

Antibiotic Resistance Pattern of Bacteria Isolated from Urinary Tract Infections in Pregnant Women

Javid Taghinejad¹ *, Mehdi Roshdi Maleki¹, Sina Karimi², Mehdi Jahantab²

1) Department of Microbiology, Malekan Branch, Islamic Azad University, Malekan, Iran

2) Microbiology section, Health Center Headquarters Laboratory, Salmas, Iran

* j_Taghinejad@yahoo.com

Abstract

Background and objective: Urinary Tract Infection is caused by the presence and growth of microorganisms in the urinary tract and is probably the most common bacterial infection in humans. Pregnant women are easily infected with urinary tract infections due to their susceptibility. The aim of this study was to evaluate drug resistance in pregnant women referred to the central health laboratory of Salmas.

Materials and methods: This cross-sectional study was performed on 2285 pregnant women who referred to the laboratory in 2019. After sampling and urine culture, antibiogram was performed. To analyze the data, Spss version 21 was used.

Results: Out of 2285 patients, 357 were infected, of which the highest number was *Escherichia coli* with 166 samples and *Staphylococcus saprophyticus* with 125 samples. The highest drug resistance was in *Escherichia coli* with tetracycline and in *Staphylococcus saprophyticus* with oxazalin. Also, among the age groups, the age group of 24-29 with 149 cases was identified as a high-risk group.

Conclusion: Antimicrobial resistance among urinary pathogens seems to be increasing. Drug-resistant *E. coli* is still considered as a major health concern so it is necessary for health care providers to acquire thorough knowledge of antimicrobial resistance pattern.

Keywords: Urinary tract infections, Drug resistance, pregnant women, Salmas

Functional Groups and Antimicrobial Activity of *Ziziphus spina-christi* Aqueous Extract on *Escherichia coli*, *Pseudomonas aeruginosa*, *Staphylococcus aureus* and *Listeria innocua*

Hassan Barzegar^{1*}, Behrooz Alizadeh Behbahani², Mohammad Amin Mehrnia², Hadi Tanavar³

1-Associate Professor, Department of Food Science and Technology, Faculty of Animal Science and Food Technology, Agricultural Sciences and Natural Resources University of Khuzestan, Mollasani, Iran

2-Assistant Professor, Department of Food Science and Technology, Faculty of Animal Science and Food Technology, Agricultural Sciences and Natural Resources University of Khuzestan, Mollasani, Iran

3-M. Sc Student, Department of Food Science and Technology, Faculty of Animal Science and Food Technology, Agricultural Sciences and Natural Resources University of Khuzestan, Mollasani, Iran

*hbarzegar@asnrukh.ac.ir

Abstract

Background and objectives: In the recent years, using different kind of herbal extracts had been considered for bacterial infection. *Sedr* or *Konar* which scientific name is *Ziziphus spina-christi* L. is native to tropical and subtropical regions. This study aimed to evaluate the presence of functional groups and antimicrobial activity of *Ziziphus spina-christi* aqueous extract on *Escherichia coli*, *Pseudomonas aeruginosa*, *Staphylococcus aureus* and *Listeria innocua* “in vitro”.

Materials and methods: In this laboratory study, extraction of *ziziphus spina-christi* L. leaf powder with maceration method was done for 48 hours. Leaf extracts antibacterial of these leaves were evaluated by four methods: Disc diffusion agar, well diffusion agar, minimum inhibitory concentration (MIC) and minimum bacterial concentration (MBC). The functional groups of *Ziziphus spina-christi* aqueous extract was evaluated by Fourier transform infrared spectroscopy (FTIR).

Results: In disc diffusion agar and well diffusion agar methods, all the concentration of *ziziphus spina-christi* L. restrained bacterial strains. The MIC was for *Escherichia coli*, *Pseudomonas aeruginosa*, *Staphylococcus aureus* and *Listeria innocua* about 64, 32, 8 and 16 respectively. The results showed that MIC of extracts was further of MBC. The main peaks of *Ziziphus spina-christi* aqueous extract factor groups were observed in wave numbers of 3390, 2974, 2933, 1715, 1606, 1419, 1307, 1274, 1059, 885, 820, 779 and 629 cm⁻¹.

Conclusion: Based on results, the *Ziziphus spina-christi* aqueous extract had desirable antibacterial effect. The results showed that Gram-negative bacteria showed further resistance against extract. Using this herbal compound could be effective to control pathogenic bacteria in food and pharmaceutical industries.

Keywords: *Ziziphus spina-christi*, Aqueous extract, Antibacterial activity, Fourier transform infrared spectroscopy

Methicillin Resistant *Staphylococcus aureus* and Vancomycin Resistant Enterococci in Hospital Sewage in Isfahan

Fatemeh Sadat Zarkesh Esfahani¹, Nasrin Amin², Fateh Rahimi^{3*}

- 1- Ph.D. Student of Microbiology, Department of Microbiology, Faculty of Biological Sciences, Islamic Azad University, Falavarjan Branch, Iran
- 2- M.Sc. Student of Microbiology, Department of Microbiology, Faculty of Biological Science and Technology, University of Isfahan, Iran
- 3- Associate Professor of Bacteriology, Department of Microbiology, Faculty of Biological Science and Technology, University of Isfahan, Iran* f.rahimi@sci.ui.ac.ir

Abstract

Background and objective: Methicillin-resistant *Staphylococcus aureus* (MRSA) and vancomycin-resistant Enterococcus (VRE) cause a wide range of infections in the hospital and community. Hospital and municipal wastewater are the most important reservoirs of these bacteria, and inefficiency of wastewater treatment systems results in the entrance of these bacteria into groundwater, surface water and drinking water of society. The aim of this study was to study the presence of MRSA and VRE isolates in a hospital sewage in Isfahan, Iran.

Materials and methods: Sampling was carried out 2 times during spring and summer 2018 from a hospital sewage in Isfahan. Samples were diluted and 100 microliters were spread on Baird-parker agar supplemented with 2 µg/ml oxacillin and m-Enterococcus agar supplemented with 4 µg/ml vancomycin and inoculated plates were incubated for 48 h at 37°C. All black colonies with halo on Baird-parker agar and red colonies on m-Enterococcus agar were collected and identified at the species level using PCR by the species specific primers. The resistance of all isolated colonies from Baird-parker agar and m-Enterococcus agar to cefoxitin and vancomycin, respectively, was tested using disk diffusion method by the guidelines of the Clinical & Laboratory Standards Institute (CLSI).

Results: A total of 185 and 110 colonies were collected from Baird-parker agar and m-Enterococcus agar plates, respectively. The results of the PCR tests revealed that none of the black colonies on Baird-parker agar were *S. aureus* and only 3 (3%) vancomycin resistant Enterococcus faecium strains were identified among all red colonies on m-Enterococcus agar plates.

Conclusion: The results of this study revealed the absence of MRSA strains and relatively low presence of VRE in the effluent of the hospital in Isfahan, which indicating the high quality and efficiency of the hospital disinfection system for complete removal of MRSA strains and relatively high elimination of VRE strains from hospital wastewater and prevent them from entering municipal wastewater. It seems that this system is not able to eliminate other bacteria such as coagulase-negative staphylococci, *Leuconostoc* and *Lactococcus*, which could be a serious threat to public health.

Keywords: MRSA, VRE, hospital sewage, Isfahan

Comparison of Virulence Genes (int, inv, spv (vir)) in *Salmonella typhimurium* and *infantis* from Clinical Cases by Multiplex PCR

Elham Siasi^{*1}, Bahareh Azadi², Sedigheh Mehrabian³.

1-Assistant professor, PhD of Genetic, Department of Microbiology, Collage of science, North Tehran Branch, Islamic Azad University, Tehran, Iran.

2- MSc degree of Microbiology, Department of Microbiology, Collage of science, North Tehran Branch, Islamic Azad University, Tehran, Iran.

3- Professor , PhD of Microbiology, Department of Microbiology, Collage of science, North Tehran Branch, Islamic Azad University, Tehran, Iran. * emi_biotech2006@yahoo.ca

Abstract

Background and objective: virulence genes in *Salmonella* are a combination of plasmid and chromosomal factors and a single genetic position would not be responsible for all biological manifestations in *Salmonella*. Considering the difference in the serotypes of *Salmonella* in terms of serious genes, the aim of this study was to compare the presence of plasmid and chromosomal virulence genes (int, inv, spv (vir)) *Salmonella typhimurium* and *Infantis* in clinical cases in children and adults by Multiplex PCR.

Materials and methods: In this study, 676 stool specimens were collected from patients referring to Imam Khomeini and Milad hospitals and 60 isolates were identified as *Salmonella*. After serotyping, 30 isolates were recognized as *Salmonella infants* and 30 isolates as *salmonella typhimurium*. By using the Multiplex PCR technique, the prevalence of spvC, invA and Int genes was studied.

Results: All investigated serotypes had invA and Int genes. 93.3% of *typhimurium* serotypes and 6/7% of *infantis* serotypes infants had SpvC gene. In 93/3% of *typhimurium* serotypes and 6/7% of *infantis* serotypes all three genes were present simultaneously.

Conclusion: virulence genes increase the pathogenicity of *typhimurium* and *Infantis* strains. Therefore, the genetic and molecular genetic isolation of these genes can help to identify the bacterial enzymes and to make effective drugs for the treatment of related diseases.

Keywords: *Salmonella typhimurium*, *Salmonella infections*, Multiplex PCR, int,inv,spv genes.