The Impact of Climatic Parameters on Prevalence of Dysentery in Shushtar

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Abstract

Background and objective: Acute infectious diarrhea is the Cause of 16/2 percent of infectious diseases in Iran. Unsuitable hygienic conditions and environmental factors such as weather parameters have crucial role. Khuzestan Province is one of the focuses the dysentery is prevalence .The purpose of this research is determining the role of climatic factors on Shushtar city, which is the fourth high Population in Khuzestan Province.

Materials and methods: The research was performed at university of Isfahan in the year 2014. The data related to disease and climate were obtained from Ahvaz university of Medical Sciences and meteorology department of Khuzestan during 2008-2013 respectively. Data were divided to time series of is 15days, monthly and seasonal. Then their relation were specified by SPSS software.

Results: Findings showed that dysentery in rural area is more prevalence than dysentery urban area, In regard to age, age group13-40 years old were more suffered from dysentery. The peak of prevalence of dysentery in autumn and spring when the balance of temperature and humidity reached desire. In addition, Almost parameters including radiation, thermal, humidity and motion weather at15day period have correlation by number of patients at this period although showed down wand trend at monthly and seasonal period.

Conclusions: Despite the interference of different factors in incidence of dysentery, climate is also the important factor for incidence of the illness and it could be used in creating a predate warning system.

Key words: Dysentery, climate, infections disease

Detection of Neospora caninum in Milk of Cows by Polymerase Chain Reaction

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Abstract

Background and objective: Recently, Neospora caninum is known as pathogens abortion in cattle. Abortion increases in live stock populations, there is a direct correlation between the reduction in the rate of protein products. The aim of this study was detection of Neospora caninum in raw cow's milk by polymerase chain reaction in Shahrekord, 2013.

Materials and methods: In this cross sectional study, 100 samples of milk from shahrekord traditional cattle were randomly collected. Then to identify the protozoa in milk samples, extracted DNA and analyzed by polymerase chain reaction (PCR).

Results: Based on polymerase chain reaction, 10 samples (10%) were infected to Neospora caninum.

Conclusions: These findings showed that PCR in milk can be used to identify infected cows and the transfer agent avoided newborn calves and other sensitive animals.

Keywords: Neospora, Vertical transmition, Milk, PCR

Associated Factors of Delayed Detection for Brucellosis on Northwestern Iran

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Abstract

Background and objective: Timely diagnosis of brucellosis especially in non-endemic areas is accompanied with delay diagnoses or mistake. This study was aimed at identifying factors associated with delay diagnoses of brucellosis in the North and North West Iran.

Materials and methods: This was a cross-sectional study. Data from the first 6 months of 1393 for all reported cases of brucellosis by health-care providers (public and private) were studied. Data on disease reporting forms were collected by health professionals in health centers. To examine the changing role of the delay in diagnosis, a logistic regression model and to evaluate the relationship between qualitative variables, chi-square test was used.

Results: In total, 2585 cases were reported by the patient care in the areas under study. Of these 1599 (62%), were male, and 2471 (95%) identified as new cases. The majority of cases 1017 (39.35%) attributed to age group of 25-44 years. Diagnostic delay significantly correlated with age and disease type (p < 0.05).

Conclusion: The findings of the study showed that more is delay in the diagnosis of new cases and the group 25-44 years. Strengthening disease surveillance and reporting system, disease transmission ways and clinical symptoms training in order to reduce the delay in diagnosis is essential.

Key words: delay diagnosis, brucellosis, Iran

Incidence Rate and Epidemiological Characteristics of Brucellosis in Qom province (2010-2014)

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Abstract

Background and objectives: Brucellosis is one of the zoonotic diseases that have always been considered a health problem in Iran. Since this disease is endemic in urban and rural areas in Qom province, this study was done to investigate epidemiology of brucellosis and its associated risk factors during $20^{1} \cdot - 7 \cdot 1^{\xi}$.

Materials and methods: This descriptive-analytical study was done, demographic and epidemiological data on patients with brucellosis were obtained from the medical records in Qom province Health Center during Y. Y. Y. The collected data were analyzed by SPSS software version 17.

Results: The mean incidence rate of brucellosis was 7 per 100000 people during $(\cdot) \cdot - (\cdot) \xi$. The greatest incidence was in 201ξ (11.85 per 100000 people), whereas the lowest incidence was in 201. (3.62 per 100000 people). Taking occupational exposure into account, the ranchers, farmers female household keepers, and students had the highest cases of brucellosis. The most age group that involved with this disease was patients over 51 years and 21-30 years. The majority of patients had Wright test titer= 1:320 in serology titration.

Conclusion: The trend of brucellosis incidence has been rising in Oom province in recent years. Nevertheless, this province is one of the regions with low incidence of brucellosis (1-27.7 per 100,000).

Keywords: Brucellosis, Epidemiology, Oom

Polymorphism in the Bordetella pertussis Virulence Factors Pertactin and Fimbriae in Iran

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Abstract

Background and objective: whooping cough is an acute and contagious infection that caused by Bordetella pertussis, a gram negative and human-specific pathogen. In the last decade, despite high vaccination coverage against pertussis in developed and developing countries, pertussis has reemerged in many countries including Iran.

Among several reason of resurgence of pertussis, one of the most important factors in outbreak of the disease might be polymorphism and genetic variation of virulence genes of bacteria. pertactin is considered as one of the important virulence factors in B.pertussis and Polymorphism in pertactin is essentially limited to region 1. Fimbriae or pillus antigens of B. pertussis have been shown to be one of the many adhesions present on the surface of the bacteria.

The purpose of this research was to study polymorphism of region 1 of prn gene and *fim3* gene in circulating isolates and compare with vaccine strains.

Materials and methods: We examined 35 isolates isolated from nasopharyngeal specimen collected in 2008-2012. These strains have also been identified by biochemical and slide agglutination tests. Region 1 of prn gene and the fim3 gene in these isolates of B. pertussis were amplified by using specific primers by PCR method. Then we sequenced genes and analyzed our results by chromas and mega4 software. We examined also vaccine strain (134).

Result: Our results showed that all examined strains have *prn* and *fim3* gene in their genome in size 600 bp and 800 bp, respectively, as a partial codon. Also 34 strains have prn 2 and fim3-2 alleles and only one strain has prn 1 and fim3-1 allele. strain 134 showed prn 1 and fim 3-1 alleles.

Conclusion: In studies that have been done in most European and American countries with high vaccination coverage, similar results have been seen and predominant alleles were prn2 and fim3-2. We also obtained *prn2* and *fim3-2* as a predominant allele in our result. This study is performed for the first time in Iran. Investigation in the world suggest that vaccination has selected for strains which are antigenically distinct from vaccine strains, also considering the importance of polymorphism genes encoding virulence and immunogenic factors of B. pertussis, it's very important to use the clinical strain that has dominant alleles of these virulence factors for production of effective vaccine against pertussis.

Consequently, it seems that more research is needed on the polymorphism of other virulence factors of *B. pertussis* in circulating strains in our country.

Key word : polymorphism ,pertactin ,fimbriae

Malaria in the Larestan City during 1998-2010

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Abstract

Background and objective: Malaria is a major public health problem worldwide, especially in tropical areas is between 300 and 500 million people affected annually by about one million people die of the disease. The purpose of this study was to investigate the epidemiology of malaria in the city sets Larestan.

Materials and methods: This study was a cross-sectional study evaluated include all recorded cases of malaria by community health center is the city Larestan years 1998 to 2010. The analysis of data was done by Excel software.

Results: A total of 1184 cases of malaria in the years 1377 to 1389, 178 cases were Iranian and non-Iranian people in 1006. Most of the cases in 1380 were 249, 65 of the transfer, the incoming 597 and 522 cases of recurrence and in terms of type, Plasmodium vivax, with 1099 cases and most cases have had.

Conclusion: the disease malaria in larestan County, trend was the bearish but because the majority of cases of the disease have been immigrants, immigrants make up especially so, controlling and monitoring the log can help organizations improve and minimize this disease have in larestan.

Key words: epidemiology, malaria, larestan

The Study of Resistance to Aminoglycosides among Escherichia coli **Strains Isolated from Different Water Sources**

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Abstract

Background and objective: Antibiotic resistance rates especially against aminoglycosides in E. coli are rapidly rising. Antibiotic-resistant bacteria such as E. coli released from humans and animals into water sources may act as a donor of antimicrobial resistance genes for other pathogenic E. coli strains. The aim of this study was to investigate the prevalence of antibiotic resistance to aminoglycosides among E. coli strains isolated from different water sources in Alborz province.

Materials and methods: The study included all E. coli strains isolated from different surface water sources in Alborz province in 2013. Bacterial strains were isolated, detected and identified by standard microbiological and biochemical tests. To screen the aminoglycosid-resistant isolates, the antimicrobial susceptibility testing was determined according to Kirby Baur assay. Susceptibility patterns of isolates were determined to lincomycin, rifampin, streptomycin, gentamicin, tobramycin, kanamycin, clindamycin, amikacin and azithromycin.

Results: One hundred E. coli strains were isolated from water sources and examined in this study. Antibiotic susceptibility testing showed that 95.7, 94.7, 93.7, 28.1, 27.08, 10.4, 7.4, 6.6 and 4.1 percentages of the isolates were resistant to clindamycin, lincomycin, rifampin, streptomycin, gentamicin, tobramycin, kanamycin, amikacin and azithromycin respectively.

Conclusion: This study reflects an increasing prevalence of aminoglycosides resistant E. coli strains circulating in water sources. Dissemination of these resistant strains is of particular concern in water sources.

Key words: Antibiotic resistance, E. coli, Aminoglycoside, water sources.

Prevalence and Risk Factors for Salmonella on Commercial Egg-Laving Farms in Iran, 2013-2014

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Abstract

Background and objective: Consumption of Salmonella contaminated eggs are responsible for many human non typhoid salmonellosis. The aim of this study was to determine the prevalence and risk factors of Salmonella contamination in commercial laying flocks in Iran.

Materials and methods: This cross sectional study was carried out between 2013 and 2014 in 20 provinces in Iran. Fecal samples were obtained from 113 laying flocks and were subjected to standard bacteriological tests for Salmonella isolation. The serotype of positive bacteriological samples were determined using serological tests and PCR. Relevant information of sampled holdings were acquired from GIS system and used for risk factor analysis.

Results: The prevalence of Salmonella contamination in laying hen holdings was 3.5%. The flock population (P = 0.021) and the number of poultry houses in the farm (P = 0.044) were major risk factors of Salmonella contamination in commercial laying flocks.

Conclusion: This investigation showed that some of the commercial layer farms in Iran are contaminated with Salmonella spp. and flock size and the number of poultry houses in a farm are associated with increased risks of Salmonella contamination. It can be concluded that regular sampling of laying flocks and establishment of proper measurements against positive flocks are necessary for ensuring the health of consumers.

Keywords: Salmonella; commercial laying flocks; prevalence; risk factor

Diversity of Variable Number of Tandem Repeats in Salmonella enterica Serovar infantis Isolated from Clinical Samples

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Abstract

Background and objective: Salmonella is a gastrointestinal pathogen with a widespread distribution throughout the word. This pathogen is considered as one of the most common and current foodborne infection in the world. The increasing incidence of infections caused by Salmonella enterica serovar infantis is concerning. Variable number tandem repeats are patterns of the repeated DNA which may have different repeats or sizes among different strains of a particular genus. The purpose of this study to assess the diversity of Salmonella enteric serovar infantis strains isolated from the clinical samples in Tehran.

Materials and methods: A total number of 20 strains of Salmonella enterica serovar infantis were analyzed by PCR with specific primers designed for SENTR3 and SE4 loci. Diversity of each loci were assessed after gel electrophoresis.

Results: The results demonstrated that SENTR3 locus showed the highest number of alleles, while the locus of SE4 showed the least number of alleles.

CONCLUSION: Since these loci showed relatively high diversity, these loci can be used as useful markers for genotyping of Salmonella enterica serovar infantis isolates in epidemiological surveys.

KEY WORDS: Salmonella enterica serovar infantis, variable number of tandem repeats, allele, PCR

Frequency and Antibiotic Resistance Patterns of Shigella Spp. in patients with Acute Diarrheic from two hospital in Kerman

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Abstract

Background and objective: Gastroenteritis is considered as one of the most common infectious diseases in the worldwide. Emerging resistance strains and increasing the number of patient suffering from gastroenteritis, particularly in less developed regions revealed a necessary monitoring surviving to determine the incidence of Shigellosis, awareness of antibiotic resistance pattern and prevention of prolonged treatment and reduce health care costs. The awareness of prevalence of Shigella Spp, evaluating the sensitivity of antibiotic resistance with aim to prevention and reduction of health care costs which are increasing.

Materials and methods: In the Cross-sectional study, during May to September 2014, a total of 130 hospital's samples had been isolated from gastroenteritis cases at two hospitals in Kerman, applying Kirby Bauer method.

Results: According to biochemical and serological tests, existences of the shigella's genus in 41 isolates (31.3%) were confirmed. In an antibiogram test, all strain was showed resistant to Sulfamethoxazole, Oxytetracycline and streptomycin, respectively, and the low degrees of resistant was to Nalidixic Acid with 12 percent. The resistance to Chloramphenicol, Gentamicin, Ampicillin, Oxytetracycline and streptomycin were 31/7%, 53/7%, 5/2%, 97/9% and 97/5%, respectively.

Conclusion: The antimicrobial resistance pattern indicated the prescription of three antibiotics including co-trimoxazole, ampicilin and tetracycline not recommended empirically. Utilization of the third generation of cephalosporin and new quinolone as the first line of treatment and the best antibiotics therapy was suggested.

Keywords: Shigella Spp., Acute Diarrhea, Antibiotic Resistance, Kerman