**ID: 2269**

**Congress: The First International Congress of Medical Bacteriology**

**Title:** Antibiotic Resistance and Distribution of Tetracycline Resistance Genes from diarrhogenic E. coli

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**Abstract:**
Introduction and Objectives: Escherichia coli, the causative agent of a number of infections, such as gastroenteritis and cystitis in non hospitalized patients and pneumonia and septicemia of mostly nosocomial origin, has obtained resistance to many antibiotics, including the tetracycline class of agents. Studying the molecular determinants of resistance in E. coli isolates will increase our understanding of the significance of commensal bacteria in the development and transfer of antibiotic resistance. The aim of this study was to determine the tetracycline resistance gene profiles of diarrhogenic E. coli.

Materials and Methods: In total, 150 diarrhogenic E. coli samples were collected from patients in 3 hospitals in southwest Iran. Isolates were tested for susceptibility to antimicrobial drugs by disc diffusion methods as described by the CLSI. PCR amplification was used to detect genes conferring resistance to tetracycline (tetA, tetB and tetC).

Results: The number of isolates showing resistance to each antimicrobial agent were: imipenem (n = 2), tetracycline (n = 20), ciprofloxacin (n = 3), nalidixic acid (n = 17), streptomycin (n = 7), gentamycin (n = 3), nitrofurantoin (n = 2), amikacin (n = 0). Of the tetracycline resistant isolates, 76.6% (115/150) were positive by PCR for tet genes, as follow: tetA (12%), tetB (64%) and tetC (6%).

Conclusion: Antibiotic resistance is widespread in diarrheagenic E. coli in patients with acute diarrhea in Shiraz, Iran. The presence of multiple virulence genes was associated with multidrug resistance and this merits further investigation. Hence, updated strategies for appropriate use of antimicrobial agents in Iran are needed.

**Key word:** Diarrhogenic E. coli, Tetracycline resistance, Iran

**Presentation:** Poster