Induction of Rat Antibody Against Surface Proteins (OmpW) of V*ibrio cholerae O1*

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Abstract

Background and objective: Cholera is an acute intestinal disease that is caused by some members of Vibrionasea family. Among more than a hundred family members, only Vibrio cholera O-1& O-139 are pathogens for human and some marine animals. Surface proteins of these bacteria are immunogenic and act as colonization factor. The aim of this study was to evaluate the induction of rat antibody against surface proteins of Vibrio Cholerae O-1 (ompW).

Materials and methods: The recombinant antigen was injected to rats according to the standard procedures. After four times of subcutaneous injection, the rat sera were collected and purified using protein G column chromatography. Then the efficiency of antibody response was determined using ELISA.

Results: Recombinant protein concentration was measured to be about 0.9 µg/ml. Rat serum response to recombinant protein was positive up to the concentration of 1/25000 in ELISA reaction. Concentrations of purified antibody were estimated about 0.78 µg/ml. ELISA responses for antibody against ompW dealing with bacterial suspension with OD_{600}= 0/5 was assessed positive to 1/25000 while they did not react with other intestinal bacteria.

Conclusion: The recombinant ompW protein was immunogenic and the produced antibody was able to identify whole Vibrio Cholerae O-1 bacteria and did not react with other related bacterial strains.

Keywords: Vibrio cholerae, Surface proteins (omp), Polyclonal antibody, Cholera

Clonal Characterization of Multidrug-Resistant A. baumannii Isolated from Imam Reza Hospital in Tabriz, Iran

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Abstract

Background and objective: Acinetobacter baumannii is an important nosocomial pathogen. Clonal dissemination of these resistant organisms has become a serious concern for clinicians and infection control specialists. This study was conducted to assess the clonal relationship of multidrug-resistant A. baumannii isolated from Imam Reza hospital in Tabriz.

Materials and methods: In total, one hundred and thirty four clinical isolates were collected during two years. All isolates were identified using standard laboratory methods and then confirmed by detection of bla_{OXA-51}-like genes which is intrinsic for A. baumannii. Antimicrobial susceptibility test was performed using the standard disc diffusion (DAD) method. REP-PCR was carried out for evaluation of the epidemiological relationship between multidrug-resistant A. baumannii isolates.

Results: All isolates were positive for bla_{OXA-51}-like gene that confirmed their identity as A. baumannii. Among 109 (81%) multidrug-resistant isolates, 91 isolates (83/5%) belonged to genotype A, 12 isolates (11%) belonged to genotype B and 6 isolates (5%) were belonged to genotype C.

Conclusion: The results of this study indicated clonal dissemination of multidrug-resistant A. baumannii isolates in the study hospital setting. Considering high potential of these resistant isolates in the hospital environment, the rapid identification and use of appropriate infection control measures are necessary to prevent further spread of infection by these organisms.

Keywords: Acinetobacter baumannii, multidrug-resistance, REP-PCR

Control Programs for Cutaneous Leishmaniasis in Central District, Qom Province, During 2010-2011

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Abstract

Background and objectives: Cutaneous leishmaniasis is the second important arthropod borne disease after malaria in Iran. This disease is endemic in some villages of rural in Qom province. This study was done in order to evaluate of control programs for CL in this province during 2010-2011.

Materials and methods: This was a semi-experimental study based on Community- trial. Based on the incidence of disease, 10 villages were selected for CL control program in rural district of Qom province during 2010-2011. Programs were done in four parts: use of bed nets impregnated with insecticides, distribution Stick Insect Repellent and environment sanitation and health education then, active screening was done.

Results: The results showed that control activities had been reduce incidence rate of disease. Incidence rate of disease have occurred from 28.3 in 2009 to 17.4 and 11.2 /1000 people of region covered with control programs during 2010-2011.

Conclusion: Based on results of this study, imply of integration methods in the control of CL, including use of bed nets impregnated with insecticides, distribution stick insect repellent and etc can have great effect in reducing the incidence of ZCL, that this situation is effective to maintain the physical and mental health of people and also reduce costs related to the diagnosis and treatment of disease.

Keywords: Leishmaniasis, Bed Nets, Stick insect repellent, **Qom**

Seroprevalence of Hepatitis A and Hepatitis E in Qom Province, 2011

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Abstract

Background and objective: Hepatitis viruses of oral-fecal origin are responsible for a high morbidity and mortality throughout the world, even if they never result in chronic hepatitis. Two viruses, the virus of hepatitis A (HAV) and of hepatitis E (HEV) are at present the cause of severe viral hepatitis of enteric origin.this study was conducted with the aim of determining the extent of seroprevalence of hepatitis A and hepatitis E in the Qom Province.

Material and methods: Totally 740 blood samples were collected from population over 15 year old in all part of Qom province. Specimens were examined for the presence of hepatitis A and hepatitis E using the EIA method.

Results: our findings revealed that prevalence rate of anti - HAV and anti - HEV IgG infection were 78.6% and15.5%, respectively. It appeared to be a statistically significant association between HAV and HEV with age groups and residence.

Conclusion: Our results showed that the presence of antibodies against hepatitis A and E in this province is very high, and vaccination against hepatitis A is not necessary now in Qom province. Also the prevalence of HEV infection is endemic in Qom province. The application of public health education to people, especially pilgrims to control and dissemination of HEV infection would be effective.

Key words: Hepatitis A, Hepatitis E, ELISA and Qom Province.

Prevalence of Hepatitis C Infections in Tabriz Prisoners

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Abstract

Background and objective: The Hepatitis C virus (HCV) is one of the leading known causes of chronic liver disease. Every day hepatitis causes massive costs and death of millions people. prisons are places for persons with high risk behavior and IV drug user population are more found in the prisons .Regarding to this fact that one of the most important ways of HCV transmission in the prisons is the use of shared needle in IDU prisoners and this persons can be dangerous to other persons who are not an IDU we decided to study on prisons of Tabriz for determination of prevalence of HCV between prisoners and relationship between this infections with high risk behavior.

Material and methods: A cross-sectional study carried out in the central prison of Tabriz- Iran in 2007 .Inmates were interviewed using standard questionnaire including demographic imprisonment history and HCV related risk behavior. Information gathered by study of documented papers and questionnaire. Blood sample tested for HCV antibody by ELIZA and RIBA test. We used statistical test “Pearson chi-square” and “T-test” to analyze this data.

Result: A total of 192 prisoners participated in our study .72%were men and 28% were women..48.7% were IV drug users 86.4% used sharing needles. 29% were HCV antibody positive. HCV are more between prisoners who use sharing needles.

Conclusion: IDU prisoners and person who used sharing needle have a high risk for HCV infections. The seroprevalence of HCV infection among prisoners in comparison with general population in Iran is very high. Regarding to the high prevalence of HCV in prisons we must decrease of this virus in prisoners and society.

Key words: Hepatitis, prison, IDU, Prevalence

Cloning and Sequencing of Gene Encoding Outer Membrane Protein LipL32 of Leptospira interrogans Vaccinal Serovar Canicola

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Abstract

Background and objective Leptospirosis is one of the most important zoonoses with worldwide distribution. LipL32 is the major leptospiral outer membrane lipoprotein expressed during leptospiral infections. Antigenic characterization of the members of the species Leptospira interrogans is a necessary step towards to understanding the interactions between leptospires and the immune system. The aim of this study was Cloning and Sequencing of Gene Encoding Outer Membrane Protein LipL32 of Leptospira interrogans vaccinal serovar Canicola

Materials and methods: Leptospira interrogans serovar Canicola (LC-RTCC2805) was used in this study which obtained from the Leptospira Reference Laboratory, Razi Vaccine and Serum Research Institute, Karaj, Iran. The bacteria were subcultured into the selective culture medium EMJH. The genomic DNA was extracted by standard Phenol-Chlorophorm method. The specific primers for proliferation of lipl32 gene were designed. The lipl32 gene was amplified and cloned into a cloning vector plasmid and transformed in competent E. coli Top10 cells. Recombinant plasmid was isolated from cells by kit.

Results: PCR amplification of the lipl32 gene using the designed primers resulted in an 835bp lipl32 gene product. The amplified gene was cloned in pJET1.2/ blunt vector and transformed into E.coli (Top10) cells. The confirmation of the recombinants was made by picking the white colonies and carrying out colony PCR amplification of the gene. The sequence was deposited in the GenBank database.The percentage identity and divergence among different leptospiral serovars was deduced using the Blast programme.DNA sequence analysis revealed that serovar Canicola (LC-RTCC2805) was most closely related to Leptospira interrogans, serovar Canicola (accession No: AB094434 and DQ092412) in GenBank with (99.6% idenditity). The serovars Canicola (accession No: AY763509) was more distantly related (99.4% idenditity).

Conclusion: The results showed that the lipl32 gene was highly conserved among pathogenic Leptospira serovars (>90% idenditity). In conclusion, the protein expressed by lipl32 gene may be used in diagnostic methods like ELISA and also can be a good candidate for recombinant vaccine against leptospirosis.

Keywords: leptospirosis, pathogenic Leptospires, cloning, lipl32 gene

qacE /qacEΔ1 in Pseudomonas aeruginosa

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Abstract

Background and objective: Pseudomonas aeruginosa is one of the most important infection agents in burn patients. The vast and irregular taking disinfectants and antiseptics such as the quaternary ammonium compound in clinical centers not only did not destroy pathogenic bacteria, but also caused resistance to those compounds in the mentioned microorganism. The goal of this research was to study the susceptibility and presence of resistance genes such as qacE and qacEΔ1 among Pseudomonas aeruginosa witch were isolated from burn patients.

Material and methods: Eighty five Pseudomonas aeruginosa were isolated from clinical sources. Susceptibility of the isolates to biocide containing didecyl diethyl ammonium chloride (Deconex) was determined by broth micro dilution and broth macro dilution. Polymerase chain reaction (PCR) was done for detection of qacE and qacEΔ1 genes.

Result: Among the Eighty five isolates, 37% of isolates showed less susceptibility and 63% of isolates was susceptible to biocide. qacEΔ1 genes were detected in 49.9% of resistant isolates but qacE genes were not seen in any of isolates.

Conclusion: More usage of biocides substances induces resistance genes and cause more resistance to biocides in Pseudomonas aeruginosa. Thus high antibiotic resistance in Pseudomonas aeruginosa and also increase the resistance to biocides substance in these bacteria cause serious problem in cure of Pseudomonas aeruginosa infections.

Keyword: **Pseudomonas aeruginosa, quaternary ammonium compound (Deconex), qacE/ qacEΔ1 genes**

Detection of Ureaplasma Urealyticum and Mycoplasma hominis in Clinical Isolates from Women with Genital Tract Infection by PCR

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Abstract

Background and objective: The Ureaplasma urealyticum and Mycoplasma hominis are known as sexually transmitted agents, causing mainly urethritis, pyelonephritis, infertility, pelvic inflammatory disease, spontaneous abortion, low birth weight, neonatal meningititis, neonatal pneumonia**,** infection of the genitourinary tract. The main objective of this study was determined the prevalence of U. urealyticum and M. hominis in women with genital tract infections were collected from Emam Khomeiny hospital at Tehran.

Materials and methods: In this descriptive study between April 2010 to December 2011, Endocervical swabs from 191 women with genital tract infections were collected from Emam Khomeiny hospital at Tehran. Obstetrician was completed the medical records in reception process. After DNA extraction from isolates, PCR amplification was used for the detection of U. urealyticum and M. hominis respectively. Results were analyzed by SPSS software and statistical tests.

Results: From the total number of specimens examined, 58 (30%) clinical isolates were positive for U. urealyticum and 52 (27%) clinical isolates were positive for M. hominis. The isolation rate of bacteria in age group between 31 to 45 years was higher than others.

Conclusion: Because of the potential effects of genital Mycoplasma on the success rate of highly specialized treatment, and its causal roles in several maternal complications of pregnancy and in neonatal morbidity and mortality, the rapid detection of U. urealyticum and M. hominis could be important and necessary. More attention needs to be paid to their role as an important etiologic factor of urogenital infections.

Key words: Ureaplasma urealyticum, Mycoplasma hominis, Genital Tract Infection, PCR

The Frequency of dupA Gene among Clinical Isolates of Helicobacter pylori and its Association with Gastro-Duodenal Diseases

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Abstract

Background and objective: Helicobacter pylori is a gram negative, spiral shaped bacterium which colonises in the human gastric tract. It plays an important etiologic role in gastric ulcers and gastroduodenal disorders. The dupA gene is one of its virulence factors that seems to cause duodenal ulcers in human hosts on the other hand some studies indicated the converse relationship between this gene and gastric cancer disease. The aim of the current study was to determine the prevalence of dupA gene of H. pylori isolated and find its relationship with gastroduodenal diseases.

Materials and methods: This cross-sectional descriptive study was performed on 150 H. pylori-positive isolates obtained from patients with dyspeptic symptoms. DNA was extracted from biopsies and the dupA gene status was determined by Polymerase Chain Reaction (PCR). Statistical analyses were performed to find any significant relationship between this virulence factor and clinical outcomes.

Results: A total of 131 H. pylori samples, 123 (94%) were confirmed to be H. pylori positive based on 16S rRNA gene. The dupA gene was found in 41 (33.33%) of H. pylori-positive samples. There was not any significant relationship between this gene and duodenal disease, however there was a reverse association between this gene and gastric cancer ($P<0.05$). Furthermore, we found significant association between the presence of dupA gene, smoke usage ($P< 0.04$) and flatulence ($P<0.03$).

Conclusion: As the results show, dupA gene can be the predictable marker for severity of gastric disorders such as gastric cancer. Similarly to what has been seen with other H. pylori virulence markers, there may be wide regional differences in the distribution of dupA. Extended molecular epidemiology researchers in other populations are recommended.

Key words: Helicobacter pylori, dupA, gastric disorders

Resistance of Atypical Mycobacterium as Pulmonary Infections Agents to the First and Second Line of Anti Tuberculosis Drugs

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Abstract

Background and objective: Non-tuberculosis mycobacterium (NTM) as environmental microorganisms which can be found everywhere. These microorganisms are one of the **major** agents of opportunistic infections in hosts have predisposing factors. In recent years, has been shown an increasing the global prevalence of NTM infections. Pulmonary disease, skin, soft tissue and

different types of infections could be caused by NTM strains. The main aim of this investigation was isolation and identification of NTM from patients with pulmonary infection and the next one was to evaluate the drug sensitivity of the first and some second line anti tuberculosis drugs agains**t** NTM strains among patients who referred to the Research Center for TB and Pulmonary Diseases of Tabriz.

Materials and methods: Out of 235 suspected patients, 15 NTM strains had been isolated as pulmonary infection agents. Identification of strains were done by standard methods by using of differential tests and effectiveness of the first line drugs (Isoniazid, Rifampin, Ethambutol Streptomycin) and the second line drugs (Ciprofloxacin, Ofloxacin, Amikacin, Kanamycin) were investigated by proportion method on Lowenstein Jensen (LJ) medium.

Results: Out of 15 NTM strains, 5 strains (34%) were found to be as Mycobacterium avium, 3 strains (20%) were Mycobacterium fortuitum, 3 strains (20%) were Mycobacterium szulgai and 2 strains (13%) were Mycobacterium gordonae و 2 strains (13%) were found to be as Mycobacterium kansasii. Out of these 25 strains: 96% to streptomycin , 89% to isoniazid, 79% to rifampin, , 79% to ethambutol, 79% to kanamycin, 42% to ofloxacin , 38% to amikacin and were 24% resistant to ciprofloxacin.

Conclusion: The findings of this investigation indicate that the highest species isolated from clinical pulmonary samples was belonged to mycobacterium avium. On the other hand Ciprofloxacin, Amikacin and Ofloxacin could be effectively used against NTM infections.

Keywords: Non-tuberculosis mycobacterium (NTM), pulmonary infections, drug resistance