
Investigation of ParE mutations in drug resistance strains of pseudomonas aeruginosa

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Abstract Background: *Pseudomonas aeruginosa* as a major nosocomial gram negative pathogen due to its intrinsic and acquired resistance to a wide spectrum of antibiotics poses a threat in clinical settings. One of the drug resistance mechanisms in *P. aeruginosa* is mutation in topoisomerase IV subunits (parC and parE). The aim of this study was investigation of parE mutations in *P. aeruginosa* isolates some Rasht hospitals and Lahijan laboratories. **Materials and Methods:** In this cross-sectional study, forty-five *P. aeruginosa* strains was isolated several Rasht hospitals and Lahijan laboratories and identified by biochemical tests. The antibiotic resistance and susceptibility of isolates was determined by Kirby Bauer method and microdilution method. Then PCR-sequencing was carried out to assess parE mutations in ciprofloxacin resistant isolates. **Results:** In this study, 45 isolates of *P. aeruginosa*, 17 isolates were ciprofloxacin resistant. The highest MIC of ciprofloxacin was determined in some strains 1024 µg/ml. in 5 ciprofloxacin resistant isolates was defined mutations S457R, A466S and V449M in parE gene. **Conclusion:** Given that mutation was found in 5 isolates in this study, it seems that mutation in parE gene can be a reason of ciprofloxacin resistance in of *P. aeruginosa* isolates in Guilan province.

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