Pertussis Epidemiology in Iran, 2006-2009

Zahraei SM*, Shahcheraghi F, Pourshafie MR, Dousti F
*zahraeicdc@yahoo.com

ABSTRACT

Background and objective: Pertussis is an acute respiratory infection with chronic paroxissmal cough. After initiation of EPI program in Iran in 1984 with more than 95% coverage of target group, burden of pertussis decreased dramaticaly in the country. In this article we discussed in detail on epidemiological aspects of pertussis in the country.

Materials and methods: According to the national guidelines for surveillance of pertussis, nasopharyngial specimen has been taken from all suspected cases and sent on transport media for lab confirmation to the Pasture Institute of Iran.

Results: Overall, 2052 suspected cases reported to the district health centers in the period of the study. The most prevalent age groups were less than 2 month, 2-11 month and 1-4 y with 22%, 36% and 24% respectively and just 10% were in above 10. 71% lived in urban areas and proportion of male and female was approximately equal. The cases reported mainly in spring and summer.In totally, 1629 clinical specimen tested in laboratory with 18 positive culture and 141 positive by RT-PCR.

Conclusion: Detection rate of suspect and confirmed pertussis cases is increasing in Iran. Althogth 90% of cases were in less than 5 y/o, however it could be due to low suspision rate of physicians to pertussis in approach of adults with chronic cough.

Keywords:**Epidemiology, Pertussis, Iran**

A^-B^+ Toxigenic Clostridium difficile Strains in Children with Cancer

Tavafi H, Sarshar M, Owlia P, Shahrokhi N*

*shahrokhi@pasteur.ac.ir

ABSTRACT

Background and objective: Clostridium difficile was recognized as a major cause of pseudo membranous colitis, antibiotic associated diarrhea and nosocomial infections. The aim of this study was to determine prevalence of A^-B^+ C. difficile isolates, among children with cancer undergoing chemotherapy by Multiplex PCR.

Materials and methods: During a period of 12 month, 105 stool samples were collected from children with cancer undergoing chemotherapy. Multiplex PCR, was performed by specific primers of tpi (teriose phosphate isomerase), tcdA, and tcdB (A and B toxins) genes.

Results: In this study C. difficile was identified in 18 cases (17.14%) patients with cancer undergoing chemotherapy. Among of positive C. difficile isolated, 13 cases (72%) were recognized toxigenic cases, as follow: 30.76% A^+B^+ (both toxin- producing), 61.53% A^-B^+ (only producing toxin B) and 7.7% were A^+B^- (only producing toxin A).

Counclusion: Our results revealed that, high prevalence of A^-B^+ toxigenic C. difficile strains in patients group. Considering these strains can lead to C. difficile associated infections, its appears to be important in order to prevention of high prevalence of this bacterium, apply rapid and reliable molecular detection methods such as Multiplex PCR is essential for preliminary screening and detection of C. difficile and its toxins.

Key words: Clostridium difficile, A^-B^+ strains, Chemotherapy, Multiplex PCR

Tetracycline Resistance Genes of Diarrhogenic E. coli in Pediatric Patients

Sarshar M*, Tavafi H, Ghorbani-Dalini S, Souod N, Kargar M, Shahrokhi N
*meysam_sarshar@yahoo.com

ABSTRACT

Background and objective: Escherichia coli is an important group of pathogens associated with diarrhea among children fewer than 5 years old. The aim of this study was to determine the tetracycline resistance genes from diarrhogenic E. coli, as well as frequency and susceptibilities antimicrobial agents in children less than 5 years of age.

Materials and methods: In this descriptive study from April to December 2010, 450 fecal specimens were collected from children at 3 hospitals in southwest Iran. Isolates were tested for susceptibility to antimicrobial drugs by disc diffusion methods as described by the CLSI. PCR amplification was used to detect genes conferring resistance to tetracycline (tetA, tetB and tetC).

Results: From the total number of specimens examined, 77(26/20%) Diarrheagenic E. coli was detected. Antibiogram analysis revealed that the highest rate of antibiotic resistance was against tetracycline (55/8%) and the lowest was amikacin (0%). From tetracycline resistant isolates, 38 cases (88.4%) were positive by PCR for tet genes, as follow: tetA found in 33(76/6%), tetB 27 (62/7%) and tetC 6 (13/9%).

Conclusion: Our results showed that the prevalence of antibiotic resistance and the percentage of tetracyclin resistance genes are high in diarrheagenic E.coli isolated from the children under the study, which is probably due to lack of diagnosis in appropriate usage of antibiotics regiments. Therefore, there is the need for updating the treatment protocol.

Key words: Diarrhogenic E. coli, Tetracycline resistance, PCR, tet genes

Knowledge and Attitude of Injecting Drug Users about AIDS

Moradi AR , Emdadi A, Sori E, Mostafavi E*

***** mostafavi@pasteur.ac.ir

ABSTRACT

Background and objective: Currently there is no effective vaccine and treatment for Acquired Immunodeficiency Syndrome (AIDS). Therefore, the only effective measure, is to increase the knowledge of high-risk populations on this disease particularly, about the modes of it's' transmission. This study is done to determine the knowledge and attitude of Injecting drug users about Aids.

Materials and methods: This is a descriptive-sectional study in which 118 persons of Injecting drug users of Bahar were used as sample in the year 2010, which were selected according to simple sampling and were studied with the help of questionnaire. Then the resulting data were analyzed by SPSS software.

Results: Results indicated that, 7/51% of Injecting drug users had poor knowledge, 39% moderate and 9.3% had good knowledge about Aids. Most of the study groups had negative attitude regarding the transmission ways and prevention of Aids. Level of knowledge had a significant relation with attitude ($P<0.05$).

Conclusion: Overall knowledge and Attitude of high school students about ATDS was low. Therefore, necessity of conducting permanent and new educational programs regarding ways of transmission and prevention of Aids in order to increase knowledge and Attitude quality and quantity of Injecting drug users is felt.

Key words: knowledge, attitude, Injecting drug users,Aids

Cutaneous Leishmaniosis Vectors by PCR in the Central County Villages, Qom province

Rassi Y, Saghafipour A*, Abai M.R,Oshaghi Sh, Mostafavi R

* abed.saghafi@yahoo.com

ABSTRACT

Background and objectives: Cutaneous leishmaniasis is a parasitic disease transmitted by sand flies and there are foci of disease in different parts in country. In Qom province, the disease is mostly having been reported from the central county, including Ghanavat and Qomrood villages. Regarding the fact that knowing the sand fly species that transmitting leishmaniasis has a key role in the disease control, this study was performed in order to identify the vectors in central county focus of cutaneous leishmaniasis.

Materials and methods: The present study was done as a descriptive cross- sectional, in 5 villages of the central county of Qom province in 2010. Sand flies were collected biweekly from indoors and outdoors, using 300 sticky traps. The samples were identified with credible keys after slide preparation. In order to identify the disease vector, 150 P. papatasi, 20 P. sergenti and 10 P.caucasicus sand flies were selected and The DNA of sand flies are extracted. The extracted DNA analyzed by Leishmania specific premiers using ITS1 PCR-amplification. The PCR products were digested by Haelll enzyme.

Results: In total 10246 sand flies (4578 from indoors and 5668 from outdoors) were collected by sticky traps and identified. In conclusion, 10 species of sand flies were recognized in the area (5 from Phlebotomus species and 5 from Sergentomyia species). The L.major infection in three caught P.papatasi out of 180 sand flies recognized. Two of the infected sand flies with unfed and one of them had been semi gravid abdominal status.

Conclusion: According to the results, phlebotomus papatasi which is the vector of the zoonotic cutaneous leishmaniasis in Iran and around the world is vector of cutaneous leishmaniasis in central county of Qom province.

Keywords: Cutaneous leishmaniasis, Vector, PCR ,Qom.

Acinetobacter and Methalo-β-Lactamase Genes

Abedin M, Shahcheraghi F*

*shahcheraghifereshteh@yahoo.com

ABSTRACT

Background and objective: β- lactamase class B, including IMP, VIM, SPM, the MBLs are read, as of mechanisms to carbapenem resistance in Acinetobacter strains are considered. This caused many problems in the treatment of bacterial infections has created. In this study, evaluate to resistance of Acinetobacter strains isolated from clinical specimens to imipenem and investigation of MBLs genes of blaSPM-I, blaVIM-I, blaIMP- I in these bacteria were done.

Materials and methods: A total of one hundred strains of Acinetobacter Tehran's Shariati and Baghiyatallah hospital, were collected. The antibiotic suspectibility by diffusion method (disk diffusion) and the minimum inhibitory concentration (MIC) imipenem with microbroth dilution method was conducted. The PCR test strains using gene-specific primers blaSPM-I, blaVIM-I, blaIMP- I was.

Results: In total, fifty imipenem-resistant Acinetobacter strains were isolated. The minimum inhibitory concentration (MIC) showed that majority of these strains MIC ≥64µg/ml to imipenem. Investigation of methalo- β- lactamase genes showed that 14% and 26% of species were harbourd blaSPM-I, blaVIM-Irespectively. blaIMP-I gene in these strains were not found

Conclusion: According to the results, Acinetobacter strains resistant to carbapenem as a serious problem in patients with these microorganisms is considered. Because of MBLs producing strains of the bacteria, The identification of strains important step in the treatment and control of nosocomial infections caused by these strains is considered.

Keyword: Acinetobacter spp, methalo- β- lactamase SPM-I , methalo- β- lactamaseVIM-I, methalo- β- lactamase IMP- I

Resistance to Ciprofloxacin, Imipenem, Ceftriaxone and Cefotaxime in Culture Positive Samples of Pediatric Patients

Barari Sawadkohi R*, Rajabnia-R, Saeidi F, Bagheri M
*sawadkohi1330@yahoo.com

ABSTRACT

Background and objective: The widespread use of antibiotics for prophylaxis or treatment of bacterial infections leading cause of resistance in bacteries . so recognition of this bacteries and bacterial resistance patterns is one of the most important factors in treatment of bacterial infections. it seems that due to widespread use of Ciprofloxacin, Imipenem, Ceftriaxone and Cefotaxime bacterial resistance for this antibiotics have been increased. So the present study was designed to determined antimicrobial resistance in bacteries that growth in culture of admitted patients in amirkola pediatric hospital.

Material and methods: In this cross-sectional study between 1389-1390 all positive culture of patients sample was collected. Bacterial resistance pattern was determined by minimum inhibitory concentration according to CSLI-2006 protocol. All data has been analyzed by spss 18.

Results: The most frequent microorganism isolated in this study was E.cloi(68.7%), staph areus (6.1%), klebsiella , Shigella and staph saprophyticus(5.1%), streptococcus(4%) , pseudomonas and entrobacter (3%). Based on the result of antimicrobial testing susceptibility to Ciprofloxacin, Imipenem, Ceftriaxone and Cefotaxime were 90.9%, 72.2%, 91.9% and 60.6%. E.coli had the most resistance rate to Ciprofloxacin (16.2%)and the most susceptibility rate to Cefotaxime(97.1%). Kellebsiela was susceptible to all antibiotics.

Conclusion: In this study the most rate of susceptibility was seen in cefotaxime and the most rate of resistance was seen in ciprofloxacin

Key words: bacterial resistance, culture positive, MIC

Antibiotic Resistance and mecA Gene among Methicilin Resistant Staphylococcus aureus Isolated from Tehran Hospitals-2008-2011

Rahimi F, Pourshafie MR, Bouzari M*, Katouli M,

* mbouzari@yahoo.com

ABSTRACT

Background and objective: Staphylococcus aureus is a common cause of infections among human and animals and known as community-acquired and nosocomial pathogen. MRSA infection has recently become a serious problem in anti-microbial chemotherapy. The aim of the study was to detect and analyze the antibiotic resistance pattern among MRSA isolated from six hospitals in Tehran in 2008-2011.

Material and methods: Totally 396 isolates of MRSA from clinical samples were collected from six hospitals in Tehran. All isolates were identified at the species level using specific primers. Susceptibility to seventeen antibiotics was determined using disc diffusion method. MIC of oxacillin and vancomycin in MRSA isolates was also done using Etest according to CLSI recommendation. PCR was used to detect mecA gene.

Results: Using PCR all isolates were confirmed as MRSA. The highest level of resistance was observed to oxacillin, penicillin, ciprofloxacin, kanamycin, erythromycin, tobramycin and amikacin respectivelyMIC results showed that 86% of isolates showed high level resistant to oxacillin (MIC≥256 µg/ml). None of the MRSA isolates were resistant to vancomycin. One hundred percent of the isolates contained mecA gene.

Conclusion: This study showed that the prevalence of MRSA isolates is lower than the other studies in Iran. MRSA isolates showed resistance to broad spectrum of antibiotics. Synercid, linezolid, vancomycin and chloramphenicol are the most effective antibiotics against MRSA infections. Detection of mecA gene is a rapid and reliable method for identification of MRSA isolates.

Key words: MRSA, methicillin, vancomycin, mecA, Tehran

Beta Lactamases and Extended Spectrum Beta Lactamases Producing Klebsiella pneumonia in Kermanshah

Eradati S, Abiri R *, Zandie N, Rezaei M, Adabagher SH

* rabiri@kums.ac.ir

ABSTRACT

Background and objective: Klebsiella pneumonia is an opportunistic pathogen belongs to family of Enterobacteriaceae. This species, like most other pathogenic and opportunistic bacteria, is resistant to many classes of antibiotics. Regarding to prompt appearance and spreading of Beta lactamases and Extended Spectrum Beta Lactamase (ESBL) producing strains, Klebsiella is becoming resistant to most members of Penam and Cephem family of antibiotics. The aim of this study was determination of Beta lactamases and ESBL producing K. pneumonia isolated in Kermanshah.

Material and methods: Following identification of isolates using biochemical tests, existence of Beta lactamases and ESBL among the strains were detected using acidometry and Double Disk Diffusion method, respectively.

Results: From 260 isolates, 247 were confirmed as Klebsiella pneumonia. Among those, 178 (72%) containing Beta lactamase and 111 (45%) possessed ESBL.

Conclusion: Our results showed the importance of Betalactamase and ESBL enzymes among Klebsiella pneumonia in Kermanshah, and the importance of precision and attention to antibiotic prescription.

Key Words: Klebsiella pneumonia, Beta Lactamase, Extended Spectrum Beta Lactamase

Sero-epidemiology of Leptospirosis in Livestock Slaughterhouses

Majd Soltani N, Khodaverdi Darian E, Dezhbord M , Moradi Bidhendi S and Khaki P*
*khaki.pejvak@yahoo.com

ABSTRACT

Background and objective: Leptospirosis is an emerging infectious disease and is considered to be the most widespread zoonotic disease in the world. The microscopic agglutination test (MAT) is the gold standard test for serological diagnosis of the Leptospirosis. The aim of this study was Epidmiological survey of Leptospira in livestock slaughterhouses of zanjan province,in iran.

Materials and methods: A total of 135 serum samples randomly collected from herds since february 2012 to june 2012. Sera were tested by MAT using live Leptospira interrogans serovars: Hardjo, Pomona, Icterohaemorrhagiae, Grippotyphosa, Canicola,Autumnalis and Serjoe .

Results: The results showed that the 44.4% livestock sera showed positive serological reaction against leptospiral antigens. The most common serovars were L, Serjoe Hardjo .L. Canicola and L. Auotomnlis with (29.27%), (17.89%)and (16.26%) respectively.

Conclusion: In positive sera the antibody titers of 1:200 (54.47%), 1:400 (27.64%), 1:800(10.57%), and 1:600(3.25%),1:3200(4.07%), were detected.In contrast to other studies in Iran, the percentage of prevalence of leptospiral infection in zanjan was almost higher after Ahwaz. The high prevalence of infection and dominant titer of 2:100 reveal that leptospiral infection in Zanjan is endemic.

Keywords: Leptospiral, Zanjan province, Cattle, MAT.