medicine, University of Tehran, Tehran, Iran
[2]Department of Food Hygiene, Faculty of Veterinary of Medicine, University of Tehran, Tehran, Iran

Prevalence of *Hepatitis B Virus* and *Hepatitis C Virus* among Haemodialysis Patients in Hamedan, West of Iran

Masoud Hamidi[1], Mahdi Khulojini[2] , Hamed Bashiri[3], Ebrahim Mohammad niaei[2] , Alireza Ahanchian[2] , Reza Shiri heris[3]

Laboratory of Shahid Beheshti Hospital, Hamedan, Iran

Abstract

Background: Patients undergoing chronic hemodialysis potentially have an increased risk of exposure to infections with viruses, such as *Hepatitis B* (HBV) and *Hepatitis C* (HCV) viruses. The aim of this study was to evaluate the prevalence of HBV and HCV for all hemodialysis patients in two dialysis units in Hamedan.

Methods: As a routine, all hemodialysis patients in Iran have biannual blood samples for assessment of serum HBsAg, HBs Abs, and HCV Abs. Data came from the dialysis units of the Shahid Beheshti and Besat Hospitals, which are all university hospitals in Hamedan city. For each hemodialysis patients, age, gender, occupation and place of residence (rural/urban) were recorded and then analyzed.

Results: Of the two hundred and four patients, three (1.5%) were found seropositive for HBsAg and seven (3.4%) for HCV Ab. There was not any relation between positive cases and age, gender, occupation and place of residence (rural/urban) ($P>0.05$).

Conclusion: Dialysis units in Hamedan that conform to policies and regulation related to infection control and isolation of HBV and HCV sero-positive cases, had significant low incidence rate for HBV and HCV sero-conversion.

Keywords: *Hepatitis B*, *Hepatitis C*, hemodialysis patients

The Prevalence of Nasopharyngeal *Neisseria* spp on Children up to Five Years Old in Tehran, Iran

Hadi Parsa[1], Seyed Davar Siadat[2], Seyed Fazlollah Mousavi[2], Pantea Jalali[3], Peyman Mokarami[1]

[1]Department of Biology, Science and medicine, Zanjan Branch, Islamic Azad University, Zanjan, Iran
[2]Microbiology Research Center and Department of Bacteriology, Pasteur Institute of Iran, Tehran, Iran
[3]Department of Biology, Science Research Branch, Islamic Azad University, Tehran, Iran

Abstract

Background: Since *Neisseria* is a strict human pathogen and patients have not been in contact with others, carriers are the major source of the pathogenic strains. This study investigated the frequency of *Neisseria* species in healthy children under five years old and the distribution of *N.meningitidis* isolated from the nasopharyngeal of them.

Methods: One-hundred nasopharyngeal samples from healthy children under five years old in Children's Medical Center (2011-2012) were cultured on modified Thayer Martin agar. Identification was performed by biochemical testing, oxidase; CTA and then species differentiation were performed by prime PCR.

Results: Thirty cases (30%) were carriers of *Neisseria* spp (39% girls and 51% boys) and 5 cases (5%) were positive for *N. meningitidis* (40% girls and 60% boys). 27% of *Neisseria* and 20% of *N. meningitidis* isolated from 1-2 year old children, 40% of *Neisseria* and 60% of *N. meningitidis* isolated from 2-3 year old children, 19% of *Neisseria* and 20% of *N. meningitidis* isolated from 3-4 year old children and 14% of *Neisseria* and 0% of *N. meningitidis* isolated from 4-5 year old children.

Conclusion: The percentage of colonization varies depending on the age group. The prominent groups were two to three years old; this rate is reduced with increasing age. The identification and detection of serotypes will enable us to estimate the magnitude of the meningitis problem in our country and would make it possible to set up the appropriate treatment measures and apply specific vaccines in our population.

Keywords: *Neisseria*, carriers, nasopharynx, PCR

Molecular Detection of *Candida albicans* DNA in Blood Samples Using Real Time PCR

Mohsen Ashrafi[1], Mojtaba Nabili[2], Ghasem Jan Babaie[3], Mohamad Taghi Hedayati[1], Tahereh Shokohi[1]

[1]Department of Parasitology and Mycology, Faculty of Medicine, Mazandaran University of Medical Sciences, Sari, Iran
[2]Department of Parasitology and Mycology, Faculty of Medicine, Mazandaran University of Medical Sciences, Sari, Iran- Social Security Organization, Golestan, Iran
[3]Department of Internal Medicine, Cellular and Molecular Research Centre, Faculty of Medicine, Mazandaran University of Medical Sciences, Sari, Iran

Abstract

Background: *Candida albicans* is a major cause of candidemia in people with impaired immunity. Blood culture is a "gold standard" for detection of candidemia but it's time consuming and has low sensitivity. We established a real-time PCR assay for the detection C. albicans in blood by Light Cycler PCR and melting curve analysis.

Methods: Five milliliter of blood samples from healthy volunteers were spiked with 10^0-10^8 C.albicans cells to determine the detection limit. DNA was extracted from whole blood using glass bead and the QIAamp DNA Blood Mini Kit. DNA fromC.albicans isolate was amplified with primers and inserted into *E. coli* (DH5α.1) by TA Cloning vector (Invitrogen).The plasmid is used for standardization and optimization. A quantitative PCR assay with the Light Cycler amplification and detection system based on fluorescence resonance energy transfer (FRET) with two different specific probes was established. To confirm precision and reproducibility of real-time PCR the intra-assay precision was determined in six repeats.

Results: No cross-reactivity of the hybridization probes to other DNA of non *C. albicans* species, bacteria and human genomic DNA with 100% specificity was observed. The minimum limit was detected one *C. albicans* cell or 10^0 CFU/ml (10fg) per PCR reaction. Real-time PCR efficiency rate for *Candida* was high (E = 1.95). Melting curve analysis of *C. albicans* showed a specific melting peak signal that was 65.76 °C.

Conclusion: Real time PCR assay is a highly specific and sensitive to detect the fungal load for early diagnosis of Invasive candidiasis.

Keywords: Invasive candidiasis, Real Time PCR, *Candida albicans*

Molecular Analysis of Coagulase Gene Polymorphism in *Staphylococcus aureus* Isolates from Clinical Samples and Health Carriers

Teena Dadgar[1], Nima Bahador[1], Abasali Imani Fooladi[2], Ezzat Allah Ghaemi[3]

Abstract

Background: The coagulase protein is an important virulence factor of *S. aureus* coagulase gene that can be used for differentiating *S. aureus*. This study was conducted to investigate the Coagulase gene polymorphism of *S. aureus* isolated from healthy carriers and patients.

Methods: A total of one hundred seventy *Staphylococcus aureus* strains collected from Gorgan. Ninety-five (66%) cases from patients and seventy five (44%) cases from healthy carriers were analyzed for the molecular typing purpose**.** To perform coagulase gene typing, the repeated units encoding hypervariable regions of *S. aureus* coagulase gene were amplified by the PCR, followed by ALUI restriction enzyme digestion of PCR product and analyzed for the RFLP.

Results: The isolates revealed 7 types of Coa gene products between 500-1200 bp and 17 distinct RFLP Patterns were obtained with AluI digests of PCR products. Majority of isolates belong to the band classes 800bp and PCR-RFLP pattern P8 (405-324bp). Coagulase gene types 6, 8 PCR-RFLP were the most common in patients. All Coa gene types were present in different source of *S. aureus* in patients. The differences in types is significant between two group of carriers and patients (P value 0.005)

Conclusion: Some PCR-RFLP patterns had specific for *S. aureus* isolated from healthy carriers, did not observe in patients**.** Therefore this method could clearly classify *S. aureus* types consisting of either patients or healthy carrier**.** With high discriminatory index value (DI: 0.9), this method proved to be useful, rapid and efficient for typing *S. aureus* strains isolated from clinical samples. The Results of this study show that Coa marker and AluI subtypes can also be used to determine the evolution of *S. aureus*.

Keywords: Coagulase gene, polymorphism, *S. aureus*

[1]Department of Microbiology, Fars Science Research Branch, Islamic Azad University, Shiraz, Iran
[2]Applied Bioligy Research Center, Baqiyatallah University of Medical Sciences, Tehran, Iran
[3]Infectious Diseases Research Center, Golestan University of Medical sciences, Gorgan, Iran

Skin Colonization with *Staphylococcus aureus* in Patients with Atopic Dermatitis

Fakhrozaman Pezeshkpoor, Mohammad Javad Yazdanpanah, Mahnaz Banihashemi, Reza Farid, Javad Ghenaat

Research center for Skin Diseases and Cutaneous Leishmaniasis, Department of Dermatology, Faculty of Medicine, Ghaem hospital, Mashhad University of Medical Sciences, Mashhad, Iran

Abstract

Background: Atopic dermatitis (AD) is a chronic relapsing condition of pruritus and eczematous lesions that affect 15-20% of the childhood population and 1-3% of adults worldwide and sixty percent of patients develop AD within the first year of life, 85% by age five. Our aim was to investigate the presence of *Staphylococcus aureus* in the skin of AD patients and compare with healthy control group.

Methods: Forty patients with AD were recruited in to our study. *S. aureus* skin colonization was determined in AD patients and controls, also skin distribution of *S. aureus* colonization was compared in three age groups of AD patients.

Results: *S. aureus* was found on the skin of 42.5% and 7.5% of AD patients and control group, respectively (p=0.0003). The most common involved skin areas with *S. aureus* colonization were face (in ≤two yrs old), flexor surfaces (in >two and ≤twelve yrs old) and extremities (in >twelve yrs old).

Conclusion: The incidence of *S. aureus* on the skin of AD patients was considerably higher rather than controls. Further studies are needed to investigate the clearance of *S. aureus* from the skin of AD patients using anti-staphylococcal treatment.

Keywords: Atopic dermatitis, *Staphylococcus aureus*, Skin colonization

Nested PCR detection of *Parvovirus B19* in patients with blood disorders from Isfahan, Iran

Razieh Nikoozad Shahraki[1,3], Mahzounieh M[2,3], Nafise Sadat Naghavi[4], Marzieh Safarpoor[3]

[1]Faculty of Bioscience, Falavarjan Branch, Islamic Azad University, Falavarjan, Iran
[2]Department Pathobiology, Faculty of Veterinary Medicine, Shahrekord University, Shahrekord, Iran
[3] Research Institute of Zoonotic Diseases, University of Shahrekord, Shahrekord, Iran
[4]Department of Microbiology, Faculty of Bioscience, Falavarjan Branch, Islamic Azad University, Falavarjan, Iran

Abstract

Background: *Parvovirus B19* has a specific tropism for erythroid progenitor cells and thus can cause a temporary infection of the bone marrow eventually leading to a transient arrest in erythropoiesis. Patients with blood disorders are at risk of severe clinical illness such as sickle cell disease, thalassemia and hereditary spherocytosis. The aim of present study was to evaluate *Parvovirus B19* infection in patients with blood disorders from Isfahan, Iran by nested PCR.

Methods: Serum samples were collected from one hundred and seven patients with blood disorders, including acute myeloid leukemia and acute lymphocytic leukemia, thalassemia and hemolytic anemia from Isfahan, Iran. Following DNA extraction from serum samples, nested PCR was conducted for detection of *Parvovirus B19*.

Results: *Parvovirus B19* was found in twenty five (23.36%) of one hundred and seven patients. Infection was established as follows: ten (18.9%) of fifty three patients with hemolytic anemia, nine (31%) of twenty nine patients with acute myeloid leukemia and acute lymphocytic leukemia, six (24%) of twenty five patients with thalassemia.

Conclusion: Rates of *Parvovirus B19* infection were extremely high. The probable reason is many blood transfusions may increase risk of infection with *Parvovirus B19*. It is recommended to evaluate donated blood for *Parvovirus B19* infection.

Keywords: *Parvovirus B19*, blood disorders, PCR

Imipenem-EDTA Disk Methods for Detecting Metallo-β-Lactamase-Producing *Klebsiella pneumuneia* in Arak

Mojdeh Safari[1], Hamid Abtahi[2]

Abstract

Background: Infections caused by *Klebsiella pneumuneia* is a life-threatening agent forimmuno-compromised patients. This gram-negative bacterium is resistant to the various antibiotics. Until now several resistance mechanisms in *K. pneumuneia* have been known, Metallo-β-lactamase (MBL) production is one of the significant mechanisms in antibiotic resistance. This study has been designed to determine frequency of MBL-producing *K. pneumuneia* in Arak.

Methods: 110 isolates were collected from clinical specimens submitted to Microbiology laboratory of University of Medical Science in Arak/Iran from May to January 2010. Antibiotic susceptibility test was done for imipenem by Disk Diffusion Methods according to CLSI (Clinical and Laboratory Standards Institute). Imipenem-resistant strains were investigated for metallo-β-lactamase production by the Combined Disk Methods.

Results: The rates of resistance were sixty one (55.4%) to Ceftriaxone, Cefotaxime fifty five (50%), ceftazidime fifty four (49%), cefoxitin twenty (18.1%), cefotetan seventeen (15.4%), meropenem thirteen (11.8%) and imipenem thirteen (11.8%). Of the thirteen Imipenem resistant isolates, seven (53.8%) were MBL producers.

Conclusion: Results illustrated half of Imipenem-resistant strains were MBL positive, and also this study suggests that metallo-β-lactamase producing isolates in hospitals maycause serious infections lead to the antibiotic therapy fails. Therefore it is important to detect MBL-producing strains due to control their transmission .In addition phenotypic detection of MBLs is not an accurate method; molecular studies could reveal more accurate data.

Keywords: *Klebsiella pneumuneia*, EDTA, Imipenem, Metallo Beta Lactamase

[1]Department of Microbiology, Islamic Azad University of Qom, Qom, Iran
[2]Molecular and medical research center, Arak University of Medical Sciences, Arak, Iran

Evaluation of Hand Hygiene Practice among Nurses in the Amiralmoemenine Hospital of Genaveh during 2011

Mojgan Ghasemi

Amiralmoemenine Genaveh hospital, Bushehr University of Medical Sciences, Bushehr, Iran

Abstract

Background: Despite all the efforts taken, hospital infections are still the largest problem in health care system and often cause serious complication in hospitalized patients. It can be prevented by proper infection control guidelines, including hand hygiene.

Methods: A descriptive cross-sectional study was performed. Ninety nurses, with stratified random sampling, conducted in this study. SPSS statistical software and descriptive statistical analysis were used.

Results: In this study, 79% were female. The mean age of cases was 29.1 ± 4.2. Their educational properties were as follows: 60% expert, 15% technicians and 25% diploma, 71% had hand hygiene training. 22% had Poor performance, 48% had moderate and 30% had good performance. There was no significant relationship between performance and demographic characteristics.

Conclusion: Results of this study suggested thorough implementation of infection control guidelines, use of protective equipment, face to face training to improve Health care service.

Keywords: Practice nurses, principals, hand hygiene

Hand Washing for the Prevention of Swine Flu Transmission Based on Protection Motivation Theory among Adolescents, Isfahan

Parastoo Yarmohammadi[1], Gholam Reza Sharifirad[2], Zohreh Rahayi[3],Mohammad Ali Morowati Sharifabad[4]

[1]Kashani hospital, Shahrekord, University of Medical Sciences, Shahrekord, Iran
[2]Department of Health Education, School of Health, Isfahan University of Medical Sciences, Isfahan, Iran
[3] Department of Health Education, School of Health, Tarbiat Modares University, Tehran, Iran
[4]Department of Health Education, School of Health, Yazd Shaheed Sadoughi University of Medical Sciences, Yazd, Iran

Abstract

Background: Respiratory infections are of great importance because of their rapid and extensive spread and their role in mortality of children, adolescents and adults. Because pandemic and swine flu are known to be transmitted via human hands, hand hygiene using both soap and water can play a vital role in preventing these infections in adolescents.

Methods: This cross-sectional study was conducted on three hundred female high school students in Isfahan in the year 2009. Random Sampling was done in several periods. Data were collected using a self-report questionnaire based on PMT (Protection Motivation Theory) constructs. The obtained data were analyzed using SPSS software.

Results: Fifty-one percent of students believed that washing hands could prevent influenza. Frequent hand washing was reported by 74% of participants. The results of this study showed that frequent hand washing with soap and water had a positive and meaningful relationship with perceived sensitivity, response efficacy and self-efficacy (P<0/01). In addition, hand washing was significantly related with achieving information about influenza.

Conclusion: Hand washing decreases the risk of getting swine flu and it is a habit among students. Aware about these habits is important in determining healthy behaviors. The results of this study showed that the application of PMT had a role in preventive behavior (hand washing) in swine flu.

Keywords: Hand washing, swine flu, Protection Motivation Theory, adolescents

Study of Sputum and Bronchoscopic Lavage for Acid Fast Bacilli in Patients Referred to Imam Khomini Hospital in Ahvaz

Mahvash Heidari, Azardokht Khosravi, Manijeh Mehdinejad, Afroz Morvaridi

Ahvaz University of Medical Sciences, Ahvaz, Iran

Abstract

Background: The diagnosis of tuberculosis is based on the detection of *Mycobacterium tuberculosis* on clinical specimens with different methods.

There are many techniques, such as molecular methods and direct examination of Acid fast stain and cultures. The most commonly used and reliable specimen for bacteriological examination is sputum for the diagnosis of pulmonary tuberculosis.

Methods: In the present study, 2872 specimens (sputum, bronchoscopic lavage) for laboratory diagnosis collected, specimens submitted for smear were stained with Ziehl-Neelsen stain and examined under the light microscope for smear examination.

Results: There were 1726 (60%) specimens from male and 1146(40%) from female patients. There were 2758 sputum specimens and 114 bronchoscopic lavage specimens. One hundred eighty three (6.4%) of total specimens were positive for acid-fast bacilli (18.6% of specimens were from lavage and 81.4% from sputum). In positive specimens 60.7% belonged to male patients.

Conclusion: The results of this study showed that acid-fast staining (Ziehl-Neelsen staining) is proper method for diagnosing all suspected cases of tuberculosis. Specimens (sputum and lavage) were more in male patients.

Keywords: Sputum, Bronchoscopic lavage, Acid fast bacilli

Disinfectant Property Evaluation of Silver Sulfide Nanoparticles Prepared by Three Different Methods and Comparing With Silver Nanoparticles in Using for Hospital Surfaces

Roshanak Salari[1], Bibi Sedigheh Fazly Bazzaz[2], Omid Rajabi[1]

[1]Department of Medicinal Chemistry, School of Pharmacy, Mashhad University of Medical Sciences, Mashhad, Iran
[2]Biotechnology Research Center and Department of Medicinal Chemistry, School of Pharmacy, Mashhad University of Medical Sciences, Mashhad, Iran

Abstract

Background: It has been a while that the level of attention towards antibacterial properties of silver nanoparticles has been grown scientifically and practically. Sulfur and sulfur nanoparticles were known as antibacterial agents previously too. So silver sulfide nanoparticles synthesis can improve both silver and sulfur nanoparticles potencies as antibacterial agents.

Methods: Available standards of CEN TC 216, which are related to the chemical disinfectants and antiseptics, were applied to evaluate and compare the antibacterial activities of nanosilver sulfide formulations (F_1, F_2 and F_3) (different in sulfur sources) made by chemical reduction and nanosilver formulation.

Results: Among F_1, F_2 and F_3, only F_3 could pass both phases of CEN TC 216 successfully. Silver nanoparticles inhibited microorganisms' growth about one logarithmic unit lower than silver sulfide nanoparticles.

Conclusion: Third formulation (F_3) showed a satisfactory bactericidal properties and its specific use in different areas such as hospital surfaces can be further assessed. Silver nanoparticles as a disinfectant had lower potency than silver sulfide nanoparticles.

Keywords: Silver nanoparticles, Silver sulfide nanoparticles, Disinfectant, CEN TC 216

Comparison Frequency of Integrons Class1 between Burn and None Burn Clinical Isolates of *Pseudomonas Aeruginosa* in Tehran

Somayeh Moazami Goudarzi, Fereshteh Eftekhar

Department of Microbiology, Faculty of Biological Science, Shahid Beheshti University, Tehran, Iran

Abstract

Background: *P. aeruginosa* was the most predominant organism in the burn patient's infection. *P. aeruginosa* infections are normally difficult to eradicate due to acquired resistance to many antibiotics via horizontal gene transfer like integrons. The present study was conducted to comparison frequency of integrons class 1 and antibiotic resistance profiles between burn and none burn clinical isolates of *P. aeruginosa*.

Methods: Seventy- seven burn isolates and thirty five nonburn isolates collected from Motahari and Shohadaye Tajrish hospitals, respectively and were identified using the standard biochemical tests and the Kirby-Bauer disk diffusion method was performed to determine susceptibility to 13 antibiotics. Detection of class I integrins was performed by the PCR method.

Results: Comparison of antibiotic susceptibility pattern showed high level of antibiotic resistance except co-trimoxazole among burn isolates ($P<0.05$). PCR results showed that burn isolates showed high frequency of integrons class I ($P<0.05$). 82.27% of burn isolates and 17.72% of non burn isolates of *P. aeruginosa* carried class 1 integrons.

Conclusion: The high frequency of antibiotic resistance and integrons class 1 was seen among burn isolates. Since infection is the most common cause of death in burn patients, it is crucial to control antibiotic resistance via prevention of integrons prevalence.

Keywords: Burn isolates, antibiotic resistance, *P. aeruginosa*, class I integron

Abundance of *S. epidermidis* and *S. aureus* from blood culture and consideration of their antibiotic resistance pattern in north-east of Iran from 2005 to 2012

Davod Bordbar, Shamsaldin Mansoori, Houshyar akbari, Ali Sadeghian, Kiarash Ghazvini

Mashhad University Medical Science, Microbiology research center, Mashhad, Iran

Abstract

Background: Surveying causative agents of infections and their antibiotic resistance pattern is an important factor for policy making in health systems. Recently many hospital pathogens showed high level resistance to antibiotics. In this study we studied antibiotic resistance pattern of *S. epidermidis* and *S. aureus* in blood infections.

Methods: During seven years, sampling was done from patients who were suspicious to blood infections and their antibiotic resistance pattern was identified by laboratory tests.

Results: Among 28000 samples of blood cultures, six hundred samples were positive for *Staphylococci*, of these, four hundred and twenty samples were diagnosed as S. epidermidis (70%), one hundred and seventy samples were *S. aureus* (28%) and the remaining (2%) were other strains of *Staphylococci*. About 93% of S. epidermidis and 96% of *S. aureus* were penicillin resistance. There were increasing resistance to other antibiotics such as amikacin, cefamandole, co-amoxiclav and oxacillin in spite of heterogeneity among all of these antibiotics.

Conclusion: *S. epidermidis* is a normal flora of the skin so it should be considered the possibility of needle tip contamination during sampling and some positive results may be related to this matter. Resistance to antibiotics was high during these years which are apprehensive for scientists.

Keywords: Ocular infection, *Staphylococcus*, resistance pattern, North-East of Iran

Isolation of *Staphylococcus aureus* and *Salmonella* in hamburgers that made by peoples at fast food restaurants in the west of Mazandaran

Mojgan Shams Nazeri[1], Jafarpoor M[1], Nazemi A[2]

[1]Department of Microbiology, Tonekabon branch, Islamic Azad University, Tonekabon, Iran
[2]Department of Genetic, Tonekabon branch, Islamic Azad University, Tonekabon, Iran

Abstract

Background: Several bacterial agents, including *Salmonella* and *Staphylococcus aureus* are involved in food contamination; the purpose of this study was to determine microbial contamination of samples, which were handmade burgers, to Iran standard limits.

Methods: One hundred samples were prepared from homemade burgers. Iran test method based on national standards for the isolation of *Salmonella* in 1810, 1-6808 for the isolation of *Staphylococcus aureus* and 5272 is the total count of microorganisms. DNA was isolated and purified. DNA molecule used to confirm they were amplified by universal SrDNA16 and amplified products were sequenced by Blast software.

Results: Fifteen percent of the samples contaminated with *Salmonella*, 48% of the samples were contaminated with *Staphylococcus aureus* and 10% of Iran's national standard was allowed for bacteria too.

Conclusion: Due to the increased consumption of home made burgers and the possibility of food-burned is eases by pathogens, it is necessary that health authorities have more control in the supply of healthy food.

Keywords: *Staphylococcus aureus*, *Salmonella*, hand made burgers

Abundance of *K. Pneumonia*, *E. coli*, *Acinetobacter*, *Enterococcus* and *P. aeroginosa* in Blood Cultures and Their Antibiotic Resistance Pattern in North-East of Iran from 2005 to 2012

Shamsoddin Mansoori, Davod Bordbar, Houshyar akbari, Ali Sadeghian, Kiarash Ghazvini

Mashhad University Medical Sciences, Microbiology research center Mashhad, Iran

Abstract

Background: Surveying causative agents of infections and their antibiotic resistance pattern is an important factor for policy making in health systems. Recently many hospital pathogens showed high level resistance to antibiotics. In this study we studied antibiotic resistance pattern of five bacteria in blood infections.

Methods: During seven years, sampling was done from patients who were suspicious to blood infections and their antibiotic resistance pattern was identified by laboratory tests.

Results: Among 28000 samples of blood cultures, six hundred forty samples were positive for *K. Pneumonia*, *E. coli*, *Acinetobacter*, *Enterococcus* and P. aeroginosa. Of these, one hundred ninety five samples (30%) were diagnosed as *K. Pneumonia*, one hundred ninety four samples (30%) were *E. coli*, one hundred forty seven samples (23%) were *Acinetobacter*, one hundred and four samples (16%) were *Enterococcus*, and the remaining (1%) were other bacteria. There were increasing resistance to other antibiotics such as amikacin, amoxicillin, cefazolin, cefotaxim, and oxacillin in spite of heterogeneity among all of these antibiotics.

Conclusion: Our results showed that *K. Pneumonia* and *E. coli* were prevalent bacteria in blood infections. Resistance to antibiotics was high during these years which are apprehensive for scientists.

Keywords: Ocular infection, *K. Pneumonia*, *E. coli*, resistance pattern, North-East of Iran

Kefir Grains Propagation Method and Investigate Kefir Drink Antimicrobial Effects on the Bacteria *Pseudomonas aeruginosa* and *Escherichia coli*

Mehraban Zeinab[1], Kelardasht Maryam[1], Danesh Maryam[2], Parsafar Somayeh[3]

[1]Department of Biochemistry, Islamic Azad University Falavarjan Branch, and young researchers club, Falavarjan, Iran
[2]Department of Biochemistry, Shahrekord University of Medical sciences, Shahrekord, Iran
[3]Department of Microbiology, Islamic Azad University Falavarjan Branch, and young researchers club, Falavarjan, Iran

Abstract

Background: Kefir is a fermented beverage that its impact in the treatment of various diseases has focused the minds of many researchers. Kefir as a rich source of food in meals by half of the world, while among the Iranians is unknown because of the shortage and high price tag kefir grains and lack of understanding of its properties. The purpose of this study was to investigate kefir Antimicrobial effects on bacteria, *Pseudomonas Aeruginosa* and *Escherichia coli*.

Methods: Two grams of kefir grains, the ratio of 1 to 100 in milk, was incubated 18 hours at 37 ° C. After filtration the seeds were separated from the beverage and were ready for re-insemination. This process was repeated a month in order to reproduce the kefir grains. Kefir drink at 20 and 37 produced and its antimicrobial effect of the diffusion method after 24 and 48 hours on two bacteria *Escherichia coli* and *Pseudomonas Aeruginosa* have been reviewed and with three antibiotics, penicillin, gentamicin and amoxicillin were compared.

Results: Kefir grains dramatically increased over the month. Antimicrobial effect also was found in kefir.

Conclusion: Proliferation of Kefir grains was shown significant growth and Antimicrobial effect with increasing temperature and fermentation time.

Keywords: kefir, antimicrobial effect, *Pseudomonas Aeruginosa*, *Escherichia coli*

Detection of Extended- Spectrum beta-lactamases TEM and SHV in *Escherichia Coli* Isolated from Clinical Specimens

Mojdeh Safari[1], Hamid Abtahi[2]

[1]Department of Microbiology, Islamic Azad University of Qom, Qom, Iran
[2]Molecular and medical research center, Arak University of Medical Sciences, Arak, Iran

Abstract

Background: The emergence and spread of resistance in *Enterobacteriaceae* are complicating the treatment of serious nosocomial infections. Many isolates of *Escherichia coli* producing plasmid-mediated beta-lactamases have been involved in worldwide outbreaks of nosocomial infection. This study was aimed to determine the survey of bla $_{TEM}$ and bla $_{SHV}$ in *E. coli* isolated from University Medical Science Hospitals in Arak, Iran.

Methods: Totally two hundred forty one samples of *Escherichia coli* isolated from three hospitals in Arak. Susceptibility to eight antibiotics was determined by Disk Diffusion Method. A combined disk assay using clovulanic acid was employed to detect the ESBL phenotype in the strains resistant to cefotaxime and ceftazidime. ESBL positive strains were further investigated for the presence of bla TEM and bla SHV genes by PCR technique.

Results: A combined disk assay was positive for 108 (80.5%) of 241 isolated *E. coli* bacteria. The DNA amplification by PCR for detection of bla $_{TEM}$ and bla $_{SHV}$ showed that 93 isolates (86.1%) carrying both bla TEM and SHV genes. The prevalence of bla $_{TEM}$ and bla $_{SHV}$ among these isolates was 101 (93.5%) and 28 (25.9%), respectively.

Conclusion: Our finding showed that the high prevalence of ESBL producing *Escherichia coli* from hospitalized patents .Therefore, to prevent the widespread of these isolates their rapid identification by clinical laboratories is highly recommended.

Keywords: *Escherichia coli*, Extended Spectrum beta-lactamase (ESBL), combined disk assay, PCR

Determination of Microbial Contamination from Wet and Dry Sweets Units Offered in the Markazi Province

Azam Khodagholi, Mojdeh Safari, Maryam Raufi

Food Control Laboratory, Deputy of Food and Drug, Arak University of Medical Sciences, Arak, Iran

Abstract

Background: Confectionary products make an important part of the country's food production. Sweets and especially wet sweets because of the ingredients, conditions, construction and maintenance have chances for contamination by various microbes. The purpose of this study was to evaluate microbial contamination of wet sweets and dry sweets, which are produced in pastry of Markazi province.

Methods: Thirty seven samples of wet sweets and one hundred and eight samples of dry sweets selected randomly from pastry of Markazi province during one year (2010-2011). Samples were transported to food control laboratory of deputy of food and drug to detect pathogenic bacteria. The results were analyzed with T test.

Results: The results showed that 48.6% of the total wet sweets samples and 32.4% of the total dry sweets samples have been contaminated by different microbes. In wet and dry sweets 88.8% and54.2% of samples to *Enterobacteriaceae*, 77.7% and 40% to *Escherichia coli*, 61.1% and 25.7% to *Staphylococcus aureus*, 27.7% and 2.8% to *Bacillus cereus*, 50% and 11.4% to mold and yeast infection respectively was more of standards set. In this study, *Salmonella* was not isolated from wet sweets.

Conclusion: Use of healthy raw materials, health awareness of people involved in the production and distribution of wet and dry sweets**,** and supervision in the preparation and maintenance of sweets is necessary for community health.

Keywords: Sweets wet and dry, Microbial contamination, *Enterobacteriaceae*

Common Pathogens in Burn Wound and Changes in Their Drug Sensitivity

Hosain Safari, Ezzatollah Rezaei, Mahboube Naderinasab

Abstract

Background: With regard to probable microbial colonization change and antibiotic resistance in our center, we conducted this study to identify a proper empirical therapy and suitable antibiotics in burn wound infections.

Methods: This study was performed on fifty nine male and female patients admitted in the burn ward of Emam-Reza Hospital, Mashhad, during a three months period, in 2009. Samples from burn wounds were taken by swab in uniform and suitable conditions, one on the 1st and one between the 3rd and the 7th days after admission. In this study, common antibiotics including ceftazidime, ciprofloxacin, cefepime, imipenem, meropenem, cefixime, piperacillin–tazobactam, amikacin and oxacillin were evaluated with the Mast discs (Mast Group Ltd., Bootle, UK).

Results: The most prevalent organisms were *P. aeruginosa* (26.7%), *Acinetobacter* (24.5%) and *Klebsiella* (22.9%).In evaluation of the antibiotic sensitivity of the bacteria; it was found that the Gram-negative bacteria grown in the patients' wound culture were in 88.9%, 76% and 21.6% of cases resistant to ceftazidime, amikacin and imipenem, respectively.

Conclusion: Changes in burn wounds' microbial colonisation and also in antibiotic sensitivity, over time, necessitate periodic evaluation of these changes in each burn center, separately. On the other hand, the growth of MDR organisms, such as *Acinetobacter*, resistant to quinolones, cephalosporins and carbapenems should be considered as a serious risk.

Burn Center, Imam Reza Hospital, Mashhad University of Medical Sciences, Mashhad, Iran

Keywords: Infection Burn wound Microbial resistance

Nasocomial Infections in the Operation Rooms of 22nd Bahman Hospital in Neyshabour

Leila Soghandi [1], Batoul Azad[2], Farhad Fathimoghadam[3]

Neyshabour Faculty of Medicine, Neyshbour, Iran

Abstract

Background: Nasocomial infection is a considerable health issue in the present century. This study was aimed to investigate the microbial causes of nasocomial infections in the operation rooms of 22nd Bahman Hospital in Neyshabour, Northeast of Iran.

Methods: In this cross-sectional study, seven hundred and forty six samples taken from operation rooms monthly were investigated for one year. Information regarding laboratory results as well as site and time of sampling and the used disinfectants were registered and analyzed using SPSS.

Results: From seven hundred forty six samples, three hundred and eighty seven (51.87%) had positive microbial contaminations and three hundred fifty nine (48.12%) were negative. Bacterial contamination was present in 98.5% of positive samples while fungal contamination was present in only 1.5%. The most common bacterial contaminations were due to *Staphylococcus saprophyticus* (48.33%), non-invasive bacilli (31%), gram-negative bacilli (9.3%), *Staphylococcus aureus* (5.16%), and *Staphylococcus epidermidis* (2.58%).

Conclusion: We concluded that nasocomial infection in this hospital was similar to other hospitals in the country but it is higher than the global standard.

Keywords: Nasocomial infection, operation room, Neyshabour

In-Vitro Antifungal Susceptibility of *Candida* Species Isolated from Blood Cultures of Burned Patients in Burns Unit of Zare Hospital, Sari, Iran, 2011

Nazanin Lotfi[1], Tahereh Shokohi[2], Zahra Nouranibaladezaei [3], Omran Ayatolah Nasrollahi[1]

Abstract

Background: Burn patients are ideal hosts for opportunistic and blood infections. Candidemia occurs in 1 to 5% of patients with major burns. The aim of this study was to determine the *Candida* species involved in candidemia in burn wounds and assess the susceptibility pattern of four antifungal agents against of them.

Methods: In a cross-sectional study, blood samples were assessed. The yeast isolated from blood cultures identified to the species level by conventional procedure and API 20C AUX. In vitro antifungal susceptibility of the *Candida* isolates to amphotricin B, fluconazole, voriconazole and caspofungin was determined using E test.

Results: Twenty two (11%) out of 200 blood cultures from 10 (18.2 %) out of 55 burned patients were positive for *Candida*. The most predominant *Candida* species was *Candida* parapsilosis (54.5%), followed by C. guilliermondii (18.1%), C. tropicalis, (13.6%) and *C. albicans* (13.6%). In this study, 86.4% isolates were related to the Candia non-albicans species. E test antifungal susceptibility testing for the yeast isolated from blood cultures showed that all of *Candida* isolates were sensitive to amphotricin B, fluconazole and voriconazole, all (100%) of C. parapsilosis and 50% of C. guilliermondii found to be resistant to caspofungin.

Conclusion: In the present study, the *Candida* isolates showed least resistance against voriconazole followed by amphotricin B. Therefore, due to broad fungicidal activity, cheapness and better availability of amphotricin B compared to voriconazole, amphotricin B can be used as first line therapy and voriconazole should be considered in amphotricin B resistant cases.

Keywords: Candidemia, burn, susceptibility test, amphotricin B, fluconazole, voriconazole, caspofungin

[1]Department of Medical Mycology, Faculty of Medical Sciences, Azad University-Tonekabon Branch, Tonkabon, Iran
[2]Deptartment of Mycology and Parasitology, Sari Medical School, Mazandaran University of Medical Sciences, Sari, Iran
[3]Burn Center, Zare Hospital, Mazandaran University of Medical Sciences, Sari, Iran

Isolation and Identification of *Brucella* Species from Blood Samples of the Patients with Brucellosis by Biochemical and PCR Methods in Hamedan

Zahra Naseri[1], Mohammad Yousef Alikhani[2], Seyyed Hamid Hashemi[3]

Abstract

Background: Brucellosis is a major cause of zoonosis and is endemic in Hamedan Province in Iran. Rapid detection of *Brucella* species by an automated blood culture system and polymerase chain reaction (PCR) may lead to an earlier diagnosis and may improve patient management. The purpose of this study was to isolate *Brucella* species from Brucellosis patients and identify different species of this bacterium in order to determine the prevalence of these species in Hamedan Province.

Methods: Fifty blood samples were obtained from Brucellosis patients with clinical symptoms of the disease in Sina Hospital in Hamedan. The samples were cultured in BACTEC medium and incubated for fourteen days. Then, the samples were cultured on *Brucella* agar for 3 days. For detection of the bacteria we used PCR (with B. melitensis-specific primer {BM,IS711}and B. abortus-specific primer{BA,IS711}) and catalase, oxidase, urease tests, Gram stain and media with various dilutions of Thionin and Fuschin dyes.

Results: Seventeen *Brucella* strains were isolated from fifty blood samples of the patients. PCR and biochemical Methods revealed that all the seventeen isolated bacteria were *Brucella melitensis*.

Conclusion: This study was to evaluate PCR technique as a diagnostic tool for *Brucella* spp in comparison to conventional bacteriological techniques. This study showed a high prevalence of Brucellosis due to *Brucella melitensis* in Hamedan Province and efforts in this region should be aimed at the eradication of this bacterium.

Keywords: *Brucella*, Species detection, PCR

[1]Blood Transfusion Research Center, High Institute for Research and Education in Transfusion Medicine, Hamedan, Iran
[2] Department of Microbiology, Faculty of Medicine, Hamadan University of Medical Sciences, Hamadan, Iran
[3]Department of Infectious diseases, Faculty of Medicine, Hamadan University of Medical Sciences, Hamadan, Iran

Diversity of Bacteroides spp. Among Patients with Gastrointestinal Disorders

Marjan Rashidan, Masoud Alebouyeh, Mehdi Ghobakhlou, Hamid Asadzadeh Aghdaei, Rasoul Bahreini, Mohammaad Reza mZali

Research center for gastroenterology and liver diseases, Shahid Beheshti University of Medical Sciences, Tehran, Iran

Abstract

Background: Bacteroides *spp.* is anaerobic gram-negative rods and dominant bacterial genus in the human colon. These pathogens are the main cause of sepsis, perforation of the large intestine, abdominal wound infections and etc. The aim of present study is to determine of diversity of Bacteroides *spp.* between patients with gastrointestinal disorders.

Methods: During January 2011 to 2012, 100 colonic biopsy samples were obtained from patients in whom colonoscopy was done**.** 25 individuals with normal results of colonoscopy and histology served as control. For bacteriological study one of the biopsy samples homogenized with tissue grinder and cultured in BBE agar at anaerobic conditions. PCRs were by universal primers for Bacteroides fragilis group, *B. fragilis*, *B. vulgatus*, *B. caccae*, *B. eggerthii*, *B. ovatus* and *B. dorei* after common biochemical identification test

Results: The results in this study showed that *B. fragilis* group is dominant among patients with gastrointestinal disorders in compare to control group (56% and 20%, respectively). 50% of these isolates belonged to *B. fragilis* (8% for the control group and 42% for the gastrointestinal disorders). The other species isolated from the patients included B. vulgatus, *B. caccae*, *B. eggerthii*, *B. ovatusand*, *B. dorei* (35%,7%,1.7%,5% and3.5% respectively).

Conclusion: Results of present study showed significant correlation between existences of *B. fragilis* species and gastrointestinal disorders. High frequency of these bacteria among the detected species, proposed its involvement in chronic inflammatory disease through carrying its pathogens that needs further study.

Keywords: Diversity, Bacteroides spp, gastrointestinal disorders

Isolation *Rhodotorula* Species from Two Educational Hospitals in Ahvaz

Sharzad Heydarinia, Zahra Seifi, Ali Zarei Mahmoudabadi

Abstract

Background: *Rhodotorula* species are common airborne contaminant fungi and also considered as normal inhabitants in the skin, lungs, urine and feces in humans. *R. glutinis* was found the commonest isolated specie both in clinical and environmental samples followed by *R. minuta* and *R. mucilaginosa*. During the last two decades several species of *Rhodotorula* are contributed with invasive mycosis among immunocompromised patients. The most common infections due to *Rhodotorula* species in literature are, fungemia associated with catheters, endocarditis, peritonitis, meningitis, keratomycosis and endophthalmitis. The aim of present study was to isolate and identify *Rhodotorula* species from environmental samples collected from two educational hospitals in Ahvaz Jundishapur University of Medical Sciences.

Methods: Six hundred samples were collected from different parts of two educational hospitals in Ahvaz. The wet and sterile cotton swabs were drawn on the studied surfaces and inoculated on Sabouraud agar plates containing chloramphenicol. All culture media were immediately transferred to the Medical Mycology Laboratory and were incubated at room temperatures for one week. During incubation times, all red-orange yeast colonies were selected and their morphology was confirmed by a microscopic examination. Yeasts were identified by the commercial system ID 32 C (bioMérieux, France).

Results: In the present study seventy two strains of *Rhodotorula* were recovered from two educational hospitals in Ahvaz *R. glutinis* (86.1%) was the most common species among the isolates followed by *R. mucilaginosa* (6.9%), *R. minuta* (4.2%) and *Rhodotorula* species (2.8%). Most of isolated yeasts were recovered from cardiology, nephrology and urology departments.

Conclusion: we can state that *Rhodotorula* have considerable distribution in critical departments and could be regarded as an important invasive mycosis.

Department of Medical Mycology, School of Medicine, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran

Keywords: *Rhodotorula*, *R. glutinis*, *R. mucilaginosa*, *R. minuta*

Comparison of Hand Washing with Surgical Scrub Brush in the Specified Time and Counting the Number of Hands Pulling on the Contamination of the Surgical Team in Jahrom Hospitals

Reyhane Rouhi Jahromi[1], Ali Kadivarnia[2]

Abstract

Background: Surgical site infections are often caused by bacteria colonized on the skin near surgical incision. Hand washing is the most important method of preventing hospital infections. This study compared effect of hand washing method with surgical scrub in specified time and counting the number of brush usage on the contamination of hands in the surgical team of Jahrom hospitals

Methods: Fifty persons of surgical team were selected by random sampling and were divided into the two groups (scrub in the specified time and counting the brush numbers). Before washing, the fingertips of both groups were sampled with a swab dipped in normal Saline. Then, both hands put in the sterile glove containing 10cc nutrient broth for 20-30 seconds. All samples were prepared by dilution 1/1000 of environment cultured on nutrient, blood and MacConky Agar. After 24-48 h incubation, the samples in terms of number and type of bacteria were investigated.

Results: All samples of hands before washing were culture positive (100%). Counting the number of colonies before and after washing showed a significant difference (p=0.01).

Conclusion: Compared the results of both methods to wash, washing with brush has a greater impact on reducing bacterial load, but brush washing gave the negative impact on skin and it consumed more time and increased accumulation of microorganisms on the damaged skin.

Keywords: Hand hygiene- Surgical team, Surgical scrub, Drawing brush

[1]Jahrom University of Medical Sciences, Department of Microbiology, Jahrom, Iran
[2]Student Research Committee, Jahrom University of Medical Sciences, Graduate Student laboratory science, Jahrom, Iran

Evaluation of Blood Culture in Media BACTEC during 90 Years of Pediatrics in Tabriz Medical Center

Shahram Abdoli Oskuie[1], Farzaneh Alikhah[1], Mohammad Ahangarzadeh Rezayee[2], Babak Abdinia[1]

[1]Depatment of Pediatrics, Tabriz University of Medical Sciences, Tabriz, Iran
[2]Depatment of Microbiology, Tabriz University of Medical Sciences, Tabriz, Iran

Abstract

Background: Infectious diseases are problematic in all around the world especially of patients. BACTEC system is an early culture method for detecting of infections.

Methods: A cross- sectional study with convenient sampling method for blood cultures from all hospitalized and outpatients was done.

Results: Of the 2640 blood cultures, 283 samples were positive. Rate of positive blood culture was 10.71%. The isolated organisms were CONS (26.9%), S.A (16.3%), *Candida* species (16.3%), klb.P (12.4%), *Streptococcus viridance* (6.4%), *E. coli* (4.9%), *Pneumococci* (2.5%), NFGNB (1.8%) *and* Brucellosis (1.1%) respectively. Detection time was less than twenty four hours for 45.9% of isolated CONS, 58.1% S.A. 84.4% of *Candida* species were detected in less than 48 hours. Detection time for 67.7% of gram-negative bacilli was less than twelve hours and 3 samples of *Brucella* grew within 83-102 hours. Most of positive blood cultures were in neonatal ward and immunocompromised patients.

Conclusions: According to these data BACTEC culture media is a better and more useful method than conventional Methods for detection of microorganisms. BACTEC can isolate organisms in shorter duration and can facilitate early and accurate diagnosis of infectious etiologic agents. It improves antibiotic utilizations.

Keywords: BACTEC, Blood culture

Prevalence of *Alloiococcus Otitidis*, *Haemophilus influenza*, *Streptococcus pneumoniae*, and *Moraxella catarrhalis* in Children Who Suffered from Otitis Media

Ahmad Farajzadehsheikh, Sajjad Aslani, Nader Saki

Department of Microbiology, School of Medicine, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran

Abstract

Background: Otitis media with effusion (OME) is one of the major causes of hearing loss in childhood. The pathogenesis still remains unclear, though it is know that closely related to bacterial infections. *Alloiococcus Otitidis*, *H. influenzae*, *S. pneumoniae*, and *M. catarrhalis* are the most common of bacterial pathogens isolated from middle ear effusions (MEEs). The aim of the present study was the determination prevalence of *Alloiococcus Otitidis*, H. influenza, *S. pneumonia*, and *M. catarrhalis* in the clinical specimens from OME.

Methods: Forty five aspirated of middle-ear effusion were collected from seventy patients (age ranged between one and fourteen years old) who suffered from Otitis media. The specimens were examined for determination of *A. otitidis*, *H. influenzae*, *S. pneumoniae*, and *M. catarrhalis* DNA by PCR method.

Results: Out of forty five middle ear effusions, 77.8% of specimens were shown DNA of at least one of the four bacteria as mention in above. The prevalence of *A. otitidis*, *H. influenzae*, *S. pneumoniae*, and *M. catarrhalis* in middle ear effusion were 25.7%, 20%, 20% and 12.8%, respectively.

Conclusions: Present study revealed that *H. influenzae*, *S. pneumoniae*, and *M. catarrhalis* continuously respectively as common pathogens of otitis media infection in children, and it support that *A. otitidis* was found to be more frequent than three other common pathogens in our region, like other countries.

Keywords: *Alloiococcus Otitidis*, *Haemphilus influenzae*; *Streptococcus pneumoniae*; *Moraxella catarrhalis*, Otitis media

Clinical Features and Long Term Prognosis of Childhood Brucellosis in North East of Iran

Toktam Mohammadpour, Mohammad Saeed Sasan, Reza Karami

Abstract

Background: Brucellosis is a prevalent disorder in children of developing countries. It has a variety of clinical manifestations but mainly presents with arthritis and arthralgia. The aim of this study is to describe the epidemiology and long term prognosis of Brucellosis in Khorasan.

Methods: This is a descriptive cross sectional study (from Nov 2003 up to Feb 2006), the subjects of which are composed of eighty four patients (prospectively from Pediatric Infectious Diseases clinic and ward of Imam Reza hospital, Mashhad, and retrospectively from Health Center of Kashmar). In this study the diagnosis of B is based on serology accompanied with clinical signs and symptoms. Our strategy for duration of treatment was to treat all patients for at least six weeks. We followed the patients by phone and if necessary by visiting in clinic in November 2008.

Results: During thirty eight months we had eighty two children with B. The mean age was 8.02 Y, and 40% of them were girls (M/F=1.21). Summer with 45.9% of the cases was the peak season. History of having unpasteurized dairy products, close contact with farm animals, living in village and B in family was found in 91.6%, 76%, 70.24% and 41.1% of the cases respectively. The presenting symptom in 79.7 %of the cases was joint pain, 72.9% had history of fever during the course of their B. Arthritis, splenomegaly and lymphadenopathy was found in 60.97%,16.9%,7.5%,of patients respectively.

The mean of ESR and WBC was 36mm/h, 8671/mm3. CRP was negative in 46.1%.The therapeutic regimen of 48.7% of our patients was Co-trimoxazole and rifampin. We followed 74. % of the patients for at least 3 years which showed the relapse rate of 6.5 % (in whole group but In Mashhad group there was no relapse). There was a case of re infection, a patient with residual sequel and one death related to B in our case series.

Conclusion: Brucellosis is still a common disease in our children and at least a risk factor for B can be found in history of almost cases of pediatric B. With at least six weeks treatment with two antibiotics and with close follow up, we can decrease the relapse rate in Ped B to zero, even without repeating the serology during or after treatment.

Subspecialty in Pediatric Infectious Diseases, Department of Pediatrics, Mashhad University of Medical Sciences, Mashhad, Iran

Keywords: Brucellosis, Children, Prognosis, Epidemiology

Genotyping of Shigella spp. Isolated from Patients

Nazanin Eftekhari[1, 2], Bita Bakhshi[1], Mohammad R. Pourshafie[3], Behnaz Zarbakhsh[4]

[1]Department of Bacteriology, Faculty of Medical Sciences, Tarbiat Modares University, Tehran, Iran
[2]Department of Biology, Faculty of Basic Science, Science and Research Branch, Islamic Azad University, Tehran, Iran
[3]Department of Bacteriology, Pasteur Institute of Iran, Tehran, Iran
[4]Department of Molecular Medicine, Pasteur Institute of Iran, Tehran, Iran

Abstract

Background: The aim of this study was to investigate the genetic diversity of *Shigella spp.* isolated from patients of two provinces in Iran with diarrhea using PFGE method.

Methods: A total of 32 *Shigella spp.* were isolated from 700 stool samples of patients with diarrhea from two provinces in Iran. The strains were indentified by biochemical tests and PCR assay. Antimicrobial susceptibility testing was performed using disc diffusion method according to CLSI guidelines. Pulsed Field Gel Electrophoresis assay (PFGE) was performed to investigate the genetics diversity of isolated strains.

Results: The antimicrobial assay showed forty five percent of isolates were resistant to 3 antimicrobial agents or more. The most prevalent resistance was seen to co-trimoxazol (93.75%) and tetracyclin (87.5%) while only one isolate (3.1%) was resistant to ciprofloxacin. The foremost resistance profile was SXT/TE/TMP (37.5%). PFGE analysis revealed clonal dissemination (62.5%) of a single clone in Tehran province while more pulsotypes dispersed in Khorasan province.

Conclusion: Comparison of PFGE pattern through standard procedures promotes the global epidemiological investigations and helps public health monitoring. Comparison with published *Shigella* pulsotypes from other countries showed similar pulsotypes in India and Korea, with identical resistance profiles which suggests dissemination of this (these) clone (s) in Asian countries.

Keywords: *Shigella*, PFGE, Genotyping

Genetic Diversity of Integrase in HIV-1 CRF35-AD Prevalent in Iran

Leila Sadeghi[1], Naser Harzandi[1], Mohammad Reza Aghasadeghi[2], Ali Mansouri[3], Rouhollah Vahabpour[2], Ehsan Mostafavi[4], Fatemeh Jahanbakhsh[5], Arash Memarnejadian[2]

[1]Microbiology Dept., Azad Uni., Karaj branch, Karaj, Iran
[2]Hepatitis and AIDS Dept., Pasteur Institute of Iran, Tehran, Iran
[3]Microbiology Dept., Azad Uni., Qom branch, Qom, Iran
[4]Epidemiology Dept., Pasteur Institute of Iran, Tehran, Iran
[5]Dept. of Virology, Tehran University of Medical Sciences, Tehran, Iran

Abstract

Background: Introduction of HAART (highly active anti-retroviral therapy) has greatly increased the survival time of HIV/AIDS patients in the word. However, the occurrence of drug-resistant strains requires new anti-retroviral drugs, one of which, an integrase inhibitor (INI), has been recently approved and used for therapy in many countries. Sooner or later INIs are to be employed in Iran. Therefore, it is important to identify basic mutant variants prior to the introduction of INIs in order to estimate their efficacy. To monitor potential drug-resistance INI mutations in Iranian HIV/AIDS patients, herein, the polymorphism of the int gene in HIV-1 CRF35_AD, which is the major prevalent type in Iran, was investigated.

Methods: A genotypic assay for 40 INI therapy-naïve Iranian patient samples infected with previously typed HIV-1 CRF35_AD was designed. Int gene was isolated by nested RT-PCR and automatically sequenced. The drug-resistant mutation sequences were assessed using the Stanford HIV databank and the International AIDS Society resistance testing-USA panel (IAS-USA). The amino acid translation of sequenced integrase fragments was compared with that of other CRF35_AD isolates already reported from Afghanistan, Pakistan and Iran.

Results: This study found no significantly different variants of the int gene region in the study population. Major mutation sites in the integrase (E92Q, F121Y, G140A/S, Y143C/R, Q148H/R/K and N155H) were not detected.

Conclusion: Our results demonstrate that INIs will be susceptible to drug naive HIV/AIDS patients in Iran.

Keywords: HIV-1 integrase, CRF35-AD, molecular epidemiology, Integrase inhibitor

Determination of Efficiency of Skin Care Agents in Improving Hand Skin Conditions Accompanied with Using Alcohol Rub

Kiarash Gazvini[1], Mahboubeh Bouri [2], Shahrzad Hadi

Abstract

Background: One of the most important reasons for not complying with hand hygiene protocols is contact dermatitis raised by using alcohol rub agents. In WHO guideline applying skin care agents has been emphasized as a useful strategy to prevent that. The aim of this study is to determine the effectiveness of using hand cream to improve skin condition of cases, as well as assessing efficiency of that on 4 indexes of skin health separately.

Methods: Trial population is divided to 2 groups of 8. The first group apply cream besides alcohol rub whereas the second group don't use. After 2 weeks they have one week break and then rolls shift. Materials needed: skin care agent, alcohol rub, Larson chart to collect data, analysis software SPSS and excel.

Results: The results showed significant difference for all 4 indexes of skin health ($p< 0.05$) between two groups. The compliance of hand hygiene between the group with skin care and without skin care is significantly different ($P< 0.05$). The satisfactions of two groups were also different during these periods.

Conclusion: This study emphasis that using skin cares which improve skin condition influence compliance of hand hygiene. Applying skin care agent is effective in improving skin condition of cases.

[1]Microbiology and Virology Research Center, Buali Research Institute, Mashhad University of Medical Sciences
[2]Razavi Hospital, Mashad, Iran

Keywords: Dermosept alcohol rub, skin care agent, hand hygiene

Effect of Aluminum Compounds (Alum) and Nanoadjuvant MMT with DNA Vaccine Containing Plasmid Encoding Surface Protein Gene 3 of *Toxoplasma gondii* RH Strains in Order to Assess Immunogenicity and Survival against Toxoplasma Infection in Animal Models

Hossein Sobati[1], Abdolhossein Dalimi[2], Bahram Kazemi[3], Fateme Ghaffarifar[2]

Abstract

Background: *Toxoplasma gondii* is the intracellular protozoan parasite responsible for animal and human toxoplasmosis. SAG3 possess an important role in attachment to target cells. SAG3 antigen is expressed at different parasite life stage such as tachyzoite, bradyzoite and sporozite. Regarding these specifications it can be used as a *Candida*te for vaccine and disease diagnosis. In this study we used complete surface antigen 3 of *Toxoplasma Gondii* as DNA vaccine.

Methods: Toxoplasma Genomic DNA extracted using phenol–chloroform method and SAG3 gene was then amplified by PCR with specific primers. The PCR products cloned into pBluescript plasmid and then confirmed by sequencing. Then this gene subcloned into pcDNA3 and after transfection of Eukaryotic cell (CHO) with this recombinant plasmid (pcSAG3), expression of this gene was confirmed by RT-PC SDS-PAGE and Western blot analysis. After wards, we investigated the efficacy of pcSAG3 with or without adjuvant Alum and MMT in female inbred Balb/c mice against toxoplasmosis. Mice were intramuscularly immunized three times at 3 weeks interval.

Results: DNA vaccine containing Plasmid Encoding surface protein gene 3 immunizations induced a long-lasting protection against a lethal challenge with the highly virulent *Toxoplasma Gondii* RH strain, whereas control groups were not protective. Anti- T. gondii IgG, IgG1, IgG2a values (OD) increased markedly in the case groups, which were significantly higher than those of control groups ($P<0.05$). The results of cytokine (IFN, IL-4) assay show that mice immunized with pcSAG3 elicited stronger Th1–type cellular immune responses than those immunized with empty plasmid, or phosphate buffer salin (high level of IFN- and low level of IL-4).

Conclusion: Our study indicated that the co–delivery of Alum and MMT enhanced the potency of DNA vaccine. These results support further investigations to achieve a multi agent anti – T. gondii DNA vaccine.

Keywords: *Toxoplasma gondii*, DNA vaccine, Alum and MMT adjuvant, surface antigen3

[1]Department of Biology, Amam Hossein University, Graduate of medical sciences Tarbiat Modares University Tehran, Iran
[2]Department of Parasitology, Faculty of Medical Sciences, Tarbiat Modares University, Tehran, Iran
[3]Department of Parasitology and Cellular and Molecular Biology Research Center, Shaheed Beheshti University Tehran, Iran

Genomic Comparison of Mycobacterium Tuberculosis Isolated from Patients in Golestan Province (North of Iran)

Khorshid Badihi[1], Nader Mosavari[2], Rooholah Keshavarz[2]

[1]Islamic Azad university of Tonekabon branch, Tonekabon-Iran
[2]PPD Production Department, Razi Vaccine and Serum Research Institute, Karaj, Iran

Abstract

Background: Tuberculosis (TB) caused by *Mycobacterium tuberculosis* with almost 9 million new cases each year remain of the most feared disease on the planet. The identification of sources of infection , routes of transmission are important part of an eradication scheme and these can be achieved by differentiation of *Mycobacterium tuberculosis* isolates by molecular typing method such as restriction fragment length polymorphism (RFLP). Golestan province after Sistan and Baloochestan has the highest number of TB patients in Iran.

Methods: In this study, RFLP technique by Alu 1 enzyme and PGRS probe were compared of genomic pattern diversity and better identify strain. Thirty six Sputum specimens were collected from smear positive patients in Golestan province. Samples were processed and cultured on Lowenstein Jensen (LJ) slant for three weeks. DNA was extracted from two samples based on van embden protocol. First PCR assay targeting 16s rRNA genes was used for identification of *Mycobacterium spp.* Whole DNA restricted with Alu 1 enzyme then DNA fragments transferred to charge positive membrane (southern blotting) and hybridized with DIG labeled PGRS probe.

Results and Conclusion: In this study, wide range of genetic diversity as twenty two different genomic patterns were obtained after digestion with Alu I and hybridization with PGRS.

Keywords: PGRS, RFLP, Alu I, M. tuberculosis, Golesta

Interleukin-8 but not Interlukin-6 Gene Polymorphisms Confers Resistance to Brucellosis in Iranian Population

Sadaf Asaei[1], Manoochehr Rasouli[1], Ali Moravej[2]

[1]Department of Immunology, Professor Alborzi Clinical Microbiology Research Center, Shiraz University of Medical Sciences, Shiraz, Fars, Iran
[2]Department of Immunology, Fasa University of Medical Sciences, Fasa, Fars, Iran

Abstract

Background: Increased level of interleukin-8 (IL-8) and interlukin-6 (IL-6) in acute human Brucellosis has been reported. Previous studies showed that the production of IL-6 and IL-8 cytokines is associated with the polymorphism of their genes. According to the important role of these two cytokines in outcome of *Brucella* infection and role of polymorphisms in cytokine production, in the present study, we attempted to clarify the probable association between IL-6 (-174 C/G) and IL-8 (-251 A/T) gene polymorphisms and susceptibility/resistance to Brucellosis.

Methods: The patient group included one hundred ninety six patients suffered from *Brucella* infection and the control group consisted of 82 healthy animal husbandmen from the same geographical area as the patients. IL-8 (-251 A/C) gene polymorphism was analyzed by PCR-RFLP and IL-6 (-174 C/G) gene polymorphism was analyzed using Allele Specific PCR.

Results: The frequency of -251 IL-8 AA genotype was significantly lower in controls compared with that in the patients (P=0.0098), while the frequencies of other genotypes (AT and TT) and alleles A and T were not significantly different among the participants. In addition, no association was found between the IL-6 (-174 C/G) polymorphism and Brucellosis.

Conclusion: In conclusion, this study indicated that the IL-8 -251 AA genotype may be considered as a genetic susceptibility factor for Brucellosis.

Keywords: Interleukin-8, Interlukin-6, gene polymorphisms, Brucellosis

Common Pathogens in Burn Wound and Changes in Their Drug Sensitivity

Hosain Safari, Ezzatollah Rezaei, Mahbobe Naderinasab

Burn Center, Mashhad University of Medical Sciences, Mashhad, Iran

Abstract

Background: With regard to probable microbial colonization change and antibiotic resistance in our center, we conducted this study to identify a proper empirical therapy and suitable antibiotics in burn wound infections.

Methods: This study was performed on fifty nine male and female patients admitted in the burn ward of Emam-Reza Hospital, Mashhad, during a three months' period, in 2009. Samples from burn wounds were taken by swab in uniform and suitable conditions, one on the 1st and one between the 3rd and the 7th days after admission. In this study, common antibiotics including ceftazidime, ciprofloxacin, cefepime, imipenem, meropenem, cefixime, piperacillin–tazobactam, amikacin and oxacillin were evaluated with the Mast discs (Mast Group Ltd., Bootle, UK).

Results: The most prevalent organisms were *P. aeruginosa* (26.7%), *Acinetobacter* (24.5%) and *Klebsiella* (22.9%).In evaluation of the antibiotic sensitivity of the bacteria; it was found that the Gram-negative bacteria grown in the patients' wound culture were in 88.9%, 76% and 21.6% of cases resistant to ceftazidime, amikacin and imipenem, respectively.

Conclusion: Changes in burn wounds' microbial colonisation and also in antibiotic sensitivity, over time, necessitate periodic evaluation of these changes in each burn center, separately. On the other hand, the growth of MDR organisms, such as *Acinetobacter*, resistant to quinolones, cephalosporins and carbapenems should be considered as a serious risk.

Keywords: Infection, Burn wound, Microbial resistance

Incidence of Mycotic and Bacterial Infections in Patients with Diabetic Foot Ulcer Refer To Diabet and Metabolic Diseases Center, Tehran, Iran

Maryam roudbary [1], Shahla Roudbar Mohammadi [1], Farideh Razi[2], Zohreh Anabestani[2], Mahmood Vahidi[1]

Abstract

Background: Diabetes mellitus is a chronic disorder that affects a large segment of the human population and is a major public health problem. Patients with diabetes represent a unique group of individuals who appear more prone to develop infections than others. Diabetic foot infections frequently result in morbidity, hospitalization and amputations. This study was designed to investigate the incidence of fungal and bacterial pathogens in diabetic foot infections.

Methods: Forty five people with diabetes and foot ulcer of grade 2 – 4, were enrolled in the study that was referred in the department of diabetic foot and metabolic disorder clinic, Tehran, Iran. Direct fresh smear, bacterial and fungal culture were performed for each patient. Fungal contaminations were confirmed by direct microscopy and/or culture on sabouraud dextrose agar and chrome agar. Bacterial infection confirmed by growth on specific media (blood agar, chocolate and macConkey agar) and was done differential tests for gram positive and gram negative bacteria. DNA extract from yeast samples was done with phenol-chloroform, lysis buffer and glass bead. PCR was done for identification of fungi by use of ITS1 and ITS4 primers. *Candida albicans* (ATCC10231) was used as standard strain. PCR reactions were denatured for 5 min at 94 0C and subjected to 40 cycles of 94 0C (30 s), 58 0C (30 s) and 72 0C (30 s). A final 7 min extension at 72 0C completed the reaction. PCR products were running on 2% agarose/TAE gels and visualized by staining with ethidium bromide.

Results: The ages of the patients were between 30 to 80 years old. Of those (80.7%) individuals were male and (20.3%) were female. *Candida* species were the most predominantly fungi that isolated from 12 patient by PCR method. Also *Candida* krusei and tropicalis were isolated. *Escherichia coli* was the predominant bacteria (40%), followed by serratia 25%, Proteus spp 10% and *Pseudomonas* spp10% , *Acinetobacter*10% and *Staphylococcus* aureus 5%, respectively

Conclusion: Our result in this study indicated that fungal infection can be observed in diabetic foot ulcer and causes a lesion with poor prognosis. Fungal infection in diabetic patient that the most of them are immunosuppressive is very important because in spite of anti bacterial therapy, they have un-healing ulcers with recurrent infections. The most common cause of mycotic diabetic foot is *Candida* species, especially *C. albicans*. We investigated the need for mycological evaluation of the non-healing diabetic foot tissues and appropriate antifungal therapy.

Keywords: Diabetes, foot ulcer, bacterial and fungal infection and PCR

[1]Department of medical mycology, faculty of Medicine, Tarbiat Modares University, Tehran, Iran
[2]Diabetes and metabolic diseases research center, Faculty of Medicine, Tehran University, Tehran, Iran

Surveying the Effects of Antimicrobial Bacteriocin Produced by *Lactobacillus plantarum* Isolated from Traditional Cheeses in Khorramabad

Enayat Ghahremani, Mahnaz mardani, Sadegh Rezapour

Faculty of medicine, Lorestan University of Medical Sciences, Khorramabad, Iran

Abstract

Background: *Lactobacillus plantarum*, lactic acid bacteria in dairy products, are heterofermentative. These bacteria can product bacteriocin against pathogenic bacteria. The purpose of this review is surveying the effects of antimicrobial bacteriocin produced by *Lactobacillus plantarum* isolated from traditional cheeses in Khorramabad city.

Methods: A total of 11 samples were collected from traditional cheeses in Khorramabad city. In the desired bacteria using phenotypic Methods (cell morphology, physiological and biochemical tests) identified and bacteriocin was extracted. Bacteriocin extracted using the method of diffusion, on the pathogenic bacteria *Pseudomonas Aeruginosa*, *Proteus vulgaris*, *Staphylococcus aureus*, *E. coli*, *Bacillus cereus* and *Bacillus subtilis*, *Streptococcus feacalis* were tested

Results: The results showed the inhibition zone in the bacteria *Pseudomonas Aeruginosa* (12mm), *Staphylococcus aureus* (10mm), *E. coli* (11mm), *Proteus vulgaris* (9mm), *Bacillus cereus* (7mm), *Bacillus subtilis* (11mm) *Streptococcus feacalis* (14mm).

Conclusion: This study showed that *Lactobacillus plantarum* had an inhibitory effect on pathogen bacteria and could improve infection or prevent infection in the body.

Keywords: *Lactobacillus plantarum*, antimicrobial effects, inhibition zone, bacteriocin

Development of Proprietary and Sensitive Real-Time PCR to Diagnosis *Brucella* Types

Ali Nazemy, Momeneh Delbisheh, Mostafa Jafarpour

Department of Biology, Islamic Azad University of Tonekabon Branch, Tonekabon, Iran

Abstract

Background: Brucellosis is a common disease among human and animals and is a public health problem in the world. The correct and quick diagnosis of the disease is an important factor for disease control and prevention. The purpose of this study was to improve the diagnosis of the Brucellosis in suspicious samples by Taq Man Real-Time PCR method.

Methods: Twenty eight positive samples (twenty, sheep blood and eight, human blood) were provided from the townships of the Mazandaran province. After DNA extraction, the reaction of TaqMan Real-Time PCR was performed based on bcsp31 gene on samples.

Results: Only twelve samples from twenty eight samples suspicious to Brucellosis were positive by use of TaqMan Real-Time PCR method.

Conclusion: Diagnosis of Brucellosis is often difficult due to nonspecific clinical findings and the lack of correct diagnosis Methods. TaqMan Real-Time PCR is an accurate method which can identify the minor amounts of the *Brucella* type bacteria. Our study showed that suspicious samples could be diagnosed as Brucellosis by Real-Time PCR.

Keywords: Brucellosis, Real-Time PCR

IJMS
Vol 37, No 3, Supplement 1, September 2012

Determination of the Pattern of Antibiotic Resistance and Identification of Extended-Spectrum β-Lactamases (ESBLs) in Enteropathogenic *Escherichia coli* (EPEC) Strains Isolated from Children with Diarrhea

Pejman Karami, Mohammad Mehdi Asalani, Mohamad Yousef Alikhani

Abstract

Background: Enteropathogenic *Escherichia coli* (EPEC) are one of the main causes of diarrhea in children less than one year old. For treatment of infections caused by this microorganism rehydration and antibiotic treatment are being used. On the other hand one of the issues that in recent years tremendously challenged medical society is the antibiotic resistance incidence and failure in treating infectious diseases. Producing Extended-Spectrum β-Lactamases (ESBLs) enzymes is one of the most important ways of resistance in this group of bacteria.

So the objective to this study was to determine the antibiotic resistance pattern and considering the prevalence rate of Extended-Spectrum β-Lactamases (ESBLs) genes coding, including TEM, SHV, CTX-M and OXA gene and insertion sequence of ISE-CP1 in Enteropathogenic *Escherichia coli* (EPEC) strains isolated from children with diarrhea.

Methods: In this study 192 strains of Enteropathogenic *Escherichia coli* (EPEC) enrolled in our study. They were isolated from children with diarrhea and antibiogram was performed to study antibiotic resistance pattern with Kirby-Bauer method with the usage of 14 different antibiotic disks. In the second phase, to confirm phenotypic strains of Extended-Spectrum β-Lactamases (ESBLs) enzyme producer, all the strains were studied with Double Disk Synergy Test (DDST) method. Finally, all the strains were examined to study molecular prevalence rate of Extended-Spectrum β-Lactamases (ESBLs) genes coding enzymes with five genes, including CTX-M, SHV, TEM, OXA and ad insertion sequence of ISE-CP1 with PCR technique.

Results: The performed antibiogram showed that these strains had the most resistance toward cefpodoxime (97%), trimethoprom (60.7%), tetracycline (58.4%) and ampicillin (45.8%). Multidrug resistance was 68.7 percent. Also these strains showed the most sensitivity toward imipenem, ceftriaxone, and ciprofloxacin antibiotics. The percentage of ESBLs prevalence in EPEC cases with DDST approach was estimated 79.7 %.Also PCR approach showed that different ESBL gene prevalence, including, TEM, SHV, CTX-M, OXA and insertion sequence of ISE-CP1, respectively are, 13.5, 11.9, 10.9, 7.3, and 61.7 percent.

Conclusion: According to the abundant prevalence of multidrug resistant strains among these bacteria it is suggested that unnecessary use of antibiotics should be strongly avoided.

Keywords: Enteropathogenic *Escherichia coli*, Extended spectrum betalactamase, Antibiogram, Antibiotic Resistance, Diarrhea

Hamedan University of Medical Sciences, Hamedan, Iran

Investigation of Urophatogenic *Escherichia coli* Phylogenetic Groups Distribution

Mahsa Mirzarazi[1], Elham Rezatofighi[1], Mahdi Pourmahdi [2], Mohammadreza Mohajeri[3]

[1]Biology Department, Faculty of Science, Shahid Chamran University of Ahvaz , Ahvaz, Iran
[2]Food Hygiene Department, Faculty of Veterinary medicine, Shahid Chamran University of Ahvaz ,Ahvaz, Iran
[3]Pathology and clinical laboratory of Dr. Mohajeri, Isfahan, Iran

Abstract

Background: *Escherichia coli* is one of the microorganisms most frequently involved in urinary tract infections (UTIs) and most Escherichia coli infections other than gastrointestinal infections are believed to originate from human fecal flora. *E. coli* strains generally fall into one of four phylogenetic groups A, B1, B2, and D and that virulent extra strains belong mainly to group B2 and, to a lesser extent, to group D, whereas most commensal strains belong to group A. The aim of this study was distribution of urophatogenic *Escherichia coli* phylogenetic Groups.

Methods: In this study 138 uropathogenic *E. coli* strains were investigated. PCR was performed with a standard protocol. In isolates related to B2 phyloghenetic group, chuA and also yja genes are positive but in D phylogenetic group yja gene is negative. In B1 and A phylogenetic groups, chuA gene is negative; however TSEP4.C2 DNA fragments in B1 is exist but A phylogenetic group has not this fragment of DNA.

Results: From 138 UPECs, 16(12%), 76(55%), 29 (21%) and 17 (12%) *E. coli* strains were related to B1, B2, D and A phylogenetic groups respectively.

Conclusion: Phylogenetic analyses have shown that *E. coli* strains fall into four main phylogenetic groups (A, B1, B2, and D) and that virulent extra strains belong mainly to group B2 and, to a lesser extent, to group D.

Keywords: Urophatogenic *Escherichia coli*, A, B1, B2 and D phylogenetic groups

Molecular Strain Typing of Mycobacterium Tuberculosis Complex by DR and IS6110

Sajad Yaghuby, Nader Mosavari , Soheila Moradi Bidhendi , Ali Asghar Farazi, Mohammad Taheri

Abstract

Background: One of the potent tools to control *Mycobacterium tuberculosis* is molecular epidemiology techniques: RFLP-IS6110 standard Technique to genotyping M. tuberculosis. The aims of this study were to identify the genetic diversity of *M. tuberculosis* population in Markazi Province, and to recognize the manner of transmission of the disease in this region.

Methods: RFLP was analyzed among 42 isolates of *M. tuberculosis* deposited in the Mycobacterial Centre from Markazi province. DNAs isolated from these strains were restricted with Pvu II, hybridized with a PCR amplified DIG-labeled 245 bp IS6110 probe.

Results: Based on the copy number, isolates were classified into four groups, (1) lacking IS6110 element; (2) low copy number (1-2); (3) intermediate copy number (3-5); and (4) high copy number (6-17). Copy number higher than 17 however was not observed in any of the isolates studied. 72 percent of the isolates showed high copy number of IS6110, 13 percent showed intermediate copy number, 10 percent showed low copy number, whereas 5 percent isolates lacked IS6110 element.

Conclusion: IS6110 DNA fingerprinting helped us to understand epidemiological links between some TB cases and this technique estimate from reactivation of latent infection transmission of the disease in Markazi Province. The low rate of clustering indicates that tuberculosis among the study population results mainly from reactivation of latent infection in this region.

PPD Production Department, Razi Vaccine and Serum Research Institute, Karaj, Iran

Keywords: IS6110, RFLP, *Mycobacterium* tuberculosis

Molecular Detection of Extended-spectrum Beta-lactamase Genes from *Pseudomonas Aeruginosa* Strains Isolated from Clinical and Environmental Samples of Shahid Beheshti Hospital in Kashan

Zahra Tavajjohi, Rezvan Moniri

Department of Microbiology and Immunology, Faculty of Medicine, Kashan University of Medical Sciences, Anatomical Sciences Research Center, Kashan, Iran

Abstract

Background: *Pseudomonas Aeruginosa* is the most common pathogen causing nosocomial infections. In this study we determined the antimicrobial susceptibility pattern and prevalence of ESBLs in clinical and environmental isolates of *Pseudomonas Aeruginosa* by phenotypic and genotypic Methods.

Methods: In this descriptive study, 100 *Pseudomonas Aeruginosa* strains isolated from different clinical and environmental specimens were used. The pattern of antibiotic resistance to eight antimicrobial agents was determined by disk diffusion method. The ESBLs producing strains were confirmed by double-disk-diffusion test. bla_{TEM-1},bla_{SHV-1}, bla_{SHV-5}, $bla_{CTX-M-1}$, $bla_{CTX-M-2}$, $bla_{CTX-M-3}$, $bla_{CTX-M-9}$, bla_{OXA-1}, bla_{GES-1} and bla_{GES-2}genes were detected by PCR.

Results: In this study piperacillin with 36% and ciprofloxacin with 16% showed the highest and lowest resistance against isolates respectively. 30 % of the total isolates were resistant to at least three classes of antibiotics. By double-disk-diffusion test, eight strains (8%) were ESBL positive. According to PCR results 8, 2, 2 and 1 isolates of ESBLs producing strains were carried bla_{GES-2}, bla_{SHV-1}, bla_{SHV-5} and $bla_{CTX-M-1}$ genes, respectively.

Conclusion: According to the PCR assays, bla_{GES-2} gene plays important role in create of imipenem resistance, was detected in the total of ESBLs producing strains.

Keywords: *Pseudomonas Aeruginosa*, ESBL, Multidrug resistant

The Clinical Spectrum of Exophiala Jeanselmei and In vitro Antifungal Susceptibility of the Species

Sadegh Khodavaisy[1], Hamid Badali[2], G. S. DE Hoog[3]

Abstract

Background: *Exophiala jeanselmei* is clinically redefined as a rare agent of subcutaneous lesions of traumatic origin, eventually causing eumycetoma. The species has been described as being common in the environment, but molecular Methods have only confirmed its occurrence in clinical samples. The first purpose of this study was the re-identification of all clinical and environmental strains maintained under the name *E. jeanselmei*. The second goal of this investigation was the evaluation of in vitro susceptibility of Exophiala species to conventional and new generations of antifungal drugs to improve antifungal therapy in patients.

Methods: Strains used in this study were obtained from the Central bureau voor Schimmel cultures, Utrecht, The Netherlands, deposited and phenotypically identified *E. jeanselmei*. The strains were verified with sequence data of the internal transcriber spacer regions (ITS) of the rDNA. In vitro antifungal susceptibility testing of eight antifungal drugs against *E. jeanselmei* (n=9) and *E. oligosperma* (n=5) employing the Methods described in the CLSI guideline (M38-A2).

Results: Identification of seventeen strains (11 clinical and 6 environmental) with sequence data of the ITS of the rDNA. Results have shown that amphotericin B MICs ranged from 0.25–2.0 and 1–2µg/ml for *E. jeanselmei* and *E. oligosperma*, respectively. Voriconazole and isavuconazole had highest MICs with complete inhibition end points with MIC 50 (1µg/ml and 2µg/ml) against *E. jeanselmei* and MIC_{50} (both 1µg/ml) against *E. oligosperma*. Itraconazole and posaconazole showed potent activity against all *E. jeanselmei* and *E. oligosperma* isolates. Posaconazole demonstrated the lowest MIC 50 (0.031µg/ml) of all azoles.

Conclusion: In vitro studies demonstrated that posaconazole and itraconazole had the highest antifungal activity against *E. jeanselmei* and *E. oligosperma* for which high MICs were found for caspofungin. However, their clinical effectiveness in the treatment of Exophiala infections remains to be determined.

Keywords: *Exophiala jeanselmei*, black yeasts, ITS rDNA, mycetoma, antifungal susceptibility testing

[1]Department of Medical Mycology and Parasitology, Tehran University of Medical Sciences, Tehran, Iran,
[2]Department of Medical Mycology and Parasitology, Mazandaran University of Medical Sciences, Sari, Iran,
[3] CBS-KNAW Fungal biodiversity Centre, Utrecht, The Netherlands

The Rate of Coagulase-Negative *Staphylococci* in 5214 Isolated Organisms from Blood Cultures in Shiraz Hospitals and their Antibiogram, 2001-2011

Marzieh Hosseini, Gholam Reza Pouladfar, Fatemeh Norouzi, Mona Zarafshanian, Mojtaba Anvarinejad, Bahman Pourabbas, Aziz Japoni, Mehdi Kalani, Mohammad Ali Dehyadegari and Nooredin Rafaatpour

Professor Alborzi Clinical Microbiology Research Center, Shiraz University of Medical Sciences, Shiraz, Iran

Abstract

Background: Coagulase-negative *Staphylococci* (CoNS) are the most common etiology of nosocomial bacteremia as well as the most common blood culture contaminant. The aim was to determine the isolation rate of CoNS in blood cultures and their antibiogram patterns in Shiraz during the three periods Jan 2001- Dec 2004 and Jan 2005-Dec 2006 and Jan 2010-Dec 2011.

Methods: All CoNS isolated from blood samples by BACTEC system in Professor Alborzi Clinical Microbiology Research Center were analyzed and antibiotic resistance was evaluated by Standard Disk Diffusion method. The samples were obtained from different wards of the hospitals in Shiraz.

Result: During three periods, 5214 positive cultures were identified and 2048 CONS (67%) isolated: 523 (47%) within 2001-2004, 483 (49%) within 2005-2006 and 1402 (45%) within 2010-2011. The susceptibility to ciprofloxacin was dropped significantly in these periods: 2001-2004, 79%; 2005-2006, 68% and 2010-2011, 43%. The susceptibility to oxacillin was also dropped in 2010-2011 period (22%) when compared to 2005- 2006 (35%). The susceptibility to vancomycin was stable (99-100%) in these three periods.

Conclusion: CoNS was the most common bacteria isolated in blood cultures in Shiraz. Although, we did not determine which isolated CoNS is a contaminant, it seems to be the most common cause of contamination of blood cultures in our hospitals. The resistance rate to various antibiotics was increased consistently over times. The vancomycin remains the drug of choice when CoNS is a true pathogen causing bloodstream infection.

Keywords: Bloodstream Infection, Coagulase-negative *Staphylococci*

Rapid Identification of Atypical Mycobacterium spp from Mycobacterium tuberculosis by PCR-RFLP Analysis of Hsp65 Gene

Azadeh Nahavandi Araghi, Mahnaz Saifi, Esmail Zabar Zadeh, Ahmad Reza Bahremand, Ali karimi, Mahrouz Dezfoulian, Elham Safar Pour

Abstract

Background: Atypical *Mycobacterium* is Saprophyte pathogens cause various infections. Some of them lead to Tuberculosis-like disease which makes it difficult to distinguish them from *Mycobacterium* tuberculosis. Conventional Methods for identification of *Mycobacterium* are time consuming. Treatment of atypical *Mycobacterium* is difficult because not only are resistant to a wide range of antibiotics, but often difficult to differentiate them from *Mycobacterium* tuberculosis. It is considered one of the important reasons for treatment failure. PCR-RFLP (PRA) method where it is a method for detecting genotyping is more accurate than phenotyping Methods.

Methods: Samples of positive cultures of *Mycobacterium* from patients referred to thePastorover91 years were tested using biochemical diagnostic tests. Strain identification Methods were performed simultaneously by (PCR-RFLP (PRA). A 644 bp region of Heat Shock Protein 65 (hsp65) was amplified by PCR. Subsequently, PCR products were digested with Ava II enzyme.

Results: With the PRA patterns of the total 100 samples positive culture in 91,33 cases(33%) of atypical *Mycobacterium* were identified using standard algorithms were classified in 8 groups.

Conclusion: The results showed PCR-RFLP (PRA) using the enzyme Ava II is a simple, fast and accurate for the general grouping of atypical *Mycobacterium* isolates from TB and with reducing time to diagnosis of atypical strains from *Mycobacterium* tuberculosis can be effective in the treatment of Mycobacterial infections.

Keywords: Rapid identification, *Mycobacterium* tuberculosis, atypical *Mycobacterium*

Karaj Azad University Cooperated with Tehran Pasteur Institute _ Tuberculosis and pulmonary research department, Karaj, Iran

The Pattern of Antimicrobial Use Mashhad Imam Reza Hospital: Retrospective Study Years 2010 and 2011

Javad Rashid, Nasrin Khosravi, Hamidreza Naderi, Irandokht Mostafavi, Fereshte Sheybani, Shahram Taherzadeh

Nosocomial Infection Control, Imam Reza Hospital, Faculty of Medicine, Mashhad University of Medical Sciences

Abstract

Background: Overuse of antibiotics increases antimicrobial resistance and the number of medicines that are no longer effective against infectious disease.

Methods: This study was conducted to evaluate the antibiotic prescribing pattern in Imam Reza University Hospital, Mashhad, Iran during a two year period between 2010 and 2011.

Results: According to the hospital patient registration system, 83634 and 87260 patients were hospitalized during the years 2010 and 2011, respectively. During these periods of time (2010 and 2011), 27.67% and 27.04% of hospitalized patients received antibiotic treatment when just 40.52% and 42.52% of whom had microbial culture results, respectively. There were no significant differences between the antibiotic drugs mostly prescribed during these two periods. The antibiotic drugs most frequently used were as follows: clindamycin (18.10%), ceftriaxone (14.95%), vancomycin (13.5%) and imipenem (12.67%).

Conclusion: According to the results of this study, it seemed that antibiotic prescribing in our center is mostly a symptom-based practice and the empirical antibiotic regimens are not deescalated according to the microbiological data. We concluded that the current practice of antimicrobial prescribing in our center may need to be reviewed.

Keywords: Antibiotic, culture, imipenem

Seroprevalence of *Brucella Canis* among Patients with Active Brucellosis

Manoochehr Rasouli[1], Mohammad Amin Behzadi[1], Mehdi Kalani[1], Asghar Mogheiseh[2]

Abstract

Background: *Brucella canis* infection is a zoonotic disease caused by a rough or mocoid, small, Gram-negative intracellular bacterium that can affect all breeds of dog and rarely human. The infection is endemic in the South and Central America; but it is sporadic in Europe and Asia. The current study was conducted to reveal the seroprevalence of *B. canis* among patients with active Brucellosis in Fars province, southern Iran.

Methods: Serum samples were taken from sixty eight patients with active Brucellosis including fifty seven male and eleven female from different areas of Fars province, Iran. The samples were examined with a commercial rapid *B. canis* Ab test kit (Anigen, Animal Genetics, Inc., Korea) base on chromatographic immunoassay. The sensitivity and specificity of the kits vs blood culture were 93% and 100%, respectively.

Results: *B. canis* antibodies were detected in 1/68 (1.47%) of patients. The history of this male individual showed that he had a chronic Brucellosis, which did not treat with routine antibiotic therapies. In addition he was a shepherd and had close contact with animals especially dogs and this may be a predisposing factor for the transmission of disease to him.

Conclusion: Limited studies showed the existence of *B. canis* infection in companion dogs in Iran; however there is no report of the infection in human and this is the first report of human *B. canis* in Iran. Considering our results, detection of *B. canis* in chronic Brucellosis patients is notable. Due to the increase in close contact of human and companion dogs in recent years, more studies are essential to demonstrate the prevalence of the disease in Iran.

Keywords: *Brucella canis*, Seroprevalence, Human, Iran

[1]Professor Alborzi Clinical Microbiology Research Center, Shiraz University of Medical Sciences, Nemazee Hospital, Shiraz, Iran.
[2]Department of Clinical Sciences, School of Veterinary Medicine, Shiraz University, Shiraz, Iran

Genome Phylogenetic Analysis of A/H1N1/ pdm09 *Influenza Virus* Isolated from Shiraz, Southern Iran

Mohammad Amin Behzadi, Mazyar Ziyaeyan, Abdolvahab Alborzi

Abstract

Background: A novel *Influenza A* virus, subtype H1N1 Which caused the first influenza pandemic of the 21st century, emerged in April 2009 and since then continues to circulate globally. In this study, we report the isolation and genome phylogenetic analysis of A/H1N1/pdm09 *Influenza Virus* from Shiraz, southern Iran.

Methods: The partial genome of the matrix protein of the A/H1N1/pdm09 *Influenza Virus* isolated from nasopharyngeal specimens during 2011 influenza season was amplified with specific primer sets and cloned in to the pTZ57R/T vector. The recombinant plasmid was sequenced by an ABI 3730 automated DNA sequencer (Applied Biosystems, USA) using the M13 universal primers. The sequence of the amplified segment was compared with reference sequences published in GenBank followed by topology analysis of the resulting phylogenetic tree using Laser gene sequence analysis software package (DNA Star, Madison, WI, USA).

Results: The data indicated that the prevalent A/H1N1/pdm09 *Influenza Virus* isolated from Shiraz had close relationship with other isolates from all around the world, although the small number of various nucleotides existed.

Conclusion: It can be concluded that the nucleotide differences in this viral genome segment may lead to the existence and prevalence of new isolates in southern Iran, although, complete sequencing of the viral genome is needed. Moreover, for rapid diagnosis of possible future pandemics, isolation and genetic monitoring of *Influenza virus*es is strongly recommended.

Professor Alborzi Clinical Microbiology Research Center, Shiraz University of Medical Sciences, Nemazee Hospital, Shiraz, Iran

Keywords: *Influenza A* virus, H1N1pdm09, Genome phylogenetic analysis, Matrix

Molecular Detection of Herpetic Ocular Infection; a Real-Time PCR Based Study

Roya Feyznezhad, Mazyar Ziyaeyan

Abstract

Background: Herpetic ocular infection caused by *Herpes Simplex* virus (HSV) is the major cause of corneal blindness in developed countries. However, in recent years the infection becomes more prevalent in developing countries and causing more blindness. Ocular herpes presents either as a primary infection, or more typically, as a recurrent disease following reactivation of the latent virus. The aim of the present investigation is to explore the usefulness of assessing eye herpetic lesion by Real-Time PCR in corneal scrapings and swab specimens.

Methods: Corneal scrapings or swab samples were obtained from 227 patients consecutively during the period from January 2009 through July 2012 in viral transport media. Viral DNA was extracted using commercial kits according to the manufacturer's instructions. The highly conserved region of HSV1 and HSV2 DNA polymerase was amplified using a TaqMan Real-Time PCR assay.

Results: The samples came from one hundred eighty nine adults and thirty eight children (129 males and 98 females; median age: 50.7 and range: 1-99 years). HSV DNA was detected in 67/227 (29.5%) corneal scrapings and swab samples submitted for analysis by Real-Time PCR. As revealed, 70.5% of the clinical samples tested were negative for HSV DNA by PCR.

Conclusion: *Herpes Simplex* virus types 1 and 2 (HSV-1 and HSV-2) DNA has been found in the corneas of suspected patients with ocular lesions. The presented data in this study reveal that TaqMan Real-Time PCR testing of corneal scrapings and ocular swab samples, as a rapid and persuaded method, can be a first-line diagnostic procedure that is useful as a supplement to history and clinical examination.

Keywords: *Herpes Simplex* Virus, Keratitis, Ocular infection, Real-Time PCR

Professor Alborzi Clinical Microbiology Research Center, Shiraz University of Medical Sciences, Nemazee Hospital, Shiraz, Iran

Incident HIV Infection among *Hepatitis C* Virus Infected patients in south of Iran

Marzyeh Jamalidoust[1, 2], Mazyar Ziyaeyan[1]

[1]Professor Alborzi Clinical Microbiology Research Center, Shiraz University of Medical Sciences, Shiraz, Iran
[2]Virology Department, Faculty of Medical Science, Tarbiat Modares University, Tehran, Iran

Abstract

Background: Because of shared modes of transmission, patients with *Hepatitis C* virus (HCV) infection are often co-infected with other types of hepatitis viruses and/or HIV. In this study, the prevalence of HIV positive patient and characteristics of HCV in this group have been described.

Methods: Two hundred eighty three HCV infected patients that have been referred to our laboratory for first time was studied after their HCV infections were confirmed by western blotting test (Trusty one step rapid test- Artron Bioresearch Inc. -Canada). HIV prevalence, HCV RNA level, and HCV genotype were determined.

Results: The weighted overall estimate of HIV prevalence was 16.51% (36 cases), with significant variability depending on risk factors. Among HCV/HIV co-infected patients, 100% were "at risk". Genotype 1 was found in 80% of infected patients. Median HCV RNA level was $3.82 \times 10_6$ IU/mL.

Conclusion: We identified incident HIV infection among HCV-infected men involved in HCV therapeutic trials in the Iran. The question of whether rates of HIV infection are truly increasing among HCV-infected patients or whether the perception of increasing incidence is attributable to enhanced ascertainment warrants further investigation.

Rapid Detection of *Herpes Simplex* Virus (Hsv) Infection in Mucosal and Cutaneous Ulcers of the Suspected Patients Referred To Nemazee Hospital, Shiraz, Iran by Real-Time PCR

Mazyar Ziyaeyan, MandanaNamayandeh

Professor Alborzi Clinical Microbiology Research Center, Shiraz University of Medical Sciences, Shiraz, Iran

Abstract

Background: The speed and sensitivity of real-time polymerase chain reaction (PCR) have made it a popular method for the detection of microbiological agents in both research and clinical specimens. For the detection and quantification of *Herpes Simplex* virus (HSV) in clinical specimens, real-time PCR has proven to be faster, more sensitive and safer than earlier Methods which included isolation of the virus in cell culture followed by immunofluorescence microscopy. The aim of this study was to detect the HSV DNA in skin samples of the suspected patients by Real-Time PCR

Methods: The study population consisted of 169 male and 148 female patients (n=317). Specimens were collected from various anatomical sites including 100 face or lips, 65 oral cavity,50 genital, 45fingers, and 57 other body parts. Cotton swabs were sent to the laboratory in buffered saline or viral transport medium. DNA was extracted using an invisorb spin virus DNA Isolation Kit according to the manufacturer's instructions. Real-Time PCR was performed on the purified DNA using a standard HSV PCR kit.

Results: The majority (52.05%) of the samples were from face, lips and oral cavity. All the genital lesions samples were taken by gynecologists. HSV DNA was detected in 33.5 of 100 patients with face or lip ulcers (33.5%), 26 of 65 patients with oral mucosa lesions (40%), 45 of 50 patients with genital involvement (90%), 40 of 45 patients with whitlow ulcers (88.8%), and in 14.2 of 57 patients with other body parts ulcers (25%).

Conclusion: Taking into account the high sensitivity, reproducibility and specificity, the Real-Time PCR assay can be used for the rapid detection of HSV DNA from skin origin clinical samples, especially in difficult clinical cases.

Keywords: *Herpes Simplex* Virus, rapid detection, PCR, skin infection

HCV Genotypes 2 and 4 Detection and Its Prevalence by Real-Time PCR in Shiraz

Sadaf Assaei, Mazyar Ziyaeyan

Professor Alborzi Clinical Microbiology Research Center, Shiraz University of Medical Sciences

Abstract

Background: *Hepatitis C* infection is now the most common cause of end-stage liver disease in many countries. HCV is classified at seven genotypes. HCV Genotype 4 has been identified as the principle genotype amongst infected individuals from the Middle East, north and central Africa although there is a low frequency of detection in populations outside these areas. This study was conducted to determine the rate of genotypes 2 and 4 infection in Shiraz, Southern Iran

Methods: During 2010 to 2012, HCV genotyping was performed on sera of 574 HCV RNA positive patients by a TaqMan real-Time PCR with four specific probes that can detect HCV genotypes 1-4. The study consisted of 501 males (87%) and 73females (7.86%). The age range was 13-79 years with the mean of 34.3 and SD=12.01.

Results: Of the 574 patients examined, only 5 patients were detected with HCV genotype 4 infections, one of whom was living and working in Arabic countries of Persian Gulf residents. One of the patients is positive for HCV Genotype 2 and he was living and working in Arabic countries too.

Conclusion: Genotypes 2 and 4 HCV infections are rare in HCV chronic infected patients in our region. Rare cases that are recognized might have been introduced from the neighboring countries.

Keywords: HCV genotype 2, HCV genotype 4, Middle East

Hepatitis B Virus Occult Infection Detection in Hemodialysis Patients Fasa, Southern Iran

Mahsa Moeini, Mazyar Ziyaeyan

Professor Alborzi Clinical Microbiology Research Center, Shiraz University of Medical Sciences, Shiraz, Iran

Abstract

Background: Occult *Hepatitis B* virus (HBV) infection is defined as the presence of HBV DNA and the absence of detectable *Hepatitis B* surface antigen (HBs Ag) in patients' sera. The aim of this study was to investigate the HBV occult infection and viral load in hemodialysis patients by quantitative Real-Time PCR

Methods: Totally 55 patients in Fasa, main center of hemodialysis, were evaluated using a Real-Time PCR to detect and analysis the quantity of HBV DNA serum. A commercial ELISA kit was used to detect serum HBs antigen in the patients. Also, water wash samples collected from 18 hemodialysis units were investigated for HBV DNA by the PCR.

Results: all the patients were sero-negative for HBs Ag. HBV occult infection was detected in only 4/55 subjects (8%) by PCR, in whom the serum HBV DNA levels were $< 5\times10^3$ copies per mL Low level HBV DNA was detected in three hemodialysis instruments.

Conclusion: The related data indicated that occult HBV infection is frequent in hemodialysis patients and they can contaminate the hemodialysis units during usage, therefore, more attention should be paid to this matter.

Keywords: Hemodialysis patients, *Hepatitis B*, occult infection, Viral load

KPC- Producer Gram Negative Bacteria among Burned Infants in Motahari Hospital, Iran: First Report from Iran

Leila Azimi[1], Abdolaziz Rastegar Lari[1], Reza Alaghehbandan[1], Masoud Mohammadpoor, Mohammad Rahbar[2]

Abstract

Background: To the best of our knowledge, this is the first report of *Klebsiella*, *Acinetobacter* and *Pseudomonas*-producing *Klebsilla pneumoniae* Carbapenemase (KPC) among burn infants in Iran. The objective of this study was to determine the phenotypic detection of these KPC among isolated Psedomonas aeruginosa, *Acinetobacter baumannii* and *Klebsiella spp.*

Methods: A cross-sectional study was performed (February to September 2011) at a tertiary burn hospital in Tehran, Iran. Sixty four strains were isolated from 20 patients. Strain and genus of isolates were confirmed, antibiotic susceptibility testing was implemented and KPC determined by Modified Hodge Test.

Results: Fifteen of thirty six strains (6 *Pseudomonas Aeruginosa*, 6 *Acinetobacter baumannii* and 3 *Klebsiella* pneumoniae) were resistant to Imipenem. Ten strains of 36 gram negative isolates were resistant to all tested antibiotics except for Colistin. Thirteen of 15 resistant Imipenem strains were confirmed as KPC-producer bacteria that isolated from 9 patients. Six of 36 isolated strains were Extended-spectrum β-lactamase (ESBL)-producing bacteria, of which 4 strains were both KPC and ESBL.

Conclusion: High percentage of Multi drug Resistant (MDR) strains in our center with positive KPC has created a major challenge in terms of mortality and morbidity. Findings of this study highlight the importance of implementation of an effective infection control strategy to prevent and decrease the prevalence of KPC-producing organisms.

Keywords: *Pseudomonas*, *Acinetobacter*, *Klebsiella*, KPC, Infant

[1]Antimicrobial Resistance Research Center, Tehran University of Medical Sciences, Tehran, Iran
[2]Department of Microbiology, Iranian Reference Health laboratory, Ministry of Health and Medical Education, Tehran, Iran

Cryptosporidium Infection in Children Who Have Relationship with Pets

Masoumeh Rostami, Fatemeh Soghra Maghsoodloorad, Farideh Tohidi, Heshmatollah Taherkhani

Department of Parasitology and Mycology, School of Medicine, Golestan University of Medical Sciences, Gorgan, Iran

Abstract

Background: *Cryptosporidium* is an important cause of diarrhoeal disease worldwide and, as several recent waterborne outbreaks have shown, poses a significant threat to public health in Iran. We identified the *Cryptosporidium spp.* in 56 positive children stool samples by direct wet smear method and Sheather's sugar flotation and stained with Modified Z.N.

Methods: The study was conducted in 7-12 year-old primary schoolchildren. Participants provided fecal samples and answered a questionnaire about their demographics and hygiene habits. The samples were examined by two Methods including direct wet smear method and Sheather's sugar flotation and stained with Modified Z.N. in the Parasitology laboratory of the Golestan University of Medical Sciences.

Results: Totally 800 stool specimens were collected from children averagely aged 9.5 years. Overall 56 children (6.9%) were infected by *Cryptosporidium* oocyst. There was significant association(p-value < 0.5) between positive *Cryptosporidium* with clinical symptoms (61%) and non-clinical symptoms (39%). 20 children (35.7%) were in contact with domestic animals such as cows and sheep. 19 children (33.9%) were in contact with dogs or cats. also16 children (28.5%) had no contact with any animal.

Conclusion: This work shows that the prevalence of intestinal parasitism is quite high among primary school students in Gorgan city and suggests an imperative for the implementation of control measures.

Keywords: Pets, *Cryptosporidium*, children

Brucella repididimo-Orchitis in Pediatric Ages Group

Mohammad Esmaeili

Department of Pediatrics, Imam Reza Hospital, Mashhad University of Medical Sciences, Mashhad, Iran

Abstract

Background: Brucellosis is a common disease in endemic areas, although epididimo-orchitis is uncommon. In endemic areas, all of the patients with epididimo-orchitis must be worked up for Brucellosis**.**

Methods: A series of twenty one patients in pediatric ages group (3-16 y) presented with epididymo-orchitis between October 1993 - 2003

Results: In 8 cases Brucellosis were diagnosed and in others (13 cases) non specific bacterial epididimo-orchitis. Brucellar group were compared with nonspecific group. The former ones were older, without lower urinary tract symptoms, lesser grade of tenderness and inflammatory sings. There were fever, leukocytosis and increased RBC sedimentation rate only in a few cases.

Conclusion In endemic areas all of the patients with epididimo-orchitis must be worked up for Brucellosis. The distinction between Brucellar and nonspecific epididimo-orchitis is essential since the treatments are entirely different.

Keywords: Pediatric ages, Brucellosis, epididimo-orchitis-children

Six Months Report of Positive Blood Cultures in Patients with Acute Leukemia in Hematology-Oncology Ward in Doctor Sheikh Pediatric Hospital from October to March, 2011

Hamid Farhangi, Abdullah Banihashem, Zahra Badiee, Ali Ghasemi, Simin Hiradfar, Mohammadreza Mosaddegh

Abstract

Background: Diagnosis of organisms that produce bacteremia and septicemia in reducing mortality especially in children with leukemia is important. Abstinence from uncontrolled use of antibiotics can prevent the occurrence of stains resistant to antibiotics. This is six months report of positive blood cultures in patients with acute leukemia in hematology-oncology ward of Doctor Sheikh pediatric hospital.

Methods: Before starting broad spectrum antibiotic blood cultures were obtained because of fever in sixty inpatient children with acute leukemia in different stages of treatment. After specific staining and biochemical tests to detect bacteria; antibiotic susceptibility test by using antibiogram disks for amikacin, gentamicin, cotrimoxazole, ampicillin, cefixime, imipenem, vancomycin, ciprofloxacin and norfloxacin were done.

Results: Mean age of the patients was 6 ± 3.8 years (7 months -14 years). Male to female ratio was 33/27. Acute lymphoblastic leukemia and acute myeloid leukemia were seen in 45 and 15 patients respectively. In this period, 158 blood cultures were obtained which 31 samples were positive. The most common organism was *Staphylococcus epidermidis* (Stp. *Epidermidis* 9 cases, *Entrococcus* 5 cases, *Acintobacter* 2 cases, gram positive bacilli 3 cases, pnumococci 2 cases, *Pseudomonas* aueroginoza 2 cases, *Klebsiella* pneumonia 1 case, *Klebsiella* oxytoka 1 case, Stp. Aureous 1 case and *Candida* 4 cases). In this study, the lowest bacterial resistance belonged to imipenem (18%) and ciprofloxacin (22%), in contrast the highest bacterial resistance was related to ampicillin (89%). All of the Stp. Epidermidis were sensitive to vancomycin but all cases of entrococci were resistant to vancomycin.

Conclusion: This study suggests that the imipenem and vancomycin can be effective in children with fever and leukemia as empirical therapy. Use of ciprofloxacin should be considered in refractory cases.

Keywords: Fever, leukemia, bacteremia

Department of Pediatrics, Doctor Sheikh Pediatric Hospital, Mashhad University of Medical Sciences, Mashhad, Iran

Assessing and Comparing Different Type of Hypochlorite Solution on Selected Intra-Hospital Bacterial Agent

Samaneh Akbarzadeh[1], Mahboubeh Naderinasab[1], Saeid Amel Jamehdar[1], Elnaz Harifi Mood[1], Maryam Kamalaldini[2], Leila Ataei[2]

[1]Microbiology and Virology Research Center, Avicenna Research Institute, Mashhad University of Medical Sciences
[2]Department of Microbiology and Virology, Imam Reza Hospital, Faculty of Medicine, Mashhad University of Medical Sciences

Abstract

Background: Hypochlorite or standard household bleach solutions have been used as a disinfectant for many years. There have many of the properties of an ideal disinfectant, including a broad antimicrobial activity, rapid bactericidal action, easy to use and low cost. Hypochlorite is lethal to most microbes and despite the increasing availability of other disinfectants, it continue to find wide use in hospitals. Furthermore, it has also clinical uses in hospitals include cleaning of environmental surfaces, disinfection of equipment and decontamination of medical waste prior to disposal. In present study we evaluate the antimicrobial activity of different household bleach of different bacteria.

Methods: Five brands of commercially available bleaches were used in this study. Different dilution of these 5 brands (1:10, 1:20, 1:50, and 1:100) was constructed and their affectivity in different time intervals (5, 10, 15 minute) was studied. Tested bacteria included *Staphylococcus arouse*, *Escherichia coli*, *Enterococcus* and *Pseudomonas Aeruginosa*.

Results: In this study we found that minimum appropriate effective concentration of all solution except first solution on *Staphylococcus arouse*, *Escherichia coli*, *Pseudomonas Aeruginosa* was 1:20 in 10 minute and about *Enterococcus* was our first solution with 1:10 concentration in 10 minute. Solution B had best bactericidal effect and its antibacterial effect was increases with increasing concentration. In this study *Staphylococcus aureus*, *Escherichia coli* are more sensitive to sodium hypochlorite than *Enterococcus*, *Pseudomonas Aeruginosa*.

Conclusion: Selecting and applying appropriate disinfectant can be effective in reducing bacterial infections.

Keywords: HCV genotype 2, HCV genotype 4, Middle East

Surveying Of Frequency of Anti-*Mycoplasma Pneumonia* IgG and IgM in 5-6 Years Old Children in Tehran

Anahita Sanaei, M Hashemi, Abdollah Karimi, R Arjmand

Department of Microbiology, Tehran University of Medical Sciences, Tehran, Iran

Abstract

Background: *Mycoplasma pneumonia* is one of important causes of respiratory infections among children. It is endemic in many countries. There is no information about prevalence of *Mycoplasma pneumonia* in Iran. One of the most specific and sensitive tests for MP evaluation is ELISA. In this study the prevalence of positive anti-*Mycoplasma pneumonia* IgM and IgG among 5- 6 years old children have been evaluated.

Methods: Among 5-6 years old children, two hundred ninety one children without any chronic disease who were to be vaccinated in health centers of Tehran enrolled in the study. Blood samples of these children were checked for anti-*Mycoplasma pneumonia* IgM and IgG by ELISA method.

Results: IgM was negative in all children. IgG was positive in 25% of children; 23% of males and 26.9% of females. There was no significant association between positive IgG and gender ($p>0.5$).

Conclusion: Recent *Mycoplasma pneumonia* infection was not detected in this study. High prevalence of positive IgG in this age group is explained by high rate of infection before 5 years old.

Keywords: *Mycoplasma pneumonia*, ELISA, IgM, IgG

Study of Bactericidal and Bacteriostatic Effect Alternating Current against *Staphylococcus aureus* and *Pseudomonas Aeruginosa*

Mehdi Mirzaii[1], Alireza Alfi[2], Piraste Noruzi[3], Fateme Davar Dust[4], Mojgan Fazli[5], Mojtaba Nasiri[6]

[1]Assistant Professor Shahroud University of Medical Sciences
[2]Assistant Professor Shahroud University of Polytechnical Sciences
[3]Master of Science student of Damghan Azad University
[4]Master of Science student of Shahroud Azad University
[5]Critic of Shahroud University of Medical Sciences
[6]Medical Student Shahroud University of Medical Sciences

Abstract

Background: The use of physical means as an aid for modern medicine in the champion against pathogenic microorganisms holds new approach that recently have begun to be widely recognized. The use of an additional physical means, alternating current and inhibit bacterial growth. The purposes of the present study were (1) to find out the best frequency of alternating currents can inhibit the growth of bacteria and (2) to determine efficacy alternating currents on disinfectant bactericidal potency.

Methods: Electric field strength of 12 and 20 V/cm at 50 KHz, 10 MHz, 20 MHz was applied continuously during course of staphylococcal and *Pseudomonas* lag phase. Then Changes in growth of bacteria investigated by time kill method. Efficacy alternating currents on current disinfectant bactericidal potency (microzed, deconex, cidex) evaluated by MIC and MBC.

Results: The best bacteriostatic effect showed due to electric field strength of 20 V/cm at 20MHz (*S. aureus* and *P. aeruginosa* decreased 1.1 log and 1 log respectively). Electric field strength of 20 V/cm at 20MHz had also the more efficacious on deconex 53 plus bactericidal potency.

Conclusion: It is necessary to find out suitable alternating current form in future. This method might be applied as a complementary to eliminate pollution of waters and increase disinfectant bactericidal potency .

Keywords: Alternating currents, frequency, bactericidal, bacteriostatic

Poster Presentations Second day

The Study of Common Microorganisms and Their Antibiotic Resistance in Burn Ward of a General Hospital, Qom, Iran

Mohammad Khodadad Motlagh

Nekuei Hospital, Qom, Iran

Abstract

Background: Burn wounds are suitable environments for the growth of various opportunistic infections. The knowledge of the common microorganisms in these infections and their antibiotic resistance are fundamental. We studied common microorganisms and their antibiotic resistance in burn ward of Nekuei Hospital, Qom, Iran.

Methods: In this study, during five months, seventy patients admitted to the burn ward of Nekuei hospital were examined. After Sampling and isolation of bacteria, biochemical standard tests for determination of microorganisms were done. Determination of antibiotic resistance was done by using disc diffusion or Kirby Bauer using these antibiotics: co-trimoxazole, vancomycin, ciprofloxacin, cephalothin, ceftazidime, amoxicillin, amikacin, gentamicin, chloramphenicol, cefazolin, cefotaxime, ceftriaxone, ampicillin, oxacillin, and imipenem.

Results: Totally, the cultures of fifty four cases (77.14%) of a total of seventy samples were positive. The most common isolated bacteria were *Pseudomonas Aeruginosa* (38.9%), *Staphylococcus aureus*, and *Staphylococcus epidermidis* (11.42%), and *Enterococcus* faecalis (9.59%). The results of the Antibiotic resistance of *Pseudomonas Aeruginosa* are as follows: amoxicillin 94.73%, amikacin 25.64%, gentamicin 30.77%, co-trimoxazole 84.62%, ciprofloxacin 48.72%, ceftazidime 51.28%, cefotaxime 58.97%, chloramphenicol 86.84%, ceftriaxone 55.26%, and imipenem 50%

Conclusion: The most common bacteria in infection of burn wound were *Pseudomonas Aeruginosa*, which was mostly susceptible to amikacin and gentamicin.

Keywords: Infection, burn wound, bacteria, antibiotic resistance

The Seroprevalence of *Helicobacter Pylori* Infection in Renal Transplant Recipients

Zakieh Rostamzadeh Khameneh, Sanaz Hatami, Nariman Sepehrvand, Zahra Shirmohammadi

Kidney Transplantation Ward, Urmia University of Medical Sciences, Urmia, Iran

Abstract

Background: *Helicobacter pylori* is a small gram-negative spiral bacillus living in the mucus layer of the human stomach, and there are evidences proving its effect on some gastrointestinal disorders. Considering the immunocompromised nature of transplant recipients due to medical immunosuppression, these patients are generally prone to viral and bacterial infectious diseases. In this study we aimed to investigate the seroprevalence of H-pylori infection among Iranian kidney transplant recipients.

Methods: Ninety one patients were selected randomly among patients who underwent kidney transplantation in Urmia, Iran. Each patient was experimented for anti-*Helicobacter pylori* IgG using ELISA method (Lake Success, NY)

Results: Forty three subjects (47.3%) were seropositive for anti-HEV IgG. There was no significant difference among the age (P=0.49), sex (P=0.22), history of blood transfusion (P=0.19), and history of hemodialysis (P=0.46) between seropositive and seronegative groups, but there was a significant difference among two groups regarding the educational status of the subjects (P=0.03), This difference was not confirmed by considering diploma as the cut point for categorizing the subjects (P>0.05). Comparing the age groups, Pearson chi-square revealed no significant correlation between HP seropositivity and increasing age (P=0.963).

Conclusion: The frequency of transplant recipients with anti-*H. pylori* IgG antibodies in our institution (47.3%) is not higher than its prevalence in the general population. This rate is lower compared to some reports from developing countries which the difference could be due to a better health and sanitation status in our setting.

Keywords: *Helicobacter pylori*, Renal Transplantation, ELISA

Evaluation of Relationship between HHV_6 Infection with Reactivation of CMV Infection in Liver Transplant Recipient in Nemazee Hospital

Ebrahim Sadeghi[1], Abdolvahab Alborzi[2], Mazyar Ziyaeyan[2], Marziye Jamalidoost[2], Mahsa Moeini[2]

Abstract

Background :*Cytomegalovirus* (CMV), the largest member of the herpes virus family, can cause infections in (50-70%) of the liver transplant recipients, of whom one third develop CMV disease. The present study seeks to investigate the development of CMV infection and its severity, following the reactivation of HHV_6.

Methods: Four hundred-ninety-two blood samples were tested for CMV-antigenemia and real time PCR was performed on the respective sera and PMNs to detect CMV infection and HHV_6. The patients were reviewed for 3 months following transplantation and those with clinical findings associated with CMV received treatment.

Results: Of the 46 studied cases, 23 (50%) were found with CMV, of which 17 exhibited the associated symptoms. As for HHV_6, 25 cases (54.3%), were detected. Among the 17 patients, 13 were symptomatic with concurrent positive results for CMV and HHV_6. It is noteworthy that in 10 cases, positive results for HHV_6 became evident 9 days earlier than CMV positive results, and the difference was significant (P=0.001). The mean antigenemia count (load) in symptomatic patients was 42.47±5.41 and significantly correlated with clinical findings (P=0.003).

Conclusion: The present findings demonstrate that HHV_6, as an independent factor, is correlated with CMV reactivation and respective clinical signs. It could then be predictive of CMV infection. The results also suggest the use of diagnostic PCR assay with quantitative real time method for CMV and HHV_6 in liver transplant recipients. Furthermore, replacement of prophylaxis and empirical therapy with pre-emptive therapy is recommended.

[1]Department of Pediatrics, Urmia University of Medical Sciences, Urmia, Iran
[2]Profoessor Alborzi Clinical Microbiology Research Center, Nemazee Hospital, Shiraz, Iran

Effects of Three Species Thymus Essential Oil on *E. coli*, *Pseudomonas aeruginosa*, *Staphylococcus aureus* and *Candida albicans* and Compare Effect of Antimicrobial Species Thymus with Ampicillin and Gentamicin

Emad Vahidi manesh

Islamic Azad University, Qom Branch, Faculty of Medical Sciences, Qom, Iran

Abstract

Background: Thymus used as a medicinal plant since 16th century. Important effective compounds in the thymus are phenolic of thymol and carvacrol. Essential oil of thymus is a yellow or purple liquid with pleasant smell and hot taste. In this study we investigate antimicrobial properties on *E. coli*, *Pseudomonas Aeruginosa*, *Staphylococcus aureus* and *Candida albicans*. Essential oil of thymus has antibacterial effects that can use in medicine and veterinary.

Methods: For comparing antimicrobial activity of thymus against bacteria and fungus with antibiotics, after extracting essential oil of thymus disk diffusion method was used. Disks of antibiotics were put on culture media and incubated for 24 hours at 37°c. Then we report Inhibitory Zone.

Results: Results of this study showed that inhibitory zone for essential oil of Thymus against *E. coli*, *Pseudomonas Aeruginosa*, *Staphylococcus aureus* and *Candida albicans* were 10, 0, 8, and 11mm respectively. Extract of Thymus daenensis has inhibitory zone of 13, 0, 10 and 13 mm for *E. coli*, *Pseudomonas Aeruginosa*, *Staphylococcus aureus* and *Candida albicans* respectively. Extract of *Thymus kotschyanus* has inhibitory zone of 11, 0, 10 and 13 mm for *E. coli*, *Pseudomonas aeruginosa*, *Staphylococcus aureus* and *Candida albicans* in order. Ampicillin as a for *E. coli*, *Pseudomonas aeruginosa* and *Staphylococcus aureus* in order to 18, 0 and 28 mm. Gentamicin antibiotic for *E. coli*, *Pseudomonas Aeruginosa* and *Staphylococcus aureus* in order to 21, 18 and 16 mm.

Conclusion: This extracts showed good antibacterial effect on *E. coli*, *Staphylococcus aureus* and *Candida albicans*, but had not much effect on the *Pseudomonas aeruginosa*.

Keywords: Thymus, disk diffusion, Ampicilin, Gentamicin, Antibacterial activity

Vibrio Cholera and Changing of Microbial Resistance Patterns in Sistan and Baluchistan Province in 1387- 1390

Alireza Salimi Khorashad[1], Seyyed Mehdi Tabatabai[2], Shahla Rudbar Mohammadi[3]

Abstract

Background: Cholera is a diarrheal disease in tropical areas which is caused by bacteria called vibrio that affects humans exclusively. And its symptoms are caused by toxins secreted by *Vibrio cholera* in the human intestine. Each man with diarrhea that o1 or o139 *Vibrio cholera* isolated from the stool by accredited laboratories has approved. *Vibrio cholera* has specific types of antigen. So, *Vibrio cholera* is divided on three types Ogava, Inaba, and Hychojyma.

This study aimed to compare changes in antibiotic resistance pattern in 1390 with the years 1387 to 1389 on patients with cholera have been conducted in areas covered by the Medical Sciences University of Zahedan.

Methods: In this descriptive study that includes all patients with cholera from early 1387 until June 1390 in areas covered by medical science university of Zahedan, rectal swab samples in the CARY-BLAIR MEDIUM working environment of all suspected patients sent to the laboratory area and do diagnostic procedures and with using the agar disc player, the use of Mueller Hinton Agar and comparison of microbial suspensions prepared with a McFarland turbidity standard, antimicrobial susceptibility testing was performed according to NCCLS recommendations. (Book) evaluated antibiotics were including co-trimoxazole, furazolidone, tetracycline, nalidixic acid, ciprofloxacin, ampicillin, doxycycline and erythromycin that the disks were prepared from the Iranian company antibody therapies. And results using the NCCLS table and other empirical data for determining the antimicrobial susceptibility had been evaluated and three of the sensitive, intermediate, and resistance were reported.

Results: Sixty four positive samples in the study of microbial susceptibility testing was done both Ogava and Inaba that samples of the year 1387, 1388 and 1389 followed by a similar pattern of allergic. Thus, all these examples of co-trimoxazole, nalidixic acid and ampicillin are resistant, have intermediate sensitivity to furazolidone and against tetracycline, ciprofloxacin and erythromycin were susceptible. While the pattern of sensitivity of three month beginning in 1390 were including sensitivity to erythromycin and ciprofloxacin, and sensitivity to tetracycline and doxycycline found no much. And the halo of blight was in intermediate range.

Conclusion: with respect to the province border with Afghanistan and Pakistan and the inevitability of incidence of cholera epidemics in the region, may the control of possible epidemics be a serious problem. And remind the need of implementation of drug sensitivity tests more than before during the epidemics, before any treatment.

[1]Research center of Tropical and Infectious Diseases, Zahedan University of Medical Sciences, Zahedan, Iran
[2]Sanitary Asistant, Director of Zahedan University of Medical Sciences, Zahedan, Iran
[3]Fungiology Group, Tarbiat Modares University, Tehran, Iran

Comparative Antifungal Effect of Extracts of *Allium ascalonicom*, *Marticaria chamomilla* (*Chamaemelum Nobile*) and *Stachys lavandulifolia* against *Candida albicans* in Vitro

Hasan Moghin, Mahmoud Rafieian, Simin Taghipoor, Najmeh Shahin Fard

Abstract

Background: Despite the increased risk for opportunistic fungal infections and the increasing prevalence of hospital infections caused by pathogenic yeasts, the fungus resistance to antifungal drugs, the discovery of antifungal compounds with high efficiency is necessary. Humanhas used of plants as medicine for centuries, and today, with advances in science, medicinal properties of them have been discovered.

The aim of this study was evaluation of antifungal activity of *Allium ascalonicum*, *Marticaria chamomilla* and *Stachys lavandulifolia* on *Candida albicans* and its comparison (In vitro).

Methods: In this study the powder of each plants were macerated in ethanol 70% and evaporated at 38˚C by percolation method. Suspension of *Candida albicans* according to McFarland is prepared, its concentration was approximately 0.5- 2.5 × 10^3 cfu/mL. Testing was performed (according to micro-broth dilution method) in 96 well micro-dilution plates. 100µl of sterile liquid sabuoraud medium was added to each well. Also 100µl from two fold concentration of extracts was added to wells and diluted serially. Finally 100µl of inoculum added to each wells. The plates incubated in 35˚C for 48 hours. Then 10µl of contents were cultured to plates with Sabouraud dextrose agar and incubated. After 48 h colonies were counted visually.

Results: MIC50% of *Allium ascalonicum*, *Marticaria chamomillae* and *Stachys lavandulifolia* were respectively 0.93, 10.59 and 41.32 mg/ml, MIC90% of them were 8.65, 16.88 and 60.55 mg/ml and its MFC were 20,20 and 65 mg/ml ($P<0.05$). The difference between *Stachys lavandulifolia* and other plants were significant ($P<0.05$).

Conclusion: The results demonstrated that *Allium ascalonicum* possessed antifungal activity against *Candida albicans*. If clinical trial approved these findings, this plant could represent a new source of antifungal agent for control of *Candida albicans*.

Medical Plants Research Center, Shahrekord University of Medical Sciences, Shahrekord, Iran

Keywords: *Candida albicans*, *Allium ascalonicum*, *Marticaria chamomillae*, *Stachys lavandulifolia*

The Frequency of Methicillin-Resistant *Staphylococcus aureus* among Hospitalized Patients in Different Wards of Two Tertiary Hospitals and a Burn Hospital, Shiraz, Iran

Zahra Hashemizadeh, Mohammad Reza Kandehkar Ghahraman *, Mohammad Javad Rahimi, Mohammad Motamedifar, Abdollah Bazargani

Department of Microbiology and Virology, School of Medicine, Shiraz University of Medical Sciences, Shiraz, Iran

Abstract

Background: *Staphylococcus aureus* is an opportunistic Gram positive bacterium. It can cause serious infections in many sites, including skin, soft tissue, lung, blood stream and cardiac valves. Infections caused by methicillin-resistant *S. aureus* (MRSA) were originally limited to hospital settings. MRSA plays a prominent role in serious infections in immune-compromised patients. Burn patients are highly prone to infections because of suppression of their immune system. It is necessary to be aware of the MRSA prevalence and to choose suitable antibiotics for treatment. The aim of this cross sectional study was to determine the frequency of MRSA isolates among hospitalized patients in a burn hospital and different wards of two tertiary hospitals in Shiraz, south west of Iran.

Methods: This study was conducted from June 2007 to June 2012. All *S. aureus* positive samples of hospitalized patients sent to the laboratory to detect methicillin resistant *S. aureus* isolates by using disk diffusion Methods.

Results: In this study, 627 *S. aureus* isolates were detected that 198 (31.5%) of them were MRSA. The most common positive cultures were sputum cultures, 106 (17%), that 70 (66%) of them were MRSA. The most common ward with positive *S. aureus* isolation was ICU, 90 (14.35%). In sum 54 (60%) of the isolated were MRSA. Most MRSA isolation, 96 (48.48%), were in Nemazee Hospital.56 (55%) of 102 *S. aureus* isolates from burn hospital were MRSA.

Conclusion: Methicillin resistant *S. aureus* is an important cause of nosocomial infections worldwide. Our data indicate that MRSA with high frequency of isolation in some hospital wards need immediate medical interventions.

Keywords: Methicillin-Resistant *Staphylococcus aureus*, Nosocomial Infection, ICU wards

Epidemiology of mecA-Methicillin Resistant *Staphylococcus aureus* (MRSA) in Iran: a Systematic Review and Meta-Analysis

Emran Askari[1], Fatemeh Soleymani[1], Arash Arianpoor[1], Seyed Meghdad Tabatabai[1], Aminreza Amini[2], Mahboobeh Naderi Nasab[1, 3]

[1]Mashhad Medical Microbiology Student Research Group, Mashhad University of Medical Sciences, Mashhad, Iran
[2]Department of Biostatistics, Mashhad University of Medical Sciences, Mashhad, Iran
[3]Department of Microbiology, Central Laboratory, Imam Reza Teaching Hospital, Mashhad, Iran

Abstract

Background: *Staphylococcus aureus* (*S. aureus*) is a prevalent pathogen worldwide. Methicillin Resistant *Staphylococcus aureus* (MRSA), which is usually multi-resistant in hospitals, has been a daunting challenge for clinicians for more than half a century. The aim of this systematic review and meta-analysis is to determine the relative frequency (R.F.) of MRSA in different regions of Iran.

Methods: Search terms "*Staphylococcus aureus*", "Methicillin", "mecA" and "Iran" were used in PubMed, Scirus and Google Scholar. Two Persian scientific search engines and ten recent national congresses were also explored. Articles/abstracts, which used clinical specimens and had done PCR to detect the mecA gene, were included in this review. Comprehensive Meta-Analysis and Meta-Analyst software used for statistical analysis.

Results: Out of 2690 results found in the mentioned databases, 48 articles were included in final analysis. These studies were done in Ahvaz, Falavarjan, Fasa, Gorgan, Hamedan, Isfehan, Kashan, Mashhad, Sanandaj, Shahrekord, Shiraz, Tabriz, Tehran and Tonekabon. Pooled estimation of 7464 *S. aureus* samples showed 52.7% ± 4.7 (95% confidence interval [CI]) of strains were mecA positive. MRSA R.F. in different studies varied from 20.48% to 90% in Isfahan and Tehran, respectively. A moderate heterogeneity (I^2=48.5%) of MRSA R.F. among studies conducted in Tehran (ranging from 28.88% to 90%, mean 52.7% [95% CI: 46.6%-58.8%]) was found.

Conclusion: According to the results of this study, MRSA R.F. in Iran is in the high range. Thus, measures should be taken to keep the emergence and transmission of these strains to a minimum.

Keywords: *Staphylococcus aureus*, MRSA, mecA gene, Meta-analysis, Iran

The synergism effect of mixture of antibiotics on the growth of *Helicobacter pylori* isolated from patient referred to Imam Reza Hospital, Amol

FatemehHabibi Nava[1], Seyed Masoud Hashemi Karouei[2], Shahriar Shafaee[3]

Abstract

Background: The incidence of gastric cancer is increasing in many counties. *H. pylori* are related to progress of diseases. The cure of the diseases is important for prevention of the process. The important point in treatment is selected suitable drug. The aim of this research is survey the synergism effect of mixture of two and or three antibiotics on *H. pylori*'s isolates.

Methods: For this aim, the sensitivity test was performed by disk diffusion method on Mueller Hinton agar contain sheep blood. The test were performed with disks contain double antibiotic (metronidazole and clarithromycin) and triple antibiotics (metronidazole, clarithromycin and ciprofloxacin). Thirty *H. pylori* samples isolated from gastric biopsy were included in this study. The size of the inhibition zone of these disks was compared with the size of the zone of inhibition disk metronidazole, clarithromycin and ciprofloxacin single.

Results: For 4 cases (13%) of *H. pylori* we haven't seen inhibition zone around disks contain single, double and triple antibiotics but in 87% of *H. pylori* inhibition zone were observed around disks contain single, double and triple antibiotics. The size of the inhibition zone in double disk and triple disk increase compare to single disk.

Conclusion: In this study we found the mix of antibiotics in double disk and triple disk have synergism effect on growth of *H. pylori* and increase the diameter of inhibition zone.

Keywords: Synergism effect, *Helicobacter Pylori*, Antibiotics

[1] Microbilogy Tonekaboon Branch, Islamic Azad University, Tonekabon, Iran
[2]Department of Mycology, Tonekabon Branch, Islamic Azad University, Tonekabon, Iran
[3]Department of pathology, Babol University Medical sciences, Babol, Iran

In-vitro Cytotoxicity Activity of New anti TB Drugs against Hela, Raji, Kga-1 and Mouse Lymphocyte Primary Cell Lines

Mehdi Zandhaghighi[1], Kiarash Ghazvini[1], Zahra Meshkat[1], Farzin Hadizadeh[2*]

Abstract

Background: Due to the increased incidence of new cases of drug resistance in *Mycobacterium tuberculosis* worldwide, research to discover new drugs against TB, is one of the major priorities of World Health Organization (WHO) and some countries like Iran. In previous study of researchers, the two active compounds:

1. N,N-Bisphenyl-4-[1-(4-fluorobenzyl)-2-methylthioimidazole-5-yl]-2,6-dimethyl-1,4-dihydropyridine-3,5-dicarboxamide (This so-called F-27)
2. N,N-bisphenyl-4-[1-(2-chlorobenzyl)-2-methylthioimidazole-5-yl]-2,6-dimethyl-1,4-dihydropyridine-3,5-dicarboxamide (This so-called Cl-33)

As new drugs for TB treatment were evaluated and their anti-mycobacterial impact on strains: *Mycobacterium* smegmatis and BCG (bacille Calmette-Guerin) is proven. MBC of the two compounds were respectively 16 and 32 micrograms per milliliter. Activity of compounds in comparison with isoniazid (32 micrograms per milliliter) was in the acceptable range.

The aim of this study was to evaluate the cytotoxicity level of two compounds: F-27 and Cl-33.

Methods : MTT Assay with different concentrations of each compound 1 - 1000 ìg / ml (two fold dilutions) was performed on cell lines (HeLa, RAJI, Kga-1, mouse lymphocyte primary cell) in vitro and Cytotoxicity level of each compound was determined. Cytotoxicity level of compounds on all cell lines are in acceptable range.

Results: IC_{50} obtained for each of the compounds was in the range 31-125 ìg / ml, which is divided as follows: Compound F-27: HeLa (>31 ìg/ml) ,RAJI (>31 ìg/ml) ,Kga-1(>62 ìg/ml) , Primary (>62 ìg/ml), Compound Cl-33: HeLa(>62 ìg/ml) , RAJI(>62 ìg/ml) ,Kga-1(>62 ìg/ml) ,Primary(>125 ìg/ml)

Conclusion: According to cytotoxicity levels for each of the compounds obtained in this study, that is lower than MBC of compounds (obtained in the previous study), can be concluded that the IC_{50} of compounds in comparison with standard tuberculosis drug (isoniazid) are in acceptable range and in the next step of research the inhibitory effects of these compounds can be measured on *Mycobacterium* tuberculosis.

Keywords: Dihydropyridine, Anti TB, MTT, cytotoxicity

[1]Microbiology Research Center, School of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran
[2]Biotechnology Research Center, School of Pharmacy, Mashhad University of Medical Sciences, Mashhad, Iran

Profile of Antimicrobial Susceptibility Isolated Microorganisms from Hospitalized Patients in PICU Ward and Detection of Methicillin-Resistant *Staphylococcus aureus* and ESBL-Producing Bacteria by Phenotypic Methods

Jalal Mardaneh[2, 3], Shahla Abbas Poor[1]

Abstract

Background: Hospital-acquired infections are a major challenge to patient. A range of gram-negative organisms are responsible for hospital-acquired infections, the *Enterobacteriaceae* family being the most commonly identified group overall. Infections by ESBL producers have been associated with severe adverse clinical outcomes that have led to increased mortality, prolonged hospitalization, and rising medical costs.

Methods: In this study sampling was performed from patients that hospitalized in PICU part of Bahrami Hospital, Tehran, with attention to involved organ. For isolation of bacteria from patient samples, culture performed on different selective and differential media. After confirmation of bacteria by biochemical tests, susceptibility testing was done by disc diffusion method. Phenotypic detection of MRSA strains was performed by use of cefoxcitin disc. ESBL producing strains were detected by ceftazidime (CAZ) and ceftazidime/clavulanic acid (CAZ/CLA) discs.

Results: Among all isolated organisms from clinical samples that transported to laboratory, the most common isolated organisms were *Escherichia coli* (24 cases), *Pseudomonas Aeruginosa* (9 cases) and *Staphylococcus aureus* (8 cases) respectively. Among 8 MRSA isolated strains from different clinical samples, 6 strains (75%) were MRSA.Among52 isolated gram negative organisms, 5 strains (9/6%) were ESBL.

Conclusion: Standard interventions to prevent the transmission of antimicrobial resistance in health care facilities include hand hygiene, the use of barrier precautions in the care of colonized and infected patients, the use of dedicated instruments and equipment for these patients. The colonized or infected patients should be isolated in single rooms or multiple rooms or areas reserved for such patients.Active surveillance screening is necessary to identify asymptomatically colonized patients who may serve as undetected reservoirs.

Keywords: PICU, Antimicrobial susceptibility, MRSA strains, ESBL-producing strains

[1]Bahrami Hospital, Tehran University of Medical Sciences, Tehran, Iran
[2]Department of pathobiology, School of Public Health and Institute of Public Health Research, Tehran University of Medical Sciences, Tehran, Iran
[3]Professor Alborzi Clinical Microbiology Research Center, Shiraz University of Medical Sciences, Shiraz, Iran

Inhibitory Effects of Bacteria *Pediococcus* Acid lactici, *Lactobacillus reuteri*, Leuconostocmesenteroides, and *Lactobacillus delbrueckii* Lactis and *Lactococcus Lactis* against Ten Species of Gastrointestinal Pathogens

Toktam Lessani[2], Majid Zare Bidaki[1]

Abstract

Background: Today the treatment of gastrointestinal diseases caused by pathogenic bacteria colonization in many countries imposes many costs on health systems. As an alternative method of treatment, the use of probiotic bacteria in infection control has been considered. Probiotics may act as bacterial normal flora interacting with pathogenic organisms. Thus, the present study was conducted to investigate the inhibitory effects of probiotic bacteria on ten pathogenic bacteria.

Methods: The antibacterial effect of probiotics *Lactobacillus rhamnosus*, *Lactobacillus fermentum*, *Lactobacillus casei*, *Lactobacillus Plantarum* and *Bacillus licheniformis* was studied against ten gastrointestinal pathogenic species including *Klebsiella* pneumonia, *Staphylococcus aureus*, *Shigella* flexneri, *Pseudomonas Aeruginosa*, *Bacillus subtilis*, *Shigella* dysenteries, *Yersinia Enterocolitica*, *Salmonella enterica*, *Escherichia coli* and *Bacillus cereus*, in two ways of disk plate and well test by using supernatant solution prepared of bacteria in a cultivable environment after twenty four hours Incubation in

Results: Maximum inhibitory effects were shown by *Lactobacillus delbrueckii lactis* and the lowest inhibitory effect was caused by lactococcu slactis in the well test. The maximum and minimum inhibitory effects were observed against *Shigella* flexneri and *Escherichia coli* respectively.

Conclusion: Results obtained show beneficial activity of probiotic bacteria against pathogenic bacteria in the digestive tract. Considering the prevalence of antibiotic resistance against bacterial pathogens, the use of alternative therapies using probiotic bacteria may be an important point.

Keywords: Probiotic bacteria, antagonistic, pathogenic bacteria

[1]Assistant professor, Medical Microbiology department, Birjand University of Medical Science, Birjand, Iran
[2]StudentLaboratory Sciences, Paramedics, Birjand University of Medical Sciences, Birjand, Iran

The Antagonistic Effects of Bacteria *Lactobacillus Rhamnosus*, *Lactobacillus Fermentum*, *Lactobacillus Casei*, *Lactobacillus Plantarumand Bacillus Licheniformis* against Several Strains of Pathogenic Bacteria

Majid Zare Bidaki[1], Toktam Lessani[2]

Abstract

Background: World Health Organization has defined probiotics as type of living microorganisms can compete with pathogenic organisms and promoting the development and quality of life by causing health effects on the host, improving immune system and evolving mucosal surfaces. No considerable research has been done in this domain in Iran. The aim of this study was to evaluate antagonistic effects of some probiotic bacteria on pathogenic bacteria.

Methods: The antibacterial effect of probiotics *Lactobacillus rhamnosus*, *Lactobacillus fermentum*, *Lactobacillus casei*, *Lactobacillus Plantarum* and *Bacillus licheniformis* was studied against 10 gastrointestinal pathogenic species including *Klebsiella* pneumoniae, *Staphylococcus aureus*, *Shigella* flexneri, *Pseudomonas Aeruginosa*, *Bacillus subtilis*, *Shigella dysenteriae*, *Yersinia Enterocolitica*, *Salmonella* enterica, *Escherichia coli* and *Bacillus cereus*, in two ways of disk plate and well test by using supernatant solution prepared of bacteria in a cultivable environment after 24 hours Incubation in.

Results: Maximum inhibitory effect was found for *Lactobacillus rhamnosus* and the lowest inhibitory effect for *Bacillus licheniformis*in the well test method. Maximum and Minimum Inhibitory effect was observed on *Shigella flexneri* and *Escherichia coli* respectively.

Conclusion: Results obtained from the culture supernatant of the probiotic bacteria are beneficial activity against pathogenic bacteria in the digestive tract, considering the prevalence of antibiotic resistance against bacterial pathogens, alternative therapies using Probiotic bacteria are more suggestive.

Keywords: Probiotic bacteria, antagonistic, pathogenic bacteria, digestive diseases

[1]Assistant professor, Medical Microbiology department, Birjand University of Medical Science, Birjand, Iran
[2]StudentLaboratory Sciences, Paramedics, Birjand University of Medical Sciences, Birjand, Iran

Consideration of Experimental Results of Antibiotic Resistance in *Acinetobacter* Positive Wound Cultures in Burn Patients: (In Men Burns Department of Mashhad Imam Reza Hospital in 1390)

Seyed Saeed Saeedi Shahri[1], Seyed Hassan Tavusi[2], Zohreh Bonakdaran[3], Armin Mahdiani[4]

Abstract

Background: *Acinetobacter* is a Gram-negative cocobacilli. During the past decade the prevalence of nosocomial infections is increasing. This is especially important in particular has had surgery and burns. In 1991 the first report of antibiotic resistance in *Acinetobacter* to carbapenem in United States, was everyone's concern. Due to *Acinetobacter* can long remain in the hospital environment and patients transfer the problem of antibiotic resistance in strains that could be considered a major risk. In this study, the antibiotic resistance of *Acinetobacter* in burn patients must be examined.

Methods: This descriptive and cross-sectional study was conducted of all patients admitted in men burns department of Mashhad Imam Reza Hospital in1390 were studied. All patients in the experimental section of the wound: direct smear and culture was performed. And then related antibiograms and antibiotic resistance were extracted. The entire information system software SPSS 15 were investigated and analyzed.

Results: 155 male patients hospitalized in men burns department of Mashhad Imam Reza Hospital. Most range between 31-40 years of age hospitalized men with 36.5% of cases.

Acinetobacter infection rate in men was 93.5% of cases. (145 cases among 155 patients)

Colony count of bacteria in the male follows: colony high: 54% - the average colony count: 19% - low colony count: 21% of cases - a rare colony count: 6%

Sensitivity of *Acinetobacter* to Colistin therapy in men was21.3% and with Amikacin was 16.5 %(with the highest percentage). 6. Antibiotic resistance in *Acinetobacter* in men of all existing drugs (amikacin-cephtazidime-ciprofloxacin-pipracillin-imipenem-meropenem) with the percentage shown above.

Conclusions: Due to the high antibiotic resistance in *Acinetobacter* and risks associated with microorganisms, it seems that many antibiotic drugs in these patients should be observed carefully and cultures of Weber ANTIBIOGRAM the wound alternately carried out.

The study has shown that the sensitivity of antibiotics is significantly higher in Colistin than other. Thus Colistin for the treatment of *Acinetobacter* infections seems very appropriate. And perhaps because of the low probability of resistance to these antibiotics were prescribed less in recent period

Keywords: Antibiotic resistance, *Acinetobacter*, Burn

[1]Internist, Mashhad University of Medical Sciences, Mashhad, Iran
[2]Professor of surgery, Mashhad University of Medical Sciences, Mashhad, Iran
[3]Master of Anesthesia, Mashhad University of Medical Sciences, Mashhad, Iran
[4]Medical student, Qeshm International University, Qeshm, Iran

The Most Common Bacteria Isolated From Ocular Infection and Antibiotic Resistance Pattern in North-East of Iran between 2005-2011

Abstract

Background: Surveying causative agents of infections and their antibiotic resistance pattern is an important factor for policy making in health systems. Recently many of hospital pathogens show high resistance to antibiotics. Antibiotic resistance among ocular pathogens is increasing in parallel with the increase seen over the year in bacteria associated with systemic infections; other contributing factor may be misuse of antibiotics. In this study we survey resistance pattern of ocular pathogens.

Methods: Bacterial specimens were isolated and identified genius and species by laboratory tests. Then, samples were tested against several antibiotics and information related 7 years were collected.

Results: Among 300 ocular infection samples that were collected from patients in Ghaem University Hospital, the five most common bacteria were isolated including: Coagulase-negative *Staphylococcus* (40%), *K. Pneumonia* (15%), *E. coli* (13%), Coagulase-positive *Staphylococcus* (12%), *P. aeruginosa* (6%), others bacteria (14%). 90% of all specimens were isolated from neonatal department that 75% of them were girls. *Staphylococcus* had high resistance to penicillin and eritromycin (over 80%). It showed heterogeneous and high resistance against cefixime, ceftizoxime, gentamycin and sulfametaxozole.

Conclusion: Probably rout of bacteria transition was contaminated hands of nurses or perinatal. Resistance to antibiotics during these years is high (74%), which is alarming.

Akram Baghani, Samira Rashidian, Maede Nakhaee, Ali Sadeghian, Kiarash Ghazvini

Microbiology and Virology research center, Avicenna Research Institute, Mashhad University Medical Science

Keywords: Ocular infection, *Staphylococcus*, resistance pattern, North-East of Iran

Ocular infection, *Staphylococcus*, Resistance pattern, North-East of Iran

Mohammad Soleimani[1], Keivan Majidzadeh[2], Amirhosein Mohseni[3]

[1]Assistant Professor of Microbiology, Tasnim Biotechnology of Research Center (TBRC), AJA University of Medical Sciences, Tehran, Iran
[2]Assistant Professor of Biotechnology, Tasnim Biotechnology of Research Center (TBRC), AJA University of Medical Sciences, Tehran, Iran
[3]Researcher of Tasnim Biotechnology of Research Center (TBRC), AJA University of Medical Sciences, Tehran, Iran

Abstract

Background: *Coxiella burnetii* is the causative agent of Q-fever, a worldwide zoonosis that has been categorized in biosafety level 3 agents. We developed a quantitative SYBR Green real time PCR assay for rapid detection of the bacterium.

Methods: 16srRNA gene was targeted and specific primers were designed using primer BLAST of NCBI. The SYBR Green Real time PCR assay was established. The test specificity was evaluated using the other bacterial genomes. Construction of positive control plasmid was carried out with cloning of the PCR product into pTZ57R/T vector. The sensitivity of the assay was tested by performing the assay on the 10 fold serial dilution of the positive control plasmid with initial concentration of 200 ng/µl. To develop the assay as a quantitative test, the standard curve was depicted based on C_t value of the serial dilutions against to the concentrations.

Results: Specific amplification of 16srRAN gene of C. burnetii was occurred in Tm of 85ºC as expected. Result of the amplification in specificity testing was negative which shows the specificity of the designed assay. The limit of detection of assay was 20 pg. After plotting the standard curve, R^2, slope and efficiency of the standard curve calculated as 0.99, 3.4 and 98% respectively. The linearity of the quantitative assay was in the range of 200 ng – 20 pg of the positive control plasmid.

Conclusion: The results showed high specificity and sensitivity of the SYBR Green Real-time PCR for rapid and quantitative detection of C. burnetii.

Keywords: *Coxiella burnetii*, diagnosis, SYBR Green Real-time PCR

Study on Resistance Level to Vancomycin in *Staphylococci* in Imam Reza Hospital-Mashhad during November 2009 until November 2010

Elnaz Harifi Mood[1, 2], Askari E[1], Mohammad Zadeh M[3], Mahboubeh Naderi Nasab[1, 2], Amin Bojdi[3], Mohammad Reza Sarveghad[3]

[1]Microbiology and Virology Research Center, Avicenna Research Institute, Mashhad University of Medical Sciences, Mashhad, Iran
[2]Department of Microbiology, Imam Reza Hospital, Faculty of Medicine, Mashhad University of Medical Sciences, Iran
[3]Department of Infectious Diseases, Imam Reza General Hospital, Faculty of Medicine, Mashhad University of Medical Sciences, Iran

Abstract

Background: *Staphylococci* are one of the most important pathogens both in hospitals and community. Vancomycin has been used from decades ago for treatment of these pathogens. In recent years, emergence and spread of *Staphylococci* with reduced susceptibility, intermediate and full resistance to vancomycin have caused problems worldwide and also in Iran. The aim of this study was evaluate the rate of vancomycin resistant among staphylococcal isolates recovered from Imam Reza hospital of Mashhad.

Methods: In this cross-sectional study which was conducted from November 2010 to November 2011, 1000 samples of *Staphylococci* were studied in two parts. In the first part, 900 isolates were screened with disc diffusion (Mast diagnostics, UK). In the second part, 100 samples were evaluated with Mast disc diffusion, 3 and 6 µgr/ml screening agar test and minimum inhibitory concentration (MIC) by E-test. Clinical data were extracted by looking into patients' records and using checklists designed by investigator himself. Data were analyzed by SPSS software.

Results: In the first part, all isolates were sensitive by disc diffusion. In the second part, E-test results showed that from 100 isolates, 96 were sensitive and 3 were intermediate resistance. One isolate was resistant to vancomycin which was found to be vancomycin resistant *Enterococcus* by laboratory diagnostic tests.

Conclusion: Fortunately, no vancomycin resistance was found in this study. Detection of isolates with intermediate resistance to vancomycin was an alarm to healthcare for controlling of nosocomial infections.

Keywords: *Staphylococcus*, vancomycin, vancomycin-intermediate *Staphylococcus aureus*, vancomycin-resistant *Staphylococcus aureus*

Genotyping Analysis of *Mycobacterium tuberculosis* Strains among TB Patients in Tehran

Mohadese Mozafari, Parissa Farnia, Mohammad Reza Masjedi, Ali Akbar Velayati

Mycobacteriology Research Centre (MRC), National Research Institute of Tuberculosis and Lung Diseases (NRITLD)

Abstract

Background: Molecular epidemiology tools are widely used in determining epidemiology of tuberculosis. Spoligotyping is a molecular epidemiology method that is used for characterization and typing of *Mycobacterium tuberculosis* complex strains. The method is based on polymorphism of the chromosomal DR locus consisting of identical 36-bp DRs alternating with 35-41 unique spacers. The objective of this study is to investigate the prevalence of *M. tuberculosis* spoligotypes in Tehran.

Methods: Two hundred and twelve M.TB strains were isolated from TB patient between 2010 and 2011 in Mycobacteriology Research centre (MRC). DNA was extracted from patient's sputum samples. PCR was performed by using of specific primers for DR region. The amplified DNA was hybridized to the spoligotyping Membrane. Hybridized DNA was detected with ECL detection kit and by exposing ECL Hyper film to the membrane. The obtained result was entered to a binary format and was analyzed using SpolDB4 database.

Results: Spoligotyping resulted in forty four different patterns. Out of two hundred and twelve M.TB strains, one hundred and eighty five strains (87.2%) were classified into seventeen clusters, and the remaining strains (12.7%) were orphan. Strains of CAS family were more prevalent than other strains (39.6%). Other prevalent families were Haarlem (20.2%), T (11.8%) and Beijing (3.3%), respectively.

Conclusion: Spoligotyping is a rapid method for simultaneously detection and differentiation of M.TB strains; it can be used effectively for molecular epidemiology studies to determine ongoing transmission clusters. However other molecular epidemiology Methods can be used for further differentiation of M.TB strains.

Keywords: Molecular epidemiology, Spoligotyping, *Mycobacterium* tuberculosis

Antibiotic Resistance among *Acinetobacter* spp. Strains Isolated from Wound Infections in North East of Iran from 1383 to 1390

Samira Rashidian, Akram Baghani, Maede Nakhaee, Ali Sadeghian, Kiarash Ghazvini

Microbiology and Virology Research Center, Avicenna Research Institute, Mashhad University of Medical Sciences, Mashhad, Iran

Abstract

Background: *Acinetobacter spp.* has become an important cause of different infections such as wound infection, due to its great ability to survive and spread in hospital setting and to develop resistance against many antibiotics. The aim of this study was to examine the resistance against antibiotics in isolates of *Acinetobacter* from wound infections during these 7 years.

Methods: During those periods, patients with wound infection in Qaem hospital identified based on NNIS and appropriate samples taken from these wounds. Then microbiological studies were performed to identify bacteria causing the infection. Antibiotic susceptibility of *Acinetobacter spp.* strains were tested by disk diffusion method.

Results: Based on NNIS guideline, 324 cases of infection were identified, 43 samples of *Acinetobacter spp.* strains were isolated; and among these samples resistance to Kanamycin and norfloxacin were increased during these period and resistance against Ampicillin, Ciprofloxacin, cefexime, Trimethoprim-sulfamethoxaxole, cefotaxime, cefazolin, gentamicin and ceftizoxime were not significantly increased. The bacterial resistance is high. The pick of *Acinetobacter spp.* was observed in 1385 and 1386.

Conclusion: Our results showed high resistance against antibiotics among *Acinetobacter spp.* isolated from wound infections. Resistance to antibiotics such as Kanamycin and norfloxacin increased because of high use of these and resistance to other noted antibiotics were reduced, perhaps because of less use of these.

Keywords: *Acinetobacter spp.* strains, Antibiotics resistance, Wound infections

Study of Urinary and Septicemia Infections in Neonatal Intensive Care Unit and Determination of Their Antimicrobial Resistance

Zahra Rajabi[1], Mehrnaz Taheri Poor[1], Jalal Mardaneh[2], Mohammad Mehdi Soltan Dallal[2,3]

[1]Department of microbiology, Islamic Azad University of science and research, Arak branch, Arak, Iran
[2]Department of pathobiology, Division of microbiology, School of public health, Tehran University of medical sciences, Tehran, Iran
[3]Food microbiology research center, Tehran University of medical sciences, Tehran, Iran

Abstract

Background: Blood streams and urinary tract infections are one of the main factors in causing illness and death in the world, especially in developing countries. On the other hand, resistance to antimicrobial agents was a global problem and knowledge of antimicrobial resistance patterns of microorganisms is important to treat the infection. The aim of this study is determination of urinary and septicemia infections in neonatal intensive care unit (NICU).

Methods: In this study, the gram negative microorganisms of blood and urine samples of hospitalized infant in NICU from Emam Hossien, Children hospital center and Bahrami hospitals during seven months isolated, and their antimicrobial resistance was studied by Kirby-Bauer test**.**

Results: Out of one hundred and five urine and blood samples, 75 gram negative bacteria were isolated, including (85/33%) urine and (14.66%) blood samples. The most isolated were: *Klebsiella pneumonia* (42.66%), *Entrobacter cloacae* (29.33%), *E. coli* (17.33%). *Klebsiella* oxytoca (6.66%), respectively.

The most sensitivity shown to merofloxacin (89.33%), ciprofloxacin (84%) and the most resistance shown to cefixim (49.33%), nitrofurantoin (40%).

Conclusion: The results show that controlling NICU is very important**.**

Keywords: NICU, Gram negative microorganisms, UTI, Septicemia

The Antimicrobial Nature of Lactobacillus Casei Culture Supernatant against Multiple Drug Resistant Clinical Isolates of *Shigella sonnei* and *Shigella flexneri* In-Vitro

Vahhab Piranfar[1], Reza Mirnejad[3], Mohammad Erfani[1], Fazlollah Mirzaei Nasab[3]

Abstract

Background: This study was carried out to evaluation of cell-free culture supernatants (CFCS) antimicrobial substance effects of *Lactobacillus casei* isolated against multiple drug resistance (MDR) clinical samples of *Shigella* sonnei and *Shigella* flexneri in vitro.

Methods: *S. sonnei* and *S. flexneri* was identified by common microbiological and serological Methods. Antibiogram with 18 antibiotics were tested for 34 positive cultures by disc diffusion method. Samples showed considerable resistance to antibiotics. Antimicrobial effects of CFCS were tested against *S. sonnei* and *S. flexneri* by agar-well assay and broth micro dilution Methods. In addition, the antimicrobial activity remained active treatment after adjust pH 7, adding Proteinase K and heating for *L. casei*.

Results: The MIC_{50} and MIC_{90} of CFCS of *L. casei* were determined, for *S. sonnei* was 3.25 and 12.5, for *S. flexneri* was 6.25 and 6.25 respectively. Standard growth curves of pathogenic *Shigella* isolates and *L. casei* were obtained and colony count procedures. According to the results of this paper, CFCS of *L. casei* highly resistant against to antibiotics, heat, Proteinase K and has so many activities against MDR *Shigella* pathogenic strains.

Conclusion: The results presented here provide an evidence for the fact that *L. casei* strongly inhibit the multiple drug resistance gastrointestinal pathogens *S. sonnei* and *S. flexneri*. In addition, all tested strains were found to possess desirable probiotic properties in vitro. *L. casei* good *Candida*tes for their application as novel probiotic strain. More the information presented in this paper unfortunately showed the *Shigella* isolates strains has complete resistance against tetracycline, streptomycin, trimethoprim/sulfamethoxazole and ampicillin. Furthermore, that all samples were Intermediate antibiotics-resistant for Ciprofloxacin and Chlortetracycline.

Keywords: *Lactobacillus casei*; *Shigella flexneri*; *Shigella sonnei*; Antimicrobial effect

[1] Department of microbiology, Tonekabon branch, Islamic Azad university of Tonekabon, Tonekabon, Iran
[2] Molecular Biology Research Center, Baqiyatallah University of Medical Sciences, Tehran, Iran
[3] Department of Biochemistry Payam-e-Noor university Taft, Yazd, Iran

Rapid and Specific Detection of Streptococcus Pneumonia by Polymerase Chain Reaction

Amin Moazami[1], Mohammad Hassan Shirazi[2], Ziba Vaise Malekshahi[3], Sara Hajikhani[2]

[1]Microbiology, Islamic Azad University science and research, Arak, Iran
[2]Department of Microbiology, Faculty of health science, Tehran Medical University, Tehran, Iran
Microbial Biotechnology, Shahed University, Tehran, Iran

Abstract

Background: *Streptococcus pneumonia* is a Gram-positive, alpha-hemolytic bacterium. *S. pneumonia* is a bacterium commonly found in the nose and throat. The bacterium can sometimes cause severe illness in children. The aim of this study was to rapid and specific detection of *S. pneumonia* by Polymerase Chain Reaction in sputum of patients suspect influenza.

Methods: Gene (blpa) selected as target sequence. Primers lead to amplify 349bp region for S. pneumonia. In this study eighty sputum specimens from patients suspect influenza sending influenza center , Faculty of Health Science, Tehran medical university were analyzed.

Results: After detection of gene (blpa) by PCR Methods, the products were analyzed on agarose gel electrophoresis. Out of eighty sample collection, *S.* pneumonia was isolated from 17(13.72%) samples were positives by PCR.

Conclusion: Because of Long culture method, detection of bacteria by PCR in sputum specimens from patients suspect influenza can be sensitive and rapid method for identify *S. pneumonia*.

Keywords: *Streptococcus pneumonia*, PCR

Study of Prevalence of ESBL type PER-1 among Isolated Entrobacter Collected from Qazvin Hospitals

Amir Peymani[1], Hamide Malikhan[2], Rahimeh Sanikhani[1], Mohammad Moini-Rad[1]

[1]Qazvin University of Medical Sciences, Qazvin, Iran
[2]Department of Microbiology, Rasht University of Medical Sciences, Rasht, Iran
[3]Gilan University, Faculty of Sciences, Department of Biology, Rasht University of Medical Sciences, Rasht, Iran

Abstract

Background: In recent years, there are increasing reports of the emergence of betalactam resistant Enterobacter isolates in clinical settings worldwide. Extended spectrum beta lactamases (ESBLs) are the most important mechanisms of betalactams resistance among Enterobacter species. The aims of this study were to determine the frequency of ESBLs-producing isolates using Double Disk Approximation Test (DDAT) and to determine the prevalence of bla $_{PER-1}$ gene among them.

Methods: One hundred non duplicated clinical isolates were collected from Qazvin hospitals. The ESBL screening was done using Disk Agar Diffusion method according to Clinical and Laboratory Standards Institute (CLSI) guideline and then ESBL production was confirmed by DDST method. The PCR assay was performed to detect the blaPER-1 gene.

Results: In total, ninety isolates were reported as non-susceptible to screening antibiotics. Amongst them fifty four (60 %) isolates were found to be ESBLs producers using double disk approximation method. Four isolates (7%) carried the bla PER-1 gene among ESBL producer by PCR method.

Conclusion: Considering the high prevalence of ESBLs producing isolates, the initial identification of them and use of appropriate infection control measures is necessary in different wards of selected hospitals.

Keywords: Enterobacter spp, ESBLs, PER-1

Antimicrobial Activity of Enterolysin an Endopeptidase among indigenous *Enterococcus Faecalis* Strains of Iran on Foodborn and Clinical Pathogens

Zeinab Hatami[1], Mitra Salehi[1], NaderMosavari[2], Marzie Eyn Namnam[1]

Abstract

Background: Enterolysin A is a large (calculated molecular weight of 34,501 Da), heat labile bacteriocin and therefore fits the general characteristics of class IV bacteriocins. Target of present study is Molecular detection of enterolysin Agene among animal isolates of *Enterococcus faecalis* for their potential as biopreservatives in food or feed.

Methods: In this study occurrence of class IV enterocin structural gene (enterolysin A) in a target of *Enterococcus faecalis* isolated from sixty three samples of different locales of Tehran animal feces have been surveyed. Enterococcal strains were isolated using Bile Aesculin Azide Agar medium and after strains purifications, *E. faecalis* species identification and occurrence of enterolysin A gene was performed by PCR method. Cell-free neutralized supernatant (of selected gene positive strains) was used to test bacteriocin production and antimicrobial spectrum of endopeptidase was assayed by diffusion Methods (disk and wall) on the gram-positive and negative indicators bacteria.

Results: Ten strains of *E. faecalis* were purified from sixty three isolated samples. Six strains of these ten *E. faecalis* strains (60%) had enterolysin A gene that they inhibited growth of indicator bacteria such as clinical strain of *Staphylococcus epidermidis*, Listeria monocytogenes, *Bacillus subtilis*, *Pseudomonas Aeruginosa* and *Salmonella typhimurium*.

Conclusion: These strains produce an endopeptidase, enterolysin A encoded by enl A, which is homologous to other cell wall lytic enzymes such as lysostaphin and zoocin A. However, unlike these enzymes enterolysin A has a broad spectrum of activity and can lyse a wide range of Gram-positive bacteria.

Keywords: *Enterococcus faecalis*, PCR, Enterolysin A

[1]Department of Microbiology, North Tehran Branch, Islamic Azad University, Tehran, Iran
[2]Razi Vaccines and Serum Research Institute, Karaj, Iran

Evaluation of Antibacterial Effects of Catechin and Carvacrol on Planktonic and Biofilm Cells of *Pseudomonas aeruginosa*

Mina Saadat[1], Shahla Roudbarmohammadi[2]

Abstract

Background: Today, bacterial biofilms contribute to 65% of nosocomial infections worldwide. One of the most common pathogens that can form biofilm is *Pseudomonas aeruginosa.* Because of ever-increasing prevalence of antibiotic resistance, it is necessary to find an antimicrobial substance to reduce contaminations. In this study we evaluated the antibacterial activity of carvacrol and catechin as herbal agents on planktonic and biofilm cells of *Pseudomonas Aeruginosa* standard strain.

Methods: Standard strains of *Pseudomonas Aeruginosa* (ATCC 27853) were cultivated in nutrient agar medium for twenty four at 37^0C. The MICs values of Carvacrol, Catechin and Imipenem as an antibiotic on *P. aeruginosa* were determined with micro dilution test. Then, the biofilm of this bacterium was formed and finally the influences of these agents on biofilm inhibition were evaluated by MTT assay.

Results: The MIC values of catechin and carvacrol and imipenem on *Pseudomonas aeruginosa* were 7.24, 1, 5 and 0.43 (µg/ml), respectively. Colorimetric assay with MTT showed that carvacrol, inhibited biofilm formation significantly.

Conclusion: Our findings showed that carvacrol and catechin can inhibit the growth of planktonic and biofilm cells of *P. aeruginosa* with significant mean difference and carvacrol do this strongly. From the results of the present study, we suggest using these agents to reduce or inhibit bacterial contamination of medical devices.

Keywords: Biofim, *Pseudomonas aeruginosa*, biocides

[1]Master Student of Microbiology, Department of basic science, Azad University, Research and Science Branch, Tehran, Iran
[2]Assistant Professor, Department of Medical Mycology, School of Medical sciences, Tarbiat Modares University, Tehran, Iran

Determining and Detecting Antibiotic Resistance of Bacteria Isolated from Sputa of Cystic Fibrosis Patients

Parisa Vali[1], Maryam Sayfipoor[2], Reza Akbari[3], Fereshteh Shahcheraghi[4], Mohammad Mehdi Feizabadi [5]

[1]Pasteur Institute of Iran, Microbiology Department, Tehran, Iran
[2]Pasteur Institutes of Iran, Microbiology Department, Tehran, Iran
[3]Pasteur Institutes of Iran, Microbiology Department, Tehran, Iran
[4]Pasteur Institute of Iran, microbiology department, Tehran, Iran
[5]Tehran University of Medical Sciences, Medical Microbiology Department, Tehran, Iran

Abstract

Background: Cystic fibrosis is an autosomal recessive genetic disorder caused by mutation in the gene encoding CFTR protein. Because repeated respiratory tract infections have been diagnosed as their major problem, obligation to identify these infections leading bacteria and determining antibiotic resistance is crucial. The purpose of this project is determining and detecting antibiotic resistance of bacteria isolated from sputa of cystic fibrosis patients.

Methods: In this study 40 sputa samples of CF patients obtained. Samples cultured in selective and non-selective media and isolated bacteria recognized by biochemical tests. The antibiotic susceptibility of isolates to cephalosporins, aminoglycosides, carbapenems was measured by Disc Diffusion and MIC method.

Results: 55 bacteria isolated from 40 sputa samples were included different species same as: *Pseudomonas Aeruginosa*(%35), *Klebsiella ozaenae*(%7.1), alcaligenes xylosoxidans (%3.5), *Achromobacter denitrificans*(%8.9), *Klebsiella pneumonia* (%3.5).In some patients more than one bacteria detected. Obtained results of antibiogram and antibiotic susceptibility tests showed the rate of resistance to cefixime (%86), ceftriaxone (%75), ceftazidime (%70) and meropenem (%7).

Conclusion: Microbial diversity and antibiotic resistance in CF patients is high. With considering above mentioned results, the most antibiotic resistancy is related to cefixime, ceftriaxone, ceftazidime and the least is related to meropenem and imipenem. In some bacteria multidrug resistance were seen, therefore usage of new antibiotics with modern and combined treatment Methods can be effective.

Keywords: Antibiotic Resistance, Microbial diversity Sputa, Cystic Fibrosis

Antimicrobial Susceptibility Pattern of Methicillin-Resistant *Staphylococcus aureus* Isolated at Center of Iran

Mohsen Rezazadeh[1,2], Ehsanollah Ghaznavi-Rad[1], Rasoul Yousefi Mashouf [3], Bita Bakhshi[4],Hossein Sarmadyan[5]

[1]Department of Medical Microbiology, Faculty of Medicine, Arak University of Medical Sciences
[2]Student research committee, Arak University of Medical Sciences, Arak, Iran
[3]Department of Medical Microbiology, Faculty of Medicine, Hamadan University of Medical Sciences
[4]Department of Medical Microbiology, Faculty of Medicine, Tarbiat Modares University
[5]Department of Infectious Diseases, Faculty of Medicine, Arak University of Medical Sciences

Abstract

Background: *Staphylococcus aureus* has been recognized as an epidemiologically important pathogen which is a great concern in hospital setting as a causative agent of nosocomial infection. Despite antibiotic therapy, staphylococcal infections occur frequently in hospitalized patients and have severe consequences. The spread of this microorganism is through contaminated hands and nose of healthcare workers. Today, main problem with *Staphylococcus aureus* is resistance to wide range of Antibiotics. There for the aim of present study is to determine the susceptibility pattern of methicillin-resistant *Staphylococcus aureus* isolated at center of Iran.

Methods: Fifty methicillin-resistant *Staphylococcus aureus* isolates were recognized. All the isolates were confirmed by phenotypic and genotypic (sa442). Antibacterial susceptibility patterns of the isolates to 17 antibiotics were determined by disc diffusion according to the method of the CLSI.

Results: The results of Antibacterial susceptibility patterns in as follows**:**mupirocin (100%), vavncomycin (96.97%), linezolid(100%), ciprofloxacin (84.90%), quinupristin-dalfoprictin (100%), rifampicin (62)%, chloramphenicol (100%), netilmicin (90%),Levofloxacin (73.53%), tigecycline (65.50%), teicoplanin (87.88%), fusidic acid (94.96%),cefoxitin (73.53%), trimethoprim-sulfamethoxazole (88.24%), tetracycline (50%), erythromycin(56.53%), clindamaycin (62%), gentamicin (73.53%)

Conclusion: In according to geographical differences in antimicrobial resistance profiles of methicillin-resistant, *Staphylococcus aureus* have a non-multidrug resistant antimicrobial profile that cause raise in empirical and directed therapy of infections caused by these strains. However, the recent study showed increasing non-β lactam resistance in HA-MRSA, provides a warning for clinicians making decisions about treatment of patients potentially infected with *S. aureus*. Continued monitoring of global epidemiology and emerging drug resistance data is critical for the effective management of these infections.

Keywords: *Staphylococcus aureus*, sa_{442}, susceptibility pattern, CLSI

Polymorphism Identification of the OmpL1 Gene of L. Interrogans Dominant Field Serovars in Iran

Mehrangiz Dezhbord[1], Pejvak Khaki[2], Majid Esmaelizad[3], Atena Zarehparvar Moghadam[4], Fariba Fotohi[5]

Abstract

Background: Leptospirosis, caused by infection with pathogenic *Leptospira* species is the most prevalent zoonotic diseases in the world. The *Leptospira* l vaccines used currently are mainly multivalent dead whole-cell mixtures made of several local dominant serovars. These vaccines, however, do not confer cross-protective immunity and may lead to incomplete, short-term immunity as well as serious side effects. Thereupon design and construction of an efficient recombinant vaccine for leptospirosis control is very important.OmpL1 is an immunogenic porin protein i.e. expressed only in pathogenic *Leptospira spp.* highly conserved OmpL1 antigen is special significance in vaccination and serodiagnosis for leptospirosis. In order to homological analysis we sequenced and compared ompL1 genes cloned from pathogenic field serovars of leptospires prevalent in Iran.

Methods: Five field serovars of pathogenic L. interrogans (*L. icterohaemorrhagiae*, *L. pomona, L. serjoe hardjo, L. grippotyphosa, L. canicola*) and one saprophytic species (*L. biflexa*) were used to inoculate into the selective culture medium and extraction of the genomic DNA by standard Phenol-Chlorophorm method. The specific primers for proliferation of ompL1gene were designed. The PCR products of pathogenic serovars were ligated in pJET1.2/ blunt vector and transformed in competent *E. coli* Top10 cells**.** The extracted recombinant plasmid was sequenced.

Results: PCR amplification of the ompL1gene using the designed primers resulted in a 963 bp ompL1gene product in all three pathogenic vaccinal serovars tested. No PCR products were amplified from the non-pathogenic *L. biflexa*. Our results showed that the ompL1gene is relatively different among dominant *L. interrogans* serovars. Minimum sequence identity of the ompL1gene was observed between *L. Grippotyphosa* and *L. Canicola* (88.4%).while, maximum sequence identity was between *L. Canicola* and *L. Sejroe hardjo* (98.9 %).

Conclusion: According to the results of this study and other researches, ompL1 gene nucleotide sequence is different within dominant *L. interrogans* serovars in Iran. Thus, the differences in nucleotide sequences in the ompL1 gene types may affect the immunogenicity of OmpL1 proteins. OmpL1 is considered as genus-specific protein antigen; hence Immune response against this protein is important in immunity to leptospirosis. This is the point that is noteworthy in design an effective recombinant ompL1 vaccine. In order to improve efficiency of ompL1 recombinant vaccine, it can be designed to include all the OmpL1 protein variants.

So the cloned gene in this study could be further used for expression and recombinant OmpL1 may be a useful vaccine *Candida*te against leptospirosis.

Keywords: Leptospirosis, Sequencing, ompL1, Homological analysis

[1] Department of Microbiology, Karaj Branch, Islamic Azad University, Karaj, Iran
[2] National Reference Laboratory for *Leptospira*, Department of Microbiology, Razi Vaccine and Serum Research Institute, Karaj, Iran
[3] Department of Biotechnology, Razi Vaccine and Serum Research Institute, Karaj, Iran
[4] National Reference Laboratory for *Leptospira*, Department of Microbiology, Razi Vaccine and Serum Research Institute, Karaj, Iran
[5] National Reference Laboratory for *Leptospira*, Department of Microbiology, Razi Vaccine and Serum Research Institute, Karaj, Iran

Synergistic Antibacterial Activity of *Capsella Bursa-Pastoris* and *Glycyrrhiza glabra* against Oral Pathogens

Saman Soleimanpour[1], Fereshteh Sedighinia[1], Akbar Safipour Afshar[2], Reza zarif, Javad Asili[1], Kiarash Ghazvini[1]

[1]Microbiology and Virology Research Center, Avicenna Research Institute, Mashhad University of Medical Sciences, Mashhad, Iran
[2]Department of Biology Islamic Azad University,Neyshabour Branch,Neyshabour,Iran

Abstract

Background: Oral infections and dental caries are still considered as serious public health problems and inflict a costly burden to health care services around the world and especially in developing countries. Herbal mouth wash compared to chemical drugs have fewer side effects and are more economical. Consequently, evolution of antibacterial effects of medicinal plants for the manufacture and use of mouth wash with minimal adverse effects and cost, using our natural resources can be important. In the present study, we evaluated the antibacterial activity of *Capsella Bursa-Pastoris* alone and also combined with *Glycyrrhiza glabra* against oral pathogens.

Methods: The antimicrobial activities of an ethanol extract of *Capsella Bursa-Pastoris* alone and in combination with *G. glabra* were tested in vitro against six reference strains of oral pathogenic bacteria. The antimicrobial activities of the extracts were examined using disc diffusion method and the minimum inhibitory concentration (MIC) determined by both broth and Agar dilution Methods and minimum bactericidal concentration (MBC) by broth dilution Methods.

Results: In this study, *C. bursa-pastoris* extract and mixed extract showed good antibacterial activity against six bacteria. No strain in this study showed resistance against these extracts.

Conclusion: *C. bursa-pastoris* is suggested as an appropriate *Candida*te to help us in order to control dental caries and endodontic infections.

Keywords: Antibacterial Activity, *Capsella Bursa-Pastoris*, *Glycyrrhiza glabra*, Oral Pathogens

Comparison of PCR-RFLP and sequencing Methods for fast detection of Isoniazid resistant isolates of *Mycobacterium tuberculosis*

Maryam Tayeboon[2], Mohammad Arjomandzadegan[1], Azam Ahmady[1], Mana Shojapour[3]

[1]Tuberculosis and Pediatric Infectious Diseases Research Center, Arak University of Medical Sciences, Arak, Iran
[2]Department of Microbiology, Islamic Azad University of Arak Science and Research Branch, Arak, Iran
[3]Research Center of Molecular Medicine, Arak University of Medical Sciences, Arak, Iran

Abstract

Background: In this study, a PCR-RFLP method for rapid detection of *Mycobacterium tuberculosis* clinical isolates resistant to isoniazid was designed and the compared by sequencing results.

Methods: In this study fifty one clinical isolates of *Mycobacterium tuberculosis* with positive culture and biochemical methods were used. PCR-RFLP method with the HPAII endonuclease was used for detection probably mutation at codon 315 of kat G gene. The results were compared with sequencing as golden standard.

Results: From fifty one isolates, seventeen strains were resistant and thirty four ones were susceptible phenotypically. As a result of molecular method, all of susceptible isolates were non mutant by PCR-RFLP method. In the other hand, 85% of all resistant strains have mutation in katG315. Results of sequencing method were proved the results of molecular method.

Conclusion: The results of this study indicate that the PCR-RFLP method can be used in routine work as a simple and rapid method for detection of resistance to Isoniazid.

Keywords: *Mycobacterium tuberculosis*, drug resistance, isoniazid, PCR-RFLP

Evaluation of Antifungal Activity of Tio2 Nanoparticles on Growth Inhibition of *Candida Dubliniensis* Biofilm Using MTT Assay

Farnoosh Haghighi[1], Shahla Roudbar Mohammadi[1], Mehdi Eskandari[2]

Abstract

Background: Nowadays, mortality and morbidity due to *Candida* biofilm infections via medical devices, such as catheter and implants, are increasing. Therefore, finding new Methods of combating such infectious agents seems necessary. Thus in this study antifungal effects of titanium dioxide nanoparticles (TiO2) on *Candida dubliniensis* biofilms were investigated.

Methods: TiO2 nanoparticles were synthesized through the hydrolysis of TiCl4 (Titanium tetrachloride).The morphology and structure properties of the product were analyzed by using scanning electron microscopy (SEM) and X-ray diffraction (XRD). MIC and MFC tests of TiO2 nanoparticles were evaluated by micro-dilution broth techniques. Biofilms of *C. dubliniensis* were developed on flat-bottomed of 96-well microtiter plates and antifungal effects of TiO2 nanoparticles were evaluated by standard MTT reduction assays for measuring metabolic activity of sessile cells within the biofilms.

Results: Concentration of synthesized TiO2 was 7.03 µg/ml. TiO2 nanoparticles were spherical with diameter between 60-100 nm. MIC90 of TiO2 nanoparticles were 0.87 µg/ml and MFC was determined 1.35 µg/ml. Biofilm inhibitory concentration of TiO2 nanoparticles was 2.73 µg/ml. The metabolic activity of sessile cells was reduced >90% at about twice the minimum inhibitory concentration of planktonic cells. findings revealing the ability of TiO2 nanoparticles to penetration of *C. dubliniensis* biofilms.

Conclusion: In this study, TiO2 nanoparticles showed significant inhibitory effects against *C. dubliniensis* biofilm compared with Fluconazole. Thus it can be a new strategy in prevention of fungal biofilms after supplementary studies.

Keywords: Antifungal effects, *Candida dubliniensis* biofilm, TiO2 nanoparticles

[1]Department of Mycology, School of Medical Sciences, Tarbiat Modares University, Tehran, Iran
[2]Department of Nanomaterial Engineering, Tarbiat Modares University, Tehran, Iran

Identification of Pandrug-Resistant (pdr)-*Acinetobacter* spp.InICUPatients of Al-ZahraHospital of Isfahan, Iran

Tahereh Motalebi Rad, Hossein Fazeli

Department of Microbiology, Faculty of Medicine, Isfahan University of Medical Sciences, Isfahan, Iran

Abstract

Background: In recent years, outbreaks of *Acinetobacter spp.* resistant to treatment, especially in ICU patients and its role as one of the major factors causing hospital infections has been-considered. The aim of this study was to evaluate the antibiotic resistance of *Acinetobacter spp.* isolates in ICU patients of Al-Zahra hospital in Isfahan.

Methods: Sixty nine isolates of *Acinetobacter spp.* were collected over four months from different clinical specimens in ICU patients and were identified using standard phenotypic method. Antimicrobial susceptibility of all isolates to eleven antibiotics(Mast, UK) was tested using the standard Kirby-Bauer disk diffusion method on two Mueller Hinton Agar plates according to CLSI guidelines (Clinical and Laboratory Standards Institute, 2011) and results were analyzed by WHONET ver5.6 software.

Results: Of sixty nine isolates, the fifty three isolates were resistant to all antibiotics (76.81%) and eight isolates had intermediate resistance to six antibiotics (11.59%) and sensitivity was observed only in nine isolates to four antibiotics (13.04%).

Conclusion: Given the high prevalence of PDR-*Acinetobacter spp.* in the hospitals, especially ICU, must take the necessary measures by the clinical governance of every hospital, for the management of correct identification of resistant strains, prescribing antibiotics and prevention of creation hospital acquired infections.

Keywords: *Acinetobacter* spp, ICU, PDR

Determination of *Mycobacterium Tuberculosis* Frequency in Patient's Samples Referred to Outpatient Clinic of Ghaem Hospital during Seven Years

Zahra Meshkat [1], Mehrangiz Khajekaramadini[2], Reza Akhavan [3], Mojtaba Meshkat[4], Saeid Amel Jamehdar[2]

[1] Women's Health Research Center, Mashhad University of Medical Sciences, Mashhad, Iran
[2]Microbiology and Virology Research Center, Avicenna Research Institute, Mashhad University of Medical Sciences, Mashhad, Iran
[3]School of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran
[4] Isalmic Azad University, Mashhad Branch, Mashhad, Iran

Abstract

Background: Nowadays, tuberculosis is known as one of the infectious diseases with a heavy disease burden. Thus the rate of decrease in disease prevalence could be a good indicator of the strength of health systems in a country. The aim of present study was to do a disease prevalence survey of tuberculosis in our local area, which could provide an accurate measure to assess how the country is moving toward the WHO standards.

Methods: We used our recorded data of the results of sputum microscopy for acid fast bacilli and the cultures for *Mycobacterium tuberculosis* to assess the tuberculosis frequency in patients referred to Outpatient Clinic of Ghaem Hospital during seven years.

Results: The presence of *Mycobacterium tuberculosis* in studied patients was 2415 (9%) with macroscopic method and 1547 (6%) with culture method. The measure of agreement between these was 48% that is statistically significant.

In this study, the microscopic method showed a specificity of 94.6% and sensitivity of 66% compared to the culture results as a gold standard method.

Conclusion: The highest frequency of *Mycobacterium tuberculosis* was in the sputum sample (5.2% and 12.6% positive results using culture and direct microscopic Methods, respectively). According to these results, we can see that although direct microscopic method is and agreeable means of screening, but the high frequency of false negative results, make it necessary to do the culture method for all the samples.

Keywords: *Mycobacterium tuberculosis*, Prevalence, Outpatient

Quantitative Suspension Test for the Evaluation of Basic Bactericidal Activity of Disept

Aghigh Ziaeemehr, Kiarash Ghazvini, Mastureh Momen Heravi, Tahereh Rashed, Mohammadtagji Malekmohammadi, Majid Akbari

Microbiology and Virology Research Center, Avicenna Research Institute, Mashhad University of Medical Sciences, Mashhad, Iran

Abstract

Background: This study specifies a test method and the minimum requirements for basic bactericidal activity of Disept as a chemical disinfectant that form a homogeneous, physically stable preparation when diluted with water. Products can only be tested at a concentration of %80 or less as some dilution is always produced by adding the test organisms and water.
This study only could apply to active substances (antibacterial biocides) and to formulations under development that are planned to be used in food, industrial, domestic and institutional, medical and veterinary areas. This study was done based on Iranian national standard (10504).

Methods: A sample of Disept as delivered (highest test concentration = 80%) is added to a test suspension of bacteria. The mixture is maintained at (20 ± 1) °C for 5 min ± 10 s (obligatory test conditions). At the end of this contact time, an aliquot is taken; the bactericidal and/or the bacteriostatic activity in this portion is immediately neutralized or suppressed by a validated method. The method of choice is dilution-neutralization. The numbers of surviving bacteria in each sample are determined and the reduction is calculated.
The test is performed using *Pseudomonas Aeruginosa* and *Staphylococcus aureus* as test organisms (obligatory test conditions).

Results: In both the bacteria *Pseudomonas Aeruginosa* and *Staphylococcus* aureous, the number of colony forming units per ml of test mixture was 105

Conclusion: For the Disept E-1 as ready to use possesses bactericidal activity in the conditions of the test. The basic bactericidal concentration determined according to this study is ready to use for both test organism *Pseudomonas Aeruginosa* and *Staphylococcus aureus* and showed a 5 log reduction or more at a this concentration.

Keywords: Disinfection, Bactericidal activity, Disept

In Silico Identification of Drug Targets in *Staphylococcus aureus* N315

Zohre Hajisharifi

Department of Science and New Technologies, Master of Microbial Biotechnology, Isfahan University, Isfahan, Iran

Abstract

Background: Methicillin/ multidrug resistant *Staphylococcus aureus* N315 causes serious infections in humans and becomes resistant to increasing numbers of antibiotics. The present study has followed an in silico way for identification of new drug targets.

Methods: DEG tools and BLAST were used for identification of essential genes number with E-score < 10-4(302) and absent in the human genome with E-score < 10-2 (170) respectively. Then the genes were classified according to their functions by KEGG pathway or DEG tolls.

Results: 170 genes were considered as promising antibiotic drug targets. We proposed that the prevention of expression of cell wall biosynthesis gene (fmhA) and 4 cell envelope biogenesis genes which either do not have human homologues is a novel approach to avoid antibiotic resistance.

Conclusion: Five genes are new drug targets.

Keywords: Methicillin/multidrug resistant, essential genes, drug targets, DEG tools, KEGG pathway

Prevalence of Apha (6), Aacc (1) Resistance Genes in *Acinetobacter baumannii* Isolates from Patients of Tabriz

Katayun Aliakbarzade[1], Safar Farajnia[2], Ashraf karimi Nik[3], Amir Peymani[3], Nasrolah Sohrabi[4]

[1]Department of Microbiology. Science and Research branch, Islamic Azad University, Kerman, Iran
[2] Biotechnology Research Center, Tabriz University of Medical Sciences, Tabriz, Iran
[3] Department of Microbiology, Ghazvin University of Medical Sciences, Qazvin, Iran
[4] Department of Microbiology, Kermanshah University of Medical Sciences, Kermanshah, Iran

Abstract

Background: In recent years, the antimicrobial resistance has been emerged as a major problem in treatment of nosocomial infections. *Acinetobacter baumannii* is one of the most important causes of nosocomial infections worldwide. This bacterium is resistant to most of available antibiotics and plays an important role in mortality of hospitalized patients. The present study investigated the prevalence of the genes encoding aminoglycoside-modifying enzymes (AME) in *Acinetobacter baumannii* strains isolated from Tabriz city in the northwest of Iran.

Methods: In this study ninety seven multi drug resistant *Acinetobacter* isolates were collected from Imam Reza hospital in Tabriz. Antimicrobial susceptibility of isolates to antimicrobial agents including gentamicin and amikacin evaluated by disc diffusion method. The AME encoding resistance genes aacC1and aphA6 was analysis by PCR method.

Results: Antimicrobial susceptibility analysis showed that the highest antibiotic resistance was to cefiexim (100%) followed by ceftizoxim (100%) and ticaracilin (100%), whereas the highest sensitivity was observed to colsitin and polymixin.The PCR results showed that forty three (44.4%) isolates contained the aacC1, forty seven (51.3%) isolates contained aphA6 and twenty seven (28%) isolated were positive for both aacC1 and aphA6 resistance genes.

Conclusion: The results of this study indicated that the genes related to AME are prevalent in the *A. baumannii* strains in the study region which highlighted the necessity of considering preventive measure to control dissemination of resistance genes.

Keywords: *Acinetobacter baumannii,* aminoglycoside resistance genes, aacC1 ،aphA6

Antibacterial Activity of *Tribulus terrestris* and Its Synergistic Effect with *Capsella Bursa-Pastoris* and *Glycyrrhiza Glabra* against Oral Pathogens

Saman Soleimanpour[1], Fereshteh Sadat Sedighinia[1], Akbar Safipour Afshar[2], Reza Zarif[1], Javad Asili[1], Kiarash Ghazvini[1]

[1]Microbiology and virology Research Center, Avicenna Research Institute, Mashhad University of Medical Sciences, Mashhad, Iran
[2]Department of Biology Islamic Azad University,Neyshabour Branch,Neyshabour,Iran

Abstract

Background: Mechanical removal of the dental plaque by antiseptic agents like Chlorhexidine is the most efficient procedure in caries prevention; however, development of resistance against antibiotics and antiseptics is a growing cause of concern which has limited the preventive measures. In the present study, we evaluated the antibacterial activity of *Tribulus terrestric* alone and also combined with *Glycyrrhiza glabra* and *Capsella Bursa-Pastoris* against oral pathogens.

Methods: The antimicrobial activities of an ethanol extract of T. terrestris alone and in combination with *G. glabra* and *C. bursa-pastoris* were tested in vitro against six reference strains of oral pathogenic bacteria. The antimicrobial activities of the extracts were examined using disc diffusion method and the minimum inhibitory concentration (MIC) determined by both broth and Agar dilution Methods and minimum bactericidal concentration (MBC) by broth dilution Methods.

Results: In this study, *Tribulus terrestric* and mixed extract showed good antibacterial activity against six bacteria. No strain in this study showed resistance against this extract.

Conclusion: *T. terrestris* and its mixture with *G. glabra* and *C. bursa-pastoris* are suggested as appropriate *Candida*tes to help us in order to control dental caries and endodontic infections.

Keywords: Antibacterial Activity, *Tribulus terrestris*, *Capsella Bursa-Pastoris*, *Glycyrrhiza glabra*, Oral Pathogens

Comparison of PCR-RFLP and Sequencing Methods for Fast Detection of Isoniazid Resistant Isolates of *Mycobacterium Tuberculosis*

Mohammad Arjomandzadegan[1], Maryam Tayeboon[2], Azam Ahmady[1], Mana Shojapour[3]

Department of Microbiology, Tuberculosis and Infectious Research Center, Arak University of Medical Sciences, Arak, Iran

Abstract

Background: In this study, a PCR-RFLP method for rapid detection of *Mycobacterium tuberculosis* clinical isolates resistant to isoniazid was designed and the compared by sequencing results.

Methods: In this study 51 clinical isolates of *Mycobacterium tuberculosis* with positive culture and biochemical Methods were used. PCR-RFLP method by the HPAII endonuclease was used for detection probably mutation at codon 315 of katG gene. The results were compared with sequencing as golden standard.

Results: From 51 isolates, 17 strains were resistant and 34 ones were susceptible phenotypically. As a result of molecular method, all of susceptible isolates were non mutant by PCR-RFLP method. In the other hand, 85% of all resistant strains have mutation in katG315. Results of sequencing method were proved the results of molecular method.

Conclusion: The results of this study indicate that the PCR-RFLP method can be used in routine work as a simple and rapid method for detection of resistance to Isoniazid.

Keywords: *Mycobacterium tuberculosis*, drug resistance, isoniazid, PCR-RFLP

Determining Antibiotic Resistance of *Pseudomonas* spp. Isolated from Different Units of the Shahid Rajaii Hospital in Tonekabon, Mazandaran, Iran

Seyyedeh Zahra Azimi, Masoud Ghane, Zahir Heshmatipour

Abstract

Background: Various species of *Pseudomonas*, especially *Pseudomonas Aeruginosa* are the most important pathogens and agents which cause nosocomial infections. One of the most significant problems which are to be raised in connection with *Pseudomonas* is their antibiotic resistance problem. The aim of this study was to determine the antibiotic resistance of *Pseudomonas* isolated from the hospital environment in Tonekabon.

Methods: Between December 2010 and June 2011, four hundred sixty samples from hospital sections were collected. Totally, sixty one strains of *Pseudomonas* were isolated from all the hospital sections. The identification of strains was performed by using biochemical tests and API20NE (Biomerieux). Then the antimicrobial resistance of *Pseudomonas* species was evaluated by disk diffusion Methods.

Results: The result obtained for antibiotic resistance of *Pseudomonas* indicate forty seven (77%) of them were resistant to nalidixic acid and ampicillin, forty four (72%) to Tetracycline, forty one (67%) to chloramphenicol, thirty seven (61%) to amoxicillin, thirty two (52%) to erythromycin, seventeen (28%) to ceftriaxone and Piperacillin, forteen (23%) to Imipenem, ten (16%) to amikacin, while they showed the least resistance three (5%) to ciprofloxacin, gentamicin and ticarcillin.

Conclusion: The information obtained from the current research showed the resistance among the various species of *Pseudomonas* and diverse strains of a species is different. Therefore, to be able to treat the infections originating from *Pseudomonas* correctly, it is required to test the drugs resistance model and then prescribe drugs for it.

Department of Microbiology, Tonekabon branch, Islamic Azad University, Tonekabon, Iran

Keywords: Nosocomial infections, *Pseudomonas*, Antibiotic Resistance

Frequency of the Resistance Genes against Aminoglycoside and Extended Spectrum Beta Lactamase (ESBL) in the *Pseudomonas Aeruginosa*

Mozghan Pourjafari[1], Masood Ghane[2], Shohre Shargh[3], Reza Golijani Moghadam[2], Zahra Azimi[1], Hoda Ghafarai[1]

Abstract

Background: *Pseudomonas aeruginosa* is a common hospitalized pathogen. Resistance of this bacterium against different antibiotics has been reported from the various regions. The objective of this study is to determine the antibiotic susceptibility of *Pseudomonas aeruginosa* strains isolated from the various wards of the hospital and the presence of the bla$_{oxa-50}$, bla$_{oxa-2}$, pstS, aadA, aadE genes.

Methods: In this study, 35 strains of *Pseudomonas Aeruginosa* were collected from different wards of Shahid Rejaei hospital of Tonekabon within 2011-2012. In order to determine the resistance of strains, antibiogram test was carried out by the method of the disk diffusion. In order to the presence of the studied genes, the Specific primers were used and the PCR technique was applied to Amplification the above genes.

Results: the results obtained for antibiotics susceptibility of *Pseudomonas Aeruginosa* isolated from hospital samples by disk diffusion method indicated that all strains were resistant to cephalexin, cephalotine, ampiciline, penicilin, amoxicilin and co-amoxycelav. Also, they showed different levels of resistant to other antibiotics including 85.7% to neomycine, 42.8% to toberamycin, 28.5% to cephteriaxon, 20% to cephtazidium and 2.8% to imipenem. All *Pseudomonas aeruginosa* isolates were sensitive 100% to ciprofloxacin, 97.2% to Gentamicin, and 94.3% to amicacin. Of total 35 studied strains, Psts, bloa oxa 50 and addE genes was observed in 35 (100%), 34 (97.1%) and 33 (94.2%) strains, respectively. Also, the aadA and bla $_{oxa-2}$ genes were not identified in none of the isolated strains.

Conclusion: With regard to the high percentage of the resistance of isolated *Pseudomonas aeroginosa* to the antibiotics of the group of the Aminoglycoside and extended spectrum beta lactamase, the accurate performance of the anti-biogram tests before the prescription of the antibiotic in the treatment of the infections resulted from these bacteria is an unavoidable necessity.

Keywords: *Pseudomonas Aeruginosa*, antibiotics Resistance, aminoglycoside, ESBL

[1]Master of Sciences, Department of Microbiology, Islamic Azad University Tonekabon Branch, Tonekabon, Iran
[2]Assistant Professor, Department of Microbiology, Islamic Azad University, Tonekabon branch, Tonekabon, Iran
[3]Assistant Professor, Department of medicine, Islamic Azad University, Challus branch, Challus, Iran

Comparison of Culture and PCR Method in Identification of *Campylobacter Coli* in Patients with Diarrhea

Mohammad Hassan Shirazi[1], Ziba Vaise Malekshahi[2], Sara Hajikhani[1]

Abstract

Background: Campylobacter is a gram-negative, spiral and microaerophilic bacterium which is a common cause of diarrhea in human acute disease. The aim of this study was to identify campylobacter infection in the patients with diarrhea through culturing and PCR method.

Methods: Stool samples from 70 patients with diarrhea were collected and dissolved in 500µl PBS and 100µl added to Preston medium was incubated overnight under microaerophilic environment at 42 °C. Then 100µl of samples were cultured in blood free campylobacter agar base medium and were incubated at 42°C under microaerophilic conditions for 48h. *C. coli* colonies were tested for biochemical characters, Gram staining, oxidase, catalase. DNA was extracted from pure bacterial cultures. The asp genes were used for identification of C. coli. Genes amplified by PCR.

Results: *C. coli* was isolated from stool samples of 12 patients by PCR (17.14%) and 4 patients by culture (5.71%).

Conclusion: The findings suggest that PCR is a rapid diagnostic tool for detecting *C. coli* infection in diarrhea patients.

Keywords: *Campylobacter coli*, culture, PCR

[1]Department of Microbiology, Faculty of health science, Tehran Medical University, Tehran, Iran
[2]Microbial Biotechnology, Shahed University, Tehran, Iran

Detection of Mutations in gyrA and katG Genes for Identification of PGG in Mycobacterium Tuberculosis Isolates in Markazi Providence

Arezoo Eshghinejad Fard[1], Mana Shojapoor[2], Azam Ahmadi[3], Mohammad Arjomandzadegan[3]

Abstract

Background: Grouping of *M. tuberculosis* isolates were assigned to one of three genotypic groups (PGGs) based on the combinations of mutations at codon 463 of katG and gyrA codon 95. Determination of strains belonging to these groups and its early detection is epidemiologically very important. This study was planned to identify principle genetic groups of clinical isolates of *M. tuberculosis*.

Methods: Thirty-tree sputum samples were collected from tuberculosis patients of the Markazi province. DNA purification from isolates was performed by using Chelex 100. The mutation in katG463 was identified by RFLP using HpaII restriction enzyme (restriction site CCGG). 194bp of gyrA gene purified from PCR product was sequenced.

Results: PCR-RFLP and digestion of 620-bp fragment in different samples showed various patterns determining the type of the mutation in katG463 in the samples. Results of sequencing codon gyrA95 in combination by results of PCR-RFLP determined type of the principle genetic group (PGG). Therefore it showed that among the 33 *Mycobacterium tuberculosis* isolates 12 samples showed PGG 1, 15 Samples showed PGG2 and 6 samples showed PGG 3. Results revealed that PGG 2 was dominant form in *M. tuberculosis* strains of Markazi Provinces by frequency of 45.5%.

Conclusion: As the results it was revealed more frequent of PGG2 occurrence among clinical strains of the Markazi provinces. Considering susceptibility of these strains to available antibiotics, this subject is noteworthy. In this work, were presented three applicable benefits from the test as: PGG typing and bacterial resistance to Isoniazid.

Keywords: *Mycobacterium Tuberculosis*, Principal Genetic Groups, gyrA, katG

[1] Department of Microbiology, Islamic Azad University, Qom Branch, Qom, Iran
[2] Research Center of Molecular Medicine, Arak University of Medical Sciences, Arak, Iran
[3] Tuberculosis and Pediatric Infectious Research Center, Arak University of Medical Sciences, Arak, Iran

The Prevalence of MRSA and MSSA Isolates and Their Antibiotic Profiles in Shiraz Teaching Hospitals

Hossein Khoshkharam Roodmajani[1], Mohammad Motamedifar[1,2], Ali Nazarialam[1], Abdollah Bazargani[1]

[1]Bacteriology and Virology group, Faculty of Medicine, Shiraz University of Medical Sciences, Shiraz, Iran
[2]Shiraz AIDS Research Center, Shiraz University of Medical Sciences, Shiraz, Iran

Abstract

Background: *Staphylococcus aureus* is the major cause of nosocomial and community acquired infections. They are transmitted easily among patients and visitors in the hospitals. Drug resistant strains are arising rapidly and thus making the treatment of infections difficult. Methicillin Resistant *Staphylococcus aureus* (MRSA) is one of the leading cause of increasing morbidity and mortality and their identification in the infected subjects is very crucial in controlling their spread and transmission.

Methods: From August 2011 to July 2012, 262 samples were collected from different clinical specimens such as sputum, wound and blood from three major teaching hospitals in Shiraz, Iran. *Staphylococcus aureus* isolates were identified by morphologic property and biochemical tests. Disk diffusion test according CLSI guideline performed to distinguish MRSA and MSSA and to detect antibiotic susceptibility to some other antibiotics.

Result: Out of 227 *Staphylococcus aureus* isolates, the percentages of MRSA and MSSA were 48. 5% and 51.1%. Antibiotic resistance to vancomycin, linezolid, gentamycin and chloramphenicol were 4.0 %, 1.3%, 40.1% and 2.2% respectively.

Conclusion: This study indicated increasing prevalence of MRSA in teaching hospitals in Shiraz. It necessitates considering Infection control strategies and additional measures to prevent the spread of MRSA bacteria especially in the hospitals.

Keywords: *Staphylococcus aureus*, MRSA, MSSA, nosocomial infections

Study of Antibacterial Effects of a New Synthetic Substance 1,1≠ - (Ethane-1, 2-diyl) Dipyridinium Dichromate(VI) Using Microplate Method

Mansour Mashreghi[1, 2], Mostafa Gholizadeh[3], Pardis Haghighi[1], Bita Khadivjam[1]

[1]Department of Biology, Faculty of Sciences, Ferdowsi University of Mashhad, Mashhad, Iran
[2]Cell and Molecular Research Group, Institute of Biotechnology, Ferdowsi University of Mashhad, Mashhad, Iran
[3]Department of Chemistry, Faculty of Sciences, Ferdowsi University of Mashhad, Mashhad, Iran

Abstract

Background: The resistance of bacteria to current medicine and emergence of new bacterial diseases urges us to synthesis new drugs. The anti-bacterial features of pyridinium compounds are proven and in this study a new derivative of compound, called 1, 1 -(Ethane-1,2-diyl) dipyridiniumdichromate (VI), is synthesized and its anti-bacterial feature has been tested on some standard bacteria using microplate method.

Methods: Above mentioned compound was dissolved in Muller-Hinton Broth medium and was diluted to a certain amount. Certain amounts of that compound and the bacteria were added to microplate wells and after seventeen hours of incubation in a temperature of 37 degrees, the Minimum Inhibitory Concentration (MIC) was measured using ELISA Reader device and the Minimum Bactericidal Concentration (MBC) was determined using microcolony assay on agar medium.

Results: The results revealed that the growth of gram negative bacteria *Pseudomonas Aeruginosa* and *Escherichia coli* is inhibited in 750 µg/ml density; whereas, for *Staphylococcus aureus* 1500 µg/ml density was inhibitory. Also MBC was matched with MIC.

Conclusion: The new synthesized compound has antimicrobial effect on both gram positive and gram negative bacteria, however, the gram negative bacteria were more sensitive than gram positive.

Keywords: Anti-bacterial features, pyridinium compounds, microplate method

Study of ethA Gene Sequence in Ethionamide Resistant Clinical Isolates of *Mycobacterium Tuberculosis*

Somayeh Moazami Gudarzi[1], Azam Ahmady[2], Mana Shojapour[3], Mohammad Arjomandzadegan[2]

[1] Department of Microbiology, Islamic Azad University of Arak Science and Research Branch, Arak, Iran
[2]Tuberculosis and Pediatric Infectious Diseases Research Center, Arak University of Medical Sciences, Arak, Iran
[3]Research Center of Molecular Medicine, Arak University of Medical Sciences, Arak, Iran

Abstract

Background: Ethionamide (ETH) is one of the second line anti-tuberculosis drugs. In this study resistance to Ethionamide in clinical isolates of *M. tuberculosis* (MTB) by a molecular method was determined.

Methods: Thirty eight MTB isolates were entered in the study. With attendance to the length of the gene to do the sequencing, three fragments from the exclusive primers collection of ETHA1, ETHA5, ETHA4, ETHA9, ETHA8, ETHA10, which are overlapped with each other, have been employed; then PCR reaction was executed. PCR products were sent to Source Bioscience Company for sequencing.

Results: Out of thirty eight isolates, twenty eight isolates were resistant to Ethionamide and 10 were pan-susceptible to drugs. Results of electrophoresis determined suitable selection of primers. Results of DNA sequencing revealed mutations in different points of the gene in the resistant isolates, while there were no any mutations in susceptible isolates to ETH.

Conclusion: According to the obtained results, it was determined that mutation in the each point of ethA gene can cause resistance to Ethionamide; therefore quick detection of resistance is possible only by complete sequencing of the gene.

Keywords: *Mycobacterium tuberculosis*, drug resistant, Ethionamide, sequence

The Effective Combination of *Lactobacilluse casei* and *Saccharomyces boulardii* in Treatment of Experimental Colitis

Sara Solki[1], Tina Didari [1], Mohammad Abdollahi[1,2]

Abstract

Background: Inflammatory bowel disease (IBD), severe form of intestinal inflammation, involves a deregulated host-microbiala interaction. Recently, probiotic therapies have been concerned to restore balance to the gastrointestinal microbiota and reduce intestinal inflammation in IBD. A number of different studies have shown the anti-inflammatory effects of the nonpathogenic yeast probiotic *Saccharomyces boulardii*and gram positive probiotic bacteria *Lactobacillus casei* in IBD. Therefore, we employed both of them for synergetic effects.

Methods: Colitis was induced by 2,4,6 trinitrobenzen sulphonic acid (TNBS) in male wistar rats. Animal were divided into seven groups (6 rats in each group) including :normal (non-colitis),control(vehicle-treated),dexamethasone as standard, treatment groups (oral administration of 1×10^8 cfu *L. casei* and mixture of (*L. casei–S. boularbii* after TNBS-induced colitis) and prevention groups (oral administrations of 1×10^8 cfu L. casei and mixture of (*L. casei–S. boularbii* before TNBS-induced colitis).The period of treatment was 10 days, then animals were sacrificed and distal colon were removed and examined for inflammatory markers including tumor necrosis factor α (TNF-α) by ELISA, myeloproxidase (MPO)and lipid peroxidation (LPO)by TBARS assay method and histopathological scores.

Results: The results indicated that combination therapy of *L. casei-S. boulardii* in contrast to *L. casei* single therapy would show more improvement in colon histopathological scores, TNF α, MPO and LPO rates in treatment group however, probiotic combination did not show positive effect in prevention group.

Conclusion: In conclusion, the synergistic effects of combination of S. boulardii and *L. casei* demonstrated that mixture of these probiotics were significantly more effective than *L. casei* in treatment protocols of IBD.

Keywords: Inflammatory markers, Colitis, Probiotics

[1]Department of Microbiology, Pharmaceutical Sciences Branch, Islamic Azad University, Tehran, Iran
[2]Faculty of Pharmacy and Pharmaceutical Sciences Research Center, Tehran University of Medical Sciences, Tehran, Iran

Identification of Panton-Valentine Leukocidin (PVL) Genes in *Staphylococcus aureus* isolated from patients of Imam Reza and Shohada Hospitals of Tabriz by Real-Time PCR

Hamed Molla-abbaszadeh[1], Haideh Mobayen[2], Hamid Mirzaei[3]

[1] Department of Microbiology, Faculty of Basic and Medical Sciences, Islamic Azad University, Zanjan Branch, Zanjan, Iran
[2]Department of Microbiology, Faculty of Medicine, Islamic Azad University, Tabriz Branch, Tabriz, Iran
[2]Department of Microbiology, Faculty of Veterinary, Islamic Azad University, Tabriz Branch, Tabriz, Iran

Abstract

Background: *Staphylococcus aureus* could produce different toxins such as alpha, beta, and gamma-toxins and leukocidin Penton - Valentine. Leukocidin (PVL) is a cellular toxin which acts against polymorphonuclear cells, monocytes, and macrophages and causes an increase in cellular membrane permeability and leukocytes lysis and tissue necrosis. This study intends to determine the prevalence of PVL positive strains of *Staphylococcus aureus* by Real-Time PCR method.

Methods: This descriptive study was done during the last 6 months of the 2011.47 *Staphylococcus aureus* strains from the clinical samples of Imam Reza Hospital and 53 strains from Shohada Hospital were collected from Tabriz- Iran. Real-Time PCR method was done by using specific primers and probes.

Results: From 100 *Staphylococcus aureus* isolates,18 strains were PVL positive. Eleven strains belonged to Imam Reza Hospital and 7 strains to Shohada Hospital isolates.

Conclusion: By regard to producing PVL-toxins in *Staphylococcus aureus* strains accounts as a serious threat for human health. Therefore, rapid and accurate diagnosis of this gene in these bacteria is necessary. So, it seems that access a rapid and repeatable method will help in rapid diagnosis and timely control of PVL- producing strains in clinical centers.

Keywords: Panton-Valentine Leukocidin, *Staphylococcus aureus*, Real-Time PCR

Isolation of *Clostridium perfringens* from Stool Sample Human and Detection of A and C Toxin Encoding Gene by PCR

Ali Rezaeyan[1], Abasali Imani Fooladi*[1], Hamid Sedighian[1], Mohammad Javad Soltanpoor[1], Ahmad Reza Jabbary[2]

Abstract

Background: *Clostridium perfringens* is a Gram-positive, anaerobic; spore-forming that was found in soil and some materials. This bacterium is common between human and veterinary as an important pathogen in nature is known. This bacterium is often found in the intestines of animals and human. In certain circumstances, cause disease with Production of extracellular toxins and enzymes in many animals and human.

Clostridium perfringens based on their ability to produce four major toxins (alpha, beta, epsilon and beta) to five types (A-E) is classified which type A can only produce alpha toxin and type C can produce alpha and beta toxins.

Methods: Type A and C these bacteria found in human. Recognition of A and C toxins encoding gene by uniplex and multiplex PCR have been done. In the present study, for the first time in Iran, we collected one hundred twenty samples isolates from human Random people who referred to the laboratory. For the culture Bacterial was used specific medium TSC agar in anaerobic condition. Two pair primers were designed for Cpa and Cpb genes, DNA extraction was performed then by uniplex and multiplex PCR tests alpha and beta toxins were identified.

Results: From one hundred twenty stool samples have studied, twenty five *Clostridium perfringens* strains isolated that from them twenty strains having alpha toxin gene and five strain having alpha and beta toxin gene.

Conclusion: The diversity of the *C. perfringens* toxinotypes probably results from the localization of the toxin genes on mobile elements or on variable regions of the chromosome. In summary, PCR provides a simple and rapid assay for detection of *C. perfringens*. It should be immediately useful in epidemiologic and diagnostic studies. So, regard to resulting of this research, method of isolation and molecular diagnostic can be used routine in clinical laboratory.

Keywords: *Clostridium perfringens*, Cpa, Cpb, PCR

[1] Applied Microbiology Research Center, Baqiyatallah University of Medical Sciences, Tehran, Iran
[2]Department of anaerobic bacterial vaccine research and Razi Vaccine and serum research Institute, Karaj, Iran

Interferon-γ Gene Polymorphisms (A+2109G) and Susceptibility to Pulmonary Tuberculosis

Mona Afraei Karahrudie[1], Parisa Farnia[2], Fateme Sheikolslami[3], Mehdi Kazempoor[4], Mohammad Reza Masjedi[5], Aliakbar Velayati[6]

[1]Mycobacteriology Research Center, National Research Institute of Tuberculosis and Lung Disease, Masih Daneshvari Hospital, Shahid Beheshti University of Medical Sciences, Tehran, Iran
[2]Mycobacteriology Research Center, National Research Institute of Tuberculosis and Lung Disease, Masih Daneshvari Hospital, Shahid Beheshti University of Medical Sciences, Tehran, Iran
[3]Mycobacteriology Research Center, National Research Institute of Tuberculosis and Lung Disease, Masih Daneshvari Hospital, Shahid Beheshti University of Medical Sciences, Tehran, Iran
[4]Mycobacteriology Research Center, National Research Institute of Tuberculosis and Lung Disease, Masih Daneshvari Hospital, Shahid Beheshti University of Medical Sciences, Tehran, Iran
[5]School of Medicine and Researcher of National Research Institute of Tuberculosis and Lung Disease, Shahid Beheshti University of Medical Sciences, Tehran, Iran
[6]School of Medicine and Researcher of National Research Institute of Tuberculosis and Lung Disease, Shahid Beheshti University of Medical Sciences, Tehran, Iran

Abstract

Background: Susceptibility to infectious diseases is influenced by genetic background and efficient cellular immune activation is responsible for protection. In tuberculosis (TB), interferon-gamma is crucial to control intracellular growth of *Mycobacterium tuberculosis* . The generally the local and systemic IFN-γ levels correlate with the severity of disease. Recent studies showed that IFN-γ play a central role in regulating the type and level of immune response in mycobacterial infections. Mutations in this gene may associate with susceptibility to pulmonary TB. The aim of this study was to investigate the frequency of IFN-γ (+2109), gene polymorphisms and its relation with susceptibility to the pulmonary TB.

Methods: Thirty patients with smear positive tuberculosis and 30 healthy controls with no history of TB were selected for these studies. Genotype of IFN-γ (+2109), was performed using PCR-RFLP method. The PCR-products were analyzed using FauI restriction enzyme. The results analyzed using SPSS and Hardy – Weinberg equilibrium method.

Results: The frequency of A/G at region+2109 in control and case groups was 16.7% and 40% respectively. Therefore the results of this study showed that a significant difference in IFN-γ (+2109) between the control and study groups ($P < 0.05$).

Conclusion: Presence of mutation in region +2109 of IFN-γ may increase the host susceptibility to *Mycobacterium tuberculosis* and genotyping of these regions can be used for screening of the high risk factor.

Keywords: Polymorphism, Pulmonary Tuberculosis, IFN-γ

Emergence of Imipenem Resistant Species of *Acinetobacter*, *Klebsiella*, and *Pseudomonas* among Six ICUs in Tehran, Iran

Maryam Razaghi, Elahe Tajeddin, Sima Sadat Seyedjavadi, Marjan Rashidan, Somayeh Jahani Sherafat, Ehsan Nazemalhosseini, Masoud Alebouyeh, Mohammadreza Zali

Gastroenterology and Liver Diseases Research Center, Shahid Beheshti University of Medical science, Tehran, Iran

Abstract

Background: During the last decade, carbapanem resistance has emerged among clinical isolates of the *Enterobacteriaceae* family, and this is increasingly attributed to the production of the β-lactamases capable of hydrolyzing carbapenems. The aim of this study is to investigate frequency of carbapenemes resistant gram-negative bacterial isolates among six ICU as a survey analysis.

Methods: Bacterial isolates were obtained from clinical (including, tracheal aspirate, urine, blood and wound swabs) and environmental sample from six ICUs in Tehran. Culture on selective media and biochemical identification tests were done according to standard Methods. The antibiotic susceptibility testing for 13 antibiotics was done by disk diffusion method according to the standard criteria for CLSI.

Results: Eight hundred thirty four different samples from clinical (27.45%) and environmental (72.54%) were collected from six ICUs in Tehran. Most frequent bacteria for clinical and environmental samples were related to *Acinetobacter* (33.2%/16.5%), *Klebsiella* sp (10.9%/1.8%), *Pseudomonas* (14.4%/1%), respectively. The results of the antimicrobial susceptibility testing indicated that, among one hundred sixty seven *Acinetobacter* sp. isolates, 92.3%, forty six *Pseudomonas* sp. isolates 54%, 33 *Klebsiella* sp. isolates 63.15% were imipenem resistant. Among these isolates 73.7% of *Klebsiella* sp., 90% of *Acinetobacter* sp. and 76% of *Pseudomonas* sp. also showed resistance phenotypes against members of Cephalosporin III, and IV families of antibiotics.

Conclusion: High frequency of imipenem resistant species of the analyzed bacteria in the studied ICUs has cleared emergence of new therapeutic challenge for treating their infections. Homology of resistance patterns between the clinical and environmental isolates also proposed their probable roles in nosocomial infections and importance of serious health care attentions at these units.

Keywords: Carbopenemase, Gram-negative bacteria, Nosocomial Infection

Unnecessary Antibiotic Therapy in Children with Diarrhea May Cause Antibiotic Resistance

Ali Khakhshour[1], Seyed Hamid Hosseini[1], Hamid Reza Kianifar[2], Seyed Ali Jafari[4], Mohammad Ali Kiani[5], Zhila Shaikhi[6]

[1]Assistant Professor of Pediatrics, North Khorasan University of Medical Sciences, Bojnurd, Iran
[2] North Khorasan University of Medical Sciences, Bojnurd, Iran
[3]Assistant Professor of Pediatrics, Mashhad University of Medical Sciences, Mashhad, Iran
[4]Assistant Professor of Pediatrics, Mashhad University of Medical Sciences, Mashhad, Iran
[5]Assistant Professor of Pediatrics, Mashhad University of Medical Sciences, Mashhad, Iran Iran
[6] Urologist, North Khorasan University of Medical Sciences, Bojnurd, Iran

Abstract

Background: Antibiotic resistance is rapidly increasing in both developed and developing countries. Diarrheal disease is a leading cause of morbidity and mortality in children that treats with antibiotics. This study was conducted to evaluate correct prescription of antibiotics in children less than five years old in hospitalized for diarrhea at Imam Reza hospital in Bojnord 1389.

Methods: A total of 292 children, aged less than five years old with diarrhea were recruited in this one group cross-sectional study. Sampling design was non-random, purposeful sampling. The clinical history, socio-demographic characteristics, physical examination findings and laboratory finding were recorded in tree questionnaires. All data were analyzed by t-test, one-way ANOVAs, chi-square and correlation using SPSS 11.

Results: 53% children were male. 73% patients had vomiting and fever.42% had abdominal pain and 24% had dehydration. Antibiotics were prescribed for 79% of patients; 70 % prescribed on antibiotics was incorrect. There was a significant relation between negative stool exam and misuse of antibiotics ($P < .05$). Kappa agreement coefficient was 0.125 that means invert relation.

Conclusion: prescription of antibiotics must be according stool culture and diagnostic tests. Most attention should be paid to common viral diarrhea in hospitalized children to prevent antibiotics resistance.

Keywords: Antibiotic resistance, Children, Diarrhea

Multidrug-Resistant *Acinetobacter* Infection in Mashhad Ghaem Hospital

Hadi Safdari

Department of Microbiology and Virology, Ghaem Hospital, Mashhad University of Medical Sciences

Abstract

Background: *Acinetobacter* infections have increased and gained attention because of the organism's prolonged environmental survival and propensity to develop antimicrobial drug resistance. Patient with multidrug-resistant (MDR) Reports isolates have increased during last decade. The aim of this study was an investigation Resistance *Acinetobacter* infection in Ghaem University Hospital, Mashhad during March 2011 to April 2012 to a few antibiotics.

Methods: Universal active surveillance cultures from the urine, wounds, endotracheal tube aspiration and sputum were performed on admission and weekly among a cohort of 4521 patients admitted to medical intensive and intermediate care units of the Ghaem Hospital.

Patients with NAUTI were identified. All culture-proven and microbiological cultures were analyzed which 102 *Acinetobacter* isolated. antibiotic susceptibility of isolates against *Acinetobacter* with different antimicrobials agents was determined on Mueller Hinton agar by the standard disc diffusion according to Clinical and Laboratory Standards Institute antimicrobial susceptibility (CLSI) , Antibiotic susceptibility was determined for *Acinetobacter* the following antibiotics: Gentamycin, tobramycin , amikacin, imipenem, cefazolin,

Results: From4521 samples cultured 102 (2.26%) strains of *Acinetobacter* baumannii were isolated among 102 *Acinetobacter*, gentamycin 19%, tobramycin 57%, imipenem 66.5 %, amikacin 60%, cefazolin 88% were Resistance.

Keywords: *Acinetobacter*, resistance, infection

Diagnosis of Ciprofloxacin and Novobiocin Resistance in *Mycobacterium* with Single Strand Conformation Polymorphism (SSCP)

Kimia Taghavi, Parisa Farnia, Fateme Sheikolslami, Mehdi Kazempoor, Mohammadreza Masjedi, Aliakbar Velayati

Mycobacteriology Research Center, NRITLD, Masih Daneshvari Hospital, Shahid Beheshti University of Medical Sciences, Tehran, Iran

Abstract

Background: The most frequent mutations associated with ciprofloxacin and novobiocin resistance in *Mycobacterium* arises from gyrA and gyrB which encode A and B subunits of DNA gyrase. The purpose of this survey was to rapid and accurate diagnosis of OFX and NOV resistance associated mutations.

Methods: In order to identify mutations in gyrA and gyrB genes clinical isolates were collected from patients attending in Mycobacteriology Research center in Tehran. 97 multi drug resistants (MDR) *Mycobacterium tuberculosis* were diagnosed. The Quinolone resistance determining regions (QRDR) of gyrA and gyrB in all 97 isolates were amplified using polymerase chain reaction and analyzed using Single Strand Conformation Polymorphism method (SSCP) method.

Results: Our results revealed that out of 97 available isolates, 91 (93.8%) were susceptible to ciprofloxacin and 6 (6.2%) were resistance. In analyzing SSCP patterns 5 different sensitive patterns and 2 different resistant patterns were seen. In testing gyrB region all isolates were susceptible to novobiocin and 2 different patterns were existed which one belonged to resistant isolates and the other to susceptible isolates.

Conclusion: SSCP is a rapid, efficient and non-radioactive method for routine detection of Fluoroquinolone resistance in *Mycobacterium tuberculosis*.

Keywords: Single Strand Conformation Polymorphism (SSCP), Ofloxacin, gyrA, gyrB

Multidrug-Resistant Tuberculosis in Foreigner Patients in Tabriz

Seyed Reza Moaddab[1], Jalil Rashedi[2], Ahad Zarei[2], Nahid Shirzad[2], Rozita Azimi[2]

[1]Research Centre for TB and Pulmonary Diseases, Paramedical Faculty, Tabriz University of Medical Sciences, Tabriz, Iran
[2] Research Centre for TB and Pulmonary Diseases, Tabriz University of Medical Sciences, Tabriz, Iran

Abstract

Background: Drug-resistant tuberculosis (TB) has raised public health concern about the global control of TB. The World Health Organization estimated that 0.5 million cases of multidrug-resistant TB (MDR TB: *Mycobacterium tuberculosis* resistant to two of the most potent TB drugs, rifampin and isoniazid) occurred in last year. Some countries have high rates of this MDR TB like Azerbaychan but the problem is universal, and the extent varies from a country to another one.

Methods: A total two hundred fifty six isolates were collected from the same number of foreigner (mostly from Azerbaychan) TB patients between 2007 -2012. Susceptibility of drug tests was done by using of Lowenstein Jansen and proportional procedure.

Results: Out of two hundred fifty six pulmonary TB patients 43% had MDR TB. MDR TB among Iranian patients in East Azerbaychan province in Iran is lower than 2%.

Conclusion: For prevention of spreading of MDR TB from foreigners to our country specially from countries like Azerbaychan which have extraordinarily high rates of MDR TB, at least traveling of MDR TB patients should be limited.

Keywords: Tuberculosis, MDR TB, foreigners' patients

Detection of *Mycobacterium tuberculosis* from Sputum Specimens by PCR and Culture

Reza Moaddab[1], Abdolnaser Rafi[2], Mohammad HoseinSoroush[3]

[1]Tuberculosis and Lung Research Center, Department of Laboratory Sciences, Paramedical Faculty, Tabriz, Iran
[2]Paramedical Faculty, Department of Laboratory sciences, Tabriz, Iran.
[3]Department of Microbiology, Medicine Faculty, Tabriz University of Medical Sciences, Tabriz, Iran

Abstract

Background: Tuberculosis (TB) remains the most serious infectious diseases and a global health problem. Early diagnosis of TB is essential to effectively treatment. The aim of this study was to compare of culture with PCR for detection of *M. tuberculosis* in sputum samples among TB suspect's patients.

Methods: In this investigation, one hundred and ten sputum samples (from the same number of patients) were decontaminated, concentrated and inoculated on Lowenstein Jensen (LJ) medium. These 110 concentrated specimens were used to PCR. Genomic DNA was extracted from concentrated samples using conventional method. The primers which used to amplify were; 5´-CCTGCGAGCGTACGCGTCGG-3´and5´- CTCGTCCAGCGCCGCTTCGG-3´. An agarose 1% gel was used for detecting of amplifications products.

Results: A total of eighteen samples demonstrated 100% concordance between culture and PCR. Two specimens were PCR positive but culture negative. Only one sample was PCR negative but culture positive. The remaining 89 specimens were PCR and culture negative.

Conclusion: PCR detected *M. tuberculosis* in 2% of culture negative TB suspected patients. Thus, this investigation has shown that PCR can be increased the diagnosis of TB from clinical specimens when used along routine culture techniques.

Keywords: *Mycobacterium tuberculosis*, PCR, Culture

Characterization of Different Species of *Clostridium Botulinum* with a Focus on Type B Toxin Gene: An In-Vitro Model

MaryamMontaseri[1], Saied Hosseinzadeh[1], Negar Panahi[2], Jafar Jalaei[3]

[1]Department of Food Hygiene, School of Veterinary Medicine, Shiraz University, Iran
[2]Islamic Azad University, Science and Research Branch, Tehran, Iran
[3]Department of Basic Science, School of Veterinary Medicine, Shiraz University, Iran

Abstract

Background: The principal pathogenic serotypes of *C. botulinum* in man are A, B and E. The toxin is a 150 kDa protein. Molecular based techniques have recently employed for the rapid and reliable identification of the MO and its toxins. Here, we have focused on the amplification of type B toxin in order to advice a new generation of botulinum toxin in an in-vitro model.

Methods: Three Lab techniques including biochemical, and mPCR were used to detect *C. botulinum* in an in-vitro model. Three pairs of primers were designed and optimized to amplify A, B and E strains in the contaminated specimens and to detect the type B toxin.

Results and Conclusion: The PCR was able to amplify 782, 205 and 389 bp genes specified for A, B and E types of the MO, respectively. At the same time, a 1280 bp type B toxin was also characterized. As a final conclusion, the molecular based techniques are currently advised to detect *C. botulinum*, its toxins and spores and could be strongly recommend to use in Food microbial Lab.

Keywords: *Clostridium botulinum*, mPCR, Biotypes, Biochemical assay, Type B toxin, In-vitro

Immunity Level to *Haemophilus Influenzae* in Beta-thalassemia Splenectomized Children

Abdolreza Sotoodeh Jahromi,
Karamatollah Rahmanian

Abstract

Background: Patients with thalassemia and asplenia are at increased risk for infection. The aim of this study was to determine the *Haemophilus influenza* type b (Hib) antibody concentration among beta thalassemic patients with and without spleen.

Methods: The Hib antibody concentration was investigated in 87 patients with thalassemia, 50 of who had undergone splenectomy. Hib antibody was determined by an ELISA kit (IBL, Germany). Subjects who had Hib antibody level ≥1.0 µg/ml as long term protection, between 0.15 to <1.0 µg/ml as short term protection and <0.15 µg/ml as no protection. Also patients with Hib antibody concentration ≥0.15 µg/ml classified as protective and who had antibody level <0.15 µg/ml as non-protective. For the analysis we used SPSS 11.5 software. A two sided p-value less 0.05 was considered statistically significant.

Results: 83.8% (31) of non-splenectomized patients had protective antibody levels against Hib whereas among asplenic patients this rate was 32.0% (16) that there was significant differences (p<0.001). Protection against Hib decreased with increase interval time after splenectomy from 64.7% in ≤60 months interval to 5.3% in >120 months interval (p=0.001). Thirty percent of the 50 splenectomized subjects had long term protection against *Haemophilus influenza* type b where as 62.2 percent of 37 subjects with spleen had long term protection (p<0.001).

Conclusion: Patients with splenectomy lower Hib antibody level than cases with spleen. Also antibody level decreased with time interval after splenectomy. Thus the vaccine recommendation seems essential for beta thalassemic splenectomized patients for increased serum Hib antibody concentration.

Department of Microbiology, Jahrom University of Medical Sciences

Keywords: *Hemophilus Influenza*, splenectomy, children, immunity

Determination of the Rate of Resistance to Quinolones and Incidence of qnrA, qnrB, qnrS Genes among ESBL Producing Uropathogenic *Escherichia coli* Strains Isolated from UTI in Children

Mohammad Yousef Alikhani[1], Iraj Sadighi[2], Fatemeh Mahini[1], Ali Rahimbakhsh[1]

Abstract

Background: Urinary tract infections (UTIs) is one of the most common bacterial infections of childhood, and *Escherichia coli* is the predominant pathogen of UTI. Extensive use of quinolone in treatment of UTI has been associated with raising level of resistance. Quinolone resistance mostly originates from chromosomal mutations. In recent years, however, plasmid-mediated quinolone resistance has been reported in several parts of the world. Plasmid borne qnrA, qnrB, or qnrS genes are responsible for this kind of resistance. In the current, we focused on assessing the prevalence of Uropathogenic *Escherichia coli* resistance to quinolone and frequency of qnrA, qnrB and qnrS in ESBLs (extended spectrum beta-lactamases) producing Uropathogenic *E. coli* clinical Isolates of Urinary Tract Infections In children.

Methods: One hundred and twenty Uropathogenic *E. coli* isolates were identified during Sep 2009 to Aug 2010 in Hamedan's Besat hospital. Identity of isolates confirmed by standard biochemical Methods .Quinolone susceptibility was determined by the disk diffusion agar method and ESBLs production was confirmed phenotypically by the combined-disk synergy test. Multiplex PCR was performed for detection of qnrA, qnrB and qnrS genes.

Result: Of 120 isolates, thirty-three (27.3%) ESBLs producing and eighty seven (71.9%) non-ESBLs producing *E. coli* were identified. 42.4% (n= 14) of producing ESBLs *E. coli* and 12.6% (n= 11) of non-ESBLs *E. coli* were resistance to ciprofloxacin (5µg). 18.2% (n= 6) and 12.1% (n= 4) of ESBLs producing *E. coli* were positive for qnrB and qnrS respectively. qnrA was not identified in any isolate.

Conclusion: Our study showed high frequency of ESBLs producing *E. coli* as well as quinolone resistance genes (qnrB, qnrS) in our area.

Keywords: *E. coli*, Quinolone, ESBL, UTI, Resistance, Multiplex PCR

[1] Department of Microbiology, School of Medicine, Hamadan University of Medical Sciences, Hamadan, Iran
[2] Department of Pediatrics, School of Medicine, Hamadan University of Medical Sciences, Hamadan, Iran

Effects of Antimicrobial and Antibiotics Resistant *Lactobacillus brevis* Isolated from Traditional Yogurt in Khorramabad

Javad Hajipour[1], Enayat ghahremani [2], Mahnaz mardani [3], Sadegh Rezapour [3]

Abstract

Background: Gram-positive rods are *Lactobacillus brevis* bacteria in dairy products that are homo fermentative done. This bacterium can produce bacteriocin against pathogenic bacteria and lower the amount of pathogenic bacteria in the body.

The purpose of this review is to survey the effects and antibiotic resistance of *Lactobacillus brevis*in dairy products (yogurt).

Methods: A total of eleven samples were collected from traditional yogurt in Khorramabad city. The desired bacteria identified using phenotypic Methods (cell morphology, Gram staining, physiological and biochemical tests) and bacteriocin was extracted.

Using the agar well, Extracted bacteriocin was examined on the pathogenic bacteria *Pseudomonas Aeruginosa*, *Proteus vulgaris*, *Staphylococcus aureus*, *E. coli*, *Bacillus cereus* and *Bacillus subtilis*. On the other hand antibiotic resistance of this bacterium was tested using Antibiogram method.

Results: The results showed that the bacteria *Pseudomonas Aeruginosa* and E. coli have intermediate sensitivity against bacteriocin, the bacteria *Proteus vulgaris* and *Staphylococcus aureus* were sensitive. *Bacillus cereus* and *Bacillus subtilis* were resistant. On the other hand, *Lactobacillus brevis* was resistant against kanamycin (30µg) trimethoprin (250 µg), intermediately sensitive against clindamycin (2µg) tetracycline (30µg) and sensitive against amoxicillin (10µg) and erythromycin (15µg).

Conclusion: *Lactobacillus brevis* has an inhibitory effect on bacterial pathogen and prevents the spread of infection in the body. These bacteria also have the appropriate antibiotic resistance against most antibiotics. Due to having these properties, dairy productions can be safely consumed.

Keywords: *Lactobacillus brevis*, antimicrobial effects, antibiotic resistance, bacteriocin

[1]Senior Student of Microbiology, Islamic Azad University branch Science Research markazi
[2]Senior Student of Microbiology, Islamic Azad University branch Science Research markazi
[3]Assistant Professor, Member of Medical Faculty, Lorestan University of Medical Sciences

Survey of Sensibility and Antimicrobial Resistance in *Escherichia coli* Isolated from Traditionally Made Ice Cream in Khoy

Kobra Eslami[1], Hamed Molla-Abbaszadeh[2], Masoud Mollazadeh[3], Nader Mohammadzadeh Gheshlaghi [2, 4]

[1]Department of Microbiology, Islamic Azad University, Lahijan Branch
[2]Department of Microbiology, Islamic Azad University, Zanjan Branch
[3]Department of Aerospace, Research Assistant, Army University of Medical Sciences, Tehran, Iran
[4]Central Laboratory of Eastern Azarbaijan Province, Tabriz, Iran

Abstract

Background: *Escherichia coli* bacteria are one of the most important intestinal pathogens which cause contagious diseases via food in humans. The object of this study is to examine the pattern of sensitivity and antibiotic resistance of *E. coli* derivations extracted from traditionally ice cream which is provided in Khoy city markets.

Methods: This survey was done in sections in first six months of the 2010 year, on 150 ice-creams collected from shops and bakery shops providing ice-cream in different parts of Khoy city and after detecting derivations of *E. coli*, using Kirby-Bauer test, their patterns of sensitivity and antibiotic resistance was determined.

Results: Forty seven strains of *E. coli* was extracted from traditionally ice cream and the results of antibiogram test indicated that highest levels of sensitivity reaction determined in following order in contact with ceftizoxim, ciprofloxacin, and ceftriaxone; the most of resistant in contact with amoxicilin, oxacilin, kanamycin.

Conclusion: Considering the high prevalence of resistance to antibiotics, rapid diagnose of resistant strains is necessary in order to select the best clinical choice and prevent their spread, also respecting the hygienic issues during the production and distribution of traditional ice cream along with knowledge augmentation of the consumers about unpasteurized products; it would be possible to reduce the number of patients affected with these infections.

Keywords: *E. coli*, traditionally made ice cream, antibiotic, Khoy

Detection of Plasmid-Mediated Quinolone Resistance Genes among Strains of *Escherchia coli* Isolated from Feces of Healthy and Diarrheic Calves

Zeinab Abiri[1], Mehrnaz Rad[2]

[1] Department of Pathobiology, School of Veterinary Medicine, Shahid Bahonar University of Kerman, Kerman, Iran
[2] Department of Pathobiology, School of Veterinary Medicine, Ferdowsi University of Mashhad, Mashhad, Iran

Abstract

Background: The animal reservoir of plasmid-mediated quinolone resistance (PMQR) is still controversial and little information is available on the prevalence of these resistance determinants in developing countries. The aim of this study was to identify PMQR in *Escherichia coli* strains isolated from feces of diarrheic and healthy calves.

Methods: In this study, one hundred strains including fifty strains of *Escherichia coli* isolated from feces of calves with diarrhea and fifty strains isolated from feces of healthy calves were examined. To determine the antimicrobial susceptibility of strains, Antibacterial susceptibility tests were conducted by a disk diffusion method, with two antibiotic disks, nalidixic acid and ciprofloxacin on Muler-Hinton agar. Resistance genes were screened by multiplex PCR and DNA sequencing.

Results: PMQR genes were detected in seven *E. coli* strains; three of them showed resistance to ciprofloxacin, and four of them were resistance to nalidixic acid. All seven strains carried qnrS. No qnrA and qnrB genes were detected among strains. All strains positive for the presence of qnr were isolated from feces of healthy calves.

Conclusions: Our findings suggest that the PMQR determinants were highly prevalent in normal flora and food animals could represent an important reservoir of PMQR. The importance of these genes are their ability to transfer and exchange among normal flora and pathogens.

Keywords: *Escherichia coli*, plasmid-mediated quinolone resistance, ciprofloxacin

The Survey of Common Bacteria and Antibiotic Resistance Determination in Urine Cultures of Patients Referred to Medical Diagnose Centers in the City of Mashhad, 2011-2012

Hasan Yazdanfar[1], Mohadeseh Khakpoor[1], Anis Iranmanesh[2]

Abstract

Background: Urinary tract infection (UTI) is a common infectious disease especially in women. Empiric therapy to treat UTI should be tailored to the surveillance data on the epidemiology and resistance patterns of common uropathogens to reduce treatment failures and emergence of bacterial resistance within the community.

Methods: This descriptive study was done on 1200 patients suspicious to UTI who referred to clinical laboratories in Mashhad, with 1390-1391. Urine sample was taken; cultured and antibiotic sensitivity pattern was assessed by Kirby – Bauer method. Demographic information of patients was also registered. Data was statistically analyzed by SPSS V.18.

Results: There were 74% women, and mean age of patients was 34.9±22.7 (±SD). Bacteriuria, Pyuria and hematuria were seen in 86.2%, 84.3% and 20.3% of patients respectively. *E. coli* (51.4%), *Klebsiella pneumonia* (9.2%) and Coagulase negative *Staphylococcus* (8.7%) were the most commonly grown pathogens. The difference between men and women considering the isolated microorganisms was statistically meaningful (p=0.001). Also the difference between age groups was significant considering pathogens (p=0.0001). Imipenem (86.7%), ceftizoxim (79%) and ciprofloxacin (75.5%) had the highest rate of sensitivity and penicillin (65.9%), tetracyclin (65.3%), Erythromycin (61.8%) had the highest rates of resistance.

Conclusion: *E. coli* remains the most common uropathogen. Antimicrobial therapy should be based on the results of urine culture and antimicrobial susceptibility test.

Keywords: Urine Tract Infection, Antimicrobial resistance pattern, sensitive

[1]Departement of Parasitology and Mycology, Faculty of Medicine, Islamic Azad University, Mashhad Branch, Mashhad, Iran
[2]Ferdowsi University of Mashhad, Mashhad, Iran

Incidence of Invasive Fungal Infections among Liver Transplant Recipients over a Period of Two Years in Shiraz, Southern Iran

Zahra Jafarpour[1], Parisa Badiee[1], Seyed Hosein Malekhosseini[2]

Abstract

Background: Invasive fungal infections after liver transplantation (LT) have resulted in high mortality and fatal complications. This study was undertaken to determine the incidence of such infections in LT recipients by real time PCR and routine Methods over two years in Nemazee Hospital.

Methods: Clinical samples were collected from the LT recipients with suspected fungal infections and examined by KOH, culture, real time PCR.

Results: From April 2010 to December 2011, 604 patients received LT at Namazi hospital, Shiraz, Iran. From the 212(35%) of suspicious patients; mean age 31.5 years, male/female ratio 126/86, the most common underlying diseases were autoimmune hepatitis, viral hepatitis, cryptogenic hepatitis, and Crigler Najjar. Three hundred fifty clinical samples of multiple sites (blood, abdomen, liver and …) were examined. According to the clinical signs and standard criteria, thirty seven samples (11.74%) revealed fungal infections consisting of 9 (2.85%) positive culture obtained with etiological agents including *Candida glabrata* (2 cases), *Aspergillus fumigatus* (2 cases), *Aspergillus Niger* (2 cases), *Mucur* (1 case), *Candida spp.* (2 cases). Also, 3(0.95%) positive KOH results were obtained including septated hyphae (2 cases) and yeast (1 case). By PCR, aspergillosis were diagnosed in 21(6.66%) and candidiasis in 4 (1.26%) recipients. The mean interval time between transplantation and the development of fungal infection was 54.2 days.

Conclusion: The clinical significance of fungal infections may be difficult to determine. Knowledge of incidence of such infections could be helpful to effective management and treatment of these conditions.

Keywords: Liver transplantation, KOH, culture, Real time PCR

[1] Prof. Alborzi Clinical Microbiology Research Center, Shiraz University of Medical Sciences, Shiraz, Iran
[2] Department of Organ Transplant Research Center, Shiraz University of Medical Sciences, Shiraz, Iran

Survey of Antibiotic Resistance Pattern of Isolated *Staphylococcus* Coagulase Negative Species from Patients with Bacteremia in Shahid Beheshti Hospital of Kashan

Mohadeseh Zarei[1], Mehrzad Erami[2], Hassan Kosha[3], Ali Mohammadi[3]

1Departmentof Microbiology, Faculty of Medicine, Shahid Sadoughi University of Medical Sciences, Yazd, Iran
[2] Master of Mycology, Shahid Beheshti Hospital, Kashan, Iran
[3] Laboratory Expert, Shahid Beheshti Hospital, Kashan, Iran

Abstract

Background: Among bacterial agents involved in bacteremia or septicemia, *Staphylococcus* Coagulase Negative has a high importance. Surviving on dry surfaces for long times, in addition to colonization on skin and nasopharynx facilitates the spreading of these bacteria. The main purpose of this study was detection of Antibiotic Resistance Pattern of Isolated *Staphylococcus* coagulase negative from patients with bacteremia in Shahid Beheshti Hospital of Kashan.

Methods: This descriptive research was carried out for all the requested blood culture samples by checklist in Shahid Beheshti Hospital of Kashan from April 2011 to March 2012.The patients' sex and antibiotic susceptibility of positive blood cultures was determined based on agar diffusion (Kirby-Bauer) method, collected from laboratory offices and then analyzed by SPSS 17 software.

Results: Forty three blood culture samples were positive. 38.3% of patients were female and 61.7% were male.
The percent of resistance of *Staphylococcus* Coagulase Negative to antibiotics were: penicillin 63.6%, cefepime 63.6%, coamoxiclav57.6%, erythromycin 54.5%, cefotaxime 33.3%, vancomycin 21.2%, clindamycin18.2%, methicillin18.2%, teicoplanin15.2%, meropenem9.1%.

Conclusions: *Staphylococcus* coagulases Negative were the most prevalent pathogen isolated from patients with bacteremia, and maximum susceptibility rate of isolated bacteria was observed for teicoplanin. However, in order to prevent the indiscriminate use of this antibiotic, routine antibiotic susceptibility test is also suggested.

Keywords: *Staphylococcus*, Bacteremia, Coagulase negative

Antibiotic Resistance and Antimicrobial Effects of *Enterococcus faecium* and *Lactococcus lactis* Isolated from Traditional Cheeses in Khorramabad

Enayat Ghahremani[1], Mahnaz Mardani[2], Samaneh Jahani[3]

Abstract

Background: Gram-positive cocci are *Enterococcus faecium* and *Lactococcus lactic* bacteria in dairy products that are homofermentative done. These bacteria can produce bacteriocin against pathogenic bacteria and lower the amount of pathogenic bacteria in the body.

The purpose of this review is to survey the effects and antibiotic resistance of *Enterococcus faecium* and *Lactococcus lactic* in dairy products (cheese).

Methods: A total of eleven samples were collected from traditional cheeses in Khorramabad city. The desired bacteria identified using phenotypic Methods (cell morphology, Gram staining, physiological and biochemical tests) and bacteriocin was extracted.

Using the agar well, Extracted bacteriocin was examined on the pathogenic bacteria *Pseudomonas Aeruginosa*, *Proteus vulgaris*, *Staphylococcus aureus*, *E. coli*, *Bacillus cereus* and *Bacillus subtilis*. On the other hand antibiotic resistances of this bacterium were tested using Antibiogram method.

Result: The results showed that the bacteria *Pseudomonas aeruginosa*, *Staphylococcus aureus*, and *E. coli* have intermediate sensitivity against bacteriocin. The bacteria *Proteus vulgaris* was sensitive. *Bacillus cereus* and *Bacillus subtilis* were resistant. On the other hand, *Enterococcus* faecium was resistant against antibiotics kanamycin (30µg) trimethoprin (250 µg), intermediate sensitive against clindamycin (2µg) tetracycline (30ug) and sensitive against amoxicillin (10µg) and erythromycin (15µg). Lactococcus lactis was sensitive against trimethoprin (250µg), Amoxicillin (10ug), tetracycline (30ug) erythromycin (15ug) and resistant against kanamycin (30µg) and clindamycin (2µg).

Conclusion: Both bacteria *Enterococcus faecium* and *Lactococcus lactis* have an inhibitory effect on pathogenic bacteria and prevent the spread of infection in the body. These bacteria also have the appropriate antibiotic resistance against most antibiotics. Due to having these properties, dairy productions can be safely consumed.

Keywords: *Enterococcus faecium*, *Lactococcus lactis*, antimicrobial effects, antibiotic resistance, bacteriocin

[1]Senior Student of Microbiology, Islamic Azad University, Sciences Branch, Research Center,
[2]Assistant Professor, Member of Medical Faculty, Lorestan University of Medical Sciences, Lorestan, Iran
3Senior Student of Microbiology, Islamic Azad University of Qom, Qom, Iran

Antimicrobial Resistance of *Pseudomonas aeruginosa* Isolated from Intensive Care Units of Isfahan Shariati Hospital

Leila Heidary, Naser Almasi, Hasan Ghajavand

Shariati Hospital of Isfahan, Isfahan, Iran

Abstract

Background: *Pseudomonas aeruginosa* is an opportunistic Gram-negative pathogen with increasing relevance in a variety of hospital-acquired infections especially among intensive care unit patients. *Pseudomonas aeruginosa* is mostly a cause of septicemia, pneumonia and urinary tract infection following hospitalization of patients with more severe illness. Multidrug-resistant isolates *Pseudomonas aeruginosa* have been reported increasingly during the last decade, probably as a consequence of extensive use of antimicrobial agents. The aim of this study was to determine antimicrobial resistance of *Pseudomonas aeruginosa* isolated from Intensive Care Units of Isfahan Shariati Hospital.

Methods: In a period of a year (2009-2010), 456 clinical samples from patients in ICUs were examined for isolation of *Pseudomonas aeruginosa*.

Results: A total of 100 *Pseudomonas aeruginosa* isolates cultured from urine, catheter wound, blood , and CSF. The antimicrobial patterns of isolates showed that 58% isolates were resistant to carbapenems (Imipenem and Meropenem), 70% to ceftazidim, 64% to amikacin, 72% to ciprofloxacin, 90% to trimetoprim sulfametoxazol and 54% were resistant to pipracilin-tazobactam. of isolates were resistant to two or more antibiotics.

Conclusion: This study showed high percentage of resistance to antimicrobial agents in *Pseudomonas aeruginosa* isolates, therefore strategies to control the spread of multidrug-resistant strains have to be designed and evaluated. In addition, new therapeutics regimes are clearly needed.

Keywords: *Pseudomonas Aeruginosa*, Antimicrobial drug resistance, Nosocomial infection

Study of Prevalence and Antimicrobial Susceptibility Pattern of *Streptococcus pyogenes* Isolated from Throat of Healthy Children in Tehran

Elnaz Parvizi[2], Gholamreza Irajian[1], Alireza Nateghian[3], Ali Ahmadi1[4], Kiana Mirsaeedi[1]

Abstract

Background: *Streptococcus pyogenes*is the major cause of pharyngitis and consequently Rheumatic fever.5-15% of healthy people are normal carriers of the organism. Erythromycin is recommended for allergic cases, although Penicillin is the first choice of drug. In recent years resistance to Erythromycin has been reported frequently. The aims of this study was to determine the prevalence and antibiotic susceptibility pattern of *Streptococcus pyogenes* isolated from throat of healthy children in Tehran.

Methods: Nasopharyngeal specimens were obtained by sterile cotton swab from throat of healthy children less than fifteen years old during six month. Samples were cultured immediately on 5%sheep blood agar plate, and after transferring to laboratory, incubated at 37 □ C in candle jar. *Streptococcus pyogenes* was identified by biochemical tests including hemolytic pattern, gram staining, and catalase, sensitivity to bacitracin and cotrimoxazole and PYR. Then Latex Agglutination Test was performed for confirmation. Susceptibility test was done for *Streptococcus pyogenes* positive cultures and, then Penicillin MIC was determined by the E-test method.

Results: Totally 609 throat swabs were collected during January to Jun 2012. Among them, 130 samples were obtained from females and the remnant from males. Finally 27(4.43%) *Streptococcus pyogenes* isolates were identified, two isolates (7.40%) from females and the remainder (92.59%) from males. All isolates were sensitive to penicillin, cefotaxim, erythromycin, and vancomycin. For tetracycline, 7.4% were resistant and 18.5% had intermediate susceptibility. Two isolates were resistant and intermediate sensitive to Ofloxasin. Three isolates had intermediate sensitivity to clindamycin and azithromycin and 2 isolates to chloramphenicol. Penicillin MICs for all isolates were ≤ 0.016 µg/ml. E test assays showed that isolates with intermediate zone to clindamycin and azithromycin by disk diffusion method were susceptible.

Conclusion: Although penicillin remains the first drug of choice for treatment of *Streptococcus pyogenes* infections but two reports about rising penicillin MIC led to determine penicillin MIC by different countries. In this study penicillin MICs were less than 0.016µg/ml. Also all isolates were sensitive to erythromycin which could be because of the small number of isolates. Resistant isolates could be found possibly in larger number of samples.

Keywords: *Streptococcus pyogenes*, asymptomatic carriers, Penicillin, Erythromycin

[1]Department of Microbiology, Tehran University of Medical Science, Tehran, Iran
[2]Department of Microbiology, Science and Research Branch, Islamic Azad University, Fars, Iran
[3]Department of Pediatrics, Tehran University of Medical Sciences, Tehran, Iran
[4]Applied Microbiology Research Center, Baghiatallah University of Medical Sciences, Tehran, Iran

Drug Resistance Pattern of *Pseudomonas Aeruginosa* Isolated from Burn Patients in Zare Hospital in Sari, 2010-2011

Mohammad Ahanjan, Soodeh Kholdi

Department of Microbiology, Medicine Faculty, Mazandaran University of medical sciences, Mazandaran, Iran

Abstract

Background: *Pseudomonas Aeruginosa* is one of the most important opportunist bacteria, that are resistant to many of antibiotics and antiseptics. *P. Aeroginosa* is causes of nosocomial infections; in this study we evaluate the sensitivity and resistance of the bacteria to many antibiotics.

Methods: Samples have been taken from wound of hospitalized patients in the burning ward of Zare Hospital. The samples transport to Amies medium and transported to Microbiology laboratory of Medicine Faculty. These samples have been cultured in the Blood agar and EMB medium and incubated of them in the 37 C for 24 h. We have done gram stain form colonies, gram negative bacilli identified and cultured in OF medium and oxidase test was done. The identified bacteria as *P. aeroginosa*, antibiogram test were compared with Mc Farland standard.

Results: 300 samples were taken, 52 persons were *P. aeroginosa* positive. Highest sensitivity belongs to ofloxacine and norfloxacine (11.5%) and imipenem (7.6%). All of another was resistant to gentamysine, tobramycin, ceftizoxime, cefepime and ceftazidime.

Conclusion: *P. aeroginosa* was isolated in this study showed resistant to tested antibiotics.

Keywords: *P. aeroginosa*, Burn patients, sari

A Study of Infection with HTLV-1 in Referring Patients to the Mousabnejafar Hospital Clinic during 2008 - 2009

Majid Hasan Zadeh, Hosain Rajabzadeh, Sara Rajabzadeh

Abstract

Background: HTLV-1 is the first human retrovirus and belongs to Oncoviruses. This virus is the etiological factor for ATL disease and so chronic neurological disease titled HAM/TSP. The restriction of regional prevalence of this virus is one of important characteristic of that. The epidemiological study and survey on spread of infection can be effective in prevention Methods planning. The purpose of this study is epidemiological survey of viral infection with HTLV-1in South Khorassan province and probable risk factors.

Methods: To gain this goal 250 Referring patients to the Mousabne Jafar hospital clinic (one of the major center of referring patients) have studied on existence or absence of HTLV-1 in one year (May 2008 – May 2009). After getting the blood of patients and separating the serums, samples have kept in -20 centigrade degree to time of experiment. Finally, samples were tested by ELISA.

Results: After of gathering and setting in the computer, the analysis of the results was done with SPSS software. However, regarding the number of 250 sample, 170 samples (65/39%) belong to cardiovascular patients , 83 samples (31/92%) belong to Hemophilic patients, 2 samples (0/77%) belong to patients with neural symptoms , three samples (1/15%) belong to patients with renal failure and 2 samples (0/77%) belong to patients with female urogenital failure . Generally, only 3 samples (1/15 %) were HTLV-1 positive and 66/66% of them belonged to Hemophilic patients and 33/33% belonged to cardiovascular patients.

Conclusion: The results showed that the infection with HTLV-1present in this region and due to that the diagnostic kits of ELISA to detect of HTLV-1 is expensive and so waste the time, should be done by considering more carefully and with focusing on probable risk factors finally, should make a decision to prevention and control of this disease in regions with high risk factors.

Mousabne Jafar Hospital Clinic, Mashhad, Iran

Keywords: HTLV-1, Hemophilic, cardiovascular, ELISA

Antimicrobial Resistance Pattern of *Staphylococcus aureus* Isolates from Outpatients of Imam Khomeini Hospital in Tehran, Iran

Mohammad Javad Nasiri[1], Samin Zamani[1], Abbas Ashrafi[2], Alireza Abdollahi[2]

[1]Department of microbiology, Faculty of medicine, Tehran University of Medical Sciences, Tehran, Iran
[2]Department of Pathology, Imam Khomeini Hospitals' complex, Tehran University of Medical Science, Tehran, Iran

Abstract

Background: *Staphylococcus aureus* is an important pathogen in human that causes different community-acquired infections. An increasing rate of antimicrobial resistance among *S. aureus* isolates may complicate therapeutic management of infection. The aim of this study was to determine antimicrobial susceptibility patterns of *S. aureus* isolates from outpatients of Imam Khomeini hospital in Tehran, Iran.

Methods: The pattern of antibiotic resistance of 284 *S. aureus* isolates from wounds, abscess, urine and other body fluids, during March 2010 to February2011, was determined by disk diffusion test as recommended by the Clinical Laboratory and Standards Institute (CLSI).

Results: Resistance of *S. aureus* to various antibiotics was as follows: erythromycin (61%), clindamycin (59%), oxacillin (40%), and gentamicin (31%). Also high susceptibility rates to vancomycin (100%), co-trimoxazole (83%), chloramphenicol (78%) and rifampin (78%) were documented.

Conclusion: According to this study, vancomycin, co-trimoxazole, chloramphenicol and rifampin revealed good activity against *S. aureus* infections. Also, these data shows that antimicrobial resistance to erythromycin, clindamycin, oxacillin and gentamicin is increasing among *S. aureus* isolates and highlights the importance of choice of appropriate antibiotics for treatment of infections.

Keywords: *Staphylococcus aureus*, Antimicrobial resistance, Tehran

Detection ofmutationininhA-15 C to T in clinical isolates of *Mycobacterium tuberculosis* resistant to isoniazid by MAS-PCR and Sequencing Methods

Roya Abkar[1], Mohammad Zolfaghari[1], Mana Shojapoor [2], Azam Ahmady[3], Mohammad Arjomandzadegan[3]

[1]Department of Microbiology, Qom Branch, Islamic Azad University, Qom, Iran
[2]Research Center of Molecular Medicine, Arak University of Medical Sciences, Arak, Iran
[3]Tuberculosis and Pediatric Infectious Diseases Research Center, Arak University of Medical Sciences, Arak, Iran

Abstract

Background: Isoniazid is the first-line TB drug. Resistance isoniazid has created many problems in the treatment of tuberculosis. Mutations that cause resistance to isoniazid (INH) are mainly occurred in codon 315 of katG gene and mabA-inhA regulatory region (-15). In this study, the need to determination of mutations in mabA-inhA promoter in routine works for the rapid detection of isoniazid resistance was examined.

Methods: From ninety eight clinical strains of *Mycobacterium tuberculosis* in the Tuberculosis Research Center, Arak, 48 strain were examined for mutations in the inhA-15 regulatory region with MAS-PCR and sequencing molecular Methods. Specific primers were used for a MAS-PCR that could detect mutant form as created 248bp band in all samples and 174bp band in the mutant strains. The results were compared with sequencing.

Result: Of 48 strains, 13 strains (27%) were susceptible and 35 strains (73%) were resistant to isoniazid. From 35 isoniazid resistant strains, 5 isolate (14.3%) and from 13 susceptible strains, one strain (7.7 %) had a mutation in the inhA-15. Results of sequencing showed full compliance with the MAS-PCR results.

Conclusion: The MAS-PCR is a simple and suitable method for rapid detection of isoniazid resistance in clinical strains of *Mycobacterium tuberculosis* in inhA-15region. Based on the results and the literature review; it is concluded that this test is valuable for determining isoniazid resistance mutations, but not provide information leading to detection of mutations in katG315.

Keywords: *Mycobacterium* tuberculosis, Drug resistant, Isoniazid, inhA-15

Evaluation of Clindamycin Constitutive and Inducible Resistance in Methicillin-Resistant *Staphylococcus aureus* Isolated from Clinical Specimen by D-Test Method in Center of Iran

Mohsen Rezazadeh[1,2], Ehsanollah Ghaznavi-Rad[1], Rasoul Yousefi Mashouf[3], Bita Bakhshi [4] Hossein Sarmadyan[5]

[1]Department of Medical Microbiology, Faculty of Medicine, Arak University of Medical Sciences
[2]Student Research Committee, Arak University of Medical Sciences ,Arak, Iran
[3]Department of Medical Microbiology, Faculty of Medicine, Hamadan University of Medical Sciences
[4]Department of Medical Microbiology, Faculty of Medicine, Tarbiat Modares University
[5]Department of Infectious Diseases, Faculty of Medicine, Arak University of Medical Sciences

Abstract

Background: Clindamycin is the selective drug in the treatment of staphylococcal infections. Erythromycin and clindamycin are two specific classes of antimicrobial agents that inhibit protein synthesis in bacterial cells. Inductive resistance to clindamycin is not detected with conventional Methods of antibiogram. Many doctors refuse to administration of clindamycin whereas all the erythromycin resistant strains are not resistant to clindamycin. The purpose of this study is determination of Inductive phenotypes of clindamycin resistance strains in methicillin-resistant *Staphylococcus aureus*.

Methods: A total of fifty clinical isolates of methicillin-resistant *Staphylococcus aureus* were tested for inductive resistance to clindamycin. Disk diffusion method was performed using erythromycin and clindamycin discs according to CLSI guidelines.

Results: D test was performed on 50 samples of methicillin-resistant *Staphylococcus aureus* that among them five isolates were negative and 3 isolates were positive for D test.

Conclusion: Performing this test, we can identify erythromycin-resistant isolates. Accurate reporting of antibiotic susceptibility can help improving the healing process. Therefore Clindamycin sensitive and erythromycin-resistant *S. aureus* should be tested for inductive resistance.

Keywords: Clindamycin, erythromycin, methicillin-resistant *Staphylococcus aureus*

Antimicrobial Susceptibility Patterns in Multidrug Resistant bacteria among *Pseudomonas Aeruginosa*, *Acinetobacter* and ESBLs Producing Bacteria in Four Tertiary-Care Hospitals in Isfahan, Iran

Armin Farhang[1], Dariush Shokri[2], Hengameh Zandi[1], Sina Mobasherizadeh[2]

Abstract

Background: Antimicrobial resistance is one of the significant problems worldwide leads to curative failure of therapy. In this study, antimicrobial susceptibility pattern of multidrug resistant bacteria among *Pseudomonas Aeruginosa*, *Acinetobacter*, and ESBLs (extended spectrum beta-lactamases) producing bacteria was investigated in four tertiary-care hospitals in Isfahan in three month in 2012.

Methods: In this cross-sectional study, Bacteria recovered from clinical specimens were identified by standard biochemical Methods. Disk diffusion method was used for determination of antimicrobial susceptibility pattern of isolated bacteria (according to CLSI guideline). ESBL assay was determined by the double-disk diffusion method.

Result: Numbers of multidrug resistant mentioned bacteria were as follows: 28*Pseudomonas Aeruginosa* strains, 26 *Acinetobacter* strains and 50 ESBLs producing bacteria (64%, 31% and 5% of ESBLs positive bacteria were *E. coli*, *Klebsiella spp.* and *Enterobacter spp.* respectively). Results showed that *P. aeruginosa* isolates were more sensitive to imipenem (66.66 %) and 33.3% were completely resistant to all tested antibiotics. In *Acinetobacter* spp, 89 % of isolated were completely resistant to all tested antibiotics. Imipenem and piperacillin-tazobactam were more effective antibiotics against ESBLs producing isolates (Imipenem: 87.5%, 77% and 80% for *E. coli*, *Klebsiella* spp and Enterobacter spp respectively and piperacillin-tazobactam: 71.87%, 77% and 80% for *E. coli*, *Klebsiella* spp and Enterobacter spp respectively).

Conclusion: High antibiotic resistant in all studied bacteria was showed that alarms an emerging public-health concern. It needs developing new antimicrobial agents and using of appropriate susceptibility testing Methods before therapy.

Keywords: Multidrug resistant bacteria, *Pseudomonas Aeruginosa*, *Acinetobacter*, ESBLs producing bacteria

[1]Department of Microbiology, Faculty of Medicine, Shahid Sadoughi University of Medical Sciences, Yazd, Iran
[2]Nosocomial Infectious Diseases Research Center, Isfahan University of Medical Sciences, Isfahan, Iran

Prevalence and Determination of Antimicrobial Susceptibility Patterns of MRSA and VRE Isolates in Four Tertiary-care Hospitals in Isfahan, Iran

Armin Farhang[1], Dariush Shokri[2], Hengameh Zandi[1], Sina Mobasherizadeh[2]

Abstract

Background: MRSA (methicillin resistant *Staphylococcus aureus*) and VRE (vancomycin resistant *Enterococcus*) are among antimicrobial resistance bacteria that cause nosocomial infections and the significant problems worldwide leads to curative failure of therapy. In this study prevalence and antimicrobial susceptibility pattern of multidrug resistant isolates of these two bacteria was investigated in four tertiary-care hospitals in Isfahan in three month in 2012.

Methods: In this cross sectional study, bacteria were recovered from clinical specimens and were identified by standard biochemical Methods. Disk diffusion method was used for determination of antimicrobial susceptibility pattern of isolated bacteria (according to CLSI guideline). E-test and MRSA screening cefoxitin disc were used for confirmatory vancomycin resistant in VRE isolates and MRSA detection respectively.

Results: Among a total of fifty four consecutive clinical isolates identified as *Staphylococcus aureus*, eighteen strains were identified as MRSA (33.3%) and among a total of eighty *Enterococcus* isolated ten strains were identified as VRE (12.5%). Results showed that Vancomycin was the effective antibiotic against MRSA isolates (100 %) and 90 % of them were sensitive to trimethoprim/sulfamethoxazole but these strains were completely resistant to other tested antibiotic contains ampicillin, tetracycline, ciprofloxacin, oxacillin and cefoxitin. VRE isolated, 33.76 % were sensitive to tetracycline but these strains were completely resistant to other tested antibiotic contains ampicillin, tetracycline, ciprofloxacin, imipenem, gentamicin, oxacillin and penicillin.

Conclusion: Our results showed high antibiotic resistant in all studied bacteria that alarm an emerging public-health concern and emphasize on emergence need for developing a treatment guideline for antibiotic consumption.

Keywords: Multidrug resistant bacteria, MRSA, VRE

[1]Department of Microbiology, Faculty of Medicine, Shahid Sadoughi University of Medical Sciences, Yazd, Iran
[2]Nosocomial Infectious Diseases Research Center, Isfahan University of Medical Sciences, Isfahan, Iran

Molecular Detection of CTX-M Group Beta Lactamases Produced by *Klebsiella pneumuneia* Isolated from Clinical Specimens of Arak University Medical Sciences Hospitals

Mojdeh Safari[1], Hamid Abtahi[2]

Abstract

Background: CTX-M is a type of extended- spectrum beta-lactamases and is an important cause of antimicrobial resistance against cephalosporins and a recent concern in treating infections caused by gram negative bacteria. *Klebsiella pneumonia* is one of the important causes of nosocomial infections that is the major carrier of the CTX-M group genes .The purpose of this study is detection of bla CTX-M group genes in *Klebsiella pneumuneia* isolated from hospitals in Arak.

Methods: Ninety samples of *Klebsiella pneumonia* from clinical specimens were collected through three Hospitals in Arak by biochemical tests. The antibiotic susceptibility isolates were determined by Disk-Diffusion Method .The Combined Disk Test was used to confirm the results. The results were compared with Clinical and Laboratory Standards Institute (CLSI). All samples were positive ESBL investigated for the presence of CTX-M genes using specific primers by PCR.

Results: Among 90 *K. Pneumonia* isolates, the highest antibiotic resistance was observed against amoxyclav (82.2%) and lowest antibiotic resistance was observed against imipenem (6.6%). Also, 57(63.3%) isolates were resistant to cefotaxime and ceftazidime. 41(71.9%) isolates were ESBL positive using the phenotypic confirmation tests. CTX-M1 positive in 36 strains (87.8%), CTX-M2 positive in six strains (14.6%), CTX-M8 positive in eight strains (19.5%) and CTX-M9 positive in nine strains (21.9%).

Conclusion: Our study revealed that there is a high frequency isolates of ESBL producing strains of *K. Pneumonia* in patients. This has a significant implication for patient managements. It is necessary for further drug resistance surveillance in our hospitals and molecular characteristics of ESBLs isolates in our country.

Keywords: *Klebsiella pneumonia*, extended- spectrum beta-lactamase, CTX-M group, antibiotic resistance

[1] Department of Microbiology, Islamic Azad University of Qom, Iran
[2] Molecular and Medical Research Center, Arak University of Medical Sciences, Iran

Antimicrobial Effects of Silver Nanoparticles on Clinical Strains Resistant to Beta-lactam Antibiotics of *Escherichia coli* and *Klebsiella pneumonia* In-vivo and In-vitro

Mojdeh Safari

Department of Microbiology, Islamic Azad University of Qom, Qom Branch, Qom, Iran

Abstract

Background: *Escherichia coli* and *Klebsiella pneumonia* are Common cause of Urinary tract and gastrointestinal infections. The widespread use of beta-lactam antibiotics developed resistance in this group of antibiotics in pathogenic bacteria through the production of beta-lactamase enzymes. In recent years the use of silver nanoparticles for antibacterial properties has been considering order to control the infection. The purpose of this study was antimicrobial effects of silver nanoparticles on *E. coli* and *K. Pneumonia* producing extended- spectrum beta-lactamases (ESBL).

Methods: In this research antimicrobial effect from concentrations 3, 6,12,25,50,100,200 ppm of silver nanoparticles was evaluated on 149 clinical strains of *E. coli* and *K. Pneumonia* ESBL positive using Well Diffusion Agar. Also anti-bacterial activity of nanoparticles was studied by determining the minimum inhibitory concentrations (MIC) and minimum bactericidal concentration (MBC) using Macro dilution. Particles of silver studied through an animal model with Balb /c mice.

Results: The results showed that silver nanoparticles had strong antimicrobial effects on the bacteria listed above. In Well Diffusion Method, inhibition zone observed in both of bacteria in concentration of 200ppm. In Macro dilution Method range of MIC and MBC were obtained 6-25 ppm respectively. In animal models was investigated significant difference in bacteria growing the spleen among the experimental groups and control groups.

Conclusion: The results show the existence of a direct relationship in increasing concentration of silver nanoparticleswith inhibition zone in bacteria listed .Therefore; they can be used for the treatment of infections caused by these bacteria as well as for covering equipment in hospitals in order to prevent contamination.

Keywords: Antimicrobial effect, Silvernanoparticles, *Escherichia coli*, *Klebsiella* pneumonia

Detection of Beta-Lactam Antibiotic Resistant *Escherichia coli* from Diarrheal Cases in Shahrekord, 2011

Davoudi Jouneghani[1], Sara Barati[1], Hossein Kaboli Boroujeni[1], Jahangir Kaboutari Katadj [2,3], Samaneh Mehrabiyan[1,3], Keyvan Farahmandi[4], Sharmin Farahmandi[1], Marzieh Tadi Beni[1], ZinatSamira Molanouri Shamsi[1], Farnoush Ansari Cholicheh[1]

[1] Faculty of Veterinary Medicine, Shahrekord University, Shahrekord, Iran
[2]Department of Basic Science, Faculty of Veterinary Medicine, Shahrekord University, Shahrekord, Iran
[3] Research Institute of Zoonotic Diseases, University of Shahrekord, Shahrekord, Iran.
[4] Faculty of Medicine, Tehran University of Medical Sciences, Tehran, Iran

Abstract

Background: Diarrheal diseases are considered a major health problem. Enteropathogenic *Escherichia coli* strains are the common cause of diarrhea in children especially in developing countries. In recent years, antibiotic resistances became one of the most important challenges in medical society for this purpose antibiotic sensitivity and resistance of strains in every geographical zone must be determined. So the present study was conducted to investigate beta-lactam antibiotic resistance patterns of *E. coli* isolated from patients with diarrhea in Shahrekord, Iran in 2011.

Methods: *E. coli* was isolated from one hundred thirty one (56%) of two hundred thirty four samples from patients with diarrhea from Hajar Hospital, Shahrekord, Iran and antibiogram tests were performed using disc diffusion method. The seven antimicrobials tested in the antibiogram were imipenem, Amoxicillin, cefotaxime, cefixime, cephalexin, oxacillin and penicillin G.

Results: Resistance of isolates to imipenem, amoxicillin, cefotaxime, cefixime, cephalexin, oxacillin and penicillin G was 32.1%, 68.7%, 71.1%, 77.9%, 80.1%, 90.8% and 94.6% respectively.

Conclusion: Antimicrobial resistances in *Escherichia coli* isolates were very high and it makes the treatment of infectious diseases difficult. So supervision on the consumption of antimicrobial agents and determining resistant strains of phenotypes and genotypes can prevent development of resistance in bacteria.

Keywords: *Escherichia coli*, antibiotic resistance, diarrhea

Determining the Patterns of Antibiotic Resistance and the Prevalence of Extended-Spectrum B-Lactamase in Strains of *Acinetobacter bnaumannii* Isolated from Clinical Samples through Phenotypic Methods

Somayeh Vafaei[1], Reza Mirnejad[2], Abbas Ali Imani Fooladi[3], Noor Amir Mozafari [4], Faramarz Masjedian[5]

[1]Department of Biology, Science and Research Branch, Islamic Azad University, Tehran, Iran

[2] Molecular Biology Research Center, Baqiyatallah University of Medical Sciences, Tehran, Iran

[3] Research Center for Applied Microbiology Baqiyatallah University of Medical Sciences, Tehran, Iran

[4]Department of Microbiology, Iran University of Medical Sciences, Tehran, Iran

[5]PhD Student Bacteriology, Tehran University of Medical Sciences, Tehran, Iran

Abstract

Background: This study determined the antibiotic resistance of *Acinetobacter baumannii* and the prevalence of strains producing extended-spectrum β-lactamase in patients held in intensive care unit of Imam Khomeini, Milad and Baqiyatallah hospitals.

Methods: This study was performed in three major hospitals in Tehran on four hundred samples during six months. After The identification of strains of *Acinetobacter baumannii* using culture and biochemical Methods, sensitivity test against fourteen antibiotics was done on one hundred isolate of *Acinetobacter baumannii* using disk diffusion method on CLIS (Clinical and laboratory standards institute). For detection of ESBL producing strains phenotypic Methods were applied using combined disks in which cefotaxime and ceftazidime disks were used alone and with clavulanic acid.

Results: According to the results of initial screening, the most common antibiotic resistance among *Acinetobacter baumanii* isolates to antibiotics were against cefepime(100%), norofloxacine (96%), ceftriaxone (95%), amikacin (95%), ciprofloxacin (93%), ofloxacine (92%), imipenem (76%), piperacillin-tazobactam (70%), meropenem (69%), gentamicin (63%), tobramycin (56%), tetracycline (51%), ampicillin - sulbactam (49%), and the lowest resistance to polymyxin B was observed. According to the combined disk test 20% of the strains were extended-spectrum β-lactamase producer.

Conclusion: Multidrug-resistant *Acinetobacter baumannii* is developing a major risk for hospitalized patients in Iran. Only twenty percent of the isolates in this study generated ESBL .Therefore, other mechanisms in bacteria such as secretory pumps and changes in Purine cause resistance. The rapid detection of these strains plays an important role in preventing their spread.

Keywords: *Acinetobacter baumanii*, Extended-spectrum β-lactamase (ESBL), Drug resistance, Antibiogram, combined disk

Frequency of Aminoglycosides Modified Enzyme Genes in Methicillin-Resistant *Staphylococcus aureus* Isolated from Clinical Specimen by Multiplex PCR in Center of Iran

Mohsen Rezazadeh[1,2], Ehsanollah Ghaznavi-Rad[1], Ali Godarzi[4], Fariba Fotoh[3], Mehrangiz Dezhbord[3]

[1]Department of Medical Microbiology, Faculty of Medicine, Arak University of Medical Sciences, Arak, Iran
[2]Student Research Committee, Arak University of Medical Sciences, Arak, Iran
[3]Islamic Azad University of Karaj, Department of Microbiology, Karaj, Iran
[4]Islamic Azad University of Qom, Department of Microbiology, Qom, Iran

Abstract

Background: Aminoglycosides are powerful bactericidal agents used in combination with betalactams, particularly in the treatment of staphylococcal endocarditis. Enzymatic drug inactivation by modified aminoglycoside enzymes are the main mechanism of drug resistance in *Staphylococcus aureus*. The main objective of this study was to determine the frequency of aminoglycoside resistance genes in methicillin-resistant *Staphylococcus aureus* by Multiplex PCR method.

Methods: In this study fifty isolates of methicillin-resistant *Staphylococcus aureus* were isolated from the patients with phenotypic tests, at the Central Hospital, Arak University of Medical Sciences. All isolates confirmed with the use of genetic Methods) PCR) for mecA and sa442 gene. The sensitivity of these strains to antibiotics was investigated in according to CLSI (Clinical and Laboratory Standards Institute) guideline. Then these strains investigated for ant, aph and acc genes by Multiplex PCR method.

Results: In this study of total 50 isolates of methicillin-resistant *Staphylococcus aureus*, aph gene found in nine (18%) isolated, acc gene in thirteen (66%) isolated and ant gene in one (2%) isolated.

Conclusion: Results from this study show increased prevalence of resistance to aminoglycoside indicating a meaningful relation between the mecA gene and resistance to aminoglycosides.

Keywords: Methicillin-resistant *Staphylococcus aureus*, CLSI, aminoglycoside resistance, mecA

The Pattern of Drug Resistance *Acinetobacter baumannii* Isolated fromClinical Specimens and Phenotypic Identified Extended-Spectrum Beta-lactamases Producing

Behnaz Deiham[1], Halvae[2]

Abstract

Background: *Acinetobacter* is Gram-negative non-fermentors causes of nosocomial infections such as ventilator associated pneumonia, urinary tract infections, bacteremia, and meningitis and wound infection. This organism is able to survive in the environment and the pollution levels will lead to spread of infection in the Hospitals.

Methods: Two-years clinical study of hospitalized patients 95 *Acinetobacter baumannii* isolates were obtained. Susceptibility testing of microbial isolates to the antibiotics gentamicin, amikacin, ciprofloxacin, ceftriaxone, cefotaxime, ceftazidime, cefepime, imipenem, meropenem and erthapenem disk diffusion method and colisitin E test method in MDR strains evaluated. The double-disk synergy test for detection of Extended-spectrum Betalactamases isolates using ceftazidime and ceftazidime/clavolanic acid disks.

Results: More isolation from the respiratory secretions of 81 isolates (85.2%) maximum resistance in BAL specimens to cefotaxime (100%), ceftazidime (95%), ceftriaxone (95%), ciprofloxacin (95%), cefepime (84.6%), gentamicin (84.6%) and imipenem (82.7%). 20% of strains were ESBL producing. Fifty three strains were Multiple Drug resistance. Colisitin resistant was not detected in any of the isolates.

Conclusion: Due to the high power transmission of drug resistance genes and biofilm formation by this bacterium, which is a factor for the acquisition and development of drug resistance genes, thus identifying by phenotypic tests in microbiological diagnosis can be controlled to a large extent and the incidence of nosocomial infections are prevented.

Keywords: *Acinetobacter baumannii*, drug resistant, ESBLs

[1]Department of microbiology, faculty of Medical Sciences, Dezful, Iran
[2] Laboratory of Teaching Hospital, faculty of Medical Sciences, Dezful, Iran

Antimicrobial Susceptibility Pattern of *Acinetobacter Baumannii* Strains Isolated From ICU Wards in Taleghani Hospital in Kermanshah, Iran

Nasrollah Sohrabi[1], Mehrdad Payandeh[1, 2], Mohammad Erfan Zare[2, 4], Samira Azizkhani[3], Atefeh Nasir Kansestani[2, 4], Amir Peymani[5] , Zohreh Amiri[6, 7]

[1] Department of Medical Lab Sciences, Faculty of Paramedicine, Kermanshah University of Medical Sciences, Kermanshah, Iran
[2] Medical Biology Research Center, Kermanshah University of Medical Sciences, Kermanshah, Iran
[3] MSc in Microbiology, Kermanshah, Iran
[4] Student Research Committee, Kermanshah University of Medical Sciences, Kermanshah, Iran
[5] Department of Microbiology, Faculty of Medicine, Qazvin University of Medical Sciences, Qazvin, Iran
[6] PhD Student of Medical Biotechnology, Faculty of Medicine, Tarbiat Modares University, Tehran, Iran
[7] Department of Biology, Faculty of Sciences, Kermanshah Razi University, Kermanshah, Iran

Abstract

Background: Nosocomial infection is a major cause of morbidity and mortality and ICU hospitalized patients are at great risk of acquiring these infections. *Acinetobacter baumannii* is one of the most frequent species involved in nosocomial infections. The most important problem associated with *A. baumannii* is intrinsic resistance to multiple antibiotics and its ability to rapidly acquire antibiotic resistance from other bacteria. The aim of this study was to determine the antimicrobial susceptibility pattern of *A. baumannii* strains isolated from ICU wards of Taleghani teaching Hospital in Kermanshah, Iran.

Methods: In this study, a total of seventy eight *A. baumannii* isolates were obtained from nosocomial infections in hospitalized patients in ICU wards. These isolates identified using standard microbiological and biochemical Methods. Antimicrobial susceptibility testing were done using disk diffusion method according CLSI standards. Data analysis was performed using SPSS software.

Result: Among seventy eight patients, 83% were male. These isolates were obtained from different clinical specimens including tracheal aspirate (83.3%), urine (9.2%), blood (5%) and wound (2.5%). The most frequent infection was pneumonia (83%). Results of antimicrobial susceptibility testing as followed below: ceftriaxone (100%), ceftizoxime (100%), trimethoprim/sulfamethoxazole (88%) ciprofloxacin (84%), ticarcillin (83%), piperacillin (80%), gentamicin (78%), meropenem (73%), imipenem (72%).

Conclusion: Results of this study showed *A. baumannii* isolates are resistant to most of the antibiotics and we must use more effective drugs such as polymixin B and colistin. Applying prevention standard guidelines is necessary to reduce the rate of these infections in ICU.

Prevalence and Antimicrobial Susceptibility Pattern of *Klebsiella pneumonia* Strains Isolated from ICU Wards in a Teaching Hospital in Kermanshah, Iran

Nasrollah Sohrabi[1], Mehrdad Payandeh[1, 2], Mohammad Erfan Zare[2, 4], Samira Azizkhani[3] , Atefeh Nasir Kansestani[2, 4], Amir Peymani[5] , Zohreh Amiri [6, 7]

[1]Department of Medical Labarotary Sciences, Faculty of Paramedicine, Kermanshah University of Medical Sciences, Kermanshah, Iran
[2]Medical Biology Research Center, Kermanshah University of Medical Sciences, Kermanshah, Iran
[3]Microbiology, Kermanshah, Iran
[5]Department of Microbiology, Faculty of Medicine, Qazvin University of Medical Sciences, Qazvin, Iran
[6] Medical Biotechnology, Faculty of Medicine, Tarbiat Modares University, Tehran, Iran
[7]Department of Biology, Faculty of Sciences, Kermanshah Razi University, Kermanshah, Iran

Abstract

Background: *Klebsiella pneumonia* is one of the most frequent species involved in nosocomial infections especially in ICU wards. ICU hospitalized patients are at great risk of acquiring these infections because of underlying diseases of patients and invasive treatment procedure. In this study we determined the antimicrobial susceptibility pattern of *Klebsiella pneumonia* strains isolated from ICU wards in a teaching hospital in Kermanshah, Iran.

Methods: A total of 51 *Klebsiella pneumonia* isolates were collected from hospitalized patients in ICU wards of a teaching hospital in Kermanshah. Identification was done using standard microbiological and biochemical Methods. Antimicrobial susceptibility testing was done using disk diffusion method according to CLSI standards. Data analysis was performed using SPSS software.

Results: Among fifty one patients, thirty nine (76%) were male. These isolates were obtained from different clinical specimens including wound (47%), tracheal aspirate (28%) and urine (25%). Results of antimicrobial susceptibility testing showed that the rate of resistance to selected antibiotics were as follows: ceftizoxime (100%), ceftriaxone (100%), cephotaxime (96%), ciprofloxacin (84%), cephalothin (95%), ticarcillin (83%), piperacillin (80%), gentamicin (78%), trimethoprim/sulfamethoxazole (62%), amikacin (46%), imipenem (43%) and meropenem (40%)

Conclusion: The results of this study emphasize on importance of gram negative bacteria specially *Klebsiella* Pneumonia in nosocomial infections in ICU wards. Development of preventive strategies to reduce the rate of these infections in ICU is necessary. The results of antibiogram showed that imipenem, meropenem and amikacin were the most effective antimicrobial agents.

Frequency of ESBL Production and Comparison Antibiotic Susceptibility Patterns between ESBL Producing and none ESBL Producing Clinical Isolates of *Pseudomonas aeruginosa* in Tehran

Somayeh Moazami Goudarzi, Fereshteh Eftekhar

Department of Microbiology, Faculty of Biological Science, Shahid Beheshti University, Tehran, Iran

Abstract

Background: *Pseudomonas aeruginosa* is an opportunistic pathogen causing severe, acute and chronic nosocomial infections in immunocompromised, catheterized or burn patients. These organisms are often resistant to most antibiotics including the extended spectrum beta-lactams mostly by producing extended spectrum beta-lactamases (ESBL). We studied prevalence of ESBL production in clinical isolates of *P. aeruginosa* and comparison antibiotic susceptibility patterns between ESBL producing and none ESBL producing isolates.

Methods: One hundred and twelve *P. aeruginosa* clinical isolates were collected from Motahari and Shohadaye Tajrish Hospitals in Tehran and were identified by using the standard biochemical tests. Combined disk diffusion test was used to screen for ESBL production and the Kirby-Bauer disk diffusion method was performed to determine susceptibility to 13 antibiotics.

Results: The **results** showed that **19.64%** of isolates were ESBL producers. Comparison of antibiotic susceptibility pattern between ESBL producing and none ESBL producing isolates revealed that the resistance rate among ESBL producing isolates were higher than none ESBL producing. This difference was statistically significant ($P < 0.05$) in case of some tested antibiotics include aztreonam, meropenem , ticarcillin, Tobramycin and carbenicillin.

Conclusion: Emerging ESBL producing *P. aeruginosa* isolates limit the therapeutic options for treatment of *P. aeruginosa* infection. Therefore, monitoring for ESBL production is recommended along with antimicrobial susceptibility tests in the clinical isolates of *P. aeruginosa*.

Keywords: *P. aeruginosa*, ESBL, antibiotic susceptibility

Class I Integron and Imipenem Resistance in Clinical Isolates of *Pseudomonas aeruginosa*: Prevalence and Antibiotic Susceptibility

Somayeh Moazami Goudarzi, Fereshteh Eftekhar

Department of Microbiology, Faculty of Biological Science, Shahid Beheshti University, Tehran, Iran

Abstract

Background: *P. aeruginosa* is one of the most common causes of life-threatening nosocomial infections. *P. aeruginosa* infections are normally difficult to eradicate due to acquired resistance to many antibiotics via horizontal gene transfer like integrons. Recent emergence of carbapenem resistant *P. aeruginosa* isolates has become a major healthcare problem. The present study was conducted to comparison frequency of integrons class 1 and antibiotic resistance profiles between imipenem-sensitive and imipenem-resistant clinical isolates of *P. aeruginosa*.

Methods: Antibiotic resistance profiles were studied in 112 clinical isolates of *P. aeruginosa* by disk agar diffusion method. Detection of class I integron was performed by the PCR method.

Results: Antibiotic susceptibility results revealed that thirty three (29.47%) were susceptible and seventy nine (70.53%) were resistance to imipenem. PCR results showed that sixty eight (86.07%) of imipenem resistant and eleven(33.33%) of imipenem sensitive *P. aeruginosa* isolates carried class 1 integron. Comparison of antibiotic susceptibility pattern showed high level of antibiotic resistance except cotrimoxazole among imipenem resistance isolates ($P<0.05$).

Conclusion: The high frequency of imipenem resistance and integrons class 1 was seen among our isolates. Since carbapenems are considered as the last drugs used for treatment of these infections, it is crucial to control imipenem resistance via prevention of integrons prevalence.

Keywords: Imipenem, antibiotic resistance, *P. aeruginosa*, class I integron

Study of the Relationships between Polymorphisms of the Co-stimulatory Genes: CTLA-4, PD-1, CD28, and ICOS with HCV Infection in Bone Marrow Transplant Patients

Mahdiyar IravaniSaadi[1], RaminYaghobi[2], Mohammad HosseinKarimi[2], Bita Geramizadeh[2]

Abstract

Background: Immuno-regulative role of co-stimulatory molecules have been affected by gene polymorphisms in bone marrow transplant patients. Also single nucleotide polymorphisms of co-stimulatory molecules may interact with viral pathogenesis. Therefore in this study the relationship between co-stimulatory molecule gene polymorphisms with *Hepatitis C* virus (HCV) infection was evaluated in bone marrow transplant patients.

Methods: In a cross sectional study EDTA-treated blood samples were collected from 72 allogenic and 59 autologous recipients of bone marrow between years 1386-1390. The genetic polymorphisms were evaluated in co-stimulatory genes including: PD-1 (1/3 G/A and 1/9 C/T), CD28 (17 C/T), ICOS (1720-T/C) and CTLA-4 (-318 C/T, 1722 T/C, 1661 A/G, 49AG) were analyzed by different in-house-PCR-RFLP protocols in bone marrow transplant patients. Also the prevalence of HCV infection was evaluated by ELISA method.

Results: The genetic polymorphisms of studied co-stimulatory molecules that have been found with higher frequency in bone marrow transplant recipients were as follows: the GG genotype of PD-1/3- G/A locus, the CC genotype of PD-1/9 -C/T locus, the TT genotype of CD28 (17 C/T) locus, the CC ICOS (1720-T/C) locus, The AA genotype of CTLA-4 1661 locus, the TT genotype of CTLA-4 1722 locus, the CC genotype of - CTLA-4 318 locus, and the AG genotype of CTLA-4 49A/G locus. HCV Ab was detected in only 2 of 72 (2.7%) allogenic bone marrow transplant patients. But HCV infection was no found in any autologous transplant patients. Any significant relationships were not detected between HCV infection and genetic polymorphisms of co-stimulatory molecules in studied patients.

Conclusion: For low prevalence of HCV infection in bone marrow transplant recipients, no significant associations were diagnosed between the genetic polymorphisms of studied co-stimulatory molecules with history of HCV infection. But different studied co-stimulatory gene polymorphisms had significant higher frequency in autologous and allogenic bone marrow transplant patients. Therefore to better define the correct role of the co-stimulatory gene polymorphisms in clinical outcome of bone marrow transplantation and pathogenesis of HCV infection need complete studies.

[1]Islamic Azad University, Jahrom Branch, Jahrom, Iran
[2]Shiraz Transplant Research Center, Shiraz University of Medical Sciences, Shiraz, Iran

Phenotypic Evaluation of Multidrug Resistance *Escherichia coli* Isolated from Zanjan Hospitals

Fahimeh Hajiahmadi, Fatemeh Hemmati,Nahid Keramati, Hesam Osali, Behzad Mansouri, Habib Zeighami

Abstract

Background: *Escherichia coli* is a common cause of children and adults urinary tract infection and diarrhea. Recently antibiotic resistance *E. coli* strains are effect on infection treatment process. The aim of this study was evaluation of Antibiotic resistance pattern of clinical isolated *E. coli*.

Methods: In this cross sectional study two hundred isolates of *E. coli* were collected from clinical samples such as urine, stool, wound and blood from 2011 to 2012 in Zanjan Hospitals. After verifying of isolates by biochemical test, Antibiotic susceptibility was determined by disk diffusion method as recommended by CLSI with regard to cefotaxime (CTX) , ceftazidime (CAZ), cefepime (CPM), imipenem (IMP), aztreonam (ATM), amikacine (AN), gentamicin (GM), ampicillin (AM) ciprofloxacin (CP) tetracycline (TE), erythromycin (ERY), cotrimoxazole (SXT), co-amoxiclav (AMC). Of this isolates, 58% were resistant to three or more agents and considered Multidrug Resistance (MDR).

Results: A large proportion of specimens were related to urine (77.60 %) and stool (17.70 %). *E. coli* isolates were resistant to most drugs. High percentages of isolates were resistant to AM (71.35), TE (46.35%), followed by SXT (48.43%), CTX (33.85%), CAZ (15.10%), ATM (46.87%), CPM (30.72%), CP (26.56%), GM (29.68%), AUG (19.27%) and AN (4.68%). IMP was the most active agent (100% susceptibility).

Conclusion: According to our results resistance to amoxicillin, cotrimoxazole and aztreonam were in the high level and this pattern can be bad alarm in treatment process and distribution of resistance strains.

Department of Microbiology, Faculty of Medical Sciences, Zanjan Medical University, Zanjan, Iran

Keywords: Antibiotic resistance, Disk Diffusion, *Escherichia coli*

The Antimicrobial Activity of Ethanol Extracts of Black Cumin (Nigella Satival) Against Antibacterial Resistant *Staphylococcus aureus*

Farideh Sarvari[1], Elham Saboori Robat[2]

Abstract

Background: *Staphylococcus aureus* is an important cause of community and hospital acquired infections. Its strains inhabit in the nose and increase the intensity of hospital infections and deaths patients. Therefore, many efforts have been done to find new compounds as a substitute for antibiotics. This study investigates the antibacterial effect of alcoholic extracts of cumin **(**Nigella satival**)** against *Staphylococcus aureus* resistant strain.

Methods: The ethanol extracts of cumin **(**Nigella satival**)** were prepared with rotary. Twenty isolates of *Staphylococcus aureus* separated from nose and throat areas and the MIC of plant extracts of cumin **(**Nigella satival**)** microtiter plate method has been investigated on *Staphylococcus aureus*.

Results: The results showed that different concentrations of ethanol extracts of cumin **(***Nigella satival***)** **(**10, 5, 2.5, 1.25, 0.62, 0.3 mg) had different effects on *Staphylococcus aureus*, and so on %58.82, %17.64 strains respectively. Ethanol concentrations of 1.25, 2.5mg of cumin **(***Nigella sativa***l)**were effective and as the MIC for each of the concentrations were considered , the concentrations of 10 ,5, 2.5, 1.25, 0.62, 0.3 respectively, a resistant of 100%,100%,%82.35,% 23.52, %23.52,%23.52 was showed.

Conclusion: Plant extracts and essential oil of cumin **(***Nigella satival***)** has antibacterial effect on *S. aureus* strains at high concentration so these compounds will be used in medical treatments.

Keywords: Antibacterial activity, *Staphyloccocus aureus*, Ethanol extracts

[1] Faculty of Science, Islamic Azad University, Science and Research Branch of fars, Fars, Iran
[2]Department of Plant Biotechnology, University of Zabol, Zabol, Iran

Prevalence of *Klebsiella oxytoca* in Antibiotic-Associated Colitis and Determination of Antibiotic Susceptibility Pattern and Prevalence of ESBLs in Isolates

Sepideh Khodaparast[1], Mohammad Yousef Alikhani[1], Seyed Fazlolah Mousavi[2], Mohammad Mehdi Aslani[2]

Abstract

Background: Colitis is a general term for a condition with the advent of diarrhea, as PMN cells accumulate in lamina propria of colon. For colitis types with bacterial origin can point to antibiotic-associated colitis. Occurrence of this type of colitis is due to toxin-producing *Clostridium difficile* that causes a pseudomembranous colitis. Another type of colitis, is antibiotic-associated hemorrhagic colitis. The main complication would be seen after antibiotic treatment by Penicillin, Beta-lactams, cephalosporins and Quinolone antibiotics. Recently, the bacterium named *Klebsiella oxytoca* is known to cause this type of diarrhea. Hence, the aim of this investigation is to survey the prevalence of *Klebsiella oxytoca* in antibiotic-associated colitis and determining the antibiotic-sensitivity and prevalence of ESBLS in the Isolates.

Methods: In this study, fecal samples collected from hospitalized patients who received antibiotic were transferred to the supportive media. Primary culture and differentiation on the specific media has been utilized to determine the strain. Finally, bacterial samples were confirmed by PCR method for detection a specific gene from *Klebsiella* oxytoca (polygalacturonase pehX gene). The pattern of antibiotic resistance has been investigated by using method of Kirby-Bauer disk diffusion. The detection of ESBLs-producing strains was done by using Ceftazidime and Cefotaxime disks antibiogram (alone or in combination with clavulanic acid).

Result: The study was carried out over fifteen months, the number of 211 samples collected from patients who had catched diarrhea one week to two months after starting antibiotics therapy were analyzed, the separation of 33 cases of *Klebsiella oxytoca* were confirmed by cultivation Methods, differential biochemical tests and specific gene PCR from other bacterial species which had been obtained from samples. Prevalence of *Klebsiella oxytoca* among children was about 41%, women 29% and men 35%. The pattern of antibiotic resistance results showed that bacteria are quite resistant to penicillin, ampicillin, amoxicillin and rifampicin. The bacteria are completely sensitive to amikacin, gentamicin, imipenem and meropenem. Susceptibility to ampicillin / sulbactam, cotrimoxazole and the group of cephalosporins is partial. There are 53% of ESBLs-producing strains were confirmed by standard Methods provided by the CLSI.

Conclusion: The research has indicated that a greater attention must be adhered to *Klebsiella oxytoca* among other pathogens which related to the digestive tract.

[1] Hamedan University of Medical Sciences, Hamedan, Iran
[2] Pasteur Institute of Iran, Tehran, Iran

Keywords: Hospitalized patients, antibiotic-associated colitis, *Klebsiella oxytoca*, antibiotic-resistance, disc diffusion

The Antibacterial Effects of Hydroalcoholic Extract of *Peganum harmala* on Standard Bacteria and Clinical Isolates

Hengameh Zandi[1], Mehdi Tabrizi zade[2], Mohammad Hossein Mosadegh[3], Fatame Akhavan Tafti[1]

Abstract

Background: Due to increased bacterial resistance to common antibiotics, tendency towards using herbal extracts is increasing. In this study, antibacterial effects of *Peganum harmala* extract were evaluated against nine Gram-positive and Gram-negative bacterial strains.

Methods: This descriptive study was performed in Shahid Sadoughi University of medical sciences. The hydroalcoholic extract was prepared from *Peganum hermala* seeds (20% concentration in water).The antimicrobial activity of the *P. hermala*extract was screened by disc diffusion and microdilution method was used for determination of MIC. The bacterial strains were *S. aureus* ATCC25923, *E. coli* ATCC25922, *P. aeruginosa* ATCC27853 and clinical isolates of *S. typhimurium*, *E. faecalis*, S. pyogenes, *K. Pneumonia*e, MRSA and *A. baumanii*. Paper discs were impregnated with 100µl of sterile *P. hermala*extract (final concentration of 1mg/disc) for disc diffusion. The inoculum size of strains was 1.5×10^8 cfu/ml. Process was repeated for 3 times. The serial dilutions of the extract (1-512µg/ml) were prepared in microtiter plates using Muller-Hinton broth for microdilution. 100µl of bacterial suspension in 1.5×10^5cfu/ml concentration was added to each well.

Results: The most inhibition zone was shown for *S. pyogenes* (30.67mm), *S. typhimurium* and *E. coli* (both 29.33mm) respectively. The least inhibition zone was for *P. aeruginosa* (17.33mm).The MIC varied from 2 to 16 µg/ml for all bacteria. The best antibacterial effect was observed against *S. pyogenes* and *S. typhimurium* (2µg/ml). The highest MIC value was recorded against *P. aeruginosa* and MRSA (both 16µg/ml).

Conclusion: Result shows that the hydroalcoholic extract of *P. hermala*could inhibit the growth of all bacteria. So determination of antimicrobial effects of *Peganum hermala* extracts on more clinical strains is recommended (in vitro and in vivo)

Keywords: *Peganum hermala*, antibacterial effect

[1] Department of Microbiology, Faculty of Medicine, Shahid Sadoughi University of Medical Sciences, Yazd, Iran
[2] Depatment Endodontology, Faculty of Dentistry, Shahid Sadoughi University of Medical Sciences, Yazd, Iran
[3] Depatrment of Pharmacology, Faculty of Medicine, Shahid Sadoughi University of Medical Sciences, Yazd, Iran

Antimicrobial Susceptibility Pattern of *Streptococcus pneumonia* Isolated from Mashhad Children, Comparison of Nasopharyngeal and Clinical Isolates

Mohammad Hadi Amirian[1], Mohammad Hassan Aelami[1], Saeid Amel Jamehdar[2], Maryam Jafariani[1], Kiarash Ghazvini[2], Mahmoud Bagheri[2], Hosein Nomani[2], Elnaz Harifi Mood[2]

Abstract

Background: *Streptococcus pneumonia* is the most common cause of morbidity and mortality, especially in children younger than five years. According to WHO reports, pneumococcal disease is the most common cause of preventable death by vaccination. Regarding to the increase of *Streptococcus pneumonia* drug resistance, we describe the antimicrobial susceptibility pattern of positive nasopharyngeal samples of children and positive cultures of admitted patients with invasive pneumococcal disease.

Methods: Three hundred children younger than five years old and fifty five admitted patients with invasive pneumococcal disease were enrolled in this study. Sampling was done from tonsils and tonsilarcrypt's. Samples transported to Microbiology laboratory in Ghaem hospital. They were cultured and on positive cultures antimicrobial susceptibility were done.

Results: From three hundred children, 19% were pneumococcal carrier in nasophrynx. The resistance rate to penicillin, erythromycine, ceftriaxone, cefataxime, cotrimoxasol, tetracycline and ciprofloxacine were 56.1% , 54%, 1.8% ,36.8%,93%,36,8% and 0% respectively. In admitted patients, resistance rate to penicillin, erythomycine, ceftriaxone, ampiciline, clindamycine, oxacilline and coamoxiclave were 17%, 24%, 3.2%, 3.7%, 24%,79,2% and 15% respectively.

There was no resistance to cefataxime, Imipeneme, doxyciline, vancomycine and amoxycilline.

Conclusion: In daycare samples, Resistance rate to penicillin and erythromycin is high and it is result of unnecessary use of antibiotics in this age group. For invasive sample regarding to low resistance rate to penicillin and ampicilline and ceftriaxone, they are good antibiotics instead of imipeneme and vancomycine.

Keywords: *Streptococcus pneumonia*, antibiotics susceptibility, nasopharyngeal isolates

[1]Department of Pediatrics, Imam Reza Hospital, Faculty of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran
[2]Microbiology and Virology Research Center, Avicenna Research Institute, Mashhad University of Medical Sciences, Mashhad, Iran

Prevalence and Phylogenetic Study of Human T-Cell Leukemia Virus Type 1 in Referred to Health Centers Torbat Hydariein the Northeast of Iran, in 2011 using ELISA/WB/PCR and Sequencing-Based Methods

Mahmoud Torkamani[1], Seyed Abdolrahim Rezaee[2], Houshang Rafatpanah[3], Baratali Mashkani[4]

Abstract

Background: Human T-cell lymphotropic virus type I (HTLV-I) is an oncogenic human retrovirus that causes adult T cell leukemia/lymphoma (ATL) and HTLV-1-associated myelopathy/tropical spastic paraparesis (HAM/TSP) in only 2-3% of infected people. It was previously shown that HTLV-I infection is endemic in Khorasan Razavi province, particularly in Mashhad and Neyshabour. The region is presently the largest endemic area for this virus in Iran due to several factors such as environment, immigration patterns and individual risk behaviors. The purpose of this study was to determine the prevalence and phylogenetic analysis of HTLV-I in Torbat-e-Heydarieh located, Northeastern of Iran.

Methods: Between April and June 2011, serum samples obtained from 400 randomly selected individuals screened for the presence of anti-HTLV-I antibodies by ELISA method (Dia.Pro/Italy). Genomic DNA was then extracted from peripheral blood mononuclear cells (PBMC) using PrimePrem^{TM} genomic DNA isolation kit, (GeNet Bio, South Korea). PCR for HTLV-I Tax and LTR region was performed using specific primers. Three out of five positive HTLV-I samples were selected for sequencing and phylogenetic analysis of LTR. The phylogenetic tree was built using PHYLM v2.4.5 integrated inside Geneious software.

Results: In the primary screening of the samples by ELISA, eight (2%) samples were positive for HTLV antibodies, from which only five (1.25%) cases (three males and two females) were confirmed to be HTLV-I by PCR. A significant correlation existed between prevalence of HTLV-I infection and increase age among positive cases. The results showed that HTLV-I in Torbat-e-Hydarieh belonged to the cosmopolitan subtype. The present study showed Torbat-e-Hydarieh may be a new endemic area for HTLV-I infection.

Conclusions: Our results demonstrated the existence of HTLV-I infection in Torbat-e-Heydarieh. Thus, routine screening among blood donors along with other strategies are needed for prevention of the virus transmission in this region. This also emphasizes on systemic HTLV-I screening of blood donors in other cities in Khorasan province.

Keywords: HTLV-I, Seroprevalence, phylogenetic, PCR, Iran

[1]Department of Microbiology, Jahrom Branch, Islamic Azad University, Jahrom, Iran
[2] Immunology Research Centre, Mashhad University of Medical Sciences
[3]Inflammation and Inflammatory Diseases Research Centre, Mashhad University of Medical Sciences, Mashhad, Iran
[4]Biochemistry and Nutrition Research Center, School of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran

Antibiotic Resistance of Microorganism Isolated from Blood Cultures of Newborns Hospitalized in Neonatal Ward and NICU with BACTEC System in 1390

Shahram Abdoli Oskouie[1], Farzaneh Alikhah[2], Mohammad Ahangarzadeh Rezayee[3], Babak Abdinia[4]

Abstract

Background: Resistance to antibiotics is a global problem. Reports of antimicrobial resistance patterns are different in various hospitals. Awareness of antimicrobial resistance in hospital is critical for treatment of infections. Determining of antimicrobial resistance pattern in microorganisms isolated in newborns hospitalized in children's medical center was the main goal of this study.

Methods: This is a cross-sectional study. Microorganisms isolated from blood cultures of hospitalized newborns with BACTEC system and their resistance to antibiotics was studied.

Result: From 106 positive blood cultures: CoNS (41.5%), *Candidia* (18.9%), *Klebsiella pneumonia* (17%), S.A(11.3%), *E. coli* (3.8%), NFGNB (2.8%), *Streptococcous viridians* and *Serratia* (1.9%) and *Acinetobacter spp.* (0.9%) was isolated. Eighteen cases of CoNS isolated in less than 24 hours.

Most gram- positive bacteria were resistant to antibiotics, erytromicin, oxacillin and penicillin (89.4%), ceftizoxim (91.2%), cefotaxim (92.9%), clindamycin (82.4%) and gram-negative bacteria cephalexin (100%), amikacin (90.4%), cefixim (89.6%), ceftazidim (86.2%), gentamicin (82.7%). Most effective antibiotic in G+ bacteria were vancomicin, choloramphenicol, rifampin and in G- bacteria imipenem, ciprofloxacin, choloramphenicol and cotrimoxazole.

Conclusion: These findings showed the high and worrying rate of resistance to third generation of cephalosporins was seen particularly in isolated bacteria. Fortunately, however, the rate of resistance to ciprofloxacin and carbapenems was low. These results emphasized the need for proper administration of antibiotics and further evaluation of antibiotic sensitivity patterns.

Keywords: Antibiotic, blood cultures, microorganism

[1]Sub specialist in pediatrics infectious diseases, Mashhad University of Medical Sciences, Mashhad, Iran
[2] ICN, Mashhad University of Medical Sciences, Mashhad, Iran
[3]Microbiologist, Mashhad University of Medical Sciences, Mashhad, Iran
[4]Specialist in Pediatrics Infectious Diseases, Mashhad University of Medical Sciences, Mashhad, Iran

High Frequency of Multi Drug Resistance Enterotoxigenic *Staphylococcus aureus* among Hospitalized Patients with Gastrointestinal Symptoms

Masoumeh Azimirad, Anahita Dezfulian, Zahra Hasani, Masoud Alebouyeh, Mohammad Mehdi Aslani, Mohammad Reza Zali

Gastroenterology and liver Diseases Research Center, Shahid Beheshti University of Medical Sciences, Tehran, Iran

Abstract

Background: Routine therapeutic use of some antibiotics is known to correlate with the risk of gastrointestinal abnormality in hospital setting. Despite established role of *Clostridium difficile* in causing such disorders, however, there are growing reports for involvement of enterotoxigenic *Staphylococcus aureus* in antibiotic-associated diarrhea (AAD). In this study we aimed to investigate any possible role of these toxigenic bacteria in progression of AAD among hospitalized patients with different gastrointestinal disorders.

Methods: Feces samples were collected from three hundred forty three diarrheal patients. All samples were cultured on specific culture media and grown isolates were identified with characteristic criteria. Antimicrobial susceptibility patterns of the *S. aureus* isolates were determined to twelve antibiotics by standard disk diffusion method according to the CLSI guideline. PCR results of cdd-3, tcdA, tcdB for C. difficile, and sea-sef for *S. aureus* were screened among all the isolates. Any association was finally determined among the patient's clinical data, antibiotic prescriptions, and presence of toxigenic isolates.

Results: *Cl. difficile* and *S. aureus* were isolated from 21% and 5.7% of the fecal samples, respectively. PCR results showed a frequency of 9.2 % (32) toxigenic *S. aureus* (41.9 % sea,5.4 % sec, and 2.7 % see) and 20(5.7 %) toxigenic Cl .difficile isolates (5.7 % tcdA and 5.7% tcdB), in these samples, orderly. Counting to grown colonies represent their presence in a count of $\geq 10^5$ CFU /gram of the stool samples. 12.4% percent of the enterotoxigenic *S. aureus* isolates showed MDR resistant profile.

Conclusion: The results of present study highlighted possible role of enterotoxigenic *S. aureus* strains in occurrence of AAD among hospitalized patients beside established role of *Cl .difficile*. High frequency of MDR resistance profiles among these isolates proposes their clinical importance in these patients.

Purification of Lactoferrin from *Bovine Colostrums* and Evaluation of Antibacterial Effect on *Pseudomonas aeruginosa*

Ramisa Sharbaf[1], Alireza Rafeiei[1], Fatemeh Moradian[2], Ali Barzegar[2]

Abstract

Background: Lactoferrin is an iron-binding glycoprotein involves a diverse range of biological activities. Lf is a major component of milk and is present in exocrine secretions such as tears, salvia, bile, and neutrophil granules. Lf has more potent antimicrobial activities with various range including both of gram negative and positive bacteria as well as antivirus activities.

Methods: In this study, antibacterial activity of Lactoferrin has been scrutinized after isolation and purification from cow´s colostrums against *Pseudomonas Aeruginosa*. After taking casein of milk, purification of lactoferrin was performed during two steps by ammonium sulfate precipitation and using cation exchange chromatography, CM-Sephadex C-50 resulting purified protein with 80 KDa molecular weight. Bactericidal samples were isolated from scald patients (Shahid Zare Hospital) then microbial activity confirmed by biochemical tests like oxidase, catalase and growth on TSI medium. Four concentration 400,500,600,700 µg/ml of lactoferrin were assayed. *Pseudomonas* colonies counted and compared with the control (without lactoferrin) as well as *E. coli* (DH5α, JM2163) as positive control was considered.

Results: our results suggest that 400µg/ml concentration of lactoferrin has the least inhibitory effect with 35% growth inhibitory on *Pseudomonas* and 700 µg/ml concentration of lactoferrin has the highest inhibitory effect with 86% . Therefore lactoferrin can effectively reduce the growth of *Pseudomonas Aeruginosa*.

Conclusion: Our result showed that all of lactoferrin concentrations have more effective inhibitory activity against *Pseudomonas aeruginosa*.

Keywords: Lactoferrin, isolation, purification, *Pseudomonas Aeruginosa*

[1]Molecular and Cell Biology Research Center, Mazandaran University of Medical Science, Iran
[2]Sari Agricultural Sciences and Natural Resources University, Sari, Iran

Changes in the Rate of Vancomycin Resistance in *Enterococci* Isolated from Blood Cultures in Shiraz Hospitals, 2001-2011

Fatemeh Norouzi, Gholam Reza Pouladfar, Mona Zarafshanian, Mojtaba Anvarinejad, Bahman Pourabbas, Aziz Japoni, Mehdi Kalani, Mohammad Ali Dehyadegari, Nooredin Rafaatpour

Professor Alborzi Clinical Microbiology Research Center, Shiraz University of Medical Sciences, Shiraz, Iran

Abstract

Background: Over the last decade, vancomycin-resistant enterococci (VRE) have emerged as nosocomial pathogens. VRE currently account for 20%–25% of all nosocomial enterococcal isolates in many reports. The aim of the present study was to determine the prevalence of vancomycin-resistant enterococci (VRE) in Shiraz during the two periods of Jan 2001- Dec 2006 and Jan 2010- Dec 2011.

Methods: In this study, all enterococci isolated from blood samples by BACTEC system in Professor Alborzi Clinical Microbiology Research Center were tested for their sensitivity against thirteen antimicrobials using disc diffusion method. The samples were obtained from different wards of the hospitals in Shiraz during the two above-mentioned periods.

Results: During the two periods, one hundred ninety five positive cultures were identified: seventy three within 2001-2006 and one hundred twenty two within 2010 - 2011. The VRE increased significantly in these periods: 2001- 2006, 19% and 2010-2011, 31%. The susceptibility to ampicillin was only 9% in forty nine enterococci isolated from blood samples in 2005-2006. High level gentamicin resistance (HLG) was seen in76% and 86% enterococci isolated from blood samples in 2001-2006 and 2010-2011, respectively. The susceptibility to linozolid was 99% in the enterococci isolated from blood samples in 2010-2011.

Conclusion: This study shows increased rate of VRE and multidrug-resistant enterococci in southern Iran. Regular surveillance of antimicrobial susceptibilities should be mandatory for more efficient empirical therapies.

Keywords: Antibiotic resistance, vancomycin, *Enterococci*

Characterization of Drug-Resistance Mutations of HIV-1 Isolates from Drug-Naive Patients in Kurdistan Province of Iran

Ali Mansouri[1], Shahoo Menbari[2], Mohammad Reza Zolfaghari[1], Leila Sadeghi[3], Rouhollah Vahabpour[4], Farzin Roohvand[4], Fatemeh Jahanbakhsh[5], Arash Memarnejadian[4*]

[1]Microbiology Department, Azad University, Qom branch, Qom, Iran
[2]Department of Pathology and Medical Laboratory Sciences, Faculty of Para Medicine, Kurdistan University of Medical Sciences, Kurdistan, Iran
[3]Microbiology Department, Azad University, Karaj branch, Karaj, Iran
[4]Hepatitis and AIDS Department, Pasteur Institute of Iran, Tehran, Iran
[5]Department of Virology, Tehran University of Medical Sciences, Tehran, Iran

Abstract

Background: The transmission of HIV-1 drug-resistant strains in drug naïve patients may seriously compromise the efficacy of a first-line antiretroviral treatment. Few studies have recently reported the prevalence of HIVDR in Iran, however, to better define this problem and assess the pattern of transmission of resistant strains surveillances should be continuously planned in various regions of the country. Herein, we assess the subtype and HIVDR mutations in drug-naïve HIV-infected persons in Kurdistan province of Iran.

Methods: Blood samples from a cohort of seventy HIV-infected drug-naïve intravenous-drug users (IDUs) refereeing to different counseling and testing (CT) centers in Sanandaj city were obtained. Complete protease (PR, codons 1-99) and partial reverse-transcriptase (RT, codons 41-240) regions from thirty samples with the lowest CD4 count were amplified by RT-PCR and sequenced. Drug resistance-associated mutations were detected using Stanford HIV DR Data bank and subtypes were determined by phylogenetic tree analysis.

Results: Certain majority of the samples were infected with HIV-1 CRF35_AD. Several major and minor RT-inhibitor resistance mutations were detected. Additionally, minor PR-inhibitor resistance mutations were found.

Conclusion: Our study revealed the existence of low level drug resistance strains circulating among drug-naïve IDUs. Continued surveillance of drug resistance is required for maximization of antiretroviral therapy efficacy in Iran.

Keywords: HIV drug resistance, CRF35-AD, molecular epidemiology, reverse transcriptase, protease

Investigation of the Role of Different Types of Donor with the IL-17, IL-21, and IL-23r Polymorphisms and HBV Ifection in Kidney Transplant Recipients

Sara Hejr[1], Mohammad Hossein Karimi[2], Ramin Yaghobi[2], Eskander Kamali-Sarvestani[3], BitaGeramizadeh[2], Jamshid Roozbeh[2]

Abstract

Background: *Hepatitis B* virus infection is one of the most important chronic viral diseases all over the world. Several studies have reported cytokine genes are associated with HBV chronicity, persistency and disease severity. The aim of this study is to investigate the role of donor status (cadaver vs. living) and in living donor's condition (related vs. none related) with IL-17, IL-23R and IL-21 gene polymorphisms in HBV infected kidney transplant patients with acute rejection.

Methods: Genomic DNA was extracted from plasma of 220 kidney transplant patients using a DNP Kit according to the manufacturer's instruction. The PCR-RFLP Methods were carried out for analyzing IL-21 C1472, IL-17 197GA single nucleotide polymorphisms. Also ARMS-PCR method was used for evaluating the IL-23R and IL-21 C5250T gene polymorphisms. The prevalence of HBV infection was evaluated by using a HBV PCR detection kit according to the manufacturer's instruction.

Results: The 60 of 220 (27.28%) studied kidney transplant patients were shown acute rejection and 160 of 220 (72.73%) them were not experience acute rejection. The HBV genome was detected in 52 of 220 (23.64%) kidney transplant patients. There was a significant association between IL-21CC (P= 0.01) and IL-21TT genotypes (0.01) with acute rejection in HBV infected kidney transplant recipients received kidney from cadaver. After classification of the donors/recipient relationships to related and non-related, there was no significant association was found between cytokine genotypes and alleles with acute rejection.

Conclusion: The results showed that CC genotype of IL-21C5250T is a genetic risk factor for development of acute rejection in kidney transplant recipients with HBV infection that received kidney cadaver.

Keywords: HBV, Kidney Transplantation, IL-17, IL-23R, IL-21

[1] Islamic Azad University, Jahrom branch, Jahrom, Iran
[2] Transplant Research Center, Shiraz University of Medical Sciences, Shiraz, Iran
[3] Autoimmune disease research Center, Shiraz University of Medical Sciences, Shiraz, Iran

Association of the *Cytomegalovirus* Infection with TNF-α Genetic Polymorphism in Bone Marrow Transplant Patients

Sanaz Salek[1], Ramin Yaghobi[2], Mohammad Hossein Karimi[2], Bita Geramizadeh[2], Mani Ramzi[3], Farshid Kafilzadeh[1], Zahra Malekpoor[2]

Abstract

Background: Cytokine genetic polymorphisms may have role on the pathogenesis of viruses and also affect bone marrow transplant outcomes. *Cytomegalovirus* infection and disease is one of the most important microbial diseases that have been treated post bone marrow transplant surveillance. Therefore in this study the correlation between cytokine genetic polymorphisms with *Cytomegalovirus* infection was evaluated in bone marrow transplant patients.

Methods: In a cross sectional study 150 EDTA-threaded blood samples were collected from 90 allogenic and 60 autologous bone marrow transplant patients between years 2005-2011. The genetic polymorphism of IL-12 gene was analyzed by an in-house-RFLP-PCR method. The genetic polymorphism of TNF-α gene was analyzed by an in-house ARMS-PCR method. The prevalence of *Cytomegalovirus* infection was evaluated by Antigenemia method in bone marrow transplant patients.

Results: *Cytomegalovirus* infection was found in 11 of 90 (12.2%) of allogenic and none of autologous bone marrow transplant recipients. Significant higher frequency of TNF-α (-308 G/A) GG genotype was found in *Cytomegalovirus* infected bone marrow transplant patients with GVHD symptoms (p=0.01). But significant higher frequency of IL-12 alleles and genotypes was not found in *Cytomegalovirus* infected allogenic bone marrow transplant patients with and without GVHD symptoms.

Conclusion: Diagnosis of the significant higher frequency of TNF-α (-308 G/A) GG genotype in bone marrow transplant patients with *Cytomegalovirus* infection and GVHD symptoms can enforce on the important role of TNF-α gene polymorphism in *Cytomegalovirus* related clinical outcomes post allogenic bone marrow transplantation.

Keywords: Cytokine, polymorphism, *Cytomegalovirus*, and bone marrow transplantation

[1]Islamic Azad University, Jahrom branch, Jahrom, Iran
[2]Shiraz Transplant Research Center, Shiraz University of Medical Sciences, Shiraz, Iran
[3]Bone Marrow Transplant Unit, Neemaze Hospital, Shiraz University of Medical Sciences, Shiraz, Iran

Identification and Determination of Antimicrobial Susceptibility Patterns in Isolated Clinical *Enterococci* in Tehran's Hospitals During 1391

Reza Mirnejad[2], Yalda Ghanbari[1], Abbasali Imani Fooladi[3], Mohammad Hossein Shahhosseini[4]

[1]Department of Biology Science and Research Branch, Islamic Azad University, Tehran, Iran
[2]Molecular Biology Research Center, Baqiyatallah (a.s.) University of Medical Sciences, Tehran, Iran
[3]Applied Microbiology Research Center, Baqiyatallah University of Medical Sciences, Tehran, Iran
[4]Department of Microbiology, Shareh Ghodes Branch, Islamic Azad University, Tehran, Iran

Abstract

Background: The objective of this study was to identify and determine antibiotic resistance of isolated clinical *Enterococcus* in Tehran's Hospitals during 1391.

Methods: 63 *Enterococcus* strain were isolated from clinical sample of patients who refer to different section of Baqiyatallah hospital. These samples identified by the common microbiology and biochemistry Methods and the irsensitivity to several antibiotics (vancomycin, teicoplanin, tetracycline, gentamicin, erythromycin, ciprofloxacin, chloramphenicol, linezolid) by the Kirby-Bauer disk diffusion method were evaluated.

Results: According to the screening test, from sixty three investigated isolated *Enterococci*, 77% belong to the *E. feacalis* species and 23% belong to the *E. feacium* species. Between these species the most resistant respectively was belong to the tetracycline(92%), erythromycin(69%), ciprofloxacin(38%), gentamycin (35%) and cloramphenicol (30%), in addition all strains were sensitive to tiecoplanin. Besides, only one strain of *E. feacalis* was resistant to the two antibiotics of vancomycin and linezolid.

Conclusion: Although investigated isolated *Enterococcus* were sensitive to tiechoplanin and vancomycin, plenty of *Enterococcus* strains resistance to vancomycin specially in Tehran's hospitals are insignificant; but, likely the increase related to the risk of high resistance of strains to the other antibiotics is possible and the order of drugs administration should be noticed.

Keywords: *Enterococcus feacalis*, *Enterococcus feacium*, Antibiogram, Antibiotics resistance

Nucleotide Changes of ERG11 Gene Causing Resistance of Vaginal *Candida albicans* Isolated against Fluconazole in Tonekabon City

Sajad Amani[2], Ayat Nasrollahi Omran[1], Ali Nazemi[3]

[1]Department of Medical Mycology, Faculty of Medical Sciences, Islamic Azad University of Tonekabon Branch, Tonekabon, Iran
[2]M.S of Microbiology, Islamic Azad University of Tonekabon Branch, Tonekabon, Iran

Abstract

Background: Drug resistance to azoles in *Candida*, especially fluconazole is due to different factors, and molecular mechanisms that created these resistances. Excess expression of number of pumping genes or creating point mutation in ERG11 gene as a target enzyme is some mechanisms. This study is evaluating nucleotide changes of ERG11 gene and is considered as one of purposed assumptions for gene resistance of *Candida* against fluconazole.

Methods: Fifty prepared samples from patients to vulvovaginitis have studied. After culturing in medium of SDA and of chrom agar the yeast has been identified. Then MIC was determined for identified yeast. DNA extracted from samples of *Candida albicans* resistance to fluconazole. The full duplicated genes ERG11through Real-time. PCR and identify fragments containing the SNP by the High Resolution. Melting point difference was the presence SYT_9color. The different groups based on the melting point of the sequence were determined by PCR-Sequencing. ERG11 gene sequences for each sample with normal sequence aligned with the software and identify the types of mutations in finally done.

Results: We have seen in the survey conducted in twenty fluconazole-resistant yeast *Candida albicans* ERG11 gene changes in amino acid. That may cause mutations in the ERG11 gene of *Candida albicans* resistant to fluconazole.

Conclusion: ERG11 gene expression has seen among *Candida albicans* of fluconazole resistance.

Keywords: *Candida albicans*, Fluconazole, ERG11 gene

Poster Presentations
Third day

New Genetic Variations of *Plasmodium Vivax* Dihydropteroate Synthase Gene

Fatemeh Soghra Maghsoodloorad[1], Nahid Hosseinzade Sardarabadi[2], Ali Haghighi[2], Latif Gachkar[3], Sharifi Sarasiabi[4], Ehsan Nazemalhosseini Mojarad[5]

[1]Dept. of Parasitology and Mycoloy, School of Medicine, Golestan University of Medical Science, Gorgan, Iran
[2]Dept. of Parasitology and Mycoloy, School of Medicine, Shahid Beheshti University of Medical Science, Tehran, Iran
[3]Tropical and Infectious Diseases Research Center, Shahid Beheshti University of Medical Science, Tehran, Iran
[4]Paramedical faculty, Hormozgan University of Medical Sciences, Bandar Abbas, Iran [5]Research Center for Gastroenterology and Liver Diseases, Shahid Beheshti University of Medical Sciences, Tehran, Iran

Abstract

Background: Molecular markers are useful to recognize mutations in *P. vivax*. This study was done to analyze mutations in *P. vivax*'s Dihydropteroate Synthetase Gene at codons 382, 383, 512,553, 585 which are related to antifolate drug resistance.

Methods: *P. vivax* was isolated from endemic areas of malaria in the border of Sistan and Baluchestan province in Iran, from June 2008 to November 2010.

Results: All forty isolated samples were analyzed for pvdhps gene using PCR, Semi-nested PCR and sequencing Methods. After sequencing analysis, one novel mutation was found at codon 459.

Conclusion: In spite of the fact that antifolate drugs are not prescribed for *P. vivax* malaria, observed mutant alleles in pvdhfr and pvdhps genes are probably due to exposure of P.vivax to fansidar drug.

Keywords: Dihidropteroate synthetase gene, *Plasmodium vivax*, Sistan and Baluchestan province

Clinical Comparison of the Effects of Periodontal Treatment with Azithromycin

Majid Reza Mokhtari, Seyyed Ali Banihashem, Fateme Farazi

Abstract

Background: Antibiotics are used adjunctively to scaling and root planning (SRP) for treatment of periodontal disease. The aim of this study was to evaluate the clinical effects of systemic Azithromycin (AZM) as an adjunct to SRP in the treatment of patients with chronic periodontitis

Methods: This study was a double-blinded, randomized clinical trial in which 49 patients with chronic periodontitis participated. Patients were randomly divided into 2 groups: The test group which received SRP plus AZM (two pills for first day, one pill (250mg) the day before scaling, and one pill a day for four days after scaling) and the control group which received SRP plus placebo with the same dose. Clinical indices including Probing Pocket Depth (PPD), clinical Loss of Attachment (LOA), Gingival Index (GI),and Plaque Index (PI) were measured at the baseline and 3, 13, and 25 weeks after treatment.

Results: The mean LOA and PPD in the test group were significantly less than the control group after twenty five weeks from baseline. There was no significant difference of other indices between the two groups at each time point. Over all, the mean LOA and PPD were less in the test group than the control group at all times. The mean PI and GI were always less in the test group except at the 3rd week from baseline. All four mentioned indices showed further reduction in the test group during time.

Conclusion: The adjunctive use of systemic azithromycin showed significant clinical benefit in the treatment of chronic periodontitis.

Department of Periodontics, School of Dentistry, Mashhad University of Medical Sciences, Mashhad, Iran

Keywords: Azithromycin, Periodontitis, Treatment

Newcastle Disease and Avian *Influenza A* Virus in Migratory Birds in Wetland of Boushehr, Iran

Mohammad Javad Mehrabanpour[1], Parvin Dokht Fazel[2], AbdollahRahimian[1], Mohammad Hosein Hosseini[1], Hosein Moein[3], Mohammad Amin Shayanfar[1]

[1]Department of Virology, Razi Vaccine and Serum Research Institute Shiraz, Iran
[2]Islamic Azad University Jahrom Branch, Jahrom, Iran
[3]Bushehr Enviroment Protection Office, Boushehr, Iran

Abstract

Background: Wild birds are considered to be the natural reservoir of *Newcastle Disease* Virus (NDV) and Avian *Influenza Virus* (AI) and are often suspected to be involved in outbreaks in domesticated birds. The objective of the present study was to determine ND and AI infection in migratory birds in the south of Iran in order to detect the possible source of these viruses to domestic poultry.

Methods: A total of four hundred forty three fecal specimens (fresh dropping and cloacal swabs) were collected from migratory and wild resident birds in the Boushehr wetlands from October 2009 to June 2010.

Results: All viruses were isolated from 3 out of 443 samples processed for virus isolation and confirmed by reverse transcriptase chain reaction (RT-PCR). NDVs were isolated from 22 (fresh fecal) samples and were identified as avian paramyxomyxovirus-1 by the results obtained from the HI test with NDV-specific antibodies and RT-PCR-method. Mortality related to NDV was reported in some chicken flocks in the south of Iran. These results, as well as other data from the literature indicate that wild birds play a minor role as a potential disseminator of NDVs and AIVS.

Conclusion: This study is the first report of NDV and AIV isolation from migratory and resident birds in the wetlands of Boushehr-Iran. In addition, our findings support the notion that wild aquatic and migratory birds may function as a reservoir for AIV and NDV in south of Iran.

Keywords: Avian *Influenza Virus*, H9, Iran, migratory birds, *Newcastle disease* virus

Two Year Monitoring of Norovirus in Children with Acute Gastroenteritis in the South of Iran

Akram Najafi[1,2], Shariat Najafi[3], Hassan Shafiei[4], Mah-Khanom Mohammadian[5]

[1]Department of Biology, Payame Noor University, Bushehr, Iran
[2]Department of Microbiology, Jahrom Branch, Islamic Azad University, Jahrom, Iran
[3]Department of Microbiology, Bushehr University of Medical Science, Bushehr, Iran
[4]Adult Emergency Room (ER), 17 Shahrivar Hospital, Borazjan, Iran
[5]Pediatric Emergencies (PE), 17 Shahrivar Hospital, Borazjan, Iran

Abstract

Background: Norovirus is one of the most common causes of acute diarrhea in both developed and developing countries, responsible for more than 50% of all gastroenteritis outbreaks around the world. This study was conducted to determine the prevalence of norovirus gastroenteritis in hospitalized children in Borazjan city, south of Iran.

Methods: In this study 375 stool samples from children aged <7 years old with severe diarrhea (>3 loose watery stools per 24 hours), admitted to Pediatrics Unit of 17 Shahrivar Hospital in Borazjan, were collected during 2008-2010. All the stool specimens were evaluated for norovirus antigen with enzyme immunoassays (EIA). Demographic and clinical data were analyzed by SPSS software.

Results: Out of total collected samples norovirus infection was detected in 47(12.53%). The highest infection rate was among children less than two years old (76.6%). Diarrhea (95.74%), vomiting (87.23%) and abdominal cramp (82.98%) were the most frequent reported clinical symptoms in children with norovirus infection. The highest of virus isolation was observed in autumn (63.83%) and the lowest in summer (6.38%) (P= 0.001). Also, there was no significant difference between the frequency of the norovirus diarrhea and the pattern of nutrition (P= 0.34).

Conclusion: Regarding to important role of viral agents in acute gastroenteritis, testing for the viral antigens may guide the clinical approach to the patients with acute diarrhea particularly in children less than two years old and during the cold seasons.

Keywords: Epidemiology, Norovirus, Gastroenteritis, Children

Prevalence Review of *Vibrio* Species Isolated from Coastal Waters of Bandar Abbas

Safora Hashemi Jokar[1], Ahmad Ali Porbabaii[2], Aref Amirkhani[3] and Mohaddeseh Khalilian[1]

[1]M.Sc, Department of Microbiology, Qom Branch, Islamic Azad University, Qom, Iran
[2]Assistant professor of Microbiology, Department of Microbiology, Qom Branch, Islamic Azad University, Qom, Iran
[3]Pasteur Institute of Iran, Department of Epidemiology, Pasteur Avenue, Tehran, Iran

Abstract

Background: *Vibrio* species have been known to be the agent of digestive and extra intestinal disorders which usually appear epidemically in some seasons of the year. In recent years, in addition to the *V. cholerae*, the role of different kinds of *Vibrio* in creation of cholerae and *pseudocholerae* diarrhea has been identified. As far as the fact that seas can be considered as one of the important ecosystems of *Vibrio* species, the aim of this study is prevalence review of *Vibrio* species in the coastal regions of south Iran in different seasons.

Methods: In this study, six hundred taken water samples of coastal waters of Bandar Abbas were evaluated from point of *Vibrio* strains in both spring and winter. For primary detection of these strains, TCBS and alkaline peptone water were used, and subsequently the final identification was carried out by biochemical tests (oxidase, motility, Indole ring, KIA and other biochemical tests such as 0% NaCl, 6% NaCl, VP and ONPG).

Results: Statistical analysis of isolated samples showed (revealed) that *V. harveyi* (2.3%), *V. cholerae* (1.7%), *V. parahaemolyticus* (1.3%), *V. furnissii* (1.2%), *V. metschinikovii* (1%), *P. shigelloides* (1%), *A. hydrophila* (0.5%), *V. vulnificus* (0.3%), *V. mimicus* (0.3%) and *V. fluvialis* (0.2%) have the highest frequency. PCR reaction was also performed to investigate the presence of ctx B gene in strains of *Vibrio cholera*e in standard conditions.

Conclusion: Based on the results no one of separated *Vibrio cholera*e had ctx B gene.

Keywords: *Vibrio*, coastal waters, ctx B gene

Isolation and Identification of *Nocardia* from Soil Samples in Isfahan Province and Study of Its Significance in Patients with Immune Deficiency

Jamshid Faghri, Samaneh Burbur

Department of Microbiology, School of Medicine, Isfahan University of Medical Sciences, Isfahan, Iran

Abstract

Background: *Nocardia* species are gram-positive, weakly acid-fast, non-motile and strictly aerobic. They serve as saprophyte bacteria in environmental sources. The presence of some *Nocardia* species in soil can widely be infectious, from skin disease to severe lung infections and in immune deficiency patients can lead to central nervous system disorders. The signs of *Nocardia* lung infection are similar to *Mycobacterium*. Therefore, identifying the influence of these bacteria especially in immune deficiency patients is very important. The aim of this study is to isolate and identify *Nocardia* from different soils in Isfahan province.

Methods: In this study *Nocardia* isolation was carried out by slip-buried method, culture on brain-heart infusion agar and Sabouraud dextrose agar medium with antibiotics, some conventional biochemical tests and Kinyoun staining.

Results: 12 out of 60 samples (20%) were positive. Their morphologies were wrinkled and chalky colonies that form filamentous branched cells which were fragmented into pleomorphic rod-shaped or coccoid elements.

Conclusion: As a result of sub-acute, acute and chronic bacterial disease in individuals with immune deficiency, isolation and identification of this bacterium is important. In comparison to other studies, it seems, *Nocardia* pulmonary infections especially in immune deficiency patients are more common that warn for the health care in such cases. Therefore, new identification Methods must be alternated with old ones.

Keywords: *Nocardia*, immune deficiency patients

Salmonella Contamination in Sausage Production in West Azarbaijan Province

Nooshin Motamadian, Mohammad Delir Rad, Amir Rahimi Rad, Elnaz Mozaffariyan, Nahideh Afrang, Neda Moradi

Food and Drug Counseling, Urmia University of Medical Sciences, Urmia, Iran

Abstract

Background: In recent years the relationship between various diseases and food has been widely studied and has achieved considerable results in this field. In the public interest to today's world, the usage of fast foods such as sausages is growing widely, due to problems of industrial societies and its consequences. However, the possibility of contamination of these products to various bacteria, including *Salmonella*, in the process of preparing, producing and maintaining these products is very high. When *Salmonella* enters from mouth to body, often cause enteritis, fever, intestinal and systemic infections for human and animals.Thus providing good food with attention to health is very important. The main aim of this paper is determination of *Salmonella* contamination in sausages with the highest consumption in the community, especially among children and adolescents.

Methods: In this study, fifty samples of sausages (25 sausages, 25 sausages) of the factories producing these products were collected in West Azarbaijan province. The test medium of peptone water (PW), Tetra Thiunate Broth (TTB), Rapaport Vassiliadis (RV), *Salmonella Shigella* agar (SSA), phenol red brilliant green agar (BGA) was used.

Results: The results indicate that all sausage samples collected in West Azarbaijan province of Iran are consistent with national standards.

Conclusion: These products are free from *Salmonella* contamination, indicating that the principles of hygiene in the production process are performed.

Keywords: *Salmonella*, Sausage, West Azarbaijan Province

Survey of Mycobacterium Tuberculosis Frequency in Tuberculosis Suspected Patients in Golestan Province

Maryam Shafipour[1*], Masoud Ghane[2], Somaye Rahimi Alang[3], Naemeh Javid[4], Sedighe Livani[4], Fatemeh Shakeri[4], Fatemeh Seyyed Bagheri[5], Ezzat Allah Ghaemi[6]

[1]Islamic Azad university of Tonekabon, Department of Microbiology, Tonekabon, Iran
[2]Islamic Azad university of Tonekabon, Department of Microbiology, Tonekabon, Iran
[3]Young Researchers Club, Islamic Azad university of Gorgan, Gorgan, Iran.
[4]Medical Sciences University of Golestan, Department of Microbiology, Gorgan, Iran
[5]Tuberculosis Center Laboratory of Golestan Province.
[6]Infection Research Center, Medical Sciences University of Golestan, Gorgan, Iran

Abstract

Background: *Mycobacterium* is one of the most pathogenic bacteria that have spread throughout the world in this way, about nine million new cases and 2-3 million deaths are reported annually around the world. The aim of this research is to investigate the frequency of *M. tuberculosis* in patients suspected of tuberculosis in Golestan province since this province is one of the main centers of tuberculosis in Iran.

Methods: Collecting of samples among 3336 suspected tuberculosis patients referred to hospitals and health center in the Golestan province for one year (2010-2011) was done. After smear preparation, acid fast staining was performed. To culture the bacteria, the Lowenstein Jansen medium was used and to identify the species of tuberculosis, various biochemical tests including morphology, pigmentation, nitrate reduction, niacin, semi-quantitative catalase, 68^{0c} catalase, tween 80 hydrolysis, tellurite reduction, tolerance to NaCl 5%, iron uptake, arylsulfatase, and growth on Macconkey agar were conducted.

Results: Among total samples collected, 319 (9.56%) samples were positive culture which 300 cases (8.99%) were identified as *M. tuberculosis* and other patients were infected with atypical Mycobacteria. Most cases observed in Gorgan city and Gonbad was the next, and most cases were in the age group above 65 years. 56.7% of tuberculosis patients were male and 43.3% were female. So there was no significant difference in terms of gender.

Collusion: In the case of Geographic distribution of the disease in the country, Golestan and Sistan and Bluchistan provinces are in the first place and Khorasan province is located in the next place. Frequency of tuberculosis in this province is estimated 35.8 per 100000 people. In most studies similar to our study, the age group of above 65 years has the highest frequency of incidence of tuberculosis.

Keywords: *Mycobacterium tuberculosis*; Tuberculosis; Golestan province; Sistan and Bluchestan province

Study of the Microbial Contamination Rate of Traditional Ice Cream Products in Tehran, March 2008- March 2011

Seyedeh Behnaz Haeri Behbahani, Elahe Shahbakhti, Vahide Moradi, Hamid Haghani Haghighi, Seyed Saeed Shariat, Jamshid Salamzadeh

Food and Drug Deputy of Shahid Beheshti Universiy of Medical Sciences, Tehran, Iran

Abstract

Background: Because of the high probability of microbial contamination of the traditional ice creams, this study designed to determine the microbial contamination of traditional ice cream products sold in Tehran from March 2008 to March 2011.

Methods: In this cross-sectional, descriptive study, the ice cream samples were collected randomly from different vendors in Tehran and were examined for their total mesophilic aerobic bacteria, *Enterobacteriaceae*, *Escherichia coli*, *Staphylococcus aureus* and mold using the specific national standards for any organism. The chi-square test, at significance level of $P<0.05$, was used to compare the level of contamination between different time periods.

Results: Ninety four percent of the samples did not meet the national microbiological standards for ice creams. Total mesophilic aerobic bacteria, *Enterobacteriaceae*, mold, *Escherichia coli* and *Staphylococcus aureus* contamination was detected in 88.1%, 100%, 73%, 23.6% and 4% of the samples, respectively. There was a significant difference between *Staphylococcus aureus* contamination of the ice creams in the Spring-Summer periods of 2008 to 2011. No other significant difference and no improvement in the microbial contamination of the ice creams during the study period were shown between different time periods in this study.

Conclusion: The high microbial load of the traditional ice creams confirms unhygienic conditions in their process of production and sale. Implementation of hygienic practices and regular control on these processes is recommended to minimize the risk of contamination.

Keywords: Traditional ice cream, microbial contamination, microbial quality

Genotyping *Salmonella* Strains Isolated from Clinical Samples in Tehran by Pulsed-field Electrophoresis (PFGE)

Zeinab Ahmadi, Reza Ranjbar, Reza Mirnjad, Meysam Sarshar

Baqiyatallah University of Medical Sciences, Molecular Biology Research Center, Tehran, Iran

Abstract

Background: Investigation of presumed outbreaks bacterial infection in hospitals often requires strain typing data to identify outbreak –related strains and genetic linkage between them. Pulsed field gel electrophoresis (PFGE) is the gold standard method for epidemiological studies of many types of bacteria e.g. *Salmonella* species that are one of the most common causes of bacterimia and gastroenteritis in human. The aim of this study was the genotyping of *Salmonella enteritidis* isolated from clinical samples in a pediatric hospital in Tehran by PFGE.

Methods: Clinical samples were obtained from different hospitals, *Salmonella enteritidis* strains were identified by biochemical and serological Methods, genetic linkage between the isolates were investigated by PFGE method.

Results: Out of forty isolates identified as *Salmonella enteritidis*, three different patterns (1a, 1b and 1c) were recognized by PFGE, 1a is the most common pulsotype including 28 isolates.

Conclusion: Results from PFGE show that the *Salmonella enteritidis* isolates with close clones are common in the studied different hospitals in Tehran.

Keywords: *Salmonella enteritidis*, PFGE, genotype

Prevalence of Pediculosis (head lice) and several of its Risk Factors in Primary School Students in Mashhad During 2010-2011

Hasan Yazdanfar, Mohsen Ghasemi, Samaneh Khalegh Nejad

Abstract

Background: Pediculusis is a global and contagious parasitic skin infection which is caused by direct contact with an infected person or indirect contact with contaminated equipments. Head louse infestation (*Pediculus humanus capitis*) is common usually between the age 6-11 years. Being aware of symptoms and prevalence of the infection, controls community in order to increase the school age popatation is effective mental health. This study was done in order to determine head lice and investigate the affecting factors on primary school girls in Mashhad was 2010-2011.

Methods: In this cross sectional study, that was conducted in 2010-2011, after coordination with the education organization of Mashhad, samples were selected randomly from twenty primary schools and from each elementary school students in several classes were selected according to the number of students. All the students were examined for infestation to louse and hair of head, back neck and car nearby to see the larve, nymph or matured louse in case of observing any of the above the cases was considered as infested, and the questionnaire was filled. Data were analyzed using Chi-Square.

Results: In 1000 examined students, 53(5/3%) persons were infected with pediculus. Analysis of results using chi2 test showed that Pediculosis has a significant relation with the number of people in the family, education and job of parents, the number of bathing per week, using shared tools, presence of personal room in homes, presence of nursing or worker in home and rate of mother's Knowledge (P< 0/05). It has an insignificant relation with grades of students, length of hair, presence of health instructor at school, use of shampoo or soap for washing their head (P>0/05).

Conclusion: The results show that prevalence of head lice in primary school girl students in Mashhad is high. Therefore to prevent and control pediculosis, promotion of individual and social health in school and increasing the awareness of parents and authorities is recommended. The role of health coach in order to monitor and control hair hygiene in students and to treat patients is necessary to prevent others from the infection.

Keywords: Pediculosis, Head lice, Primary School, Mashhad

Departement of Parasitology and Mycology, Faculty of Medicine, Islamic Azad University, Mashhad Branch, Mashhad, Iran

Epidemiology of Common Burn Wound Infections (In Women Burns Department of Imam Reza Hospital, Mashhad in 1390)

Seyed Mohammad Motamedolshariati[1], Mohammad Hassan Aelami[2], Zohreh Bonakdaran[3], Khosro Lotfian[4], Armin Mahdiani[5], Ali Khursand Vakilzadeh[6]

Abstract

Background: Burning is one of the most difficult conditions in the medical system that the patient's body can cause psychological, social and economic damaged. Burns due to the destruction of skin tissue that the body's first line of defense is the patients are very susceptible to infection. Can burn wound infection due to bacteria - fungi and viruses can cause burns and wounds a suitable environment for the growth of different species of bacteria is considered. So it is still one of the most important factors for mortality in patients hospitalized for burn wound infection.

Methods: Epidemiological study of microorganisms involved in the perception and wound infections were admitted to the study. And cross-sectional descriptive study was conducted of all patients admitted to the women burns department of Mashhad Imam Reza hospital in1390, were studied. All patients in the experimental section of the wound: direct smear and culture was performed. And then the system software SPSS fifteen were investigated and analyzed.

Results: The total number of burn patients hospitalized in 1390, was 302. The frequency of positive cultures grew organisms of patients was as follows: *Acinetobacter*: 198 cases (65.5% of cases) *Pseudomonas aeroginosa*: 80 cases (25% of cases) *Klebsiella*: 57 cases (18% of cases) *Staphylococcus aereus*: 50 cases (15.5% of cases) *Enterobacter aerogeneus*: 14 cases (4% of cases) Gram positive bacilli: 9 cases (3% of cases) *Escherichia coli*: 9 cases (3% of cases) *Proteus mirabilis*: 6 cases (2% of cases) *Candida*: 4 cases (1% of cases) Coagulas negative *Staphylococci*: 2 cases (0.5% of cases) *Citrobacter freundii*: 2 cases (0.5% of cases)

Conclusion: Considering the necessary barrier against microorganisms burned patients have been entered and during hospitalization are highly susceptible to infections, we examined the frequency of existing organisms. Previous studies conducted in various articles on the epidemiology of *Pseudomonas Aeruginosa* infection in the burned patient always has the first word, but today seems to be caused by *Acinetobacter* infections is higher than the incidence and prevalence of other microorganisms from the analysis of also shows a statistically significant difference. Therefore it is appropriate for all patients at frequent antibiogram performed according to the results of antibiotic sensitivity, antibiotic resistance and appropriate to prevent an increase in patients with *Acinetobacter* epidemiologic be burned.

Keywords: Wound infection, burned, *Acinetobacter*

[1]Professor of Reconstructive Surgery, Mashhad University of Medical Sciences, Mashhad, Iran
[2]Pediatrician, Mashhad University of Medical Sciences, Mashhad, Iran
[3]M.s of Anesthesia, Mashhad University of Medical Sciences, Mashhad, Iran
[4]B.s. of nursing, Mashhad University of Medical Sciences, Mashhad, Iran
[5]Chinese Medicine Department, School of Traditional and Complementary Medicine, Mashhad University of Medical Sciences, Mashhad, Iran

Mines Shiga Toxin *Escherichia coli* O157:H7 Strains May be Associated with Diarrhea and Hemolytic Uremic Syndrome

Maryam Moshiri[1], Yahya Tahamtan[2]

[1]Department of Microbiology, Jahrom Branch, Islamic Azad University, Jahrom, Iran
[2]Razi Vaccine and Serum Research Institute, Shiraz, Iran
Site of research: Razi Vaccines and Serum Research Institute, Shiraz, Iran

Abstract

Background: *Escherichia coli* O157 has been linked to a spectrum of disorders, including watery and bloody diarrhea, hemorrhagic colitis (HC) and Hemolytic Uremic Syndrome (HUS).It has ability to produce shiga toxin (stx). Detection of pathogenic *E. coli*O157 that does not produce stx is the objective of this study.

Methods: A total of 225 recto-anal mucosal swabs from healthy cattle in Fars province were screened in 2010-2011. Detection was performed on TSB and SMAC agar plates. PCR was conducted with sorbitol positive and negative bacterial colony.

Results: In addition, from 225 stool specimens, ten samples from ten different cattle were positive with O157 antiserum. Multiplex PCR assay showed that four *E. coli* O157 did not carry the gene for either stxs, whereas two *E. coli* O157 with mines stx harbored a chromosomal eae gene encoding intimin regards as a human pathogen, as well as the rfb O157 genes.

Conclusion: We are unable to state with certainty that stx had no role in causing the diseases. The previous data support the role of stx as a cause of bloody diarrhea. Stx does not appear to be necessary for all manifestations of the *E. coli* O157:H7 diseases. HUS might result from non-stx factors produced by *E. coli*O157:H7. Hypothesis raise the possibility that other properties of *E. coli*O157:H7 might also be sufficient to produce HUS.

Keywords: *E. coli* O157, Cattle, Stx

Studying the Prevalence of Pulmonary tuberculosis in Patients of Boo-Ali Hospital, Zahedan City between March and February 2010

Fariba Azarbooyeh[1], Roghie Gholizadeh Doranmahalleh[2], Mohammad Momeni[3], Taregh Bamedi[4]

[1]Department of Biology, Faculty of Science, Payame Noor University, Zahedan, Iran
[2]Department of Biology, Faculty of Science, Azad University, Zahedan, Iran
[3,4]Laboratory Sciences, Azad Islamic University of Zahedan, Zahedan, Iran

Abstract

Background: Pulmonary tuberculosis is one of the oldest and most well- known human diseases which have been with man since ancient times. The incidence of TB has been increasing over the past decades.

Methods: Studying the prevalence of pulmonary tuberculosis in patients of Boo-Ali Hospital in Zahedan city was done during March to February 2010. This study is descriptive and periodic which utilizes the existence of epidemiological data of patients who came to this hospital. This study employs SPSS and EPi6 softwares and square approach to analyze the obtained data.

Results: Based on this work, 180 patients in 2010 who suffered from pulmonary tuberculosis are known in the mentioned hospital. 4020 specimens were tested, of which 373 samples had a positive smear and 180 specimens had a negative smear sample (positive culture). From gender distribution point of view, 62 patients (36%) are males and 118 ones (64%) are female.

Conclusion: This study shows that the amount of positive smears of pulmonary tuberculosis is more than negative ones.

Keywords: Pulmonary tuberculosis, positive smear, negative smear, prevalence, Zahedan

Epidemiology of Tuberculosis and other Related Factors in the Province of North Khorasan, Iran; 2005-2010

Hamidreza Shoraka, Seyed Hamid Hosseini, Atefeh Avaznia, Rezvan Rajabzadeh, Marzieh Mohamadzadeh, Omid Eslami

Abstract

Background: Tuberculosis is a chronic infectious disease caused by *Mycobacterium tuberculosis* and is the single most important factor which causes death by infectious diseases. Anti-tuberculosis drug resistance has already created a major challenge in treatment of tuberculosis.

Methods: This study was a descriptive-analytic study conducted in patients with diagnosed tuberculosis in the years 2005-2010. Data related to patients suffering from tuberculosis (pulmonary and extra pulmonary) was provided by the Tuberculosis Office, Department of Disease control, Province of North Khorasan. Data were analyzed using SPSS 16 software.

Results: Six hundred and sixty nine cases of tuberculosis have been reported in North Khorasan during the years. 90.6% of the patients were newly diagnosed cases. The prevalence of the disease in the years studied was 10.6, 9.6, 13.1, 7.2, 8.14 and 17.14 respectively. 74/8% of patients had pulmonary TB, 25/2% had a removed lung and 56/8% were smearing positive. Sex ratio was 0/84 which means that a greater number of patients are females, 54/1% of smear positive pulmonary tuberculosis patients. Most patients with sputum smear test results were 3 + (44/7%) and between symptoms and diagnosis and early treatment of smear positivity were a significantly relevance.

Conclusion: There has been an increase in the spread of bacillus tuberculosis from patients to the healthy population of the province. In this province it takes an average of 6 months from the onset of symptoms to diagnosis. This can play an important role in the spread of the disease, highlighting the importance of early diagnosis.

Bojnord University of Medical Sciences, Bojnord, Province of North Khorasan, Iran

Keywords: Epidemiology, North Khorasan, Tuberculosis

Enteroviruses in Acute Myocardial Infarction

Toktam Mohamadpoor[1], Mayam Sadat Nabavinia[2], Aida Gholoobi[3], Maryam Sadat Alavi[1], Zahra Meshat[4, 5]

[1]Faculty of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran
[2]Department of Biotechnology, Faculty of Pharmacy, Mashhad University of Medical Sciences, Mashhad, Iran
[3]Department of New Sciences and Technology, Faculty of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran
[4]Microbiology and Virology Research Center, Mashhad University of Medical Sciences, Mashhad, Iran
[5]Women Health Research Center, Mashhad University of Medical Sciences, Mashhad, Iran

Abstract

Background: Myocardial infarction (MI) is a main cause of mortality worldwide. Several studies suggested that some infectious agents including viruses are associated with the pathogenesis of atherosclerosis and myocardial infarction (MI). Furthermore, several reports suggested a potential role of human enteroviruse as a possible risk factor in the pathogenesis of MI. The aim of present study was to evaluate the presence of enteroviruses genomes in patients with acute MI.

Methods: We investigated the presence of enteroviruses genomic RNA in the peripheral blood of one hundred fifteen patients with acute MI hospitalized in the Coronary Care Unit of Imam Reza and Ghaem Hospitals (Mashhad) by RT-PCR using the virus specific primers.

Results: The subject's mean (±SD) age was 63.5 (±9.4) years (range: 38-82) and 38.3 % were female. Of 115 patient specimens, three (2.6%) were positive in RT-PCR.

Conclusion: Based on the results of this study, the prevalence of enteroviruses in MI patients is considerable. More investigations are needed to determine the causal role of enteroviruses in MI.

Keywords: Myocardial infarction, Enteroviruses, Polymerase chain reaction

Rooming in and Nosocomial Sepsis in NICU of Imam Reza Hospital

Ashraf Mohammadzadeh[1], Khalil Farivar[2], Ahmad Shah Farhat[3]

[1,2,3]Neonatal Research Center, Imam Reza Hospital, Faculty of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran

Abstract

Background: Many studies showed that rooming has an effect on reducing nosocomial sepsis, cross sectional infection, diarrhea and mouth candidiasis. The aim of this study was the effect of rooming in on nosocomial sepsis.

Methods: All newborn admitted to NICU of Imam Reza hospital, were elected for prevalence of nosocomial sepsis in two years. After establishment of NICU (1991), there was no rooming in because of a limited appropriate place for mothers, but one year after that we did it successfully. Therefore we compare nosocomial sepsis one hour before and after rooming in.

Results: Forty of 911 (4.4%) in 1992 and 19 of 928 (2%) in 1993 had nosocomial sepsis (P=0.01, Z= 2.86). Both two groups were similar in sex, gestational age and birth weight. The most common organism was antrobacteria (57.5%) and auros estaphylococus (10%) in 1992 and antrobacteria (68%) and antrococ (10%) in 1993.

Conclusion: This study showed that rooming in reduced nosocomial sepsis (50%).

Keywords: Nosocomial sepsis, prevalence, newborn

Study of One Hundred Blood Culture Positive Neonatal Septicemia at NICU of Imam Reza Hospital, Mashhad, Iran

Ahmad Shah Farhat[1], Ashraf Mohammadzadeh[2], Gholamreza Khademi[3], Farid Mirzaie[4]

Neonatal Research Center, Imam Reza Hospital, Faculty of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran

Abstract

Background: Septicemia is one of the most dangerous diseases in newborns which cause neonatal mortality. There is no definitive laboratory test except blood culture for its diagnosis. We studied the laboratory test results of septicemia at NICU of Imam Reza hospital.

Methods: This retrospective study was done on batteries, type ESR, CBC and mortality of one hundred blood culture positive neonatal sepsis at NICU of Imam Reza hospital, Mashhad, Iran.

Results: This study showed that the most common bacteria were *Staphyllocous* and *Kleibseilla pneumonia* 22% respectively. WBC and ESR changes were seen in about 37.5% and 50% respectively. The mortality rate was 22% that most of them were in the first week after birth.

Conclusion: The bacteria of our study is different than other countries and WBC, ESR changes were in about half of the patients.

We must revise our empirical antibiotics. WBC and ESR are not definite and reliable lab tests in neonatal sepsis.

Keywords: Neonatal, Sepsis, laboratory

Detection of Serum Antibodies against Measles, Mumps and Rubella after Primary MMR Vaccination in Children

Sedigheh Rafiei Tabatabaei*, Abdol-Reza Esteghamati, Fatemeh Fallah, Raheleh Radmanesh, Farideh Shiva, Abdollah Karimi

Pediatric Infections Research Center, Shahid Beheshti University of Medical Sciences, Tehran, Iran

Abstract

Background: Measles, mumps and *Rubella* vaccine (MMR), is administered in a 2-dose protocol in Iran; the first dose is scheduled at twelve months of age. To determine the efficacy of MMR vaccine, IgM and IgG antibody levels were tested 4-7 weeks after primary vaccination.

Methods: A cross sectional study was performed on healthy children 12-15 months of age vaccinated at health centers affiliated with Shahid Beheshti University of Medical Sciences in Tehran from January to April 2009. Children with negative vaccination and/or clinical history for measles, mumps or *Rubella* were administered the first dose of MMR Live attenuated Vaccine. IgG and IgM antibodies were checked by enzyme linked immunoassay in serum samples 4-7 weeks after vaccination. A child was considered seropositive if antibody levels were higher than the assay cut-off level set by the ELISA kit.

Results: Samples from 240 children were checked for measles and *Rubella*; rates of seropositivity were as follows: Measles serum IgM level was higher than the assay cut-off in 71.7% of samples, and IgG in 75.8%; *Rubella* serum IgM in 71.7% and IgG in 73.8%. 190 blood samples were checked for mumps antibodies; Mumps serum IgM and IgG were positive in 68.9% and 95.3%, respectively, of our vaccine recipients. No significant relationship was found between seropositivity and age/gender.

Conclusion: IgG and IgM antibody levels were below the assay cut-off levels against measles and *Rubella* in approximately one-fourth of the children 4-7weeks after primary MMR vaccination.

Keywords: MMR vaccine, immunogenicity, measles, *Rubella*, mumps

The Relationship between Alginate Production with exoA and algD Genes in Clinical Samples of *Pseudomonas Aeruginosa*

Abdolamir Ghadaksaz[1], Abbas Ali Imani Fooladi[2], Maryam Hosainzadeh[3]

Abstract

Background: *Pseudomonas Aeruginosa* is an opportunistic nosocomial pathogen which causes serious chronic infections in immune compromised and cystic fibrosis patients. Alginate and exotoxin A are two virulence factors that are produced by algD and exoA genes, respectively. Alginate is a mucoid exopolysaccharide polymer which protects bacteria from host immune response. Exotoxin A is an extracellular enzyme which has functions such as inhibition of proteins synthesis. The aim of our study was to investigate the presence of these two genes in *P. aeruginosa* strains isolated from various clinical samples from the Baqiyatallah Hospital.

Methods: A total of 110 *P. aeruginosa* strains isolated from various clinical samples were used in this study. Phenotypic assay of alginate production was performed by Carbazole method. Also we designed two sets of specific primers for PCR to detect the presence of algD, exoA genes.

Results: Phenotypic assays showed that most of clinical strains have alginate producing ability. Also a significant relationship was obtained between phenotypic and genotypic assays in all alginate producing strains.

Conclusion: As a result, due to high frequency of algD gene, it can participate as an important virulence factor. Also because of significant association between the presence of exeA gene and the amount of alginate production, the importance of this gene is increased. Therefore our future investigation must be focused on molecular processes involved in exotoxin A and alginate production to recognize effective causes.

Keywords: *Pseudomonas Aeruginosa*, alginate, exotoxinA

[1]Department of Microbiology, Science and Research Branch, Islamic Azad University, Tehran, Iran
[2]Corresponding author: Applied Microbiology Research Center, Baqiyatallah University of Medical Sciences (BMSU), Tehran, Iran Email: imanifouladi.a@gmail.com
[3]Department of Microbiology, School of Basic Sciences, Islamic of Azad University, Zanjan, Iran

Studying Bacterial Infection of Urinary System in Mahmoud Abad

Sajad hosseinzadeh[1], Ashkan Ghasemi[1], Jafar Hosseinzadeh[1], Majid alipour[2]

Abstract

Background: Urinary system infection has still been regarded as one of the most important problems of women and men, despite the development of science and technology. The Enterobacters which usually cause urinary system infection consist of *E. coli*, S. saprophyticus, *Pseudomonas*, proteus and enterococci. Among these factors, *E. coli* is known as the most important pollution in humans. *E. coli* is the usual factor of Food poisoning. We tried to study the prevalence of this disease and clarify the importance of controlling and preventing it.

Methods: This study was performed on 213 patients suffering from urinary system infection. These people referred to Shohada hospital in Mahmoud Abad during the year 1390. The samples were cultured by EMB, blood Agar, SIM, TSIA, and were tested by IMVIC TEST, Urease test, Malonate test and were stained in gram.

Results: 143 out of 213 persons (67.13%) were infected by *E. coli* in which 73% were female. 43 out of the other 70 persons (32.86%) were infected by other bacterial Factors. 34 persons (48.57%) were infected by saprophyticus, 19 persons (27.14%) by *Pseudomonas*, 11 persons (15.71%) by proteus and 6 of them (8.57%) by enterococci. Maximum infection percentage (39%) was in the ages 40 to 65.

Conclusion: Regarding to the results, direct effect of *E. coli* bacteria in urinary system infection was for rural living women because of environmental condition and lack of hygiene in this area. This problem can be solved by hygienic notifies and avoiding consumption of raw meat, non-pasteurized milk and fruit juice, Sausages sliced, sausages, raw vegetables and unwashed salad lettuce.

Keywords: Infection, bacteria, Mahmodabad

[1]Young Researchers Club, Islamic Azad University, Babol Branch, Babol, Iran
[2]PhD in Biocellular and Biomolecular Medicine, Islamic Azad University, Babol Branch, Babol, Iran

Serologic Prevalence of Human Toxoplasmosis in Miyaneh City: Chemiluminescence Method

Jaber Davoudi[1], Meysam Nasrollahpour[2], Shahrokh Shirazi[3], Majid Zamani[4], Nayer Hanifeh Nikabad[5]

[1]Department of Veterinary Pathobiology Islamic Azad University Miyaneh Branch, Miyaneh, Iran
[2]Student of Medicine Department of Medicinal Science Islamic Azad University Tabriz Branch, Tabriz, Iran
[3]PhD student in Veterinary Parasitology Islamic Azad University of Scince and Research Tehran Branch, Tehran, Iran
[4]PhD in Clinical Pathobiology Diagnostic Laboratory in the Private Sector, Miyaneh, Iran
[5]Student Veterinary Laboratory Sciences Islamic Azad University Miyaneh Branch, Miyaneh, Iran

Abstract

Background: Toxoplasmosis is among the most common causes of human parasitic infections and other warm-blooded vertebrates, which has extensive worldwide distribution. The purpose of this study was to determine the level of human toxoplasmosis infection in Miyaneh city in 1389.

Methods: In this cross - sectional study of serum, two hundred admitted men and women to city level laboratories in the mid 1389 were randomly selected after completing a questionnaire, and the presence of IgG and IgM antibodies against *Toxoplasma Gondii* was investigated. The results were statistically analyzed using the Chi square test.

Results: Of 200 blood samples examined, 82 samples, 41% had IgG and 16 samples, 8% had IgM antibodies to meet the 68 patients with chronic infections and 14 infections were acute or sub-acute toxoplasmosis. The results showed that between toxoplasmosis and education level, age, marital status and occupation statistical relationship exists between gender, but individuals, contact with cats, soil, half-cooked meat, how to wash vegetables and history of hospitalization had no significant relationship.

Discussion: The results shows that high prevalence of Toxoplasma in Miyaneh is about the same prevalence of IgG and IgM positive shifter, somewhat higher than rates reported in similar studies conducted in the northwest region. This can be partly due to high sensitivity and specificity of quantitative Chemiluminescence technique than other Methods in the diagnosis of Toxoplasma Serology.

Keywords: Toxoplasmosis, seroprevalence, IgG, IgM, Miyaneh, Chemiluminescence

Identification of Class 1 Integron-Associated Gene Cassettes in *Salmonella enterica Serovar Typhimurium* Isolated from Human and Poultry

Farzaneh Firoozeh[1], Fereshteh Shahcheraghi[2], Taghi Zahraei-Salehi[3], Mohammad Mehdi Aslani[2], Vahid Karimi[4]

[1]Department of Microbiology and Immunology, School of Medicine, Kashan University of Medical Sciences, Kashan, Iran
[2]Department of Microbiology and Microbiology Research Laboratory, Pasteur Institute, Tehran, Iran
[3]Department of Microbiology, Faculty of Veterinary Medicine, University of Tehran, Tehran, Iran
[4]Department of Clinical Sciences, Avian Diseases Section, Faculty of Veterinary Medicine, University of Tehran, Tehran, Iran

Abstract

Background: *Salmonella enterica* serotype Typhimurium is a common cause of the food borne gastroenteritis. Food producing animals especially poultry, are the potential reservoirs of non-typhoidal *Salmonella*. The emergence of multi-drug-resistant (MDR) *Salmonella* serovars can complicate therapy. Integrons as mobile genetic elements can facilitate wide dissemination of resistant genes. Here we investigated the Class 1 integron-associated gene cassettes in *Salmonella Typhimurium* isolated from human and poultry clinical specimens.

Methods: A total of one hundred and eight *Salmonella* isolates comprising fifty eight human isolates and 50 poultry isolates were used in this study. Multiplex PCR was used to identify *Salmonella enterica* serovar Typhimurium. The antimicrobial resistance patterns of *Salmonella Typhimurium* isolates was determined by the agar disk diffusion test according to CLSI. PCR assays and DNA sequencing were used to identify gene cassette contents of class 1 integrons in resistant *Salmonella Typhimurium* isolates.

Results: In this study, 11 of 108 *Salmonella* strains, identified as *Salmonella Typhimurium* including three human and eight poultry isolates. Five (62.5%) and three (100%) poultry and human *S. Typhimurium* isolates were multidrug-resistant respectively. By PCR and sequencing, 37.5% poultry S. Typhimurium isolates and 66.6% human *S. Typhimurium* isolates were found to carry class 1 integrons and the gene cassette arrays aadA1, aadA6-orfD were identified.

Conclusion: Our study showed the high prevalence of class 1 integrons among *S. Typhimurium* isolates in human and poultry in our area. MDR was found to be strongly associated with the presence of integrons, so integrons play a crucial role in development of multi-drug resistant phenotype in *Salmonella* serovars.

Keywords: Integron, gene cassettes, *Salmonella Typhimurium*, multi-drug-resistance (MDR)

Determination of Highly Sensitive CRP (hs-CRP) in CSF for Differentiation of Bacterial from Aseptic Meningitis in Patients Admitted to Infectious Department of Ghaem and Imam Reza Hospitals

Mohammad Reza Keramati[1], Mohammad Hadi Sadeghian[2], Hosein Ayatollahi[3], Zahra Badiee[4], Hosein Shakibayi[5], Ali Moghimi Roudi[6]

[1]Associate Professor of Hematopathology, Cancer Molecular Pathology Research Center, Mashhad University of Medical Sciences, Mashhad, Iran
[2]Associate Professor of Hematopathology, Mashhad University of Medical Sciences, Mashhad, Iran
[3]Associate Professor of Hematopathology, Mashhad University of Medical Sciences, Mashhad, Iran
[4]Associate Professor of Hematology, Mashhad University of Medical Sciences, Mashhad, Iran
[5]Blood Transfusion Center, Mashhad, Iran
[6]Medical Student, Mashhad University of Medical Sciences, Mashhad, Iran

Abstract

Background: Bacterial meningitis is a fatal disease with considerable mortality and morbidity. To prevent its serious complications and mortality, urgent diagnosis and treatment is necessary. Symptoms of meningitis in different urgent patients vary and microbiological results of CSF analysis have low sensitivity and may not differentiate bacterial and aseptic meningitis. So, we need other laboratory markers for differential diagnosis. One important marker that could respond quickly is hs-CRP.

Methods: This study was done on forty patients admitted to Imam Reza and Ghaem hospitals with meningitis which LP was necessary for them. In order to determine the range of hs-CRP in CSF, 0.5-1ml of each specimen was sent to the control laboratory of Ghaem hospital.

Results: The average of hs-CRP was 2.36 in bacterial meningitis group, 1.175 in aseptic meningitis group and 1.1 in undetermined meningitis. Based on Kruscal Wallis test, the average of hs-CRP in these three groups was significantly different (p-value=0.000). Based on Pearson correlation test, there was direct linear relationship between amount of CSF protein and increasing hs-CRP (P- Value= 0.028).

Conclusion: If hs-CRP results are average or high, the diagnosis of bacterial meningitis is proposed, and clinicians should care for the presence of inflammatory or infectious process in other sites of the body. It is also important to measure hs-CRP in CSF and blood samples simultaneously.

Keywords: hs-CPR, CSF, Meningitis

Detection of Norovirus in Stool Samples by RT-PCR in five Centers in Iran

Fatemeh Fallah[1,2], Latif Gachkar[2], Farzaneh Jadali[1], Rafiei Tabatabaei[1], Narges Esmaeilnejad[1], Sadaat Adabian[1]

Abstract

Background: Gastroenteritis often includes stomach pain or spasms, diarrhea and/or vomiting, with no inflammatory infection of the upper small bowel, or inflammatory infections of the colon. It can be transferred by contact with infected food and water.Often something like an infection by viruses or less often by bacteria, their toxins, parasites, or an adverse reaction to in the diet or medications can cause inflammation.

Norovirus causes at least 50% of gastroenteritis cases resulting from foodborne illness. They are important human pathogens, which cause epidemic acute viral gastroenteritis. Current techniques used for detection of noroviruses in stool samples include multi-step viral RNA extraction and purification followed by reverse transcriptase-polymerase chain reaction (RT-PCR).

Methods: Two thousand and one hundred and seventy stool samples were tested from patients with acute Gastroenteritis that was either stored at −80 ˚C and tested retrospectively, or tested immediately after viral nucleic acid extraction in a prospective manner, including outbreaks of gastroenteritis that occurred from 5-disease center in Iran.

Results: RT-PCR was evaluated with 2170 stool samples containing 90 (4.14%) Norovirus-positive (0.97% Tehran, 0.64% Tabriz, 0.18% Mashhad, 1.57%Shiraz, 0.78%Bandar Abbas). The RT-PCR was validated with published primers for Norovirus (JV12/JV13). In both retrospective and prospective settings, the RT-PCR was equally sensitive and specific in detecting Norovirus.

Conclusion: This novel RT-PCR is an attractive technique for the rapid, specific, and cost-effective laboratory diagnosis of non-rotavirus acute gastroenteritis. RT-PCR was enough specific and sensitive for Norovirus detection.

Keywords: RT-PCR; Diagnosis of acute gastroenteritis; Norovirus

[1]Pediatric Infection Research Center, Shahid Beheshti University of medical science, Tehran, Iran
[2]Infectious disease and tropical medicine research center, Shahid Beheshti University of medical science, Tehran, Iran

Role of the Lewis and ABO Blood Group Antigens in *Helicobacter pylori* Infection

Mohammad Reza Keramati

Hematology Lab, Cancer Molecular Pathology Research Center, Imam Reza Hospital, Faculty of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran

Abstract

Background: *Helicobacter Pylori* (*H. pylori*) infection is a major risk factor for chronic gastritis, and gastric cancer. Some findings show increased frequency of these diseases in O blood group and secretors (expressing Le^b antigen), but some other findings have not characterized any relation between blood groups and this infection. Because of the fact that *H. pylori* infection and gastric cancer are common in Iran, the assessment of the pathogenesis of this infection in relation to these blood groups could be important.

Methods: In a cross sectional study, we determined the ABO and Lewis, Le^a and Le^b, blood group antigens by the tube method and anti-*H. pylori* IgG by enzyme linked immunosorbent assay in 171 Iranian blood donors, Mashhad, Iran during 2010. Differences between the Lewis and ABO phenotypes with *H. pylori* infection were tested by exact chi-square test. A P-value < 0.05 was considered as significant.

Results: *H. pylori* infection was determined in 76.6% of persons (n=131). The most common Phenotype in the ABO blood groups was O (33.9%) and in the Lewis blood groups was Le (a-b+) (54.7%). The frequencies of the ABO, Lewis and secretion phenotypes didn't reveal any significant difference between infected and non- infected persons.

Conclusion: We didn't find any significant difference between the Lewis, ABO and secretion phenotypes with *H. pylori* infection.

Keywords: ABO Blood groups, Lewis, *Helicobacter pylori*, Secretor phenotype

Definite Identification of *Leishmania major*, the Main Cause for Cutaneous Leishmaniasis, Using Nested PCR Method in Abarkouh District of Yazd Province

Narmin Najafzadeh[1,2], Parviz Parvizi[2], Alireza Zamani[1,2], Aref Amirkhani[3]

[1]Department of Microbiology, Islamic Azad University, Science and Research Branch of Fars, Iran
[2]Molecular Systematic Laboratory, Parasitology Department, Pasteur Institute of Iran, Tehran, Iran
[3]Department of Epidemiology, Pasteur Institute of Iran, Tehran, Iran

Abstract

Background: *Leishmania major* from *Trypanosomidae* family, *Leishmania* genus, is the main cause of Zoonotic Cutaneous Leishmaniasis (ZCL) in Iran. *L.major* is transmitted to human as an accidental host via *Phlebotomus papatasi* sandflies and the reservoirs for the disease are rodents of *Gerbilidae* family. Since Abarkouh district of Yazd province is a focus of ZCL in Iran, we have designed this study to firmly identify the main vector of the disease through molecular tests.

Methods: Sandflies were collected using sticky paper, aspirators and CDC miniature light traps. After dissection head and abdominal terminal was mounted for morphological identification and the rest was used for DNA extraction. *Leishmania* parasites were detected using Nested PCR, targeting ITS-rDNA gene, and were confirmed after sequencing.

Results: Of five hundred thirty six sandflies captured from Abarkouh district during 2010-2011, 150 of them were identified as female *Phlebotomus papatasi*. Which 20 of them were infected by *Leishmania* and after performing RFLP and sequencing 15 of them were confirmed to be *L. major*.

Conclusion: According to results of this study, *L. major* was definitely confirmed in *P. papatasi*. The 5 positive samples have not yet been identified as *Leishmania major*. The existence of more than one *Leishmania* parasite in the main vector of the disease is probably circulating in Abarkouh district of Yazd.

Keywords: *Leishmania major*, *Phlebotomus papatasi*, Identification, Abarkouh

Seroprevalence of *Cytomegalovirus and Rubella* Infections among Pregnant Women in Urmia Province, 2011

Arezoo Bozorgomid[1], Morteza Motazakker[2], SimaOshnouei[3]

Abstract

Background: Different viral infections are major sources of serious complications among congenitally infected children. The aim of present study was to investigate immune status of pregnant women for *Cytomegalovirus* (CMV) and *rubella* in Urmia province, North West of Iran.

Methods: A cross-sectional survey was conducted among 320 pregnant women who attended health centres of Urmia University of Medical Science during 2010-2011. Serum samples were tested for *Rubella*-specific IgG and anti-CMV IgM and IgG antibodies using LIAISON Chemiluminescence Immunoassay method.

Results: A total of 16 (5%) pregnant women were found to be susceptible to *Rubella* infection and the seropositive rate related to prior infection was 95%. 314 out of 320 (98.12%) pregnant women were seropositive for CMV-IgG and 7(2.2%) were seropositive for CMV-IgM.

Conclusion: Majority of pregnant women immunized against *Rubella*, therefore this province is recognized as a low risk region for Congenital *Rubella* Syndrome (CRS). In Urmia province, IgG seroprevalence is similar to other developing countries while IgM seroprevalence rate is very close to developed countries.

Keywords: *Cytomegalovirus*, *Rubella*, pregnancy

[1]Department of Parasitology and Mycology, Urmia University of Medical Sciences, Urmia, Iran
[2]The Reproductive Health Research Centre, Urmia University of Medical Sciences, Urmia, Iran
[3]Department of Epidemiology, Urmia University of Medical Sciences, Urmia, Iran

Study of Interleukin-10-1082G/A Polymorphism in Patients with *Hepatitis C* Virus

Samaneh Sepahi[1], Mitra Ahadi[2], Homan Mosanan Mozaffari[3], Seyed Mousalreza Hoseini[2], Hamid Reza Sima[3], Hasan Vosoghinia[2], Mohammad Reza Sarvghad[4], Abbas Esmaeelzadeh[3], Sina Rostami[1], Sina Gerayli[1], Hosain Nomanee[5], Hamed Hatami[6], Zahra Meshkat[7]

[1]Department of Biology, Faculty of Sciences, Ferdowsi University of Mashhad, Mashhad, Iran
[2]Department of Internal Medicine, Ghaem Hospital, Mashhad University of Medical Sciences, Mashhad, Iran
[3]Department of Internal Medicine, Imam Reza Hospital, Mashhad University of Medical Sciences, Mashhad, Iran
[4]Department of Infectious Disease, Imam Reza Hospital, Mashhad University of Medical Sciences, Mashhad, Iran
[5]Microbiology and Virology Research Center, Mashhad University of Medical Sciences, Mashhad, Iran
[6]Department of Laboratory Sciences, School of Paramedical Sciences, Mashhad University of Medical Sciences, Mashhad, Iran
[7]Women's Health Research Center, Mashhad University of Medical Sciences, Mashhad, Iran

Abstract

Background: IL-10 promotes the production of cytokines by Th1 cell clones. Determining polymorphisms may help choosing the appropriate antiviral treatment. The aim of this study was to determine IL-10- 1082 G/A polymorphism among *Hepatitis C* Virus (HCV) infected individuals in Mashhad, North-east of Iran.

Methods: Thirty five HCV- positive patients with different disease severities were enrolled in the study. Blood samples were taken from individuals. Next, DNA was extracted from peripheral blood mononuclear cells (PBMCs). Amplification Refractory Mutation System (ARMS) PCR, a method for determining single nucleotide polymorphisms (SNP), was used to study IL-10 1082G/A polymorphism.

Results: Of thirty five individuals, 12 had GG, 11 had GA and 12 had AA genotypes at position 1082.

Conclusion: Frequency of different genotypes (AA, GG or GA) seems to be same at position 1082. However, since control group (healthy individuals) has not yet been studied for interleukin-10 (-1082G/A) polymorphism, no comprehensive conclusion could be drawn.

Keywords: *Hepatitis C* virus, Interleukin-10, 1082G/A, Polymorphism

Serotyping of Prevalent *Escherichia coli* Isolated in Faghihi Hospital, Shiraz, Iran

Hosein Khoshkharam Roodmajani[1], Amir Hassanzadeh[1,1], Mohamad Motamedifar[1,2]

[1]Bacteriology and Virology Group, faculty of Medicine, Shiraz University of Medical Sciences, Shiraz, Iran
[2]Shiraz AIDS Research Center, Shiraz University of Medical Sciences, Shiraz, Iran

Abstract

Background: *E. coli* is the common cause of urinary tract infections (UTI) and accounts for 90% of first UTI in young women. It is the common etiologic agent of meningitis in infants. Few studies have been done in Shiraz to serotype *Escherichia coli* according to O antigen.

Methods: In this study from August 2011 to June 2012, 115 suspected samples of *E. coli* were collected from different clinical specimens such as urine and blood in Faghihi hospital as a major teaching center in Shiraz. They were identified by morphologic properties and biochemical tests. Identification of 4 O serogroups was done by a direct slide agglutination test using specific antisera (Bahar Afshan-Tehran, Iran).

Results: Of 105 *E. coli* samples, the percentages of the poly III (O44, O125, O128), poly II (O86, O127) and poly I (O26, O55, O111) serogroups were 26.7%, 4.8% and 2.85% respectively. Poly IV serogroup (O20, O114) was not identified in our samples.

Conclusion: This study indicated that three O antigen serogroups (poly III, II and I) were prevalent in Faghihi hospital and as these strains were important as the etiology of clinically observed infections, we suggest the application of diagnostic tests for serogrouping of *E. coli* strains in bacteriologic laboratories to chase those important isolates for preventative strategies.

Keywords: *E. coli*, O antigen, Serotypes

Frequency of *Chlamydia Trachomatis* Infection in Women with Cervicitis in Kermanshah

Alisha Akya[1], Mirshamsedin Hosseini[2], Masoud Olfati[3], Reza Mirnejad[4]

[1]Associate Professor, Faculty of Medicine, Kermanshah University of Medical Sciences, Kermanshah, Iran
[2]Master Student of Medical Microbiology, Kermanshah University of Medical Sciences, Kermanshah, Iran
[3]Associate Professor, Faculty of Medicine, Kermanshah University of Medical Sciences, Kermanshah, Iran
[4]Associate Professor, Center for Molecular Biology Research, Baghiatellah University, Tehran, Iran

Abstract

Background: Sexually Transmitted Diseases (STD) are among the common infectious diseases in various countries. One of the most common bacterial agents for STD is *Chlamydia trachomatis*. The molecular techniques are used to diagnose this bacterium and have a high sensitivity and specificity. This study aimed to test the frequency of *Chlamydia trachomatis* infection in women with cervicitis in Kermanshah.

Methods: Two hundred and fifty five women with cervicitis who referred to medical centers in Kermanshah were included in this study. Endocervical samples were obtained using Dacron swabs and put in BPS buffer and carried to the Lab. The clinical symptoms of patients were also recorded. *Chlamydia trachomatis* was detected using specific primers and PCR technique.

Results: From 255 samples, C. trachomatis was detected in 8 samples (3.1). The prevalence of infection was higher in women under 25 years old.

Conclusion: This study showed that the prevalence of *Chlamydia trachomatis* infection in Kermanshah is relatively low which is consistent with the results of studies in other Middle East countries.

Identification of *Salmonella enteritidis* by a Multiplex PCR Assay from Different Birds in Various Regions of Iran

Marzieh Eyn-nam nam*[1], Mitra Salehi[1], Nader Mosavari[2], Zeinab Hatami[1], Roya Razavipoor[1]

Abstract

Background: Most *Salmonella* serotypes were isolated from infected individuals, are *Salmonella enterica* serovar Enteritidis which is reported in previous studies. The purpose of this study was to isolate *Salmonella* of different birds and identification of *Salmonella enteritidis* using multiplex-PCR method.

Methods: Samples used in this experiment, respectively, were collected from North and West aviculturesof Iran and also several Maintenance centers for birds in Tehran. Initially identified were performed by biochemical tests. Genomic DNA of standard strains of *Salmonella* and other bacteria were extracted.Then For accurate identification of species, all three pairs of primers were added simultaneously to the main mix (Master Mix).Proliferation was performed in pre-programmed thermal cycler. Finally, the electrophoresis of PCR products was examined.

Results: Review of electrophoresis bands of the samples tested, and standard strains with desired size, makes it clear that Primers used are proprietary. Because, they did not create another product with none of the Gram-positive and-negative bacteria specially other *Enterobacteriaceae*.

Conclusion: By using this method; it is possible to identify the several pathogens in a sample simultaneously, and mixed infections can be diagnosed. Based on this study, Multiplex PCR will be considered as an accurate and relatively rapid method to detect and differentiate *Salmonella enteritidis* from other species of S*almonella* and other Enterobacteriaceae.

Keywords: *Salmonella* enteritidis; Genome; Multiplex PCR

[1]Department of Microbiology, North Tehran Branch, Islamic Azad University, Tehran, Iran
[2]Vaccines and Serum Research Institute of Razi, Karaj, Iran

Respiratory Viral Infections in Iranian Patients with Exacerbation of Chronic Obstructive Pulmonary Disease

Seyyedeh Somayeh Hosseini[1*], Behrooz Emamzadegan[2], Fatemeh Roodbari[3], Hamidreza Jamaati

Abstract

Background: Chronic obstructive pulmonary disease is a major cause of morbidity and mortality worldwide. There is increasing evidence that implicates viral infections as a major risk factor for exacerbations of chronic obstructive pulmonary disease (ECOPD).The aim of this research was to study the epidemiology of viral infections in exacerbated patients with chronic obstructive pulmonary disease.

Methods: In this descriptive cross-sectional study respiratory syncytial viruses (RSV), *Influenza Virus*es A, B and C, Para *Influenza Virus*es 1, 2 and 3, *picornaviruses*, *corona viruses, adenoviruses*, HMPV (human metapneumovirus) and human bocavirus (HBOV) were screened using nested PCR from 111 sputum, nasal lavage, and throat wash samples of patients with COPD exacerbation.

Results: A total of 43.24% of samples were positive for under study viruses. *Influenza Virus*es, RSV, *parainfluenza*, *picornaviruses*, *corona viruses*, *adenoviruses*, HMPV and HBOV were detected in 3.6% (2 cases had type A and 2 cases had type C), 2.7% (all had type B), 1.8% (all had type 1), 21.6% (12 had rhinovirus and 12 had enterovirus), 17.12% (8 cases had OC43, 10 cases had 229E, and 1 case had NL63), 5.4%, 0.9% and 0.9% of under study patients, respectively. A total of 13 cases had co-infections.

Conclusion: This study is the first research on investigation of wide spectrum respiratory viral infection in patients with ECOPD in Iran. *Picornaviruses* and *corona viruses* were detected to be the most common cause of infection. Viral infection can be detected in chronic obstructive pulmonary disease exacerbation and this highlights the need for continued research by using a variety the viral agents.

Keywords: COPD exacerbation, viral respiratory infection, COPD, human *metapneumovirus*, *human bocavirus*

[1]Department of microbiology, Islamic Azad University, Jahrom branch, Jahrom, Iran
[2] AJA University of Medical Sciences, Tehran, Iran
[3] Department of Biology, Faculty of Basic Sciences, University of Mazandaran, Iran
[4]Tobacco Prevention and Control Research Center, NRITLD, Masih Daneshvari Hospital, Shahid Beheshti University of Medical Sciences, Tehran, Iran

Detection of Brucellosis by Serological Methods in Suspected Cases in Mashhad, Iran

Samaneh Saedi, Morteza Sedighpur, Zohreh Mirbagheri, Nasrin Sadeghi, Alireza Pur Reza A, Kiarash Ghazvini, Hadi Safdari

Microbiology and Virology research Center, Avicenna Research Institue, Mashhad University of Medical Sciences, Mashhad, Iran

Abstract

Background: Brucellosis is still a major healthcare problem with various clinical signs and diagnostic Methods. The aim of this study was to estimate the prevalence of Brucellosis among suspected cases in Mashhad during 2011 – 2012.

Methods: This study was performed in Mashhad, since April 2011 to May 2012. Sera were obtained from one hundred sixty six patients suspected of *Brucella* and some Sera were collected from ten healthy donors for control. Rose Bengal Test (RBT) as the initial screening test, wright and 2ME tests as the standard tests were performed to assign antibody titer and then IgG and IgM were evaluated by ELISA (Enzyme Linked Immunosorbent Assay).

Results: Among one hundred sixty six serum samples, Rose Bengal Test detected forty (%24) serum positive. Then wright and 2ME tests performed on these samples which detected sixty (%36) positive cases. ELISA was carried out on all one hundred sixty six cases and detected eighty two (%42) IgG positive with high titer, ELISA IgM detected twenty two (%13) sera positive and ten controls had a negative ELISA.

Conclusion: According to the results, *Brucella* remains endemic in this region. ELISA results and following-up the negative sera in screening tests with ELISA reveal that RBT has low accuracy in detection of Brucellosis in chronic phase. But ELISA IgM results were consistent with this agglutination test. After performed screening tests on suspected cases it is better wright and ELISA to be done.

Keywords: Brucellosis, ELISA Test, 2ME- wright

RFLP, Sequencing and Phytogenic Analysis of ITS-rDNA and Microsatellite; Methods for Firm Identification of *Leishmania* Parasite in Vectors, Reservoirs and Suspected Patients of Zoonotic Cutaneous Leishmaniasis in Turkmen Sahara, Iran

Parviz Parvizi[1*], Asad Mirzaei[2], Narmin Najafzadeh[3], Ahmad Baghaei[1], Mona Roshanghalb[1], Soheila Rohani[4], Heshmatolah Taherkhani[5], Mahin Farahmand[6]

[1]Molecular Systematic Laboratory, Parasitology Department, Pasteur Institute Iran
[2]Medical Faculty, Ilam University of Medical Science, Ilam, Iran
[3]Department of Microbiology, Islamic Azad University, Sciences and Research Branch of Fars
[4]Parasitology Department, Medical Faculty, Shahidbeheshti University of Medical Sciences, Tehran, Iran
[5]Parasitology and Mycology Department, Medical Faculty, Golestan University of Medical Sciences, Golestan, Iran
[6]Parasitology Department, Pasteur Institute Iran

Abstract

Background: Turkmen Sahara in Iran is one of the main foci of Zoonotic Cutaneous Leishmaniasis. Although lots of studies have been done in the area on vectors, rodent reservoirs and human hosts using routine laboratory Methods, there is no record of a vast molecular investigation on all of those aspects altogether. *Leishmania* parasites were detected simultaneously on those cases targeting ITS-rDNA and microsatellite genes.

Methods: DNA samples were extracted from samples of thorax and abdomen of sandflies, rodent ears, and lesion of suspected patients. ITS-rDNA and microsatellite genes were amplified. *Leishmania* species were identified using BsuRI enzyme and RFLP Methods. *Leishmania* species were confirmed using sequencing, phylogenic analyses and molecular software.

Results: *Leishmania major, L. turanica*, and *L. gerbilli*, and also new specie close to *L. gerbilli* were identified in sandflies. *L. major* and *L. turanica* were isolated from rodents and human in endemic areas of ZCL in Turkmen Sahara. *Leishmania* species were firmly identified. More new haplotypes of *L. major* were found in sandflies.

Conclusion: After Comparison between *Leishmania* sequences of our results and those registered in GenBank; *L. major*, *L. turanica* and *L. gerbilli*, were accurately identified and proved by RFLP, sequencing ITS-rDNA and microsatellite genes followed by phylogenic analysis, separations of *Leishmania* species were impossible with conventional Methods.

Keywords: ITS-rDNA gene, sequencing, RFLP, phylogenetic analysis, *Leishmania* species

Evaluating the Immunity against *Rubella* Before and After Mass Vaccination in Mashhad

Hamid Ahanchian, Elham Ansari, Reza Faridhosseini, Ali Khakshour, Farahzad Jabbari, Monireh Anhanchian, Mohammad Taghi Shakeri

Assistant Professor of Pediatrics, North Khorasan University of Medical Sciences, Bojnurd, Iran

Abstract

Background: *Rubella* is an exanthematatous disease of childhood, presenting with rash, fever and lymphadenopathy. In the absence of pregnancy, it is considered a mild suffering which poses no serious threats. If infection prevails during pregnancy, probability of fetal infection and congenital *Rubella* syndrome is high especially in the first 12 weeks. Prevention of Congenital *Rubella* Syndrome is the main goal of *Rubella* immunization.

Methods: On December 2003, a mass campaign for measles-*Rubella* vaccination was carried out in Iran during a rather huge plan, and more than 33 million dose of vaccine were administered to the 5- to 25-year-old populations. The present study was performed to compare immunity against *Rubella* among high school girls in Mashhad, Northeast of Iran, before and after measles-Rubella mass vaccination to evaluate Rubella vaccine-induced immunity.

Results: Before mass vaccination, 89 out of 120 samples revealed a protective antibody titer (74%) and 31 cases had a lower antibody titer than the protective level (26%). After mass vaccination, 114 out of 120 samples revealed a protective antibody titer (95%) and 6 cases did not (5%).

Conclusion: The difference was significant ($P<0.001$) which shows effectiveness of mass vaccination that caused a raise in the level of immunity from 74% to 95%.

Keywords: Immunity, Mass vaccination, Mashhad, *Rubella*

Genetic Diversity of the Apical Membrane Antigen1 (AMA1) Ectodomain as a Vaccine *Candida*te Antigen in Iranian *Plasmodium falciparum* Population

Masoumeh Sepehri[1,2], Akram Abouie Mehrizi[1], Ahmad Raeisi[3], Mehrdad Hashemi[2], Navid Dinparast Djadid[1], Sedigheh Zakeri[1]

Abstract

Background: Malaria is the most important infectious disease in the world's tropical and subtropical countries. For success in malaria elimination program in the endemic areas, the use of an effective vaccine is necessary in combine to the current tools of malaria control. Although *Plasmodium falciparum* apical membrane antigen 1 (PfAMA1) is regarded as a leading malaria blood-stage vaccine *Candida*te, but antigenic polymorphism may cause to parasite escape from host immune system and can affect vaccine efficacy. Therefore, it could be useful to identify the level of polymorphisms in ama-1 gene in Iranian P. falciparum clinical isolates in order to design an effective regional PfAMA1 malaria vaccine.

Methods: Blood specimens were collected from 50 P. falciparum patients at the Malaria Health Center in Chabahar. The Pfama-1gene was amplified by using specific primers in PCR reaction and sequenced. The obtained ama-1gene sequences were aligned and compared with ama-1 sequence of 3D7 strain.

Results: Molecular analysis of the ama-1ectodomain sequences of Iranian *P. falciparum* isolates revealed 10 different allelic forms. In addition, 38 nonsynonymus SNP were found in ectodomain of ama-1 gene.

Conclusion: The current investigation was the first molecular analysis study on ectodomain of ama-1 gene in *P. falciparum* clinical isolates from Chabahar in Sistan and Baluchistan province. The results indicate limited antigenic diversity, and thus support the potential utility of the PfAMA-1 in designing polyvalent vaccine constructs.

Keywords: Malaria, *Plasmodium falciparum*, polymorphism, apical membrane antigen 1

[1]Malaria and Vector Research Group (MVRG), Biotechnology Research Center (BRC), Pasteur Institute of Iran (PII)
[2] Islamic Azad University of Pharmaceutical Sciences
[3]National Program Manager for Malaria Control, Ministry of Health and Medical Education

Interleukin-2 Expression in Lupoid and Usual Types of Old World Cutaneous Leishmaniasis

Vahid Mashayekhi Goyonlo[1], Hesameldin Elnour[1], Klas Nordlind[2]

[1]Rsearch Center for Skin Disease and Cutaneous Leishmaniasis, Dermatology Department, Emam Reza Hospital, Faculty of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran
[2]Unit of Dermatology and Venereology, Department of Medicine, Solna, Karolinska Institutet, Stockholm, Sweden

Abstract

Background: Interleukin (IL)-2 has a central role in T cell-dependent immune responses.To determine and compare the IL-2 expression in lupoid and usual types of Old World Cutaneous Leishmaniasis (OWCL), using immunohistochemistry.

Methods: Fourteen paraffin-embedded specimens of lupoid and twelve specimens of usual types of OWCL were used. A murine monoclonal anti IL-2 antibody was used for staining by Envision technique.

Results: There were strongly stained discrete foci of staining through inflammatory infiltrates of dermis and also in basal layers of epidermis and adnexal structures, with a distinctive pattern of hot spot activity foci (mean of 9.3±6.6 versus 8.2±7.0 foci per HPF for lupoid and usual types respectively). The expression of IL-2 had no correlation to pattern of granulomatous inflammation (tuberculoid, sarcoidal or mixed suppurative).

Conclusion: IL-2 takes part in the immunologic response of granulomatous reaction of OWCL and is not statistically different between lupoid and usual types (P=0.6791).

Keywords: Leishmaniasis, IL- 2, Granulomatous reaction

Effects of Antimicrobial and Antibiotics Resistant *Lactobacillus brevis* Isolated from Traditional Yogurt Khorramabad City

Javad Hajipour[1]*, Enayat Ghahremani [2], Mahnaz Mardani [3], Sadegh Rezapour [4]

Abstract

Background: *Lactobacillus brevis* is a Gram-positive rod in dairy products that are homofermentative. This bacterial can produce bacteriocin against pathogenic bacteria, as they cause the loss of pathogenic bacteria in the body. The purpose of this study is to evaluate *Lactobacillus brevis* in dairy products (yogurt) and antibiotic resistance of this bacterium.

Methods: A total of eleven samples were collected from traditional yogurt Khorramabad and identified using phenotypic Methods (cell morphology, Gram staining, physiological and biochemical tests) and bacteriocin were extracted. Extracted bacteriocin were examined on the pathogenic bacteria (*Pseudomonas Aeruginosa*, *Proteus vulgaris*, *Staphylococcus aureus*, *E. coli*, *Bacillus cereus* and *Bacillus subtilis*) using agar well diffusion method. In other hand antibiotic resistance of this bacteria using Antibiogram method were tested.

Result: The results showed that the bacteria *Pseudomonas Aeruginosa* and E. coli have intermediate sensitive against produced bacteriocin. *Proteus vulgaris* and *Staphylococcus aureus* were sensitive and *Bacillus cereus* and *Bacillus subtilis* were resistant. *Lactobacillus brevis* were resistant against antibiotics kanamycin (30ug) trimethoprin (250 ug) and were intermediate resistance against clindamycin (2ug) tetracycline (30ug), were sensitive against amoxicillin (10ug) and erythromycin (15ug).

Conclusion: *Lactobacillus brevis* has an inhibitory effect on pathogenic bacteria and could prevent infection in vivo. These bacteria also have the appropriate antibiotic resistance against most antibiotics that due to having this benefit effects in dairy produce can having consumption and increases safety against pathogenic bacteria.

Keywords: *Lactobacillus brevis*, antimicrobial effects, antibiotic resistance, bacteriocin

[1]Senior Student of Microbiology, Islamic Azad University branch Science Research markazi, Iran
[2]Senior Student of Microbiology, Islamic Azad University branch Science Research markazi, Iran
[3,4]Assistant Professor, Member of Medical Faculty, Lorestan University of Medical Sciences, Iran

Evaluation of *Brucella* spp. Contamination of Non-Pasteurized Milk in Qom Province Using PCR Technique

Reihane Ajili[1], Mohamad Soleimani Dorjagh[2] and Mohammad Reza Zolfaghari[2]

[1]Department of Microbiology, Qom Branch, Islamic Azad University, Qom, Iran
[2]Assistant professor of Microbiology, Department of Microbiology, Qom Branch, Islamic Azad University, Qom, Iran

Abstract

Background: Brucellosis is an infectious disease that can be transmitted to human and Animals, and is caused by *Brucella* strains. Brucellosis is one of the infectious diseases that have an important significance due to its commonness between human and animal.

This disease incurs numerous losses to economy in many countries like Iran. Therefore in case of not diagnosing it on time, it could be so harmful to animal husbandry and medical care industry. In view of conventional constraints for diagnosing Malta-fever, such as low sensitivity, low accuracy, time consuming process of diagnosing and pseudo -positive and negative results, in this study we used PCR as a sensitive, exclusive, fast and inexpensive diagnosing method.

Methods: One hundred milk samples were studied by a chain reaction of the omp$_2$ gene which is exclusive to *Brucella*.

Results: PCR Electrophoresis of omp$_2$ gene showed a band of 400 widths. The PCR cloning was validated through sequencing and 10% contamination of the samples was shown.

Conclusion: Using PCR molecular method could reduce needed cost and time for diagnosis of Malta-fever.

Keywords: *Brucella*, Brucellosis, milk, Polymerase Chain Reaction

Application of Counter Current Immuno-Electrophoresis Test Using Native Antigens for Diagnosis of Suspected Patients to Hydatidosis; a Five Years Study and Survey at Shiraz Medical School

Sadjjadi Seyede Fatemeh.[1], Kazemian Sakineh[2], Sadjjadi Seyed Mahmoud[2]

Abstract

Background: Hydatidosis is one of the most important parasitic diseases between human and animals all over the world, including Iran. Diagnosis of hydatid cyst is mainly based on serological and imaging techniques. Different serological Methods have been used for determination of antibody in patients with hydatid cyst including indirect haemaglutination (IHA), complement fixation (CF), Immunoelectrophoresis (IEP), Indirect-fluorescent antibody test (IFAT), radioimmunoassay (RIA), enzyme linked immunosorbent assay, (ELISA), agglutination with latex particles (LA) and Counter Current Immuno- Electrophoresis test(CCIEP); of which CCIEP is an easy and simple method. CCIEP is based on the movement of antibodies and antigens in a semi solid medium such as a gel by the electric current. In our study, sheep hydatid cyst fluid was used as antigen and it was applied for suspected patients for several years including our survey time, five years.

Methods: A total of 1330 suspected patients were referred to the helminthology laboratory at Shiraz Medical School over a period of 5 years, 2004-2009 (1383 to 1388). Their demographic data including age, sex, location and history of surgery for the cyst and the result of CCIEP test were reviewed and analyzed with SPSS 15 software.

Results: The mean age of patients was 44 years old. Minimum and maximum age of patients was 3 and 90 years old, respectively. Distribution of patients according to sex was 39.4 percent males and 66.6 percent females. A total of 31.6 percent of those who underwent a surgery had a positive result of CCIEP. The CCIEP positive test in these patients could be due to elevated levels of immunoglobulin after the surgery or cyst rupture and release of protoscoleces during surgery. It is also possible a few small cysts have been neglected during the surgery.

Conclusion: In conclusion, the results show that CCIEP test for the patients with a history of hydatid cyst surgery will be useful. As based on the literature, a total of 11 to 30 percent of patients may have hydatid cyst relapse after surgery; so the CCIEP positive test should be considered seriously and these patients should be evaluated in terms of relapse of hydatid cysts.

Keywords: Hydatid cyst, CCIEP

[1]Department of Biology, Faculty of Sciences, Shiraz University, Shiraz, Iran
[2]Department of Medical Parasitology and Mycology, School of Medicine, Shiraz University of Medical Sciences, Shiraz, Iran

Investigating of Toxoplasma Antibodies in Women Referred to Abouzar Health Clinic in Zahedan for Marriage consultation

Mohammad Jafari Modrek[1], Malihe Metanat[2], Somayeh Jahani[3]

Abstract

Background: Toxoplasmosis, an infectious disease of worldwide distribution, is caused by the protozoan *Toxoplasma gondii*. One-third of primary Toxoplasmosis occurs during pregnancy and leads to trans-placental transmission and involvement of the fetus with devastating calcification of brain cells and death in utero. If we know the percentage of immune women, who are going to get married, we can determine the occurrence of abortion, stillbirth and fetal death due to Toxoplasmosis and also congenital Toxoplasmosis. We made our plan to determine the prevalence of *Toxoplasma* infection in women referring to the Abouzar consulting center for pre-marriage tests in Zahedan.

Methods: Two hundred and fifty women who are going to get married aged between 13-31 years old have been selected through a simple sampling for this cross-sectional and descriptive study. 2ml blood was obtained from the venous and antibodies were assessed by ELISA method.

Results: The results showed that the general prevalence of positive cases was 18%. IgG was 17.2% and of IgM was 0.8%. There was no relation between positive cases, education and way of meat consumption. But there was a relation with age.

Conclusion: Moreover, 80% of women in Zahedan city were seronegative before marriage and they were prone to acute toxoplasmosis during their future pregnancy. Therefore considering this fact and trying to omit its risk factors especially before pregnancy is very important. It seems necessary to detect immune system resistance against parasite with special Lab tests before marriage, and to consult and interact with health education program.

Keywords: *Toxoplasma Gondii*, Zahedan, IgG, IgM

[1]Asistant Professor, Department of Parasitology, Mycology and Entomology, BouAli, Central of Research Tropical and Infection Disease, Zahedan University of Medical Sciences, Zahedan, Iran
[2]Associate Professor, Bou Ali, Central of Research Tropical and Infection Disease, Zahedan University of medical Sciences, Zahedan, Iran
[3]Department of Microbiology, Islamic Azad University, Falavarjan Branch, Isfahan, Iran

Comparison of ELISA and Immunofluorescence Methods to Diagnose Toxoplasmosis in Pregnant Women in Mashhad

Hasan Yazdanfar, Anis Iranmanesh, Nahid Alizadeh

Abstract

Background: The most important diagnostic Methods for Toxoplasmosis are serological IFA (Indirect fluorescent assay) and ELISA (Enzyme Linked Immunoadsorbent Assay). The aim of this study is to compare the sensitivity and specificity of these two serologic techniques in diagnosing Toxoplasmosis in pregnant women in Mashhad Azad University hospital during 2011.

Methods: In this observational study 167 pregnant women who referred to Mashhad Azad University hospital were randomly included. Blood samples were obtained and examined for Toxoplasma antibodies with ELISA and IFA kits. The results were analyzed with paired t test and SPSS16 (the first degree error is 0/05).

Results: The mean age of patients was 26.7±5.63 years old and means gestational age was 38.26±5.81 weeks. ELISA test for 100 patients (59.9%) was negative and for 67patient (40.1%) was positive. IFA test was negative for 110 patients (65.9%) and positive for 57 patients (34.1%). Sensitivity of ELISA was 96.4 and it is specificity was 89%. Positive predictive value was also determined as 82% for ELISA.

Conclusion: Although the results of two techniques in this study were similar, but ELISA is preferred because it is less expensive, faster and easier to do. We suggest using ELISA to diagnose toxoplasmosis in pregnant women.

Department of Parasitology and Mycology, Medical School, Islamic Azad University, Mashhad Branch, Mashhad, Iran

Keywords: Toxoplasmosis, sensitivity, specificity, ELISA, IFA, pregnant women

Serological Study of Toxoplasmosis by IFA and ELISA in Pregnant Woman Admitted to Hospitals of Islamic Azad University, Mashhad

Hasan Yazdanfar[1], Nahid Nadalizadeh[1], Anis Iranmanesh[2], Mohamadreza Khakzad[2], Sima Nayeban[2]

Abstract

Background: Toxoplasmosis is one of the most common parasitic infections in fetus and immunocompromised patients which is caused by an intracellular parasite named *Toxoplasma gondeii*. In pregnant women it leads to abortion or irreversible lesions. The aim of this study is to compare the sensitivity and specificity of two serologic techniques, IFA (Indirect fluorescent assay) and ELISA (Enzyme-linked immunoadsorbent assay) in diagnosing toxoplasmosis in pregnant women in Mashhad Azad University hospitals during 2010.

Methods: In this observational study 367 pregnant women who referred to Mashhad Azad University hospitals were randomly include. Blood samples were obtained and were examined for toxoplasma antibodies with ELISA and IFA kits. Results were analyzed with paired t test and SPSS16 to compare (the first degree error is 0.05).

Results: Mean age of patients was 26.7+/- 5.63 years and mean gestational age was 38.26+/-5.81 weeks.108 patients (29.3%) had a history of one abortion and 9(2.4%) had multiple abortions. In the history just two patients had contacts with cat (1.2%) and 360(98.2%) patients had not. In this study 312 patients (85%) were living in the city and 37 patient's (10.2%) were living in village and there were no history of 18(4.8%) remained patients locations. The ELISA tests for 220 patients (59.9%) were negative and for 147 patients (40.1%) were positive. The IFA test was negative for 242 patients (65.9%) and positive for 125 patients (34.1%). The sensitivity of ELISA was 96.4 and it is specificity 89%. Positive predictive value was also determined as 82% for ELISA.

Conclusion: Although the results of two techniques in this study were similar, but ELISA is preferred because it's less expensive, faster and easier to do. We suggest using ELISA for diagnosing toxoplasmosis in pregnant women.

Keywords: Toxoplasmosis, Sensitivity, Specificity, ELISA, IFA, Pregnant women

[1]Department of Parasitology and Mycology, Faculty of Medicine, Islamic Azad University, Mashhad Branch, Mashhad, Iran
[2]Ferdovsi University, Mashhad, Iran

Neonatal Sepsis in NICU of Imam Reza Hospital in Mashhad

Somayeh Sadat Hashemian, Ashraf Mohammadzadeh, Ahmad Shah Farhat, Fereshte Yazdanpanah

Neonatal Research Center, Imam Reza Hospital, Faculty of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran

Abstract

Background: Newborn infections are serious causes of mortality and morbidity in NICU around the world. Coagula negative *Staphylococcus* is the most common cause of sepsis (48%). The aim of this study was to determine prevalence and causing organism of the sepsis, also resistance to prescribed antibiotics for the sepsis in this NICU.

Methods: All newborn with positive blood culture admitted to NICU during first 4 month of 1391 were enrolled.

Results: During the study 10 of 216 NICU admissions (4.6%) had positive culture. In 3 preterm newborn (30%) coagula positive *Staphylococcus* was determined in first day of life. Two newborn (20%) after exchange transfusion for jaundice had positive culture with entrococus and klebsiela. Four newborn that referred from other hospitals had coagula positive *Staphylococcus* and *Entrobacter* sepsis. Therefore the most common organism was coagula positive *Staphylococcus* (63%), *Entrobacter* (18%) and the others were *klebsiela*, *entrococus* and *pseudomonas*. 54% were preterm and the most common resistance to antibiotics was to cephotaxim, cefipim, penicillin, erythromycin, clindamycine.

Conclusion: This study showed that coagula positive *Staphylococcus* was the most common cause of sepsis with high resistance to antibiotics. More attention should be paid to the policy for this infection in NICU.

Keywords: Sepsis, organism, antibiotic resistance

Incidence of Cutaneous leishmaniasis Among Student of Elementary Section in Mashhad During 2009-2010

Hassan Yazdanfar, Rabeae Feizi, Morteza Esmaely

Abstract

Background: Cutaneous leishmaniasis is an important disease in our country, that according to reports of CDC, the numbers of affected persons are 20 thousands annually. In Mashhad, this disease exists as endemic in different foci and each year new focus are created in city. The purpose of this study was to determine the incidence rate of cutaneous leishmaniasis among boy students of elementary section of Mashhad and the effect of age, education grade, home type, building outside and lace of door and windows on the disease.

Methods: In this study 4157 students from 15 elementary schools during nine months of 85-86 were investigated and clinically examined. And for all of healthy and affected students questionnaires are completed. Students with scars are registered in related place in the questionnaire and obtained results are analyzed by statistical software SPSS.

Results: Incidence rate by forty eight affected persons, was 1.15% which 13 person (0/31%) had acute ulcer and 35 persons (0/84%) had scar. The most common age of affliction is more than nine years (mean 10 years) and fifth grade has the most or the damages are in the face. By regarding number of damages, affected persons by one wound are most common and from then only 27 percent of persons had a travel history to infected regions. From the view of home and door and windows lace installation, there is no meaningful difference. But from the view of building outside there is meaningful difference (P value <0/05) and is indicator of high incidence in building with out weal appearance had acute ulcer and 35 persons (0/84%) had scar.

Conclusion: Results obtained from the study show that although pollution rate of Mashhad first area is lower than other areas but disease incidence relative the previous studies in this area have increased which may be a good guidance for control and prevention of disease incidence for officials.

Department of Parasitology and Mycology, Faculty of Medicine, Islamic Azad University, Mashhad Branch, Mashhad, Iran

Keywords: Cutaneous leishmaniasis, Anthroponotic, scar, student, Mashhad

Large-Scale Culture of *Pseudomonas aeruginosa* for LPS Extraction and Detoxification as Vaccine *Candida*te

Faezeh Najafzadeh[1], Reza Shapouri[2], Mehdi Rahnema[3]

Abstract

Background: *Pseudomonas Aeruginosa* lipopolysaccharide is a key factor in virulence as well as both innate and acquired responses, that is used in construction of conjugated vaccines against it is infections. The purpose of this study is extraction of *Pseudomonas aeruginosa* LPS and it's detoxifying to preparation of antigen for produced vaccine.

Methods: After mass cultivation of bacteria and precipitate preparation, LPS was extracted with modified hot phenol method and the phenol, heat and centrifuge were used, aqueous phase was extracted and by addition of 1/2 volume in cold ethanol and TCA, the supernatant had dialyzed for 24 hours and LPS was precipitated with three times of volume in ethanol. LPS electrophoresis had done in polyacrylamide gel in the presence of SDS and then gel was isolated and stained by silver nitrate. The detoxify, LPS dissolvedina minimum amount of NaoH and after heat in gat 100° C was dialyzed for two days.

Results: Investigations showed that the modified hot phenol method with three phases of aqueous, phenol, and precipitate, the aqueous phase was considered because *Pseudomonas Aeruginosa* LPS is existence in here, and then adding ethanol, TCA and dialysis had done, a clear halo was observed by the addition of three times of volume in ethanol that LPS was isolated by centrifugation. Extraction with LAL method was tested for pyrogeny and toxicity testing and non-pyrogenesis and non-toxicity were approved.

Conclusion: The results of electrophoresis showed LPS intact bands in silver nitrate staining and toxicity test showed non-toxicity of LPS, the results using of this antigen as *Pseudomonas* infections against vaccine makes it possible.

Keywords: *Pseudomonas Aeruginosa*, Extraction, Detoxify, LPS, modified hot phenol, Electrophoresis

[1]Postgraduate student, Department of Microbiology, Zanjan Branch, Islamic Azad University, Zanjan, Iran, najafzade_f@yahoo.com
[2]Assistant Professor, Biologic Research Center, Zanjan Branch, Islamic Azad University, Zanjan, Iran
[3]Associate Professor, Biologic Research Center, Zanjan Branch, Islamic Azad University, Zanjan, Iran

Prevalence of *Legionella* by PCR in the Martyr Beheshti Hospital, Yasuj

Seyyede Maryam Mohammadinasab[1], Seyyed Abdol Almajid khosravani[2], Farshid Kafil Zade[3], Alborz Jahangiri Sisakht[4], Leyla Jafarpoor[5], Negin Sherafati[6]

[1]Microbiology, Basic Sciences, Islamic Azad University, Jahrom, Iran
[2]Yasuj University of Medical Sciences, Yasuj, Iran
[3]Microbiology, Basic Sciences, Islamic Azad University, Jahrom, Iran
[4]Department Microbiology, Yasuj University of Medical Sciences, Yasuj, Iran
[5]Microbiology, Basic Sciences, Islamic Azad University, Jahrom, Iran
[6]Microbiology, Basic Sciences, Islamic Azad University, Kazeroun, Iran

Abstract

Background: *Legionella pneumophilla* is a gram-negative bacterium which causes Legionellosis. *Legionella pneumophilla*is one of the most common factors in the incidence of nosocomial infections. Bacteria transmitted through the air particles and water resources and will involve the respiratory system. Hospital environments and the place of people at risk have high potential for growth and spread of these bacteria. The ventilation and cooling systems in recent years has caused the outbreak. Considering these problems, and due to increasing cooling systems in most places we need a fast and reliable method for detection.

Methods: After complete the questionnaire for 126 patients, the blood samples and sputum samples were collected. Then Gram stain and PCR was performed.

Results: Of the 126 samples, 35.7% men and 64.3% female and their average age was forty four years. Including chest pain 84.9%, 96% phlegm, dyspnea 87.6% and 46.6% had a history of respiratory infections, results PCR 7 patients (5.5%) were positive.

Conclusion: The results of this study coincide with clinical symptoms confirming the positive PCR Resources *Legionella pneumoniae* were caused by this bacterium can be important in terms of research and realized that PCR is a fast method to detect pneumonia can have good results in treating pneumoniae prior to wasting time.

Keywords: PCR, Sputum, *Legionella Pneumophila*, Pneumonia

Diagnostic Value of Sputum Smear Microscopy for Tuberculosis

Mohammad Reza Haghshenas, Farhang Babamahmoodi, Farzaneh Fakhraei

Mazandaran University of Medical Sciences, Sari, Iran

Abstract

Background: Tuberculosis (TB) is one of the most serious diseases in the world and leads to death of more than 2 million people annually. Diagnosis of TB is based on the detection of *Mycobacterium tuberculosis* (MT) in clinical samples with different Methods. Microscopy of smears is done directly from sputum, therefore in this study we tried to identify MT in patients who referred to Razi Hospital (North of Iran) during 2009- 2011.

Methods: Sputum specimens from 114 patients were collected 3 times, into screw-cop tight containers and MT was identified using both smear and culture techniques. After liquefaction, sputum samples with 5% sodium hypochlorite (Naocl) solution were compared and evaluated.

Results: The mean age of patients was 50+/- 30 (range 20 to 80) years. 63.2% (72 patients) were male and 36.8% (42 patients) were female. Results showed that sensitivity of smear concentration technique in samples were 52%, 57% a 58% respectively.

Conclusion: The study indicates that microscopy technique of smear is a rapid test to diagnose MT in the sputum samples. This way can help to start treatment in near 60% of patients that play a key role in controlling TB.

Keywords: Diagnostic study, Tuberculosis, Smear, *Mycobacterium Tuberculosis*

Evaluating Levels of TNF-a and IL-6 in Patients with Hydatid Cyst before and One Month after Surgical Operation Using ELISA

Mohamad Taghi Khezri[1], Majid Hasanzadeh[2]

Abstract

Background: *Cystic echinococcosis* (CE) or hydatid cyst is a severe parasitic disease caused by metacestodes (larval stage) of the tapeworm *Echinococcus granulosus*. This parasite has a cosmopolitan distribution and can infect human and a wide range of animals. Humans can act as accidental intermediate hosts. This parasite in humans triggers a humoral and cellular response. Cytokines play an important role in the human immunological response, but the exact role of cytokines in the human immune response against parasites, especially against *Echinococcus granulosus* remains unclear. In this study IL – 6, TNF–a and IgG levels in blood serum of patients with liver and lung hydatidosis were evaluated by ELISA method before and after surgical treatment.

Methods: Blood sample were collected from twenty patients with CE before and one month after surgical operation. Those patients who had not other inflammatory disease or not receiving corticostroide drugs were included in this study. CRP tested by quantitative method and IL-6, 'TNF–a' and IgG levels in serum of patients were evaluated by commercial ELISA kits.

Results: Data from hydatid patients before and one month after surgical operation were compared. Before surgical removal of the cysts, serum cytokine levels increased and declined rapidly one month after it. Significant correlation between levels of TNF-α and IL-6 showed that TNF-a declined by the time that fibrosis layer is formed.

Conclusion: These results suggest that in liver and lung hydatidosis, cytokine production contributes to the host defense mechanism against the extracellular parasite and in patients that TNF-a and IL-6 activity is undetectable in sera and do not display any immune response against parasitic antigen, the risk for re-infection may increase.

Keywords: *Cystic echinococcosis* (CE), IL-6, TNF–α, ELISA

[1]Master of parasitology, Torbat Heydarie University of Medical Sciences
[2]Member of Torbat Heydarie University of Medical Sciences

Evaluation of Toxoplasmosis Seroprevalence among 2609 Women of Childbearing Age Attended in Shahid Beheshti Hospital, Hamedan

Masoud Hamidi, Mahdi Khulojini, Hamed Bashiri, Ebrahim Mohammad Niaei, Alireza Ahanchian, Sima Tavakoli, Hadi Samadian, Reza Shiri heris

Laboratory of Shahid Beheshti Hospital, Hamedan, Iran

Abstract

Background: *Toxoplasma Gondii* (*T. gondii*) is an intracellular protozoan parasite that infects roughly a third of the world population. The aim of this study was to evaluate the prevalence of seropositivity against *T. gondii* among childbearing age women who attended the Shahid Beheshti Hospital of Hamedan.

Methods: Sample population was the women referred for marriage consultation to Hamedan Marriage Consultation Center During one year (23 September 2010 -23 September 2011). They were transferred to the laboratory of Shahid Beheshti Hospital for antibody determination. The prevalence of toxoplasma antibodies (IgG and IgM) was determined by ELISA method. The association between the seroprevalence and the variables age, education level and place of residence (urban/rural) was analyzed.

Results: Of the 2609 women sampled, 513 (29.6%) were found seropositive for anti-Toxoplasma IgG and 51 (2%) for anti-Toxoplasma IgM. There was not any relation between positive cases and age ($P>0.05$) but a significant relation was observed between IgG antibody and education level ($P<0.05$) and IgG antibody and place of residence ($P<0.05$).

Conclusion: Our study showed that according to this study 72.6% of these women were sero negative. This rate is high so a large percent of childbearing age women are prone to acquisition of active infection and there is an elevated risk of primary infection during pregnancy and the potential for congenital infection.

Keywords: Toxoplasmosis, childbearing age, Hamedan

Antimicrobial Resistance Patterns of *Escherichia coli* Isolates from Clinical Samples of Outpatients in Imam Khomeini Hospital, Tehran, Iran

Shahrzad Zamani Taghizadeh Rabe[1], Mahmoud Mahmoudi[2], Ahmad Emami[3], Ali Ahi[4]

Abstract

Background: *Escherichia coli* is the most common cause of urinary tract, wound, ear and other infections in humans. Antimicrobial resistance in *E. coli* not only in hospitals but also in the community has become an important public health problem. In response to these concerns, improving antibiotic prescribing and monitoring antimicrobial resistance has become an important strategy to reduce antibiotic resistance in *E. coli*. The aim of this study was to determine the antimicrobial susceptibility patterns of *E. coli* from clinical samples of outpatients in Imam Khomeini hospital, Tehran, Iran.

Methods: A total of 1200 samples from urine, wounds, eye discharge and other body fluids were analyzed, during 2010-2011, for identification of bacteria. Antimicrobial susceptibility testing was determined by disk diffusion method according to the current Clinical Laboratory and Standards Institute (CLSI) guideline.

Results: *E. coli* was isolated from 265 (22.08%) samples. The highest isolation rate was obtained from urine samples 112(42.26%). The extent of resistant to co-trimoxazole, ceftriaxon, ciprofloxacin and ampicillin/sulbactam, by disk diffusion method was 65%, 61%, 60% and 47%, respectively. However, significantly high degree of sensitivity rates to imipenem (99 %), piperacillin/tazobactam (96%), were recorded.

Conclusion: According to our study, high level resistance of *E. coli* to co-trimoxazole, ceftriaxon, ciprofloxacin and ampicillin/sulbactam was observed. This represents significance of regular monitoring of antimicrobial susceptibility before empiric antibiotic therapy. To overcome this problem, control of widespread use of antimicrobial drugs in medical centers is recommended.

Keywords: *Escherichia coli*, Antimicrobial resistance, Tehran

[1]Department of microbiology, Faculty of medicine, Tehran University of Medical Sciences, Tehran, Iran
[2]Department of Pathology, Imam Khomeini Hospitals' complex, Tehran University of Medical Science, Tehran, Iran
[3,4]Imam Khomeini Hospitals' complex, Tehran, Iran

Comparison of Intestinal Helminthic Infections in the Period of thirty Years in Patients Referred to Parasitology Lab of Imam Reza Hospital in Mashhad

Elham Poustchi, Abdolmajid Fata, Fariba Berenji, Bibi Razieh Hoseini Farash, Alireza Abbasian, Maryam Nakhaee, Majid Ganjbakhsh, Robabeh Izadi Jahan Parvar, Mahmood Parian

Abstract

Background: Intestinal helminthic infections are one of the major health problems that are endemic in many parts of our country. This infection can have effects on people and especially children that malnutrition and lack of physical growth can be seen in them. Aim of this study was to compare the prevalence of helminthic infections in three years of early decade of sixties with three years during 88-90 in patients who are referred to parasitology lab of Mashhad Imam Reza hospital.

Methods: This analytic-descriptive study, performed on 4344 patients in three years of early decade of sixties and in 2337 people during the three years of 1390-1388. They were referred to above laboratory after clinical inspection because of gastrointestinal symptoms or periodic health check and their samples were examined by direct examination and concentration (flotation) Methods.

Results: The results show that the number of positive helminthic cases in first three years of sixties decade were 738 (17%) and during 1389-1390 were 5 cases (0.2%). In the first three years of sixties, the highest prevalence belonged to *Hymenolepis nana*, with 376 cases (50.9%) and then 167 patients with *Ascaris lumbricoides* infection (22.6%). Number of patients with *oxyuriasis* was 77 (10.4%) and *Trichuris Trichiura* with a prevalence of 67 cases (9%). *Trichostrongylus* in 22 patients (2.9%), infection with hook worms in 16 cases (2.1%) and larvae of *Strongyloides* were observed in 4 patients. During 1388 - 1390, only 5 cases were positive, three cases for *H. nana* and two cases were related to *Oxyuriasis*.

Conclusion: One of the achievements of the health system after the Islamic Revolution is significant reduction in the prevalence of intestinal helminthic infections, especially soil-borne diseases, which can show that community awareness and knowledge about the transmission of these diseases has markedly increased and prevention and controlling measures are also well done. But training on control and prevention should be considered about worms that can infect humans directly, such as *Hymenolepis nana* and *Enterobius vermicularis*.

Parasitology and Mycology Department, School of medicine, Mashhad University of Medical sciences

Keywords: Intestinal helminthic infections, parasitology lab of Imam Reza hospital, Mashhad

Evaluation of Acute Flaccid Paralysis Cases Reported in the Area Covered by the HealthCenter 3 of Mashhadin 1390

Shiva Mirakhorlu, Arabnejad, Zahra Yazdandoost, Alireza Akbri

Expert diseases Mashhad health center3, Mashhad University of Medical sciences

Abstract

Background: An acute viral infection with a range of infections ranging from asymptomatic aseptic meningitis, paralysis and death. Fatality rate in the form of polio paralysis is usually less than 5%, and death often occurs due to Sporadic cases of epidemics often occur in summer and autumn And polio occur at any age But most patients are children and adolescents Reservoir is the only human virus and the abiotic environment in the short term disappears Respiratory and fecal-oral transmission.

Methods: Incross-sectional study of 90 survey forms were completed for the cases reported from hospitals and analyzed with Excel software program.

Results: The cases of 43/5% of the city of Mashhad 56/5% to other city has been 5/1% below one year of age7/6% age1-2 years 41% 2-5 years 46/2% over 5 years of age has been updated Onset of paralysis on 4/38% has been associated with fever and all cases were reported from hospitals And 61/5% had completed the ir vaccination And 4/56% of polio cases has been completed in less than 4 days Most cases have been reported in summer and winter times.

Conclusion: The population covered by this center Expected incidence of acute flaccid paralysis and the number 2 in the15000 population is under fifteen years Mashhad region has identified three more waiting too Sensitive indicator of the hospitals for timely reporting Patient care for active and important step to wards the eradication of polio is Thank praised the hospital staff and training that should be aimed more accurately considered.

Keywords: Polio, Education, Follow-up, Vaccinations

Immunity to *Hepatitis B* Virus in Vaccinated Medical Students

Abdolreza Sotoodeh Jahromi[1], Alireza Makarem[2], Mohammad Reza Farjam[1], Karamatollah Rahmanian[1]

[1]Department of Immunology, Jahrom University of Medical Sciences, Jahrom, Iran
[2]Department of Immunology, Student Research Committee, Jahrom University of Medical Sciences, Jahrom, Iran

Abstract

Background: *Hepatitis B virus* (HBV) has worldwide prevalence and more than 1/3 of people in the world are HBs Ag positive. HBV causes chronic hepatitis, acute hepatitis, chronic cirrhosis and hepatocellular carcinoma in adults and children. The aim this study was to evaluate immunity to HBV vaccine in vaccinated medical students.

Methods: This study was done on 135 medical students of Jahrom University of medical science who had been vaccinated three times. The obtained serum was tested by ELISA method to determine for Anti-HBs antibodies.

Results: In this study 13 (9.6%) subjects had anti-HBs titer of 10-100 (mIU/ml) and 122 (90.4%) subjects had anti-HBs titer of >100 mIU/ml. There was no correlation between immunity level and age, sex, BMI, time after last vaccination.

Conclusion: Although immunity to *Hepatitis B* was in protective level among all participants, assessment of immunity in healthcare workers after complete vaccination is recommended.

Keywords: HBV, Immunity, Medical students

IJMS
Vol 37, No 3, Supplement 1, September 2012

Properties of Essential Oil "*Myrtus communis*" to Inhibit Fungal Growth, Isolated from ICU Award Patients

Nahid Shoaie[1], Parisa Mohammadi[1], Shahla Roudbar Mohammadi[2]

Abstract

Background: Today, yeast cells exhibit enhanced resistance to the most chemicals and antifungal drugs. For this reason identification new antifungal product with fewer side effects and without cause resistance drugs is one of main aims of scientists. The object of this study is to find natural compounds in treatment of fungal infections in patients with fragile immunosystem in ICU award.

Methods: In this study fifty five clinical sample from patients of ICU award of Army Family Hospital in Tehran was assayed. Then essential oil of plant was obtained and concentration ofMyrtus communis essential oil was measured. The Minimum Inhibitory Concentration (MICs), MIC50, MIC90 of essential oil was determined according to CLSI protocol by serial microdilution method and MFC of this natural product was examined.

Results: Our results showed that all of isolated yeasts were sensitive to essential oil Myrtus communis and amount of MIC50 in *C. albicans, C. tropicalis, C. glabrata* and *C. krusei* was15/62, 7/8, 62/25 and 31/25 µg/ml, respectively.

Conclusion: Essential oil *Myrtus communis* has appropriate antifungal effect against isolated yeasts although the amount of MIC was different for all isolations. Further investigation must be done to use this product as an antifungal drug in patients with weak immune system.

Keywords: *Myrtus communis*, MIC, fungal infections

[1]Department of Biology, Faculty of Science, Alzahra University, Tehran, Iran
[2]Tarbiat Modares University of Medical Science, Tehran, Iran

New Variants of *Helicobacter pylori* cagA in Iranian Patients with Gastric Disorders

FarzamVaziri[1,2], ShahinNajarpeerayeh[1], MasoudAlebouyeh[2], TabasomMirzaei[2], NaderMaghsudi[3], MohsenJanmaleki[4], HabibollahPeirovi[4], MohammadRezaZali[2]

[1]Department of Bacteriology, School of Medical Sciences, Tarbiat Modares University, Tehran, Iran
[2]Gastroenterology and Liver Diseases Research Center, Shahid Beheshti University of Medical Sciences, Tehran, Iran
[3]Neuroscience Research Center (NRC), Shahid Beheshti University of Medical Sciences, Tehran, Iran
[4]Nanotechnology and Tissue Engineering Research Center, Shahid Beheshti University of Medical Sciences, Tehran, Iran

Abstract

Background: *Helicobacter pylori* CagA is the first bacterial oncoprotein to be identified in relation to human gastric cancer. The carboxy terminal region of CagA is characterized by the presence of a unique EPIYA motif, which is present in multiple numbers. Four distinct EPIYA segments, A to D, have been identified, that are important determinants of the virulence of CagA in *H. pylori* infections. The aim of this study was to determine the polymorphism of EPIYA segments of *H. pylori* CagA in an Iranian population.

Methods: A total of 71 isolates from patients with different gastroduodenal disorders were studied. Genotyping of the cagA variable EPIYA motif was determined by polymerase chain reaction and sequencing for all the cagA positive isolates. The resulting DNA sequences were translated in frame and analyzed using Gene Runner and CLC Sequence Viewer software.

Results: Out of 44 cagA positive isolates, the EPIYA motifs of ABC (30 isolates), ABCC (4 isolates), ABCCC (one isolate), mixed types (6 isolates) and new types (3 isolates) were detected. In these new types the sequences before EPIYA were similar to segment A, whereas the sequences after EPIYA was similar to segment B.

Conclusion: The structure of the 3′ region of the cagA gene (which contains EPIYA motifs) in our Iranian isolates is Western type (EPIYA C), which is in contrast to Asian countries such as Japan that Eastern type cagA (EPIYA D) is dominant. Emergence of the new EPIYA motif as the first report in the world is of major concern.

Keywords: *Helicobacter Pylori*, cagA, EPIYA motif

A Survey of Bacterial Contamination (Anaerobic and Aerobic) of Acute Cutaneous Leishmaniasis and Effect of Its Eleimination on Course of Lesions among Patients Referring to Clinic of Leishmaniasis, Ghaem Hospital from 1387-1389

Pouran Layegh, Kiarash Ghazvini, Fakhrozaman Pezeshkpoor, Mohammad Taghi Shakeri, Fatemeh Hadian, Akram Momenzadeh

Research center for Skin Diseases and Cutaneous Leishmaniasis, Department of Dermatology, Faculty of Medicine, Ghaem hospital, Mashhad University of Medical Sciences, Mashhad, Iran

Abstract

Background: Colonization of aerobic and anaerobic microbial agents on cutaneous leishmaniasis (CL) lesions especially acute erosive ulcerative ones has been considered in previous studies; there has been conflicting results about healing process of lesions with antibiotics. The purpose of this study was a survey of bacterial contamination (aerobic and anaerobic) of acute cutaneous leishmaniasis and effect of its elimination on improvement of results among patients.

Methods: This survey was an interventional study that has been done on 84 acute cutaneous leishmaniasis patients. Clinical individual information was recorded into questionnaire and approximately half of the patients with positive culture results were treated with antibiotics. Improvement rate was evaluated in the fallowing visits based on changing of induration's size of lesions according to therapeutic physician.

Results: Eighty four patients were evaluated, 22.6% had negative culture results and 77.4% had positive ones, and the most common pathogenic germ was *Staphylococcus aureus* (52/3%) and *Staphylococcus epidermidis* (9/5%); which among these 34.5% received antibiotics treatment. Among lesions with improvement rate 75–100%, 36.1 % had antibiotics treatment and 63.9% had not (P= 0/403).

Conclusion: With respect to the results of this study, we concluded that the most common pathogen was *Staphylococcos aureus* and elimination of simultaneous microbial agents did not have any considerable influence on improvement rate of cutaneous leishmaniasis lesions.

Keywords: Acute cutaneous leishmaniasis, Anaerobe, Aerobe, Antibiotics

Evaluation of Incidence of Herpes Family Viruses in Skin Lesions of Pemphigus Patients

Mahnaz Banihashemi, Masoud Maleki, Fakhrozaman Pezeshkpoor, Amir Hoseni Jafariyan, Mohammd-Taghi Shakeri, Mohammadreza Sharghi, Sara Hashemzade

Research center for Skin Diseases and Cutaneous Leishmaniasis, Department of Dermatology, Faculty of Medicine, Ghaem hospital, Mashhad University of Medical Sciences, Mashhad, Iran

Abstract

Background: Pemphigus is a group of blistering skin diseases that is related to auto antibodies against desmoglein 1, 3. Many reports have shown that HSV1, 2, VZV, EBV, CMV, HHV8, and HIV are triggering agents for activating and exacerbating pemphigus. In this study we want to evaluate the frequency of HSV1, 2, HHV8 and EBV in paraffin-embedded specimens of new case pemphigus patients with immunohistochemical method.

Methods: Thirty patients with pemphigus (twenty cases pemphigus vulgaris, ten cases pemphigus foliaceus) were included. Ten specimens from free margin of excised melanocytic nevus as a control group were obtained. Immunohistochemical staining for HSV1, HSV2, HHV8 and EBV was done. Statistical tests including chi-square test and kruskal-wallis test were done.

Results: Statistical differences were observed in frequency of positive staining for HSV1 in skin lesions of *pemphigus vulgaris, foliaceus* and control (P=0.041), in *foliaceus* positive staining for HSV1, was significantly more than *vulgaris* and in both groups was more than control group. There was no statistical difference in frequency of positive staining for HSV2, HHV8 and EBV in skin lesions of *Pemphigus vulgaris*, foliaceus and control but presence of HHV8 was detected in 30% of *Pemphigus foliaceus* and 15% of vulgaris patients. There was no evidence for any of these viruses in control group.

Conclusion: At the end, based on results of previous studies and our research significant prevalence of HSV1 was observed in lesions of pemphigus patients especially pemphigus foliaceus patients.

Keywords: *Herpes Simplex* viruses, *Epstein - Barr virus*, Pemphigus, Immunohistochemistry

Molecular Detection of *Escherichia coli* O157 from Patients with Diarrhea in Shahrekord in 2011

Sara Barati[1], Jahangir Kaboutari Katadj[2,3], Hossein Kaboli Boroujeni[1], Hossein Tahmasby[1,3], Samaneh Mehrabiyan[1,3], Vida Najafzadeh[1]

[1]Faculty of Veterinary Medicine, Shahrekord University, Shahrekord, Iran
[2]Department of Basic Science, Faculty of Veterinary Medicine, Shahrekord University, Shahrekord, Iran
[3]Research Institute of Zoonotic Diseases, University of Shahrekord, Shahrekord, Iran
Site of research: Faculty of Veterinary Medicine, Shahrekord, Iran

Abstract

Background: *Escherichia coli* O157:H7 is responsible for outbreaks of human intestinal diseases and fatal haemolytic-uraemic syndrome worldwide. Considering the importance of *Escherichia coli* O157:H7, the present study was conducted to PCR detection of *Escherichia coli* O157:H7 from patients with diarrhea in Shahrekord.

Methods: Altogether 234 fecal samples were collected from patients with diarrhea in Shahrekord. In the laboratory, samples were streaked onto cefixime Tellurite Sorbitol MacConkey agar as selected plating media. Suspected colonies to *E. coli* O157:H7 were tested by polymerase chain reaction (PCR).

Results: *E. coli* was isolated from 131 (56%) of 234 the samples. *E. coli* O157: H7 was not found in any samples.

Conclusion: The present study indicates that other infectious agents may play a role to cause human diarrhea in this region. Complementary studies on the cause of human diarrhea in this region are recommended.

Keywords: *Escherichia coli* O157:H7, diarrhea, PCR

Evaluation of Patient Suspected to Primary Immunodeficiency in Mashhad, Northeast of Iran

Hamid Ahanchian[1], Reza Farid, Abdolali Kharazmi, Farahzad Jabbari Azad, Abdolkarim Hamedi, Fatemeh Behmanesh

Mashhad University of Medical Sciences, Mashhad, Iran

Abstract

Background: Primary Immunodeficiency disorders are heterogeneous group of illnesses that predispose patients to recurrent infection and serious complications. Early diagnosis and treatment of these disorders reduce their complications

Methods: This epidemiological study was carried out between September 2009 During the study, all patient suspected to immunodeficiency were evaluated clinically and immunologically as needed.

Results: Forty one cases were evaluated in witch most of them had normal immune system. Eleven patients had primary immunodeficiency. The most common immunodeficiency was antibody defect following by phagocyte defects. The most presenting sign was pneumonia.

Conclusion: Primary immunodeficiency disorders are rare conditions with severe morbidity and morbidity. Early diagnosis and management can significantly reduce their complications.

Keywords: Recurrent infection, Primary immunodeficiency, Early Diagnosis

Survey of Microbial Contaminated Cream Puffs Distributed in Kermanshah Confectionaries

Sina Sadat Emami, Pegah Kargar Ghomshe, Behjat Namaki, Roya Montazeri

Kermanshah University of Medical Sciences, Kermanshah, Iran

Abstract

Background: Cream puffs are widely used in the society. They also count for a huge amount of food products; however, the contaminations available in the pastries are literally or even sometimes higher in proportion to that of pastry itself. Regard tohigh consumption and susceptibility to microbial contamination, this study was conducted to determine the frequency of contamination in cream puffs.

Methods: In this descriptive cross-sectional study 120 samples of cream-puffs were investigated in Kermanshah food and cosmetic laboratory. Coliforms, *E. coli*, *Bacillus cereus*, *Staphylococcus aureus*, yeast and molds were identified in samples by conventional microbiological tests.

Results: Result of this study showed that from 120 cream puffs, the level of contamination for coliforms was 33.75%, *E. coli* 22.5%, *Bacillus cereus* 16.5%, *Staphylococcus aureus* 15%, Mold 13.5% and Yeast 30%. They were all higher than the Standard defined by the Iranian National standards.

Conclusion: As result revealed, the rate of bacteria, Mold and Yeast contamination in cream puffs were high. This contamination rate may be due to non-pasteurized cream, persons who deal with making cream puffs or contamination during transportation. With notice to high cream puffs consumption in the society, persons who deal with and places which present it must be notified more.

Keywords: Cream puffs, Microbial contamination, Coliforms, *Escherichia coli*, *Bacillus cereus*, *Staphylococcus aureus* and Yeast and molds, Kermanshah

Study of Relation of Skin Squamous Cell Carcinoma and *Human Papilloma Virus*

Mohammad Javad Yazdanpanah[1], Nooryeh Sharifi [1], Saied Amel Jamehdar[2], Ali Sadeghian[2], Elnaz Hosseini[1]

[1]Research Center for Skin Diseases and Cutaneous Leishmaniasis, Department of Dermatology, Faculty of Medicine, Ghaem hospital, Mashhad University of Medical Sciences, Mashhad, Iran
[2]Microbiology and Virology Research Center, Avicenna Research Institute, Mashhad University of Medical Sciences, Mashhad, Iran

Abstract

Background: Numerous environmental risk factors may play a role in pathogenesis of cutaneous squamous cell carcinoma (SCC), including ultraviolet radiation (UV), chemical carcinogens, x-radiation, burns and *human papilloma virus* (HPV). Previous studies have shown that skin infection with HPV is highly prevalent in general population. The objective of the current study was to assess the association between HPV infection and SCC.

Methods: A total of thirty five patients with the previous diagnosis of SCC and 35 controls without skin cancer were enrolled in the study. Using standard protocols, DNA was extracted from the archived tumor biopsies of SCC patients. The presence of HPV DNA was determined using polymerase chain reaction (PCR) assays. To determine the high-risk/low-risk HPV genotypes, HPV DNA genotyping assay was employed.

Results: We found that HPV infection was not significantly more prevalent in the SCC patients compared with controls (p =0.09). In SCC patients, 60% of HPV infected tumor biopsies had high-risk HPV genotype, whereas no high-risk HPV genotype was detected in controls.

Conclusion: Our data revealed no further evidence of an association between HPV infection and SCC.

Keywords: *Human Papilloma virus*, Squamous Cell Carcinoma, Polymerase Chain Reaction

Recto-Vaginal Colonization of Group B *Streptococcus* in Pregnant Women in Arak

Tayebeh Khoshkhoutabar[1], Hamid Abtahi[2], Soleyman Zand[3]

[1]Department of Basic Sciences, Islamic Azad University of Arak, Arak, Iran
[2]Associate Professor of Microbiology, Faculty of Medicine, Arak University of Medical Sciences, Arak, Iran
[3]Clinical Instructor, Faculty of Nursing and Midwifery, Arak University of Medical Sciences, Arak, Iran

Abstract

Background: Group B *streptococcus* (GBS) is one of most common causes of sepsis and meningitis in neonates and of invasive diseases in pregnant women.

Methods: Recto- vaginal samples obtained from 100 pregnant women were inoculated to Todd-Hewith broth containing supplements. After re-inoculation onto sheep blood agar, group B *Streptpcocci* were identified by colony morphology, Gram stain, beta hemolysis, different biochemical test.

Results: 11(11%) of 100 pregnant women were GBS carrier; 4(36.34%) and 7(63.6%) positive for rectal and vaginal swabs, respectively.

Conclusion: Given the prevalence of 11 percent between Group B Streptococcus colonization, and infection risks of early neonatal screening for pregnant women, 35 weeks Vbalatrbh Aran is recommended to prevent infection.

Keywords: GBS, Neonatal sepsis, Recto-Vaginal colonization, Pregnancy

Serological Diagnosis of Hydatid Cyst Disease Using Complement Fixation Test in Patients Suspected of Hydatidosis in Yazd

Mohammad Hossein Anvari Tafti[1], Alireza Torki[2]

[1]Department of Medical Parasitology and Mycology, School of Medicine, Shahid Sadoughi University of Medical Sciences, Yazd, Iran
[2]Mater Student, Department of Medical Microbiology, School Medicine, Shahid Sadoughi University of Medical Sciences, Yazd, Iran

Abstract

Background: Cystic hydatid disease (Hydatidosis) is the most serious tape-worm infection common in the cattle and sheep raising area of the world. Hydatidosis in men (as an accidental host) is caused by infection with the ova containing larval stage of *Echinococcus spp.* In the last decade different techniques have been employed for serological diagnosis of hydatid disease, such as IHA, IFA, ELISA and CFT (Complement Fixation Test). The immunologic technique used in this study was CFT.

Methods: This survey is a laboratory study of cases. Sixty seven patients who were diagnosed with hydatid cyst disease are suspected on clinical examination and were referred to medical diagnostic laboratories for serological survey. Serum samples from patients were prepared in the laboratory and semi-quantitative method using commercial kits lyophylized antigens of hydatid cyst disease were tested. The Information of age, sex, date and laboratory diagnosis was recorded in the checklist and then data were analyzed using SPSS software.

Results: In a total of sixty seven patients suspected with hydatidosis, 8.35% (twenty four cases) were male and2.64% (forty three patients) female, 9% (six cases) had positive and 91% (sixty one cases) had negative test. Four patients had positive serum titer of 1.8 and two had 1.16. Positive cases were observed in females 6.11% (five cases) and male17.4% (one case). Most cases of positive tests (5.9%) were observed in over fifty years old patients.

Conclusion: Results indicate that outbreak of the disease in the city of Yazd is relatively low and in clinical diagnosis, the disease maybe confused with other similar diseases. CF titre greater than or equal to 1.8 usually indicates current infection and reliable prognosis following treatment is given by CF.

Keywords: Hydatidosis, *Echinococcosis*, Complement Fixation Test

Occurrence and Characteristics of Class 1 Integrons in Clinical Isolates of *Pseudomonas Aeruginosa* in Tehran

Somayeh Moazami Goudarzi, Fereshteh Eftekhar

Department of Microbiology, Faculty of Biological Science, Shahid Beheshti University, Tehran, Iran

Abstract

Background: *Pseudomonas Aeruginosa* is a frequent nosocomial pathogen that causes a wide range of opportunistic infections and nosocomial outbreaks. Recently, more and more bacterial resistance has been found to be associated with integrons. The aim of this study was to investigate dissemination and characterization of class 1 integrons as well as the antibiotic susceptibility patterns of *P. aeruginosa* clinical isolates.

Methods: One hundred and twelve *P. aeruginosa* clinical isolates were collected from two Hospitals in Tehran and were identified using the standard biochemical tests and the Kirby-Bauer disk diffusion method was performed to determine susceptibility to 13 antibiotics. Detection of class 1 integrons and Amplifications of internal variable regions (IVRs) of class 1 integrons were performed by the PCR method.

Results: The resistance rates were between 63.39% and 93.75%. The prevalence of class 1 integrons was 70.53%. Amplifications of internal variable regions (IVRs) of class 1 integrons revealed three different arrays (0.8, 1.3, and 1.7 kb) with different distributions in clinical isolates.

Conclusion: High prevalence of class 1 integrons with limited diversity of IVRs in clinical isolates of *P. aeruginosa* and high rates of antibiotic resistance among these isolates suggests the high potential of this structure to be transferred among bacteria by the horizontal gene transfer apparatus.

Keywords: *P. aeruginosa*, integrons class 1, internal variable regions, antibiotic resistance

Identification of the Various Species of Leptospira in the Environmental Soil and Water Samples Obtained From the Native Regions in the Northern Parts of Iran

Sona RostampourYasouri, Masoud Ghaneh, Reza Golaijanimoghaddam

[1]Department of microbiology, Tonekabon Branch, Islamic Azad University, Tonekabon, Iran

Abstract

Background: Leptospirosis is one of the most significant common diseases between human and animals which are prevalent throughout the world. This disease is a native disease in Gilan and Mazandaran provinces and the risk of the infection with the strains of pathogen is high.

Methods: Seventy samples of water and soil were collected from the suburbs of the Tonekabon Township located in the northern parts of Iran during spring of 2012. In order to isolate the *Leptospira* spp from the water and soil, the membranous filters with two different pores were employed. The filtered liquid was inoculated in/ against the EMJH medium and incubated in the 30°C for 1 month. After the enrichment, bacterium's DNA was extracted by the phenol chloroform method. In order to diagnose pathogenic spp and saprophytic spp of the *Leptospira*, duplex-PCR hybridization and 16S rRNA and Lip32 primers were used.

Results: Of total seventy collected samples of water and soil with the aid of duplex-PCR technique, 18 strains were identified, out of which 16 strains were diagnosed as saprophyte and 2 strains as pathogen. Therefore, prevalence rate of this bacterium in the studied region was evaluated 25.7%.

Conclusion: Duplex-PCR technique can be used to identify the *Leptospira* spp in water and soil samples. Because of using the mentioned primers, this method is able to differentiate between the saprophytic and pathogenic *Leptospira*.

Keywords: *Leptospira*, water and soil samples, Northern part of Iran

Cloning of 55kDa *Brucella melitensis* Cell Surface Protein in pET-22b and Its Periplasmic Expression in *Escherichia coli* Host

Mahnaz Shahbazi[1], Nima Khoramabadi[2], Haniyeh Aghababa[2], Jalil Fallah Mehrabadi[2], Amir Bakhtiari[1]

[1]Department of Biology, School of Sciences, Shiraz University of Medical Sciences, Shiraz, Iran
[2]Department of Bacteriology, Faculty of Medical Sciences, Tarbiat Modares University, Tehran, Iran
[3]Department of Microbiology, Faculty of Sciences, Islamic Azad University-Karaj Branch, Karaj, Iran
[4]Bacteriology Department, Tarbiat Modares University, Karaj, Iran

Abstract

Background: Induction of cell mediated immunity is the key aim of developing any kind of immunogenic component against *Brucella*. Development of cell-mediated immunity depends on the bacterial outer membrane proteins hence production and immunological evaluation of these molecules is of great value in designing subunit vaccines. Here we report the cloning of 55kDa B. melitensis cell surface protein (BCSP55) in pET-22b and its periplasmic expression in *E. coli* host.

Methods: bcsp55 gene was amplified with Prim Star HS DNA polymerase, cloned in pJET1.2 and sequenced. Bcsp55 then was subcloned in pET-22b and re-sequenced. Expression of recombinant BCSP55 was achieved by induction of pET22b-bcsp55 in E coli BL21 by IPTG. Protein expression was assayed by SDS-PAGE analysis of periplasmic fraction of induced host and confirmed by western blotting.

Results: Sequencing results confirmed the proper cloning of the BCSP55 in the recombinant vector pET22b-bcsp55. SDS-PAGE showed the expression of the protein in the periplasmic fraction of the host. Western-blot results confirm the expression of recombinant BCSP55.

Conclusion: 55kDa B. melitensis cell surface protein was expressed as soluble in the peripasmic space of *E. coli* which facilitates its purification and makes it possible to use it in vaccine research projects.

Keywords: Brucellosis, *Brucella melitensis*, BCSP55, pET-22b

Evaluation and Comparison of the Effect of Ozonated Olive Oil on Three Species of *Candida* (Albicans, Glabrata, Kruzei) in Culture Media with Clotrimazole Cream

Omid Rajabi[1], Fariba Berenji[2], Roshanak Salari[1], Nazanin Minoochehr[1]

[1]Department of Medicinal Chemistry, School of Pharmacy, Mashhad University of Medical Sciences, Mashhad, Iran
[2]Department of Microbiology, Faculty of medicine, Mashhad University of Medical Sciences, Mashhad, Iran

Abstract

Background: *Candida* is most important fungal pathogen in humans with weak immune system. Recently the prevalence of new infections with *Candida* species is increasing. Ozone is an allotropic form of oxygen with high oxidation power. In this study, the effect of ozonated olive oil compared with clotrimazole on three species of *Candida* (C. albicans, C. glabrata and *C. krusei*) in saboraud dextrose agar (SDA) media was evaluated.

Methods: Different concentrations of ozonated olive oil with different concentrations (166.66, 200, 233.33, 266.66, 300mg/ml) in culture media were prepared and poured in some plates separately. Plates without ozonated olive oil were used as negative control. Plates containing different amount of clotrimazole (1, 2, 3, 6 and 8µg/ml) were considered as positive control. All plates were incubated at 37ºc for 72 hours and observed for fungal growth in their status every 24 hours.

Results: Our study showed that the minimum inhibitory concentration (MIC) of ozonated olive oil for *Candida krusei* was less than 500mg/3ml and for *Candida albicans* and *Candida krusei* were 600mg/3ml and 700mg/3ml respectively. Clotrimazole inhibited all *Candida* species in concentration much lower than ozonated olive oil.

Conclusion: Considering the inhibitory effect of ozonated olive oil on *Candida* growth in the media, it is a Candidate for topical antifungal drugs such as clotrimazole.

Keywords: *Candida albicans- Candida krusei- Candida* glabrata- Olive oil- ozone- Clotrimazole

Prevalence of Pathogenic Intestinal Parasites in Patients with Gastroentritis Admitted in Emam Reza Hospital, Mashhad

Robabeh Izadi jahnparvar[1], Abdolmajid Fata[1, 2], Fariba Berenji[1], Mehdi Parian[1], Maede Nakhaee

Abstract

Background: Parasitic infections have always infected human populations throughout the centuries and are still major health problems in developing countries. The present study was performed to survey the prevalence of parasitic infections among gastroenteritis patients admitted to Imam Reza Hospital in Mashhad during a solar year.

Methods: About six hundred stool samples of the patients admitted in Imam Reza hospital due to gastroenteritis were studied during 2010-2011. Before microscopic examination, the samples were inspected for physical characteristics. Direct smear method performed for identification of live protozoa trophozoites, cyst, ova, taenia tape worms and nematode larvae. Floatation and Sedimentation concentration Methods also performed to identify weak infestations.

Results: The results showed that, 46 (9.66%) of the samples were infected with pathogen and nonpatogen intestinal parasites. 24 (4%) *Giardia*, 4 (0.66%) *Blastocystis hominis*, 2 (0.33%) *Hymenolepis nana*, 4 (0.66%) *Trichomonas hominis*, 6 (1%) *Enterobius vermcularis*, 2 (0/33%) *Taenia saginata* were observed. *Giardia lambelia* was the most frequent parasite among the children.

Conclusion: Such studies on the intestinal infections suffering from gastroenteritis can make great contributions for their treatment and planning for hygiene and public health.

Keywords: Intestine parasite, Gastroenteritis, Giardia, *Enterobius verrmicularis*, *Blastocystis hominis, Hymenolepis nana*

[1]Deptartment of Medical Parasitology and Mycology, School of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran
[2]Research Center for Skin Diseases and Cutaneous Leishmaniasis, School of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran

Seroprevalence of *Hepatitis E Virus* among Healthy Population in Fars Province, Iran

Sadaf Asaei, Mazyar Ziyaeyan, Mahsa Moeini

Professor Alborzi Clinical Microbiology Research Center, Shiraz University of Medical Sciences, Nemazee Hospital, Shiraz, Iran

Abstract

Background: Enterically transmitted acute viral hepatitis is caused predominantly by *Hepatitis A virus* (HAV) and *Hepatitis E virus* (HEV). The main route of HEV transmission is oro-fecally. The prevalence and the pattern of HEV infections vary different geographical regions and different populations in the world and are closely associated with respective economic and cultural status. This study was conducted to determine prevalence of the HEV infection among different age groups and genders, in Fars province, southern Iran.

Methods: Totally, three hundred and fourteen plasma samples were collected from healthy individuals referred to Motahari clinic in Shiraz during 2011-2012, their ages ranging between 1 to 85 years, mean ± standard deviation: 26 ± 2.1 years, (91 males and 223 females). The presence of HEV total Ab and HEV IgM in plasma were detected by commercial ELISA kit (Dia. Pro Diagnostic Bioprobes, Milan, Italy). The differences of HEV total Ab and HEV IgM among different age groups and genders were analyzed by SPSS software (Version 16, SPSS Inc, Chicago, Illinois).

Results: 189/314 (59 %); 48(25.1%) male female were positive by ELISA for HEV total Ab and HEV IgM, respectively. Also, 0(0%) male and 2(100%) female were positive for both of HEV total Ab and HEV IgM. Statistical analysis showed that there were no significant difference between the frequency of HEV total Ab and HEV IgM positive group and their genders (P> 0.05). The frequency of HEV total Ab positive group was significant in different age groups; however it was not similar in the HEV IgM one.

Conclusion: Considering the results of this study the frequency of HEV infection was not different between both genders; however it was increased with age. Moreover, comprehensive studies are needed to determine the prevalence of HEV in similar populations. It will be helpful to demonstrate the pattern of the infection in Iran and necessary for future health strategies.

Keywords: Seroprevalence, *hepatitis E virus*, Shiraz, Iran

Molecular Association between *Human herpesvirus-8* and/or High Risk *Human papiloma Virus* and Laryngeal Carcinoma

Nima Mohammadian Roshan, Amir Hossein Jafarian, Hossein Ayatollahi, Kiarash Ghazvini, Ebrahim Akbari, Saeed Akhlaghi

Mashhad University of Medical Sciences, Mashhad, Iran

Abstract

Background: Each year more than 159000 new cases of laryngeal cancer are diagnosed globally and more than 9000 cases die due to this malignancy. Viral infections are a known risk factor for this malignancy. Thus, this study is aimed to evaluate the role of HPV-16/18 and HHV-8 infection in patients with laryngeal cancer.

Methods: In this case-control study sixty formalin fixed paraffin embedded samples of laryngeal cancer and twenty two of normal larynx tissue from pathology department of Qaem Hospital, Mashhad, Iran were studied. After validating the diagnosis samples were evaluated for the detection of HPV-16/18 and HHV-8 DNA using PCR technique. The data were registered and analyzed using SPSS 18.0.

Results: The average age for patients and controls was 61.29±11.89 and 55.77±10.10 respectively. Fifty-four patients (90%) patients and sixteen (72.7%) controls were male. PCR results detected no HPV-16/18 DNA in both groups. Although there were two positive HHV-8 samples in both laryngeal cancer and normal larynx samples no significant relation was present (P=0.292).

Conclusion: We found no significant relation between the infection with HHV-8 or HPV-16/18 and existence of laryngeal cancer. However, more complementary studies are required to reevaluate our results using more samples and better detection techniques.

Keywords: HPV-16, HPV-18, HHV-8, Laryngeal cancer

Diagnosis Methods of *Entamoeba histolitica* and Comparative Study the Report of Amoebiasis before and after Training of Laboratory Staff

Komeil Mazhab jafari[1*], Sharif Maraghi [2], Mazinani mojtaba[3]

[1]M.Sc student of Parasitology, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran
[2]Student Research Committee Jundishapur University of Medical Sciences, Ahwaz, Iran
[3]Professor of Parasitology, Department of Parasitology and mycology, Ahvaz Jundishapur University of Medical Sciences, Ahvaz, Iran
[4]Department of Biology Islamic Azad University,Neyshabour Branch, Neyshabour,Iran

Abstract

Background: Amoebic dysentery is a major health problem in tropical and subtropical regions of world and cause morbidity and mortality annually worldwide. Amoebiasis is misdiagnosis with non-parasitic disease cause diarrhea such as shigellosis. In this study the rate of *E. histolitica* reported before and after training of staff in the central laboratory of a hospital in Ahwaz was assessed.

Methods: Three thousand and seven hundred and forty three stool samples were collected from the patients referred the laboratory from June 2009 to December 2010 and examined for intestinal parasitic infection and the results were recorded. After the training of staff, 4807 stool samples from June 2010 to December 2011 were collected and examined for intestinal parasitic infection and the results were compared with those achieved before training.

Results: Two hundred fifty four (6.70%) out 3743 stool exam were reported cyst and trophozoite of *E. histolitica*. After training the staff, 48(0.99%) out of 4807 were reported as *E. dispar* and no *E. histolitica* was observed.

Conclusion: As *Entamoeba histolitica* and *e. dispar* cysts are morphologically similar and the their differentiation is by using molecular Methods, and *E. dispar* is not a pathogen amoeba and also the puss cells seen in the stool of patients with shigellosis quite similar to *E. histolitica trophozoits*. It is necessary to train the staff working in the department of parasitology and deliver accurate results to the physician for appropriate treatment.

Keywords: *Entamoeba histolitica*, dysentery, laboratory, error, diagnosis, training

Study of *Pityriasis versicolor* in the Patients Referred to the Medical Mycology Laboratory of Imam Reza Hospital, Mashhad

Ali Naseri, Abdolmajid Fata, Majid Ganjbakhsh

Abstract

Background: *Pityriasis versicolor* is a superficial infection of stratum corneum caused by species of the genus *malassezia*. This infection is common in most parts of the world. *Pityriasis versicolor* is undoubtedly one of the commonest of the superficial mycoses. The epidemiology of the disease is poorly understood because only a few large studies that provide sufficient resolution have been documented, providing detailed figures on the prevalence of the skin disease. The prevalence of this infection varies in different geographical locations. The aim of this study was to determine the prevalence of *pityriasis versicolor* and site of infection in Mashhad, Iran.

Methods: This study was conducted for a period of five years during January 2006 to February 2011. A total of three hundred eighty Patients clinically suspected to have pityriasis versicolor that were referred to the Medical Mycology Laboratory of Imam Reza Hospital, Mashhad University of Medical Sciences, were studied. Samples were taken from different sites of the patient's body by scrapping of the skin lesions and scotch tape method. All collected specimens were analyzed by direct microscopy. Microscopic examination was carried out using 15% KOH and methylene blue stain.

Results: From three hundred eighty patients suspected to having *pityriasis versicolor* eighty four cases suffered from this infection; among them forty four cases (52%) were female and forty cases (48%) were male, ranged in age from six to fifty six years. The most commonly infected age groups, was twenty to twenty (29.6%) years old. The lesions of *Pityriasis versicolor* in order of frequency were distributed in skin surface as follows: chest, neck, face, back, abdomen, groin and axillae.

Conclusion: *Pityriasis versicolor* is still one of most important superficial fungal infections in Mashhad; promotion of public health care and self-hygiene and knowing the frequency of this disease may play an important role in controlling the infection.

Department of Medical Mycology and parasitology, Imam Reza Hospital, School of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran

Keywords: *Pityriasis versicolor*, Mashhad, superficial fungal infection

Cloning, Expression and Purification of Penicillin-Binding Protein from Methicillin-Resistant *Staphylococcus aureus* as Vaccine Candidate: Study on Immunogenicity in Balb/C Mouse

Setareh Haghighat[1], Davar Siadat[2], Medi Rezayat Sorkhabadi[3], Abbas Akhavan Sepahi[4], Mohammadreza Aghasadeghi[5], Mehdi Sadat[5], Mohammad Hassan Pouriavali[5], Mehdi Mahdavi[6]

[1]Islamic Azad University, Sciences and Researches Campus, Basic Science College, Tehran, Iran
[2]Department of Microbiology, Pasteur Institute of Iran, Tehran, Iran
[3]Islamic Azad University-Pharmaceutical Sciences Branch, Tehran, Iran
[4]Department of Microbiology, Islamic Azad University, North Tehran Branch, Tehran, Iran
[5]Department of Hepatitis and AIDS, Pasteur Institute of Iran, Tehran, Iran
[6]Department of Virology, Pasteur Institute of Iran, Tehran, Iran

Abstract

Background: Methicillin-resistant *Staphylococcus aureus* (MRSA) is the major pathogen involved in nosocomial infections which lead to high rates of morbidity and mortality. The resistance mechanism of *Staphylococcus aureus* comprises change of binding proteins to penicillin. Vaccine strategy may be useful in controlling of infection. The aim of this study was design and production of recombinant protein PBP2a, as a vaccine Candidate in a murine model.

Methods: A 250bp fragment of mecA gene was amplified by PCR from *S. aureus* COL strain and then cloned into prokaryotic expression vector pET-24a. For expression of recombinant protein, pET24a-mec plasmid was transformed into competent *E. coli* BL21 (DE3) cells. Recombinant protein was over expressed with 1 mM isopropythio-β-D-galctoside (IPTG) and affinity purified by Ni-NTA agarose. SDS-PAGE and western blotting were performed for protein expression confirmance. In order to Mice immunization, 20µg of recombinant PBP2A, subcutaneuslly injected three times with three weeks intervals. After Bleeding, specific antibodies were evaluated by ELISA.

Results: Cloning of mecA was confirmed by colony-PCR, enzymatic digestion and sequencing. SDS-PAGE and western blot analysis showed that recombinant protein with molecular weight of 13 kDa is expressed. Also, high titer of antibody against PBP2a in vaccinated mice compared to control group developed.

Conclusion: Results suggest that the PBP2a recombinant vaccine induced specific antibodies against methicillin-resistant *Staphylococcus aureus* and can be used as a suitable vaccine Candidate.

Keywords: Methicillin-resistant *Staphylococcus aureus*, PBP2a, recombinant vaccine

Genetic Characterization of Iranian *Plasmodium vivax* Populations by Using Apical Membrane Antigen 1 Marker

Hengameh Sadeghi[1,2], Akram Abouie Mehrizi[1], Majid Nojavan[2], Navid Dinparast Djadid[1], Sedigheh Zakeri[1]

Abstract

Background: *Plasmodium vivax* exists in sympathy with *P. falciparum* in south easthern part of Iran. Present study was undertaken to evaluate and compare genetic diversity and population structure of *P. vivax* in natural isolates using sequences analysis of apical membrane antigen 1 gene (Pvama-1).

Methods: In this study blood samples (n = 70) were collected on admission from patients diagnosed with vivax malaria in Chabahar, Sistan and Baluchistan Province, Iran. Template of parasite deoxyribonucleic acid (DNA) was obtained by phenol/phenol-chloroform extraction and ethanol precipitation. The genetic diversity of the gene encoding the AMA-1protein was investigated by sequencing the entire gene in 25 isolates using PCR-sequencing Methods.

Results: The Pvama-1 gene was successfully amplified from genomic DNA purified from seventy collected samples and was equal in size (1523 bp). The amino acid sequence data of Pvama-1 in all twenty five sequenced samples demonstrated nucleotide changes, leading to non-synonymous mutations at 22 positions compared to Sal-I sequence (accession no:AF063138), leading to 15 different allelic forms. However, limited variation has been found in B and T cell epitopes.

Conclusion: PvAMA-1 has been the most promising vaccine target antigen to date. Sequence data generated from this study showed that PvAMA-1 is a good Candidate to be included in designing an effective vivax malaria vaccine. Having such information on local malaria parasites is an important factor and prerequisite in understanding the epidemiology of malaria as well as implications for the development of acquired immunity and for local anti-malarial vaccine research.

Keywords: *Plasmodium vivax*, malaria

[1]Malaria and Vector Research Group (MVRG), Biotechnology Research Center (BRC), Pasteur Institute of Iran, Tehran, Iran
[2]Azad University of Urmia, Urmia, Iran

Rapid Identification of *Mycobacterium Avium Complex* (MAC) Culture Isolates at Species Level

Azadeh Nahavandi Araghi, Mahnaz Saifi, Esmaeil Jabarzadeh, Ahmadreza Bahremand, Mehrooze Dezfoulian, Morteza Masoomi

Karaj Azad University*, Cooperated with Tehran Pasteur Institute, Tuberculosis and Pulmonary Research Department, Iran

Abstract

Background: *Mycobacterium avium complex* (MAC) is an opportunistic infection caused by species of *Mycobacterium* which is responsible for severe illnesses in immunosuppressed individuals but rarely affects others. MAC is the most common cause of infection by nontuberculous Mycobacteria (NTM) in patients with AIDS. *Mycobacterium avium* complex (MAC) consists of two species: M avium and M intracellulare; because these species are difficult to differentiate, they are called *Mycobacterium avium-intracellulare* (MAI). MAC is the atypical *Mycobacterium* most commonly associated with human disease. The definite diagnosis is usually made by isolation of the organisms from culture. Cultures require 2 to 6 weeks which is time consuming. Since these pathogens are life threatening, its early diagnosis is important.

Methods: A method based on PCR-RFLP (PRA) using a region of the Heat Shock Protein 65 gene was developed for rapid and exact identification of *Mycobacterium avium complex* (MAC) to the species level. Using conventional biochemical tests, 28 samples of atypical *Mycobacterium* were selected from cultures**.** Chromosomal DNA was extracted. A set of primers were used to amplify 644 bp hsp65 DNA. After confirming the successful amplification, PCR products were subjected to restriction enzyme digestion by AvaII. Digestion was performed over night at 37 'C. Following digestion, mixtures were electrophoresed in agarose gel.

Results: Eight *Mycobacterium avium complexes* (MAC) were identified. Intracellulare was distinguished from *M. avium*, because it had a unique AvaII PRA pattern. According to patterns, 3 samples belonged to M. avium and 5 samples belonged to *M. intracellulare*.

Conclusion: This method not only enables identifying of *Mycobacterium avium complex* (MAC), but also can divide *M. avium* and *M. intracellulare* to the species level by AvaII digestion. The results suggest that this novel PRA offers a simple, rapid, and accurate method for identification of *Mycobacterium avium complex* (MAC) culture isolates at species and subspecies level.

Keywords: Rapid identification, *Mycobacterium avium complex*, MAC, AvaII

Frequency of etA, etB andtsst-1 Virulence Genes in Community Associated Methicillin-Resistant *Staphylococcus aureus* Isolated from Arak University of Medical Sciences

Hamid Kazemian[1,2], Ehsanollah Ghaznavi Rad[1], Alireza Japoni-nejad[1], Mohsen Rezazade[1], Mahsa Tabibnejad[1]

[1]Department of Medical Microbiology, Faculty of Medicine, Arak University of Medical Sciences, Arak, Iran
[2]Student Research Committee, Arak University of Medical Sciences, Arak, Iran

Abstract

Background: *Staphylococcus aureus* is the most important causes of community and hospital infections. Enterotoxin (ETA, ETB), and toxic shock syndrome toxin 1 (TSST1) is a very important virulence factors and the part of pyrogenic toxin super-antigens. Outbreaks of dangerous strains producing TSST-1 are an important issue in the community. The purpose of this study was to identify tsst genes in *Staphylococcus aureus* strains isolated from students of Arak University of Medical Sciences.

Methods: In this study, 568 nasal swab specimens were collected from students using of sterile swabs. After performing the conventional test 82 samples were identified as *Staphylococcus aureus*. With performing phenotypic tests (In according to the CLSI guideline) five strains were identified as methicillin resistant *Staphylococcus aureus* (CA MRSA). PCR method were done for sa442 (Diagnostic marker for *Staphylococcus aureus*) gene as final confirmation. Bacterial strains were analyzed for ETA, ETB and TSST genes by PCR technique.

Results: The results are as following: frequency of etA, etB and tsst-1 were 35%, 22% and 43% respectively

Conclusion: The results of this study indicate a high prevalence of ETA ،ETB ،TSST genes in isolates of this region. These strains can also act as a reservoir for transfer of antibiotic resistance genes to hospital strains that it could endanger public health.

Keywords: Methicillin-resistant *Staphylococcus aureus*, etA, etB, tsst-1

Evaluation of a Multipelex PCR Assay for Simultaneously Rapid and Accurate Detection of *Neisseria meningitidis*, *Haemophilus influenzae* Type (b) and *Streptococcus Pneumoniae* in CSF Specimens

Safiyeh Ghafel

Department of Microbiology, Faculty of Medicine, Hamadan University of Medical Sciences, Hamadan, Iran

Abstract

Background: Acute bacterial meningitis is an important infectious disease of the neonatal and children. In general, the number of cases of bacterial meningitis whose etiologic agent is not identified by conventional procedures is still significant. Therefore rapid and accurate laboratory diagnosis of bacterial meningitis has major importance for management of such patients. This study describes the evaluation of a multiplex PCR assay for rapid and accurate detection of *Neisseria meningitidis*, *Streptococcus Pneumoniae* and *Haemophilus influenza*e type B, which globally account for 90% of cases of bacterial meningitis.

Methods: One hundred forty CSF specimens after processing were cultured on proper culture media supplemented with necessary cofactors and other additives and diagnosis process was proceeding by biochemical procedures at species level of any each three organisms. Multiplex PCR assay was performed in the single-tube assay with three primers designated based on the ctrA gen for *Neisseria meningitides*, ply gene for *Streptococcus Pneumoniae* and bex gene for *Haemophilus influenza*e type b targets, respectively as well positive and negative standard controls.

Results: In multiplex reactions, the detection limits of DNA for *Haemophilus influenza*e, *Neisseria*. *Meningitidis* and *Streptococcus Pneumoniae*, as determined in repeated experiments, were very low (about 5 pg, 5 pg and 10 pg, respectively). In this study the sensitivity of PCR reactions in compare with culture is very high.

Conclusion: In general, the number of cases of bacterial meningitis whose etiologic agent is not identified by conventional procedures including culture method is still significant. In the other hand rapid, accurate and inexpensive diagnosis of bacterial meningitis is critical for patient management, as well as for prevention and public health intervention. Overall, this single-tube PCR assay is a simple, reliable and easily implemented method for the confirmation of bacterial meningitis, and is a rapid and cost-effective way of analyzing large numbers of samples.

Keywords: Diagnosis, *Haemophilus influenza*e, meningitis, *Neisseria meningitidis*, PCR

Comparison of Group B Streptococcal Colonization in Pregnant Diabetic and None Diabetic Women

Farideh Akhlaghi[1], Mojtaba Mazinani[2]

Abstract

Background: Group B *streptococcus* is a main cause of perinatal infections and neonatal sepsis. GBS is also a major cause of bacteriemia in pregnant women. Colonization of recto-vaginal tract with GBS is a risk factor associated with chorioamnionitis and transmission of the infection to the infant. Neonatal exposure to high concentrations of GBS, mainly during vaginal delivery, leads to colonization of the lung airways and subsequent onset of severe diseases like pneumonia, sepsis and meningitis. GBS is present in the genitourinary tract of 10% to 40% of pregnant women and can induce early-onset neonatal disease (sepsis, meningitis or pneumonia) during the first week of life and late-onset neonatal infection within the first 12 weeks of life. Maternal-intrapartum chemoprophylaxis is able to prevent the transmission of GBS to the newborn and to reduce the frequency and the severity of early onset disease. Because of high colonization of GBS in normal pregnant women, aim of this study was to evaluate the influence of maternal diabetes as a risk factor and comparison colonization of group B *streptococcus* in diabetic and non-diabetic pregnant women.

Methods: In this prospective study fifty pregnant women with diabetes mellitus include both pregestational and gestational diabetes (Case group) and forty three pregnant women without diabetes (control group) between thirty three and thirty seven weeks of gestation were recruited. Three samples for Group B streptococcal culture detection were obtained from each subject in the following order: perinea sample, vaginal sample, and an anorectal sample. All had singleton gestations, negative tests for human immunodeficiency virus, and intact membranes at enrollment. Data analyzed with Pearson chi-square and fisher exact test and comparison between two groups was done. P value less than 0.05 was considered significant.

Results: Most site of the GBS colonization in all women was vagina (11.8%). Colonization of group B *streptococcus* in control group includes vagina (7%) perineum (0.3%) and rectum 0.3%) and in case group include vagina (16%) perineum (16%) and rectum (16 %). Although comparison was shown higher vaginal colonization rate in case group (16%versus7%) but difference was not significant (p=0.154).The prevalence of group B *streptococcus* colonization in gestational diabetes was 20% and higher than pregestational diabetic women. Among women with pregestational diabetes, the prevalence of group B *streptococcus* colonization was 15% in none insulin dependent diabetic women and 10% in insulin dependent diabetic women (P> 0.05). Comparison between two groups was shown high rectal colonization in diabetic group and difference was significant (p=0.027).

Conclusion: Pregnant diabetic patients have higher carriage rates of group B streptococcus (GBS) in rectum than non-diabetic pregnant women and diabetes is a risk factor for group B *streptococcus* colonization during pregnancy.

Keywords: Group B *streptococcus*, Diabetic pregnant women, Non diabetic pregnant women, vaginal colonization, Perineal colonization, Rectal colonization

[1]Associate Professor of Obstetrics and Gynecology, School of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran
Site of research: Women health research center
[2]Department of Biology Islamic Azad University,Neyshabour Branch,Neyshabour,Iran

Sensitive Quantification of *Hepatitis B Virus* by Taq-Man Real-Time PCR Assay

Saeid Amel Jamehdar[1], Mohammad Derakhshan[1], Mehdi Parian[2], Hossein Nomani[1]

Abstract

Background: *Hepatitis B virus* (HBV) is a serious and worldwide problem that can lead to severe illnesses such as fulminant hepatitis, chronic hepatitis, liver cirrhosis, and hepatocellular carcinoma (HCC). According to WHO reports, approximately 2 billion people have been infected with this virus globally and the infection is persistent in over 400 million individuals. Quantitative measurement of HBV DNA levels in plasma has become the most reliable method used for assessment of the infection presence as well as to monitoring of the response to treatment. In the present study, a sensitive and reproducible Real time-PCR assay was developed to quantify HBV DNA using a Taq-Man probe.

Methods: The primers and probe corresponding to HBV pre-core region was used for HBV DNA quantification. A 140 bp fragment from this genomic region of HBV was cloned and serial 10 fold dilutions of plasmid DNA were used as an external DNA standard curve. The intra- and inter-assay reproducibility of this assay was determined. Finally, the performance of this assay was evaluated by analyzing 25 quantified samples by COBAS Amplicor HBV DNA monitor test.

Results: In this assay, the lower limit of detection was 1 DNA copy/reaction. The median coefficient of variation of inter- and intra- experimental variability was 3.8% and 10.1 % respectively. Comparison of the real-time PCR quantitation results from 25 clinical plasma samples with those obtained by COBAS Amplicor HBV DNA monitor kit revealed a significant correlation (r = 0.91).

Conclusion: These findings suggest that our Real Time PCR assay combines high sensitivity and reproducibility for HBV DNA quantification and it will be useful for monitoring HBV-infected patients in routine diagnostic laboratories and in clinical practice.

Keywords: HBV, Real Time PCR, Taq-Man probe, Quantification

[1]Microbiology and Virology Research Center, Avicenna Research Institute, Mashhad University of Medical Sciences, Mashhad, Iran
[2]Biotechnology Research Center, Pasteur Institute of Iran, Tehran, Iran

Epidemiology and Antimicrobial Susceptibility of Strains Isolated from Tracheal Tubes of Patients Suffering from Respiratory Disorders Admitted to University Hospitals of Tehran in Year 2011

Fatemeh Ashrafian[1,2], Hossein Dabiri[1], Mehrdad Gholami[1], Shadi Aghamohammad[1], Hossein Goudarzi[1], Maryam Nouri[1], Alireza Salimi Chirani[1]

Abstract

Background: Tracheal tube is one of the most important equipments having a role in transmitting of nosocomial infections and identification of different microbes transmitted through this route and seems to be important for prevention and control of these infections. The aim of this study is to investigate the prevalence and antimicrobial susceptibility of strains isolated from tracheal tubes of patients suffering from respiratory disorders admitted to university hospitals of Tehran in year 2011.

Methods: In this survey, 472 samples of tracheal tubes isolated from hospitalized patients of different wards were collected and cultured on standard media. Colonies were identified using differential tests. Assessment of antibiotic resistance and susceptibility of isolated bacteria was done on MHA medium with Kirby-Bauer method according to CLSI guidelines.

Results: Out of 1000 samples of tracheal tube, 472 samples grew on culture media. Among microorganisms isolated, *Staphylococcus aureus* (34.7%), *Klebsiella spp.* (25.8%), *Acinetobacter spp.* (18.2%), *Pseudomonas spp.* (8.5%), *Escherichia coli* (5.3%), *Enterobacter spp.* (1.7%), *Enterococcus* (1.1%) and *Proteus* (0.4%) were found. Antibiotic susceptibility of bacteria to 18 frequently used antibiotics was evaluated. *Staphylococcus aureus* had the highest sensitivity to linezolid (100%) and sulfamethoxazole (86%) and *Klebsiella* to cefotaxime (90%) and amikacin (81%). *Acinetobacter spp.* showed the highest resistance to cefotaxime (100%) and imipenem (96%).

Conclusion: According to the results obtained, the rate of tracheal contamination (47%) is high in Tehran University Hospitals and nosocomial microorganisms (i.e. *Staphylococcus aureus*, *Klebsiella*, *Acinetobacter* and *Pseudomonas Aeruginosa*) are the most contaminating pathogens of tracheal tubes. Based on results of antibiotic susceptibility testing, rate of resistance is high and implementing of preventive and infection control policies seems to be necessary.

Keywords: Nosocomial infections, Tracheal tubes, Antibiotic susceptibility

[1]Microbiology Department, Shahid Beheshti University of Medical Sciences, Tehran, Iran
[2]Student Research Committee, Shahid Beheshti University of Medical Sciences, Tehran, Iran

Trends in the Rate of Antibiotic Resistance of *Streptococcus Viridans* Isolated from Blood Cultures in Shiraz Hospitals, 2001-2011

Maneli Aminshahidi, Gholam Reza Pouladfar, Fatemeh Norouzi, Mona Zarafshanian, Mojtaba Anvarinejad, Bahman Pourabbas, Aziz Japoni, Mehdi Kalani, Mohammad Ali Dehyadegari and Nooredin Rafaatpour

Professor Alborzi Clinical Microbiology Research Center, Shiraz University of Medical Sciences, Shiraz, Iran

Abstract

Background: Despite the overall low virulence of *Streptococcus viridans*, they may cause infective endocarditis, contributed to polymicrobial abscess, and invading the bloodstream during the state of neutropenia. The aim was to determine the prevalence of *Streptococcus viridans* isolated from blood cultures in Shiraz during three periods of Jan 2001- Dec 2004, Jan 2005- Dec 2006 and Jan 2010- Dec 2011.

Methods: All *Streptococcus viridans* isolated from blood samples by BACTEC system in Professor Alborzi Clinical Microbiology Research Center were evaluated. Samples were obtained from different wards of the hospitals in Shiraz during the three above-mentioned periods. Antibiotic susceptibility tests were performed using Disk diffusion method.

Results: Of 5214 isolated organisms, 142 (3%) *Streptococcus viridans* isolates were identified: 56 within 2001-2006 (3% from 2115 isolates) and 86 within 2010-2011 (3% from 3099 isolates). As results show, 99% of the strains were susceptible to vancomycin. The susceptibility to ciprofloxacin decreased significantly from 73% to 35% within 2001-2006 and 2010-2011, respectively and the susceptibility to gentamicin and penicillin decreased from 32% to 16% and 50 to 25% within the same period

Conclusion: The rate of *Streptococcus viridans* isolation did not change significantly during the study period. Vancomycin remains the drug of choice in empirical therapy. Analysis of antimicrobial susceptibility testing showed an increase in the resistance rate over time in Shiraz.

Keywords: Antibiotic resistance, Bacteraemia, *Streptococcus viridans*

Toxoplasma gondii Infection in Women of Child Bearing Age of Isfahan, Iran: A Population-Based Study

Nasser Mostafavi[1], Behrooz Ataei[2], Zari Nokhodian[3], Majid Yaran[4], Anahita Babak[5], Leila Jalali Monfared[6]

[1]Assistant Professor, Growth and Development Research Center, Isfahan University of Medical Sciences, Isfahan, Iran
[2]Associate Professor, Infectious Diseases and Tropical Medicine Research Center, Isfahan University of Medical Sciences, Isfahan, Iran
[3]B.Sc. Research Assistant, Infectious Diseases and Tropical Medicine Research Center, Isfahan University of Medical Sciences, Isfahan, Iran
[4]MT, PhD, Infectious Diseases and Tropical Medicine Research Center, Isfahan University of Medical Sciences, Isfahan, Iran
[5]Community and Preventive Medicine Specialist, Infectious Diseases and Tropical Medicine Research Center, Isfahan University of Medical Sciences, Isfahan, Iran
[6]MD, Infectious Diseases and Tropical Medicine Research Center, Isfahan University of Medical Sciences, Isfahan, Iran

Abstract

Background: Toxoplasmosis is a worldwide infection with important consequences in developing fetuses. We conducted an epidemiological survey on seroprevalence of toxoplasma infection in the entire population of women of child bearing age in Isfahan Province.

Methods: In a cross-sectional study in 2010, 217 women in the age range of 10-50 were randomly selected from among participants in another study on hepatitis A in the entire population of the Isfahan province. The blood samples examined for the presence of IgG anti-*Toxoplasma Gondii* antibody by a commercial ELISA kit (Dia-Pro, Milan, Italy). The data were analyzed using the Statistical Package for Social Sciences for Windows version 15 (SPSS Inc., Chicago IL.). Chi-square and Fisher´s exact tests were employed to examine the antibody status in different age, marriage, education, and residence groups.

Results: The overall prevalence of *Toxoplasma Gondii* infection was 47.5 %(103/217). The peak age of infection acquisition was in the range thirty to forty in rural areas and 20-30 in urban districts. The theoretical estimate of congenital toxoplasmosis would be 1.1% in the 30-40 in rural area while in urban regions this estimate is 1.29% in the age group of 20-30.

There was no significant association between residence, education, and marriage groups on the one hand and chance of *Toxoplasma Gondii* infection in the participants on the other hand.

Conclusion: The findings of the study suggest a moderate prevalence of *Toxoplasma Gondii* infection, but a high prevalence in ages of high reproductive activities, which necessitates an active strategy for the prevention of congenital toxoplasmosis in the province.

Keywords: Prevalence, Toxoplasmosis; Iran, Women, Child bearing age

Association of Interleukin-17 Gene Variants with Susceptibility to *Helicobacter pylori*-Associated Gastroduodenal Diseases among Iranian Population

Ali Moravej[1], Manoochehr Rasouli[2], Mehdi Kalani[2], Kouhpayeh SA[3]

[1]Department of Microbiology, Fasa University of Medical Sciences, Fasa, Fars, Iran
[2]Department of Immunology, Professor Alborzi Clinical Microbiology Research Center, Shiraz University of Medical Sciences, Shiraz, Fars, Iran
[3]Department of Pharmacology, Fasa University of Medical Sciences, Fasa, Fars, Iran

Abstract

Background: *Helicobacter Pylori* is the main cause of chronic active gastritis, which can lead to peptic ulcer disease, gastric adenocarcinoma, and gastric mucosa-associated lymphoma. According to the important role of IL-17 in pathogenesis of inflammatory diseases and effect of IL17 gene polymorphisms on its production, we investigated the associations between nine SNPs in the IL-17A gene and the risk of *H. pylori* related chronic active gastritis and peptic ulcer disease.

Methods: The study groups included 100 patients suffered from chronic active gastritis and 50 patients with peptic ulcer disease in addition to 226 healthy individuals as control group. Alle and genotypes of IL-17 at nine polymorphic sites were compared among study groups by PCR-RFLP.

Results: The results showed that the distribution of A allele at position rs3819024 was significantly more frequent in the gastritis patients than the controls (P=0.0003) and was significantly more frequent in the ulcerative gastritis patients than the controls (P=0.0001). In addition, the frequency of homozygous rs3819024GG was significantly more frequent in the controls than the gastritis patients (P=0.0008) and was significantly more frequent in the controls than the ulcerative gastritis patients (P=0.0005).

Conclusion: It can be suggested that some IL-17 genetic variants can affect resistance or susceptibility to *H. pylori*-associated gastroduodenal diseases among Iranian patients.

Keywords: IL-17, Genetic polymorphisms, gastritis, *Helicobacter Pylori*, Iran

Drug Susceptibility of Different Antimicrobials on Methicillin Resistant *Staphylococcus aureus*, Isolated from Patients

Mohammad Reza Bojary[1], Marzieh Fattahi Dolat Abadi[1], Mitra Ranjbar[2], Mahboubeh Sattarzadeh[3], Zahra Aghasi[1], Pavaneh Hamed Nasimi[1]

[1]Antimicrobial Resistance Research Centre and Department of Microbiology, Faculty of Medicine (Hemet paradise area), Tehran University of Medical Sciences, Tehran, Iran
[2]Hazrat Rasul and Firozgar General Hospitals, Tehran University of Medical Sciences, Tehran, Iran
[3]Shahid Motahari Burn Hospital, Tehran University of Medical Sciences, Tehran, Iran

Abstract

Background: *Staphylococci spp.* are the most prevalent causes of infection in humans, as well as, methicillin resistant *Staphylococcus aureus* (MRSA) strains which are known as common pathogenic agent in hospitals. The aim of this study was to determine the drug susceptibility of different important clinical antimicrobial agents against MRSA strains.

Methods: For this study 236 *S. aureus* strains isolated from in and out patients of Hazrat Rasul Akram and Shehid Motahari educational hospitals in Tehran, Iran, of which 152 strains were confirmed to be methicillin resistant applying oxacillin disk (Mast Co.) by using disk diffusion method. Antimicrobial susceptibility test was performed on MRSA strains only according to CLSI, for vancomycin, erythromycin, tetracycline, gentamicin, and ciprofloxacin.

Results: The results showed that the MRSA isolated strains prevalence was 64.4%. Their resistance to erythromycin, tetracycline, gentamicin, and ciprofloxacin was 34.5%, 23.8%, 11.9%, and 10.7% respectively. In patients, the MRSA strains were sensitive to vancomycin. The prevalence of the MRSA strains in male patients was more.

Conclusion: It seems that increasing the resistance against the MRSA strains is due to high use of the antimicrobial drugs in ours hospitals. Therefore because of high prevalence of MRSA strains, these strains should be controlled specifically in hospitals.

Keywords: MRSA strains, Methicillin, MIC, antibiotics

Antibiotic Sensitivity Pattern of Community Associated Methicillin-Resistant *Staphylococcus aureus*

Maryam Rezaei, Rezva Moniri

Kashan university of Medical Sciences, Kashan, Iran

Abstract

Background: Community associated-methicillin resistant *Staphylococcus aureus* infections are an emerging problem in Iran and many parts of the world. CA-MRSA may become a serious problem for the clinicians in the near future. The aim of this study was to determine antibiotic sensitivity pattern of CA-MRSA**.**

Methods: A cross-sectional study was conducted in eight hundred and ten patients referred to emergency ward in Shahid Beheshti hospital in Kashan. We used sterilized nasal swabs to collect nasal bacteria. Nasal specimens were further recognized as *S. aureus* strains by standard biochemical tests, and being sensitive or resistant to methicillin determined by disk diffusion method. MIC of oxacillin in MRSA isolates were examined by E-test. We also determined the susceptibility of MRSA isolates to ten antibiotics including: amikacin, penicillin, clindamycin, gentamicin, vancomycin, ciprofloxacin, cefoxitin, SXT, erythromycin, tetracycline by using disk diffusion method according to recommendation of CLSI.

Results: Two hundred ninety six out of eight hundred and ten (36.5%) of isolates were *S. aureus***.** Thirty out of two hundred ninety six (10.13%) *Staphylococcus aureus* isolates were recognized as MRSA. Twenty three (76.7%) out of the MRSA strains showed high MICs level (MIC ≥ 256 µg/ml) and seven (23.3%) out of them showed intermediate MICs level (MIC ≥ 32 µg/ml). All of them were resistant to more than one antibiotic. The CA-MRSA isolates were susceptible to various classes of antibiotics. The highest and lowest rate of susceptibility was shown to vancomycin (100%) and penicillin (0%).

Conclusion: This study showed high MIC of oxacillin in MRSA isolates. A high proportion of resistance to different antibiotics was found among CA-MRSA isolates, signifying that the aspect of CA-MRSA has been changed in epidemiological features.

Keywords: *Staphylococcus aureus*, antibiotic susceptibility, MRSA, CA-MRSA

Serological Study of *Cytomegalovirus* in Recipients of Liver and Kidney Transplantation

Sadaf Asaei, Mazyar Ziyaeyan

Professor Alborzi Clinical Microbiology Research Center, Shiraz University of Medical Sciences

Abstract

Background: *Cytomegalovirus* (CMV) was first isolated from the salivary gland and kidney of two dying infants with cytomegalic inclusion bodies and reported in 1956. Positivity of CMV serology in donor-recipient is associated with rejection, graft survival, and CMV infection especially in the group of positive donor /negative recipients.

Methods: A total of one hundred seventy three liver transplants and sixty four kidney transplant recipients were included in the study. Anti-CMV IgG titers were determined by commercially available enzyme-linked immunosorbent assay (Dia. Pro Diagnostic Bioprobes, Milan, Italy).

Results: One hundred and sixty-five of the liver transplant patients (98.2%) possessed IgG antibodies against *human Cytomegalovirus* and all of the kidney recipients had anti-CMV antibodies.

Conclusion: As the results revealed, all the recipients, except for three one to three year old children who received liver transplants, had the anti-CMV antibodies. Therefore, weekly quantitative PCR assay is recommended for monitoring CMV and initiating pre-emptive therapy. It is also suggested that prophylactic treatment begin for the limited number of negative recipients following transplantation.

Keywords: *Cytomegalovirus*, Transplantation, serology, IgG

Estimation of *Cytomegalovirus* Seroprevalence in Donor-Recipients of Bone Marrow Transplantation

Sadaf Asaei, Mazyar Ziyaeyan

Professor Alborzi Clinical Microbiology Research Center, Shiraz University of Medical Sciences, Shiraz, Iran

Abstract

Background: *Cytomegalovirus* (CMV) disease continues to be a major and life-threatening complication in recipients of solid organ and bone marrow transplants (BMTs). CMV may cause deadly interstitial, pneumonitis, esophagitis, gastritis, colitis, hepatitis, fever, leukopenia, and a severe wasting syndrome. The aim of this study was evaluation of patients in order to assess their risk of post-transplant CMV reactivation and disease.

Methods: A total of 57 bone marrow transplant recipients and thirty two donors were included in this study. IgG against CMV in donor and recipients were analyzed by a commercial ELISA kit (Dia. Pro Diagnostic Bioprobes, Milan, Italy)

Results: All cases of bone marrow transplant recipients and also all evaluated donors had IgG antibodies against *human Cytomegalovirus*.

Conclusions: As demonstrated, all bone marrow donors and recipients had antibodies against CMV. Therefore, there is no risk of CMV primary infection among the recipients. However, CMV reactivation is certain in recipients. Monitoring the respective cases for CMV using sensitive molecular assay like quantitative PCR is recommended.

Keywords: Transplant recipients, serology, IgG, *Cytomegalovirus*

Effect of Recombinant Human Granulocyte Colony Stimulating Factor on Prognosis of Sepsis in Preterm Infants Hospitalized in NICU of Ghaem Hospital

Reza Saeedi, Hossein Akhavan

Department of Pediatrics, Ghaem Hospital, Faculty of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran

Abstract

Background: Despite recent progresses in the development of new antimicrobial medications and the use of intensive care Methods, neonatal sepsis and its complications are one of the most important causes of mortality and morbidity in the neonatal period, especially in the premature neonates. This may be due to the increasing resistance to the antimicrobial agents. The cellular and humeral defense mechanisms are not fully developed in neonates, and neutrophils have some quantitive and qualitive defects in this group. Nowadays, there is a growing interest in the adjuvant therapies such as some cytokines like G-CSF in the treatment of neonatal sepsis.

Methods: Fifty premature low birth weight neonates that were admitted to the nICU ward with the clinical diagnosis of sepsis were enrolled in the study. The study population was divided to the case and control groups. We compared the outcome of G-CSF administration to the case and placebo (normal saline) administration to the control group.

Results: No statistically significant difference was found in most of the assessed parameters between the case and control groups. The only exceptions were peripheral blood leukocyte count and absolute neutrophil count that were significantly higher in the case group, but these were not associated with any clinical and laboratory improvements such as decrease in the complications, mortality, average length of hospital stay, etc.

Conclusion: According to this study and other similar studies, the routine administration of G-CSF as an adjuvant therapy for neonatal sepsis in the non-neutropenic premature neonates is not recommended.

Keywords: Recombinant human granulocyte colony stimulating factor, early onset neonatal sepsis, Low birth weight neonate, premature neonate

Phenotypic Detection of ESBL and MBL Produced by Multi-Drug Resistant *Pseudomonas aeruginosa* Strains Isolated from Burned Patients Admitted to Motahari Hospital, Tehran, Iran

Leila Azimi[1], Babak Asghari[1], Ebrahimzadeh Namvar[1], Fariba Bazmi[2], Bahar Khansari[1], Abdolaziz Rastegar Lari[1]

[1]Antimicrobial Resistance Research Center, Tehran University of Medical Sciences, Tehran, Iran
[2]Motahari Hospital, Tehran University of Medical Sciences, Tehran, Iran

Abstract

Background: *Pseudomonas Aeruginosa* is an important opportunistic pathogen causing nosocomial infections, especially in immunocompromised patients such as burned patients. *Pseudomonas Aeruginosa* is potentially resistant to the different broad-spectrum antibiotics due to its ability to produce ESBL and MBL.

Methods: In the present study during a period of 6 months, 22 strains of multidrug-resistant (MDR) *Pseudomonas Aeruginosa* were isolated from both male and female burned patients hospitalized for at least one week in Motahari hospital in Tehran and were screened by Disc diffusion and Double disc method to determine the ability of producing ESBL and MBL.

Results: among all strains, 18% were ESBL positive indicates a significant zone size enhancement (≥5 mm) with cefotaxime and ceftazidime plus clavulanic acid discs when compared with the plain cefotaxime or ceftazidime discs. 38% of strains were MBL positive showed at least 7 mm difference between the inhibition zone around the imipenem discs alone in comparison with imipenem plus EDTA discs and at least 5 mm difference between the inhibition zone around imipenem plus EDTA discs and EDTA discs alone.

Conclusion: Based on our results, the rapid spread of resistance among bacterial populations because of the extensive use of antibiotics is a matter of concern for the optimal treatment of the patients, particularly in burn wards and determination of ESBL and MBL production of MDR *Pseudomonas Aeruginosa* strains seems to be essential.

Keywords: ESBL, MBL, Multi-Drug Resistant *Pseudomonas Aeruginosa*, Burned, Tehran, Iran

ESBL and MBL Mediated Resistance in *Acinetobacter baumannii*; A Global Threat to Burn Patients

Parisa Armat[1], Parviz Owlia[1,2], Leila Azimi[1], Babak Asghari[1], Morovat Taheri Kalani[3], Abdolaziz Rastegar Lari[1,4]

[1]Antimicrobial Resistance Research Center, Tehran university of Medical Sciences, Tehran, Iran
[2]Department of Microbiology, Faculty of Medicine, Shahed University, Tehran, Iran
[3]Department of Microbiology, School of Medicine, Ilam university of Medical Sciences, Banganjab, Ilam, Iran
[4]Department of Microbiology, Tehran University of Medical Sciences, Tehran, Iran

Abstract

Background: The aim of this study was to determine the prevalence of Extended Spectrum Beta-Lactamase (ESBL) and Metallo Beta-Lactamase (MBL) in isolated strains of *A. baumannii* from burned patients.

Methods: The 126 *A. baumannii* isolates were collected from 76 both male and female burned patients admitted to burn unit in Motahari hospital Tehran. The susceptibility test was done by the disk combination disc test and disc diffusion method was performed to confirm the producing of ESBL and MBL isolates in accordance with CLSI standard guidelines.

Results: Twenty-one percentages of ceftazidime-resistant *A. baumannii* isolates were found to be ESBL producer. Thirty-nine percentage of imipenem-resistant isolates produced MBL.

Conclusion: Prolonged duration of hospitalization of burned patients made an important contribution to the incidence of resistant bacteria. The utility of an accurate surveillance for ESBL and MBL in *A. baumannii* isolated from burned patients as an important step for successful antimicrobial treatment in future.

Keywords: *Acinetobacter baumannii*, Extended-spectrum β-lactamase (ESBL), Metallo-β-lactamase (MBL), burned patients

Determining the Resistance Pattern of Isolated *Acinetobacter baumannii* from Hospitalized Burned Patients in Motahari Hospital, Tehran

Abdollah Ardebili[1,2], Hajar Mohammadi-Barzelighi[1], Mayam Beheshti[1,2], Maliheh Talebi[2], Morovat Taheri Kalani[3], Abdolaziz Rastegar Lari[1,2]

[1]Antimicrobial Resistance Research Center, Tehran University of Medical Sciences, Tehran, Iran
[2]Department of Microbiology, Faculty of Medicine, Tehran University of Medical Sciences, Tehran, Iran
[3]Department of Microbiology, School of Medicine, Ilam University of Medical Sciences, Banganjab, Ilam, Iran

Abstract

Background: *Acinetobacter baumannii* is an important human pathogen which is highly regarded in recent years. These bacteria are a leading cause of therapeutic resistant nosocomial infections especially in burned or hospitalized patients at intensive care ward. The aim of this study was isolating the *Acinetobacter baumannii* species from wounds of burned patients and determination of antimicrobial resistance pattern of these bacteria for selective antibiotics.

Methods: Isolates were collected from patients and transferred to the laboratory under standard condition. Bacteria were isolated and purified by conventional culture Identification of bacteria to the species level was performed by standard biochemical tests. The isolates were identified as *Acinetobacter baumannii* subsequently tested for antibiotic resistance by disk diffusion agar method to 17 various antibiotics. Test carried out on Muller Hinton agar (MHA) plates and incubate at 35◦C for 18hrs.The minimum inhibition concentration were determined for 5 common therapeutic antibiotics.

Results: Out of 65 clinical *Acinetobacter baumannii* isolates collected from hospitalized patients, 61 (94%) were Multi Drug Resistance (MDR). Ceftazidime and aztronam (98%) were the most active antibiotics against *Acinetobacter baumannii*. The highest minimum inhibition concentration was seen for ceftazidime, cefepime and ciprofloxacin.

Conclusion: The results of this study confirm the high prevalence of *Acinetobacter baumannii* resistant isolates and its therapeutic problems in Iran. Determination of resistance patterns of these bacteria according to MIC can be helpful in treatment of patients, especially burned patients. So, determination of MIC is necessary in especial cases.

Keywords: *Acinetobacter baumannii*, Antibiotic resistant, Minimum Inhibition Concentration

Identification and Survey of Microbial Resistance of Isolated *Burkholderia cepacia* and *Stenterotomonas maltophia* in Burn Infections

Shida Asadpoor[1], Hassan Salimi[1,2], Fariba Bazmi[3], Mohammad Mehdi Soltandallal[1,4], Elnaz Rastegar Lari[1], Abdolaziz Rastegar Lari[1]

[1]Antimicrobial Resistance Research Center, Tehran university of Medical Sciences, Tehran, Iran
[2]Department of Industrial and Environmental Biotechnology, National Institute for Genetic Engineering and Biotechnology, Tehran, Iran
[3]Motahhari Hospital, Tehran University of Medical Sciences, Tehran, Iran
[4]Food Microbiology Research Center, Tehran university of Medical Sciences, Tehran, Iran

Abstract

Background: *Burkholderia cepacia* and *Stenterotomonas maltophia* as opportunistic microorganisms have a significant role in nosocomial infections, especially in burned wounds. Mechanism of their resistance to therapeutic antibiotics related to produce Extended Spectrum Betalactamase (ESBL) cause complications for treating. The aim of this study was determine the antiobiotic resistant, screening and identification of ESBL-producer *Burkholderia cepacia* and *Stenterotomonas maltophia* from different clinical specimens of Motahari hospitals in Tehran.

Methods: In the present study, 360 *Burkholderia cepacia* and *Stenterotomonas maltophia* collected from 106 patients, from Motahri hospital. Isolated strains identificated by specific microbiology tests such as oxidase, DNase, SIM, OF, TSI and confirmatory tests such as O-nitrophenyl-ß-D- galactoside (ONPG), lysine decarboxilase and sucrose and lactose oxidation and fermentation. Antibiotic susceptibility testing conducted according to Clinical and Laboratory Standards recommendation and ESBL by combination disc.

Results: Twenty-one *Burkholderia cepacia* were confirmed according to microbiology tests. The most of resistance observed for cefotaxime. Colistin is the only effective antibiotic affected on all isolated bacteria. From the total 21 Burkholderia cepacia 24% were shown to produce ESBLs by phenotypic test.

Conclusion: Obtained results showed severe problems for physician to treat infections related to resistant Burkholderia cepacia specially the species that can produce Extended Spectrum Beta Lactamase.

Keywords: *Burkholderia cepacia, Stenterotomonas maltophia*, burn infections

Circumcision for the Prevention of Urinary Tract Infection in Preschool Boys

Mohammad Esmaeili

Pediatric Nephrologist, Mashhad University of Medical Sciences, Mashhad, Iran

Abstract

Background: Urinary tract infection (UTI) is common in childhood with serious sequela. Among infants, boys are more likely to develop UTI. The aim of this study was to determine circumcision effects in decreasing UTI incidence and the appropriate age of circumcision.

Methods: During a seven year period prospective study, one hundred and sixty six boys less than six years old with UTI, allocated into two groups. They had not any urinary tract abnormalities. In the first group 79 boys ranging from 2 months to 5.5 years of age (mean 11.3 ± 3.1 mo) were circumcised after UTI treatment and then observed for a six month period with taking urinalysis (U/A) and urine culture (U/C) 1-2 monthly. The second group, as control subjects, included 87 boys aged from 40 days to 5.5 years (mean 12.1 ± 3.4) after treatment of UTI, which were followed for a 6 month period with taking U/A and U/C, then circumcised and followed for another 6 month period. Incidence of UTI in the first group (circumcised) and the second (uncircumcised period) was compared using Chi-square test. For comparing the incidence of UTI in the second group (6 months before and 6 months after circumcision) we used Mc nemar method.

Results: There was significant difference (P=0.009) in occurrence of UTI in the first and second group. There was also significant difference (P<0.0001) in the incidence of UTI 6 months before and after the circumcision in patients in the second group.

Conclusion: The present study indicated that circumcision decreases the risk of UTI in boys, which is independent to the age. Therefore, circumcision should be considered in newborns and any patient with UTI or urinary tract abnormalities. Routinely performing cystourethrography in boys with first attack of UTI without urinary tract abnormalities (proven by history, physical examination and sonography) is questionable and needs further studies.

Keywords: Urinary tract infections, circumcision, boys, male infants, cystourethrography

Reducing the Risk of Microbial Keratitis by Developing Antimicrobial Contact Lenses

Bahman Khamneh Bagheri[1], Bibi Sedigheh Fazly Bazzaz[1], Ahmad Mohajeri[2], Bijan Malaekeh-Nikouei[3]

[1]Biotechnology Research Centre, School of Pharmacy, Mashhad University of Medical Sciences, Mashhad, Iran
[2]Pharmaceutical Research Centre, School of Pharmacy, Mashhad University of Medical Sciences, Mashhad, Iran
[3]Nanotechnology Research Centre, School of Pharmacy, Mashhad University of Medical Sciences, Mashhad, Iran

Abstract

Background: Microbial keratitis (MK) is a serious complication of wearing contact lens. In order to control the risk of MK many approaches such as selecting a safe lens wear are being pursued. Development of contact lenses which possess antimicrobial properties would be desirable as a mean to control the risk of MK. The aim of this study was to prepare silver impregnated antimicrobial contact lenses to prevent bacterial infection in eyes.

Methods: Different amounts of silver nanoparticles were added to the mixture of monomers which used to synthesize the lenses (groups A-F). The resulting lenses were soaked in solution of sodium hypochlorite in water (5%). Then lenses were placed into of Mueller Hinton Broth media containing 10^4 CFU//ml *Pseudomonas Aeruginosa* (ATCC15442) and *Staphylococcus aureus* (ATCC6538), and incubated at 37° C. After 6, 24, 48, and 72 hours each sample was added to quenching agent. To enumerate living bacteria the pour plate method was used.

Results: The results showed that lenses which were prepared with 2 mg silver nanoparticles (Group B) had a significant effect on both *S. aureus* (after 24 h) and *P. aeruginosa* (after 6 h). But it didn't reduce the number of *S. aureus* at 48 and 72 h while lenses which were prepared with 5 or 7 mg silver nanoparticles (Groups E, F respectively), had significant effect on both types of bacteria at all times.

Conclusion: Due to proper efficacy in reducing the number of both types of bacteria at 24 h, Group B was selected as suitable lenses in comparison to other groups.

Keywords: Antimicrobial properties, Contact lens, Microbial keratitis, Silver nanoparticles

Antimicrobial Effectiveness Test: Interaction of Cyclodextrins and Preservatives in Fluorometholone Eye Drop

Vahid Soheili[1], Bibi Sedigheh Fazly Bazzaz[2], Bijan Malaekeh-Nikouei[3], Kobra Mohammadian[1]

[1]Medicinal Chemistry Department, School of Pharmacy, Mashhad University of Medical Sciences, Mashhad, Iran
[2]Biotechnology Research Centre and School of Pharmacy, Mashhad University of Medical Sciences, Mashhad, Iran
[3]Nanotechnology Research Centre and School of Pharmacy, Mashhad University of Medical Sciences, Mashhad, Iran

Abstract

Background: Cyclodextrins (CDs) are cyclic oligosaccharides with a hydrophilic outer surface and hydrophobic central core. In pharmaceutical products, CDs particularly are used as drug carriers to improve drug dissolution and to enhance drug absorption. It has been shown that presence of CDs can result in reduction of antimicrobial effectiveness of preservatives. Therefore, to find an optimum combination of preservatives in fluorometholone eye drop, the interaction between commonly used preservatives, benzalkonium chloride (BZCl) or methyl paraben (MP), with synthetic CDs (HP γ-CD or SBE β-CD) in the presence or absence of EDTA, as a preservative potentiator, was investigated.

Methods: The tests requisites including preparation of media and inoculums, and procedure were performed according to the 51 general chapter of USP 2010, antimicrobial effectiveness testing. Briefly 20 ml of mixed samples in different test tubes was inoculated with 0.1 ml of 10^8 CFU/ml of each microorganism (*Escherichia coli*, *Pseudomonas Aeruginosa*, *Staphylococcus aureus*, *Candida albicans* and *Aspergillus niger*). In duration of 28 days and at weekly interval, the reduction in number of CFU/ml was counted. Calculation was performed according to USP.

Results: Application of CDs can result in reduced effectiveness of BZCl and MP, even in the presence of drug molecules. The only exception was HP γ-CD 5% solution with BZCl and EDTA, which was effective against tested microorganisms either in the presence or absence of drug molecules.

Conclusion: The solution of HP γ-CD 5% with BZCl 0.02% and EDTA 0.1% was introduced as best carrier for dissolving fluorometholone to apply as an eye drop.

Keywords: Benzalkonium chloride, Cyclodextrins, EDTA, Fluorometholone, Methyl paraben

Early Diagnosis of Late Neonatal Sepsis by Measuring Interleukin 10: a Case Control Study

Hassan Boskabadi[1], Gholamali Maamouri[2], Jalil Tavakol Afshari[3]

Abstract

Background: Late-onset sepsis is estimated for high morbidity and mortality in neonates particularly in developing Countries. Serum interleukin 10 (IL-10) levels predict late-onset sepsis in neonates prior to positive blood Culture yields.

Methods: Eighty eight neonates, with a gestational age of twenty eight to forty weeks, and suspected of infection 72 hours post-partum, were recruited into the study. They were categorized on the basis of their clinical presentation, laboratory parameters and blood culture results into: 1) cases [definitive infection (with positive blood or/and cerebrospinal fluid (CSF) cultures) or clinical sepsis (clinical and laboratory evidence of infection, but without positive blood or CSF cultures)] 2) controls (physiologic hyperbilirubinemia or routine feeding) For each neonate, samples were taken for serum IL-10, C-reactive protein (CRP), blood culture and other laboratory tests. Receiver-operating characteristic (ROC) curves were used for determination of thresholds for the sepsis group versus healthy neonate group.

Results: Serum IL-10 and CRP were significantly higher in the order of definitive infection > clinical sepsis > healthy controls respectively. Using cut off values for IL-10 as >14pg/ml, sensitivity, specificity, positive predictive values (PPV) and negative predictive values (NPV) were 0.77.7, 0.87.8,0.73.6, 0.90, respectively. Serum IL-10 levels in non-surviving neonates (138.6pg/ml) were higher than in survivors (34.62 pg/ml).

Conclusion: IL-10 may be a valid and early predictive marker of neonatal infection and high IL-10 levels are also associated with more severe infection.

Keywords: Early sepsis marker, Interleukin-10, Neonate, Sepsis, CRP

[1,2]Department of Pediatric, Neonatal Research Centre, Ghaem Hospital, Mashhad University of Medical Sciences (MUMS), Mashhad, Iran
[3]Department of Immunology, Immunology Research Centre, Bu-Ali (Avicenna) Research Institute, MUMS, Mashhad, Iran

The Role of Probiotics in Prevention of Antibiotic Associated Diarrhea in Children

Ali Jafari, Hamid Ahanchian, Ali Khakshour, Hamidreza Kianifar, Mohammad Ali Kiani, Elham Zamani

Department of Pediatrics, Ghaem Hospital, Faculty of Medicine, Mashhad University of Medical Sciences

Abstract

Background: Antibiotic treatment is known to disturb gastrointestinal microflora, which results in a range of clinical symptoms--most notably, diarrhea. This is especially important in children, for whom antibiotics are prescribed frequently Antibiotic-associated diarrhea (AAD) is a common complication of antibiotic use. There is growing interest in probiotics for the treatment of AAD and *Clostridium difficile* infection because of the worldwide availability of probiotics as dietary supplements. Researchers inclined to use probiotics in order to prevent AAD so that they can achieve better compliance in complete the course of antibiotic therapy. The aim of this randomized, placebo-controlled, double-blind trial was to assess the efficacy of probiotic Protexin for prevention of AAD.

Methods: From May 2010 to November 2011, a total of 219 patients (aged six months to fourteen years) with respiratory tract infection/and or otitis media who had begun receiving antibiotics were randomized to receive Protexin or placebo for seven days. Patient's mother recorded bowel frequency and stool consistency daily for seven days. The primary outcome was the proportion of patients who developed AAD within 7 days of enrollment.

Results: No significant different found in sex, age, source of infection, type of antibiotics between groups (P>0.05). There are no significant different found between two groups for loose stool for bowel habit or prevalence of diarrhea (P.0.05)

Conclusion: The Probiotocs (Protexin) we studied did not show a statistically significant reduction in AAD compared with placebo based on analysis for the entire subject group. Our overall rates were consistent with previously reported AAD rates.

Keywords: Probiotics, Diarrhea, Antibiotics

Comparative Study of Oropharyngeal Candidosis in Children with Lymphohematopoietic Malignancies and Control Group

Zahra Badiei[1], Fariba Berenji[2], Nona Zabolinejad[3], Soraya Kakhi[4]

Abstract

Background: Almost 100 of *Candida* species are introduced so for and *Candida albicans* is the most common subtype but according to high prevalence of immune suppressed patients, recently some new species of *Candida* have become pathogen. In this study, we have evaluated the incidence of fungal infections and the frequency of different species of *Candida* in children with lymphohematopoietic malignancies.

Methods: During one year (July 2009- July 2010), 102 patients with lymphohematopoietic malignancies and 50 persons (control group) at Dr sheikh hospital, were examined for *Candida* with direct sampling of oropharyngeal cavity, Fresh smears with 10% KOH were prepared and examined directly under the microscope and also another slide with Gram staining. For fungal cultures, all samples were incubated on isolation media Sabouraud dextrose agar (SDA, Himedia Laboratories). For positive samples of Candida chromagar Himedia was used.

The culture tubes were incubated at 25^{0C} and 37^{0C} and examined daily for six weeks.

Results: Among 102 patients and 50 healthy children as our control group, mean age of patients was 7, and mean age of control group was 4/5 years old. 66% of case group were male and 33% were female. In control group 56% were male and 44% female. The most common *Candida* species which are cultured were *C. Albicans* (55.1%), *C. spp* (25.8%), *C. Glaberata* (12.06%), *C. Krusei* (1.7%) respectively in case group. In control group the most common species were Ca. spp (46.1) and Ca. albicans (33.38%).

Conclusion: *Candida albicans*, *spp*, *Glaberata* were the more common species of *Candida* among our patients. *Candida spp.* Continues to be the most common fungal pathogen in patients with cancer, so that for prevention of fungemia and fungal pneumonia, every effort should be made to prevent these infections in pediatric cancer patients.

Keywords: Lymphohematopoietic malignancies - Candidosis - oropharyngeal, children

[1]Pediatric hematologist oncologist, Doctor Sheikh pediatric hospital, Mashhad, Iran
[2]Pathologist, Emam Reza Hospital Mashhad, Iran
[3]Pathologist, Dr Sheikh pediatric hospital, Mashhad, Iran
[4]Medical student, Mashhad University of medical sciences, Mashhad, Iran

A Survey of Relationship between Human Herpesvirus-8 and Plasma Cell Myeloma by PCR Method

Mohammad Hadi Sadeghian[1], Hossein Ayatollahi[1], Mohammad Reza Keramati[2], Bahram Memar[3], Saeid Amel Jamehdar[4], Maryam Mohamadnia Avval[1], Maryam Sheikhi[1]

[1]Department of Hematology and Blood Bank, Cancer Molecular Pathology Research Center, Faculty of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran
[2]Neonatal Research Center, Imam Reza Hospital, Department of Pathology, Ghaem Hospital, Faculty of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran
[3]Department of Pathology, Department of Pathology, Ghaem Hospital, Faculty of Medicine, Mashhad University of Medical Sciences, Mashhad, Iran
[4]Microbiology and Virology Research Center, Avicenna Research Institute, Mashhad University of Medical Sciences, Mashhad, Iran

Abstract

Background: Plasma cell myeloma (PCM) is a neoplasm of plasma cells, primarily occurring in the bone marrow. Human herpesvirus-8 (HHV-8) is a member of the gamma herpesvirus family. Some authors suggested the potential role of this virus in development of PCM. The aim of this study was to find any relationship between HHV-8 with PCM by using polymerase chain reaction (PCR) method.

Methods: This case-control study was performed in the molecular pathology section of our hospital and was conducted on 30 formalin-fixed, paraffin-embedded bone marrow biopsies of PCM and 30 normal bone marrow tissues. After preparation of the thin sections, Deoxyribonucleic acid (DNA) was extracted by non-heating procedure. The PCR for detection genome of HHV-8 was carried out by using commercial kit and theirs products were run by electrophoresis. Statistical analyses were done by using SPSS software.

Results: No HHV-8 Virus DNA Band was detected by PCR of the tissue extracts from FFPE blocks of multiple myeloma samples, while one of the controls showed DNA band of the corrected molecular weights. By using Fisher's exact test no statistical differences were found between two groups.

Conclusion: Our report adds to the body of evidence that HHV- 8 is not correlated with MM and against a major role of HHV-8 infection in the pathogenesis of clonal plasma cell proliferation.

Keywords: *Human Herpesvirus-8*, Multiple Myeloma, Polymerase Chain Reaction

The Comparison of Human papillomavirus in Bronchogenic Carcinoma and Non-Carcinomatous Patients

Amir Hossein Jafarian, Abbas Ali Omidi, Kiarash Ghazvini, Mohammad Tohidi, Hadi Tohidi, Nema Mohamadian Roshan, Samaneh Boroumand-Noughabi

Abstract

Background: Lung cancer is the leading cause of cancer death worldwide. *Human papillomavirus* (HPV) has been proposed as a possible carcinogenic factor in lung cancer. Various evidences through several distinct lines of research support this issue. There has been a considerable heterogeneity between different countries and regions concerning HPV frequency among lung cancer patients.

Methods: To study the difference of HPV 16/18 infection in lung cancer patients and non-cancer controls we conducted this study to verify whether there was a similar HPV prevalence pattern in lung tumor patients and its subtypes from the North-East of Iran to those of Mazandaran province.166 paraffin-embedded samples from 92 lung cancer patients and 74 non-cancer controls were analyzed by Polymerase Chain Reaction (PCR) for HPV16/18 infection.

Results: The data showed that 9 of 92 lung tumors had high-risk HPV DNA compared with 1 of 74 non-cancer controls (9.8% vs. 1.4%, P=0.044). High-risk HPV had an OR of 7.9(95% CI 0.97-63.98, p=0.044) for lung cancer incidence and 9.52 (95% CI 1.11-81.65, p=0.019) for squamous cell carcinoma (SCC) compared with 3.84(95% CI 1.94-7.58, p<0.001) and 5.5(95% CI 2.28-13., p<0.001) of smoking status for lung cancer and SCC respectively. Adjusted by smoking and age the risk of lung cancer and SCC was 15.87 (95% CI 1.75-143.86, p=0.014) and 36.22 times (95% CI 3.08-425.10, p=0.004) higher for patients with positive HPV16/18 infection than negative, respectively. Meanwhile smoking increased the risk of lung cancer and SCC by 3.21(95% CI 1.51-6.83, p=0.002) and 4.9 (95% CI 1.79-13.39, p=0.002) respectively when adjusted by HPV and age. Also high-risk HPV positivity was more frequent among lung cancer patients under 50 than those older than 50(p=0.013)

Conclusion: This result suggests that HPV infection is relatively low among Khorasany lung cancer patients comparing to other regions, but of great impact on lung cancer development.

Department of Pathology, Ghaem Hospital, Faculty of Medicine, Mashhad University of Medical Sciences, Mashhad University of Medical Sciences

Keywords: lung cancer, *Human papillomavirus*, Polymerase Chain Reaction, Iran

Association of *Epstein-Barr virus* DNA with Lung Carcinoma

Amir Hossein Jafarian, Abbas Ali Omidi Ashrafi, Kiarash Ghazvini, Nema Mohamadian Roshan, Mehdi Karimi Shahri, Abbas Tabatabaee, Mahmoud Bagheri, Samaneh Boroumand-Noughabi

Department of Pathology, Ghaem Hospital, Faculty of Medicine, Mashhad University of Medical Sciences

Abstract

Background: Lung cancer is the leading cause of cancer death worldwide. Apart from the classic etiologic role of smoking, a variety of other contributing factors, including viral infection, have been suggested in tumor genesis. Among viral agents, *Epstein - Barr Virus* (EBV), the first known human oncogenic virus that has been linked to some lymphomas, lymphoepithelial tumors and carcinomas seem to be good *Candida*te. In this study we aimed to investigate the association of this virus with lung carcinomas.

Methods: A total number of 90 formalin fixed paraffin embedded lung tissues including 46 cases of lung cancers (18 squamous cell carcinomas(SCC), 18 adenocarcinomas and 12 small cell carcinomas) and 42 non tumoral samples (control group), all diagnosed during 2004-2010, were retrieved from the pathology archive of Quaem Hospital(Mashhad, Iran). Following DNA extraction, polymerase chain reaction was performed using EBV- Eph PCR kit (AmpliSense, Russia). The positive cases were studied immunohistochemically for expression of virus late membrane protein (EBV- LMP-1) in tumoral tissues.

Results: Five of our cases, including four SCCs and one adenocarcinoma and two control samples showed positive reaction in PCR. All positive cases showed diffuse staining with LMP-1 in immunohistochemistry.

Conclusion: We found a significant difference in presence of EBV genome in cases of lung SCC comparing to other lung lesions (P=0.02). According to our data EBV is not at major play in the non lymphoepithelioma like cancers of lung in general, but may have a role in the tumor genesis of some lung squamous cell carcinomas.

Keywords: Lung, cancer, EBV infection, Polymerase Chain Reaction

Microbial Culture and Sensitivity Pattern in Urinary Tract Infections in Children: Experience with 281 Urine Cultures in Sanandaj

Jafar Soltani, Abubakr Afura

Abstract

Introduction: Urinary tract infections (UTIs) have been considered as an important risk factor for the development of vesicoureteral reflux and renal injury. Optimal empirical therapy of UTIs requires accurate knowledge of local susceptibility patterns, which vary with organism.

Methods: This cross-sectional study was conducted from January 2007 to September 2011 in Sanandaj in order to determine prevalence of bacterial types and the antibiotic resistance of urinary pathogens. Children aged less than 12 years who had signs and symptoms of UTI were selected. Urine samples were obtained by sterile urine bags (at least 2 consecutive positive cultures), suprapubic aspiration and midstream sampling in older children. Sensitivity was measured by the disc diffusion method using the NCCLS protocol.

Results: A total of 281 positive urine cultures of children meeting inclusion criteria were included. 90% were females, and 28.1 were younger than one year. The most prevalent urinary pathogen was Escherichia coli (239 cases, 85.4%). Other organisms were *Staphylococcus epidermitis* (6 cases, 2.1%), *Enterococcus spp*. (3 cases, 1.1%), *Citrobacter spp*. (4 cases, 1.4%), *Enterobacter spp*. (9 cases, 3.2%), *Klebsiella spp*. (14 cases, 5%). *E. coli* had a resistance rate of 67.7 to trimethoprim-sulfamethoxazole, 19.7% to cefixime, 28.3% to cephalexin, 38% to cephalothin, 33.8% to nalidixic acid, 4.8% to nitrofurantoin, 70% to ampicillin, 20.4% to gentamicin, 16.2% to amikacin, 14.7% to ceftriaxone, and 22.7% to cefepime.

Conclusion: There were a high percentage of antibiotics resistances in Sanandaj. A national program is needed to provide judicious use of antibiotics and lower the bacterial resistance rates.

Department of Pediatrics, Faculty of Medicine, Kurdistan University of Medical Sciences

Keywords: Urinary tract infection; etiology; bacteria; drug resistance

A

B

C

D

E

F

G

H

I

J

K

L

M

N

O

P

R

S

T

V

Y

Z