

Distribution of the parC , parE and qnrB genes among ciprofloxacin resistant E.coli isolates U.T.I.

marjan iran zad*, Dr. Mojdeh Hakemi vala,

Abstract Distribution of the parC , parE and qnrB genes among ciprofloxacin resistant E.coli isolates U.T.I. **Introduction:** E.coli is the most frequent agent of urinary tract infections (UTIs). Chromosomal or plasmidic resistant to Ciprofloxacin as the most common antibiotic in UTI treatment is increasing. The aim of this study was determination the frequency of parC , parE and qnrB genes among ciprofloxacin resistant E.coli isolates UTIs. **Method and Materials:** 80 E.coli isolates were collected UTIs of Imam Khomeini hospital patients during 2013. All isolates were subjected to antimicrobial susceptibility testing by standard disk diffusion method according to CLSI2014 guidelines. The frequency of parC and parE genes determined by PCR. Further sequencing was done on PCR products by Bioneer company. **Results:** Based on the antibiogram 77/5% of isolates were resistant to ciprofloxacin. The size of PCR bands was: 265bp for parE, 389 bp for parC and 268bp for qnrB. Also, the frequency of these genes among ciprofloxacin resistant isolates by PCR were: 92/5% for parC, 91/3% for parE, and 0% for qnrB .After sequence alignment some mutation were detected and gene submission were done in NCBI. **Conclusion:** This study showed that the role of mutated chromosomal resistant genes are more important to plasmidic genes in emergence of ciprofloxacin resistant E.coli strains.

Keywords : Keywords: E.coli, UTI, ciprofloxacin

[Islamic Azad University, Rasht Branch - Thesis Database](#)
[دانشگاه آزاد اسلامی واحد رشت - سامانه بانک اطلاعات پایان نامه ها](#)