Abstract Book

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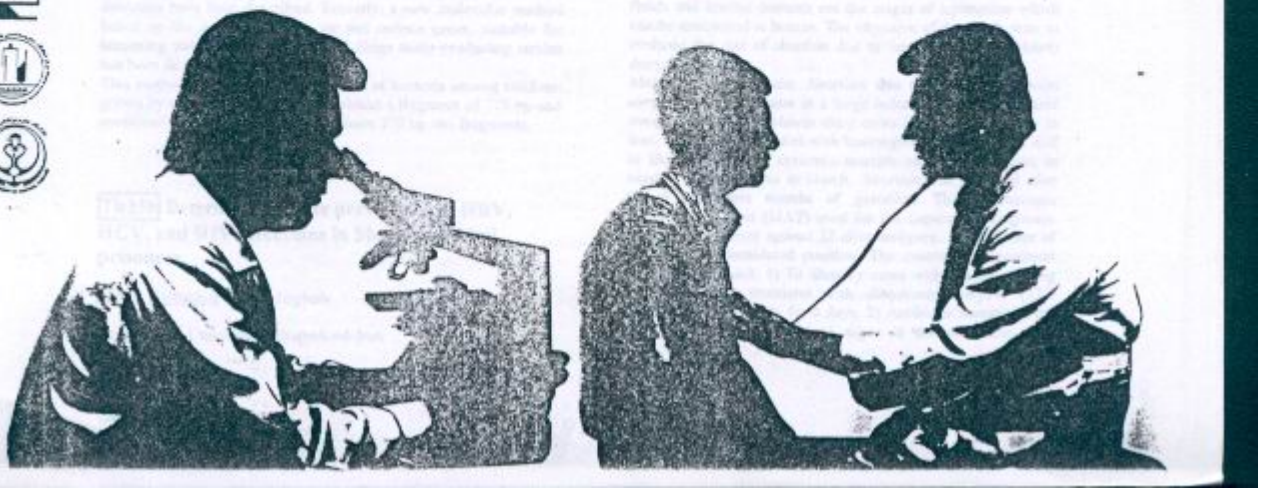
برگزار کننده : مرکز تحقیقات میکروب شناسی بالینی استاد الوزی
دانشگاه علوم پزشکی شیراز



hosts, including humans. However, only six to eight species of Cryptosporidium have been named: *Cryptosporidium parvum, C. muris, C. wrairi, C. felis, C. meleagridis, C. baileyi, C. serpentis,* and *C. nasorum*.*C. parvum* is the species that infects immunocompetent humans and most mammals. During spring and summer in 1385, 200 fecal specimens collected from children at the breast (Below 2 years) for periodic study and weight and stature. Then fecal specimens prepared whit floating and concentrating methods whit saturated sugar solution and provided smear and used modified acid-fast staining for detection.

From 200 fecal specimens ,13 specimens contained cryptosporidium parvum oocytes (6.5%), from 200 achieved fecal specimens ,115 number of specimens related to boys and 85 number of fecal specimens related to girls, from statistical viewpoint there is no relation between sex and infection ($p>0.05$). 3 number of positive specimens related to age group of 0-6 mounths.the 8 number of positive specimens related to age groups of 12-18 months. infection related to children below one years old that was a significant relation ship from statistical viewpoint ($p<0.05$).

Th257 Identification of Escherichia coli O157:H7 by Sorbitol MacConkey Agar and TSB containing cefixime and tellurite and comparison with PCR

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Selective culture media such as sorbitol-MacConkey agar supplemented with cefixime and potassium tellurite (CT-SMAC) are developed as the first selective medium for the screening and isolation of *E. coli* O157:H7. Because of the inability to ferment sorbitol, *E. coli* O157:H7 form colorless colonies on SMAC and can be distinguished from most of the remaining intestinal *E. coli* strains that ferment sorbitol and grow as pink colonies. Some *Enterobacteriaceae* present in cattle faeces, such as *Proteus, Providencia, Hafnia, Enterobacter,* and *E. hermanii*, also grow to form colorless colonies. Moreover, some of these species share common epitopes with the O157 antigen. It seems that modification of SMAC medium is necessary to isolate *E. coli* O157:H7 from faeces.

We have improved Trypticase soy broth (TSB) and SMAC agar selectivity for *E. coli* O157:H7 by the supplementation with cefixime (0.25 mg L^{-1}) and potassium tellurite (12.5 mg L^{-1}) (5 times more than original CT-SMAC) to create cefixime-tellurite-SMAC (CT-SMAC), which largely inhibits the physiological flora. However, sorbitol fermentative O157: H- STEC is sensitive against high tellurite concentrations and fails to grow on the medium.

From these viewpoints, the role of selective agar plates in isolating *E. coli* O157:H7 for preparation molecular methods is very important. Some molecular methods based on shiga toxins detection have been described. Recently, a new molecular method based on the detection of the *stx* and *intimin* genes, suitable for screening and isolation of potential Shiga toxin-producing strains has been developed.

This method has allowed the detection of bacteria among coliform grown by using specific primers to detect a fragment of 779 bp and combined with a nested PCR which have 372 bp stx_2 fragments.

Th258 Determination the prevalence of HBV, HCV, and HIV infections in Shahrekord jail prisoners.

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Background: Viral infection is one of the main causes of blood born microbial complications in jail prisoners with or without drug addiction. Viruses like hepatitis type B (HBV) and hepatitis type C (HCV) viruses, and also human immunodeficiency viruses (HIV), may have a high prevalence in these persons.

Objectives: In this research the history and prevalence of HBV, HCV, and HIV infections were determined in jail prisoners of shahrekord.

Materials and Methods: In this retrospective study, blood samples of 600 jail prisoners were collected. For determination the prevalence of these viral infections, and anti-HBV, anti-HCV, and anti-HIV antibody titers were assayed by ELISA techniques. In this community all the data were statically analyzed by Instat software for determining the possible correlation of some risk factors in HBV, HCV, and HIV infections.

Results: Anti-HBV, anti-HCV, and-HIV antibodies were diagnosed in 90 (15%), in 76 (13%), and in 5 (1%) blood samples respectively. The high rate of HBV (35%) and HCV (23%) infections were detected in 30-34 age group, and also for HIV (2.3%) infections in 18-24 age group. Significant correlations were detected between HBV infections with tattooing and route of transmission, and between HCV infections with drug addiction, types of addicted drug, and age group. Significant correlation was also detected between HIV infections and age of prisoners.

Conclusion: For high prevalence of HBV, HCV, and HIV infections in jail prisoners with and/or without drug addiction, and for significant correlations of these viral infections with some risk factors like: tattooing, addiction, types of addicted drug and age of prisoners; suggest the need of completed research focused on these blood born viral infections in jail prisoners.

Th259 The survey of leptospiral abortion rate in Holstein dairy cows

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Introduction: Leptospirosis is an important infectious zoonotic disease which occurs by members of the genus *Leptospira*. The pathogenic *Leptospires* are classified into one species of *Leptospira interrogans* (*L. i.*) containing over 212 serovars arranged into 23 serogroups. Abortion is one of the important signs of leptospirosis. Infected aborted fetus, fetal fluids and uterine contents are the origin of leptospires which can be transmited to human. The objective of this study was: to evaluate the rate of abortion due to leptospirosis in Holstein dairy cattle.

Materials & Methods: Abortion due to leptospirosis were surveyed during 2 years in a large industrial dairy cattle herd complex with 760 Holstein dairy cows in Ardabil province in Iran. The disease initiated with haemoglubinuria in a male calf in October. Clinical systemic mastitis signs were shown in most of milking cows in March. Abortion was occurred after the 5th or more months of gestation. The Microscopic Agglutination Test (MAT) used for the *Leptospira* diagnosis. Sera were screened against 22 alive antigens. A MAT titer of 1:100 were considered positive. The control and treatment strategies included: 1) To identify cows with clinical finding and subsequent treatment with dihydrostreptomycin (12.5 mg/kg, IM) twice daily for 3 days. 2) Antibiotic therapy of the entire herd with no clinical signs at the one time with

dihydrostreptomycin (25 mg/kg, IM). 3) Vaccination of all cows with *Leptospira* bacterin contained mentioned infected below serovars and repeated after 6 months then followed by annual revaccination. 4) Implementation of tight hygiene management such as reduction of rat and wildlife population, and keeping the corrals in dry condition. 5) Prescription of doxiciellin (100mg weekly) for personnel who worked in the dairy cattle herd for leptospirosis prevention.

Results: The MAT showed that the cows were infected by *L. I. Pomona, Hardjo, Grippothyposa, Icterohaemorrhagiae* and *Canicola* serovars. Totally, the rate of abortion due to the disease was 7.14%. The titer of MAT was between 1:100 to 1:3200. The signs of the disease showed in 357(85.46%) and 49(12.06%) of dairy cows during the first and second year of outbreak, respectively. During the first and second year, 26(6.4%) and 3(0.73%) out of 406(53.42%) evidenced dairy cows aborted, respectively. All of the aborted cows were retained fetal membrane.

Conclusion: The incidence of the disease is high. The frequency of abortion is lower than infection. *L. I Hardjo* and *Pomona* may cause abortion in dairy cattle. Dairy cows can be infected by different specific and non-specific leptospira serovars. Wild-life species such as rodents and cornivars can excrete leptospires for most of their life. The disease can be limited by using the related tight sanitation strategies such as reduction of natural hosts, immunization, treatment the animals with signs of the disease. Control of leptospirosis can reduce the economical losses. Since, the disease is an acquired occupational hazard, it is essential to be educated everybody in dairy cattle herds for reducing the risk of exposure to such pathogen.

Th260 Evaluating *Helicobacter pylori* virulence markers among Iranian patients with different gastrointestinal diseases

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Background: *Helicobacter pylori*, has been categorized as a carcinogen by IARC in 1994. Hp infection rate varies in different parts of the world and it is decreasing due to improvement of diet, freezing foods and effective antibacterial treatments. This microorganism colonizes the human gastric mucosa and causes chronic gastritis, peptic or duodenal ulcer disease and gastric cancer in some subjects. Vacuolating cytotoxin (*vacA*) and cytotoxin-associated gene (*cagA*) and its protein (CagA) are two key pathogenic factors in Hp strains. VacA protein possesses two distinct regions: signal sequence (s) and middle region (m) which are highly heterogenic among different Hp strains isolated from different parts of the world. Signal sequence has two types, s1 and s2 and the middle region has two types, m1 and m2, too.
cagA represents a genetic marker for cag Pathogenicity Island (cag PAI) and is present in nearly 70% of Hp strains. Its protein is associated with severe diseases in western countries whereas in East Asia its presence is more prevalent and has no association with clinical outcomes. *cagA* gene is highly heterogenic in its sequence. It can be detected by gene-specific PCR for either 5' or 3' variable or constant regions.

Objectives: The goal of this study is to evaluate the most prevalent Hp genotypes and host immune responses toward Hp virulence markers among Iranian GC and non GC patients.

Material and methods: Sampling. Biopsy sampling or stomach resection was performed after obtaining informed consent from defined locations including Cardia, Body, Antrum and Pylorus in non GC subjects and Upper, Middle, Down, Tumor and its border sites from resected stomachs in GC patients. Blood samples were taken before endoscopy or gastric operation. Serum samples were collected via centrifugation and stored at -20°C for further studies.
Hp isolation. Specimens were cultured on selective agar media under microaerophilic conditions. Identity confirmation of the isolated microorganisms as *H. pylori* was performed via urease, catalase, mobility and gram staining tests. 107 non GC subjects and 36 GC cases who were Hp positive via Culture were entered into this study.
PCRs. Genomic DNA was extracted according to standard protocols and Hp specific PCR was performed using *ureC* specific primers. *cagA* status and genotype of *vacA* were identified by PCRs with gene-specific published primers.
Serological studies. Western blotting was performed using Helicoblot 2.1 strips. Sero reactivity to Hp and its virulence markers were interpreted via the manufacturer's criteria.
Statistical analysis. The obtained results were entered into SPSS package (v 11.5) statistical analysis.

Results: *vacA* genotyping. The most prevalent observed genotype of *vacA* in Hp strains isolated from non GC and GC groups were s1m2 (38.3%) and s1m1 (52.8%), respectively. There were multiple infections in some of the cases which resulted to isolating Hp strains with different *vacA* genotypes from different parts of the stomach. s2m1 genotype of *vacA* was only observed in one of the non GC subjects.
cagA status. There was no association between *cagA* gene status and disease outcome as nearly all isolates were *cagA* positive ($p=0.211$). Multiple infections were observed in some cases (14.5%) (some isolated from defined sites were cagA+ and some were cagA negative).
Serological findings. Hp sero-positivity was observed in 113/121 (93.4%) of non GC subjects and 97/101 (96%) of GC cases. Host responses toward Hp virulence markers (mainly CagA and VacA) were different between the two studied groups. Significant association was found between simultaneous or independent presence of antibodies to CagA and VacA proteins ($p<0.05$). On the other hand, host antibody responses to 35kDa and 37kDa antigens were more frequent in non GC subjects (40%, 49.2% vs 22.8% and 33.7%) and were inversely associated with GC.

Conclusion: This study shows that s1m2 and s1m1 genotypes of *vacA* are the most prevalent Hp infecting strains among non GC and GC groups, respectively. This data is in agreement with our previous reports and those reported by other Asian countries. On the other hand, our results reveals that sero-reactivity toward CagA protein instead of its gene status seems to be suitable marker in screening Hp infected population for risk of gastric cancer development. Antibody responses to 35kDa and 37kDa antigens were more frequent in non GC subjects and were inversely associated with GC. Larger groups of patients should be studied before drawing a firmed conclusion.

Th261 The effect of magnetic field on antibiotic resistance of S.Aureus

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Objectives: Nowadays, studying the biologic effects of magnetic fields (MF) regarding their security and safety, and also medical, therapeutic and pharmacologic user seem to be of important value. This study aimed at scrutinizing the effect of static MF on antibiotic resistance of *S. Aureus*.
Methods: This prospective, case - control study was conducted to evaluate the effect of static MF with low intensity (0.5 mt) on the growth rate and the antibiotic resistance of *S.Aureus* sensitive to tetracycline and gentamicin.The studied