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**Title:** Detection of genes encoding aminoglycoside modifying enzymes (aac(3)-IIa, ant(2′′)-Ia and aph(3′)-Ia) in Uropathogenic Escherichia coli isolated from urine by PCR

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**Abstract:** Introduction: Urinary tract infection is among most occurring bacterial infections. Escherichia coli is the most prevalent etiologic agent of urinary tract infections isolating from 80% of cases. Aminoglycosides are potent bactericidal agents inhibiting bacterial protein synthesis by binding to the 30S ribosomal subunit. E. coli have acquired multiple resistances to a wide range of antibiotics such as aminoglycosides. Enzymatic alteration of aminoglycosides by aminoglycoside-modifying enzymes is the main mechanism of resistance to these antibiotics in E. coli. The aim of this study was detection of genes encoding aminoglycoside modifying enzymes (aac(3)-IIa, ant(2′′)-Ia and aph(3′)-Ia) in uropathogenic Escherichia coli isolated from urine by PCR.

**Materials and Methods:** Two hundred seventy six urinary isolates were collected from Tehran Heart center. Isolates were characterized through standard microbiological tests. Antibiotic susceptibility patterns of confirmed isolates were determined by disk diffusion method for gentamicin, amikacin, tobramycin, kanamycin and netilmicin according on CLSI guidelines. MICs of target antibiotics were determined by agar dilution method. All isolates were screened for the presence of the AMEs genes using the PCR method.

**Results:** The results of disk diffusion for Gentamicin, Tobramycin, Kanamicin, Amikacin and Netilmicin were 21.01%, 24.63%, 23.18%, 3.62% and 6.15%, respectively. The agar dilution’s results (MICs) were 66.19% for Gentamicin. The aac (3)-IIa was the most frequent gene (78.87%) among the isolates and after that the ant(2′′)-Ia and aph(3′)-Ia genes were detected in 47.88% and 23.94% of the isolates, respectively.

**Discussion:** Most of the resistant UPEC isolates harbor modifying enzymes which shows the impact of the mechanism in aminoglycoside resistance. Similar to other reports worldwide, aac(3)-IIa was the most frequent resistance gene in these isolates.

**Keywords:** Escherichia coli, Aminoglycoside modifying enzymes, aac(3)-IIa gene, UTI

**Presentation:** Poster