

Prevalence of Non-qnr Genes in *Escherichia coli* Resistant to Ciprofloxacin Isolated from Urinary Tract Infection in Ilam and Tehran (Milad) Hospitals

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Background & Objectives: Extensive use of quinolones has been associated with raising level of resistance. In the current study, we focused on assessing the prevalence of *Escherichia coli* resistance to quinolones and frequency of non-qnr genes.

Methods: One hundred and fifty *Escherichia coli* isolates were identified during Mar.2007 to Apr.2012 in Ilam hospitals and Milad (Tehran) hospital. PCR was performed for detection of ParE, ParC, gyrB, acc(Ib)cr genes.

Results: Of 150 isolates, sixty nine isolates (46%) were resistance to ciprofloxacin. Frequency of ParE, ParC, gyrB, acc(Ib)cr, were 76.8%(53 isolates), 78.54%(26 isolates), 71.01%(49 isolates) and 95.65%(66 isolates) respectively. Among non-qnr genes resistance to ciprofloxacin aac(Ib)cr had high frequency (95.65%). 21.3 % (32 isolates) had all four genes together. Three genes (ParC, gyrB, acc(Ib)cr) were seen in 31.8%(22 isolates). Two isolates (2.8%) had one gene (acc(Ib)cr) only.

Conclusion: Our study showed high frequency of non-qnr quinolone resistance genes in Ilam and Tehran (Milad) hospitals.

Keywords: Ciprofloxacin; ParE; Resistance; Aac(Ib) cr