The Viewpoints of General Practitioners Owning a Private office in North and East of Tehran about Barriers and Problems of Reporting of Communicable Diseases in 2011

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Abstract

Background and objective: Effective Prevention and control of infectious diseases requires the surveillance system for developing efficient procedures for the priority infectious diseases. According to the less than expected reports and lack of studies on problems and barriers of reporting, this study was done with the aim of identifying the barriers and problems of surveillance system, the suitable way and time of education, the believes, the requirements and the expectations in order to improve the quality and quantity of surveillance system in the viewpoint of general practitioners (GPs) who have privet office in the north and east metropolitan area of Tehran.

Materials and methods: This cross sectional study was performed with the participation of GPs undertaking their private practices around the Shahid Beheshti University in the north and east of Tehran in 2011. The sample size was 336 GPs and the sampling method was simple random. Data was collected by questionnaire and interview.

Result: A total of 336 GPs participated in the study. 131(39%) of them were male, and 205 (61%) were female. The mean age of females was 36.6 ± 6 years and for males was 41.1 ± 8.6 years. The barriers to reporting included: lack of patients consent for report (26.5%), lack of adequate information by heath centers (23.8%), uncertainty of diagnosis (22%), lack of feedback of health centers (21.7%) and lack of sufficient time (21%), conflict over patient privacy (18.5%), lack of knowledge to reporting, not clearly defined reporting necessity, feeling the reports as useless 12.5%, not known identity of report giver 11.5%, not proper working time of health centers (9.8%), inappropriate behavior with referred patients (8.6%), disconnected or busy phone (8.6%), concern for missing patients (7.4%), to avoid adverse consequences of reporting (7.1%) and long distance between private office and health center (3.3%). Except uncertainty of diagnosis between two sex, which the number of female were mentioned more than male (p=0.014), there were not seen statistically significant for other options.

Conclusion: The study showed that mentioned problems and barriers by GPs owning a private office who participated in this study indicate the inadequate understanding of the objectives of surveillance system and reporting activities. It seems that the most important reason of the above situation is the lack of a systematic education and an insufficiency of the activities of health centers.

Keywords: Reporting, ODiseases Report, Surveillance, General Practitioners

Molecular Study of Extended-Spectrum Beta-Lactamases among Enterobacter spp. Isolated from Teaching Hospitals in Tehran and Qazvin, Iran

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Abstract

Background and objective: Enterobacter spp. are members of the family Enterobacteriaceae. In recent years, there are several reports showing the high prevalence of beta-lactam resistant among these organisms. Different types of beta-lactamase enzymes have been identified in Enterobacter spp., which Extended-Spectrum Beta-Lactamases (ESBLs) are very important among them. The ESBL-producing isolates capable to hydrolyze extended spectrum penicillin's and cephalosporins. The aims of this study were to determine the prevalence of ESBLs and to detect of blaTEM and bla_{SHV} genes among ESBL-producing Enterobacter spp. isolates.

Materials and methods: A total of 107 Enterobacter isolates were collected from Tehran and Qazvin hospitals. Isolates were identified by standard microbiology and biochemical methods. All isolates were screened for ESBLs production by agar disk diffusion method using ceftazidime, cefotaxime, aztreonam, cefpodoxime and ceftriaxone discs and then were confirmed by combined disk method. ESBLs-positive isolates were tested for bla_{TEM} and bla_{SHV}-ESBLs genes.

Results: Of the 107 isolates, 58 isolates (54.2%) showed the reduced susceptibility to the screening antibiotics. 51 isolates (47.6%) were ESBLs positive by combined disks method. Twenty eight isolates (54.9%) contained bla_{TEM} genes and 2 isolates (3.9%) harbored the bla_{SHV} genes.

Conclusions: This study showed the high prevalence of ESBLs in Enterobacter spp. isolated from the clinical specimens in studied hospitals. The initial identification of ESBL-producing isolates and use of appropriate infection strategy is essential to control the more spread of these organisms in selected hospitals.

Keywords: Enterobacter, Extended Spectrum Beta-Lactamase, combined disk method

Antibiotic Resistance Pattern and Prophage Typing of Methicillin Resistant Staphylococcus aureus Strains Isolated from Chicken Husbandries in Tehran

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Abstract

Background and objective: Staphylococcus aureus is a common cause of infection among human and animals and known as community-acquired and nosocomial pathogen. Most of the isolates contain lysogenic phages which are responsible for production of various virulence factors. All staphylococcus isolates are classified in 6 groups according to their sensitivity to 27 known lysogenic phages. The aim of this study was to analyze different prophage types, antibiotic resistance pattern and detection of mecA gene in meticilin resistant S. aureus (MRSA) strains isolated from a poultry farm in Karaj.

Materials and methods: Totally 110 isolates of MRSA from poultry samples were collected from 1 laving flocks in Karaj. All isolates were identified at the species level using specific primers. Susceptibility to 19 antibiotics was determined using disc diffusion method according to guidelines of Clinical Laboratory and Standard institute (CLSI). Minimum inhibitory concentration (MIC) of oxacillin and vancomycin in MRSA isolates were also detected using Etest according to CLSI recommendation. Primers for identification of 6 classes of prophages were used in a Multiplex-PCR assay. Plaque and spot assays were used to show the presence of lysogenic prophages. mecA gene was detected using specific primers.

Results: Using PCR all isolates were confirmed as MRSA. The highest antibiotic resistance was observed to penicillin (100%) and followed by ciprofloxacin (100%), erythromycin (100%), amikacin (100%) and kanamycin (100%). None of the isolates were resistant to fusidic acid, nitrofurantoin, vancomycin, linezolid and synercid. Very high (MIC≥128 µg/ml) levels resistance to oxacillin was observed in 83.5 % of the isolates. Four different prophage types were found in MRSA isolates. Out of the total MRSA isolates, 81 and 19 percent of the isolates contained 4 and 3 different prophage types, respectively.

Conclusion: High diversity of prophage phages was found in MRSA isolates. Prophage segment from SGF prophage type was common in the MRSA isolates indicating the ability of these isolates to produce enterotoxins and other virulence factors. High prevalence of different classes of prophages encoding a variety of virulence factors and high oxacillin resistance provide an important role for phages in the evolutionary development of virulence factors and also diversity in methicillin resistance cassette in MRSA isolates. Presence of these highly virulent isolates with high resistance to first and second lines of treatments is a potential treat for public health.

Key words: MRSA, prophages, SGF, poultry

Clostridium difficile Carriage Rate in Outpatients with Inflammatory Bowel Diseases

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Abstract

Background and objective: Closteridium difficile is a gram positive, anaerobic and sporeforming bacillus. Inflammatory bowel disease or IBD includes Crohn's disease and ulcerative colitis. Inflammation of the intestinal mucosa in these patients can be as a risk factor for colonization of Clostridium difficile. The purpose of this study was to analysis of Clostridium difficile carriage in the IBD outpatients.

Materials and methods: Stool specimens were obtained from 50 outpatients with IBD. Stools were cultured on selective media under anaerobic conditions. Filtered extract of bacteria was exposed to HeLa cell culture for analysis of toxin production after identification of Clostridium difficile isolates.

Results: The results showed that 3 IBD patients (6%) had stool cultures positive for Clostridium difficile. Stool cultures were negative in all patients with Crohn's disease. All 3 patients had ulcerative colitis. Only one isolate was positive for toxin production.

Conclusion: The ulcerated colitis than Crohn's patients had higher carriage. In general IBD outpatients carriage rates for Clostridium difficile was low.

Keywords: Clostridium difficile, Inflammatory bowel disease, outpatients, Stool culture, cell culture

Molecular Typing of Mycobacterium tuberculosis by IS6110-RFLP Method

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Abstract

Background and objective: Molecular genotyping methods are important in detecting the dominance of transmission or reinfection in a population. IS6110 – RFLP typing remains the international accepted standard and continues to provide new insights in the epidemiology of mycobacterium tuberculosis infections. Genetic basement of IS6110 is because of different copies and places in different mycobacterium species genomes.

Materials and methods: During one year study genotyping of 100 of M. tuberculosis (M.t.) isolates from patients referred to Pasteur Institute of Iran were accomplished with IS6110-RFLP typing method. The IS6110 DNA probe was prepared with amplification of 245 bp-fragment using PCR method. This fragment was purified and labeled by digoxigenin. Enzymatic digestions were accomplished on extracted DNA of all Mycobacterium tuberculosis isolates using PvuII enzyme. After hybridization and detecting procedures the RFLP patterns were analyzed with GelcomparII software.

Result: According to the obtained dendrogram 35 common types (CT) and 17 single types (ST) and 3 predominant CTs were detected. We could not find any meaningful relation between antibiotypes and genotypes. Four MDR TB strains isolated among studied population.

Conclusion: According to our study the finding that 3 prevalent genotypes constituted 21% of the isolates show limited transmission rate among studied population. On the other hand high diversity among the rest of genotypes maybe due to newly acquired TB which is urgent need for TB control program. This will be value when compared with other characteristics such as level of virulence or antibiotic resistant pattern of isolates. Because of the different antibiotic resistant patterns in predominant common type isolates and the presence of MDR isolates among these types the monitoring of TB patients during antibiotic therapy is essential for prevention of spreading MDR-TB isolates in population.

Keywords: Mycobacterium tuberculosis, Molecular Typing, RFLP

Antibiotics Profile of Klebsiella pneumonia, Araad Hospital.Tehran.2008-2010

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ABSTRACT

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

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

Results: Most of Klebsiella pneumoniae strains isolated were from urine samples every three years and the lowest of Klebsiella pneumoniae strains from bronchial samples. The most amount of sensibility to Cefotaxime, Imipenem and Amikacin and the most amount of resistant were seen to Gentamicin, Ceftriaxone and Ciprofloxacin.

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

Key words: Antimicrobial Resistance, Antibiotics, Klebsiella pneumoniae, Araad hospital.

Fauna and Monthly Activity of Anopheles Mosquitoes in Mahshahr **District, Khuzestan Province. 2013**

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Abstract

Background and objective: Anopheles mosquitoes are the sole biologic vectors of malaria. Research on the anophelinaemosquitoesfauna and monthly activity is important in some aspects such as, in vector control. In this study, species composition and monthly activity of anopheles mosquitoes inMahshahr district has been studied.

Materials and methods: Larvae and adult mosquitoes were captured in a descriptive study from selected villages. Adults were captured using total catch and hand catch methods, also larvae were captured by Ladle handling method. Larvae and adults were identified microscopically using illustrated keys for Iranian mosquitoes.

Results: Totally 1746 larvae and 1167 adults of Anopheles mosquitoes were captured. Four species were identified as the Anopheles fauna in five villages consisting of Anophelesstephensi (70.55%), An. pulcherrimus (1.16%), An. dthali(5.60%), An. superpictus(22.69%). The peak of activity of Anopheles larvaeis in June and September and its monthly activity is in April to January.

Conclusion: Anophelesstephensiwhich is main malaria vector in different parts of the world and Iran, having high potential fortransmission and possibility of establishing a transmission cycle with low abundance is the characteristics of this species. Specific studies such as determination of biting and resting habits and host preference of adult mosquitoes in this area is recommended.

Key words: Fauna, Monthly activity, Anopheles mosquitoes, Mahshahr, Khuzestan

Epidemiolgy of Pulmonary Tuberculosis of Smear Positive in Kurdistan Province (Iran)

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Abstract

Background and objective: TB is major problem worldwide and it is estimated one third of the world population are already infected and each year 9 million people develop full blown tuberculosis of these 3 million die of the disease, annually. The aim of this study was to investigate the Epidemiolgy of pulmonary tuberculosis of smear positive in Kurdistan Province (Iran) during 2002-2010.

Materials and methods: All cases of smear positive TB occurring in Kurdistan province during the years of 2002-2010 was included into this study. Data on the different variables were abstracted from the patients' file and entered into the computer. For each patient demographic data, clinical data were collected. Descriptive analyses were done using SPSS software. Statistical tests including t-test and γ^2 were used. P-value of less than 0.05 was considered as criteria for statistical significancy.

Results: Totally, 694 cases were diagnosed. 59.5% of them were females, 80.9% married and 51.1% were urbans. Mean age of patients was 58.7 \pm 17.7 years. The most were in age group 40-70 years. The most of them were housewife (43.5%). 1.5% had jail experience, 9.9% were smoker and 2.3% had dependence to opoids. Prevalence of disease varied between 3.7 (the least in 2004) and 7 (the most in 2009) per 100000 people. Most clinical symptoms were cough 'dyspnea loss of appetite, loss of weight, sweetness, fatigu, fever, hemoptesia and chest pain.

Conclusion: Our findings indicate that there high prevalence of TB in the studied population. It is necessary to follow up case finding, prevention and treatment of TB in the health care system of Kurdistan Province so that an appropriate condition for the decrease of TB incidence would be provided.

Key words: pulmonary tuberculosis, smear positive ' Epidemiolgy' Kurdistan

Bacterial Flora in the Mouth of Venomous and Non-poisonous Snakes before and after Eating

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Abstract

Background and objective: Snake bite is a public health problem in tropical and subtropical countries. Snake problem is not only lead to poisoning but also because of the snake's mouth pathogens may be caused infection in the victims. This study was conducted to identify mouth bacteria in poisonous and non-poisonous snakes.

Materials and methods: 11 non-toxic and poisonous snakes were examined before and three weeks after eating food in two stages. Bacterial samples from the oral cavity with a sterile swab were cultured on of blood agar and Mac Kanky medium. Gram staining was performed on all colonies. appropriate test methods were used for identification of gram-negative and positive bacteria.

Results: Coagulase-negative Staphylococcus was the most common bacteria by 34.5 and Pseudomonas was less by 3.1 percent. Then the order, Salmonella (18.8%), Escherichia coli, Providencia (each 12.5%), Proteus, Enterococcus, Bacillus (each 6.2%) were identified in the snakes.

Conclusion: Our results indicate that oral cavity is contaminated to the bacteria in non-toxic and poisonous snakes. Thus, probable infection should be considered in addition to toxicity in victims.

Key words: Bacterial contamination, Mouth, Poisonous Snakes, Non-poisonous snakes

Molecular Detection of Campylobacter jejuni by Using a Specific Locus

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Abstract

Background and objective: Campylobacter is one of the most common causes of diarrheal in human. Hence, specific and rapid detection of Campylobacter jejuni have many importances in disease diagnosis and treatment. In this study, finding of specific locus for specific detection of Campylobacter jejuni was surveyed.

Materials and methods: In this study, multiple sequence alignment was used to finding a Campylobacter jejuni specific locus, and then primer designing was done by Primer3 software. DNA extraction was done by modified STET method and polymerase chain reaction was carried out as usual.

Results: The results of multiple sequence alignment were showed a specific and conserve locus in genome of campylobacter jejuni. By designing a primer using this locus, a specific amplicon was observed in the PCR.

Conclusion: Whereas virulence and hippurate genes are not specific to campylobacter jejuni, using specific locus of campylobacter jejuni is reliable for absolutely diagnosis of this species.

Keywords: Campylobacter jejuni. Enteritis, PCR, Specific primer