

Integron and Genotype Patterns of Quinolones-resistant Uropathogenic *Escherichia coli*

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Background & Objectives: Uropathogenic *Escherichia coli* are the most common cause of urinary tract infections, and quinolones-resistant strains cause growing concern in developing countries. This study provides relevant data in relation to the molecular epidemiology of these isolates with respect to the distribution of integron among them and in doing so, to control the infections and adopt efficient strategies.

Methods: This study was performed on 96 strains of *E. coli* isolated from patients with community acquired urinary tract infections in Jahrom, Iran. Having determined the antibiotic susceptibility patterns, Isolates were resistant to quinolones (Ciprofloxacin, Norfloxacin and Nalidixic acid) screened for integron classes by PCR. Then the genetic patterns of the strains were compared by pulsed field gel electrophoresis.

Results: of the 96 samples, 30 were resistant to at least one of the above mentioned antibiotics. Integrons were detected in 20.8%, 25%, and 25% of the Nalidixic acid, Ciprofloxacin and Norfloxacin resistant isolates, respectively. By using pulsed field gel electrophoresis among the 30 samples, we obtained 30 genetic patterns.

Conclusion: The patterns revealed no clonal relationships between the strains. The gene cassettes observed in class 1 and class 2 integrons did not correlate completely with the quinolone resistance observed in these isolates.

Keywords: Genotype Patterns ; *Escherichia coli*; Quinolones-resistant ; Uropathogenic

