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# Investigation of gyrB mutations in ciprofloxacin resistance strains of *Pseudomonas aeruginosa* in Guilan province

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**1544/5000 Abstract** *Pseudomonas aeruginosa* is an important opportunistic pathogen in immunocompromised patients. This bacterium shows the intrinsic and acquired resistance to antibiotics. An important mechanism of resistance to fluoroquinolones in *Pseudomonas aeruginosa* The mutation in gyrB is a type II topoisomerase subunit. The aim of this study was to evaluate gyrB gene mutations in cyproforoxacin-resistant *Pseudomonas aeruginosa* isolates in Guilan province. In this study, 69 isolates of *Pseudomonas aeruginosa* different specimens including burn, urine, prosthetics and respiratory secretions were identified by biochemical methods. Sensitivity and resistance to antibiotics were determined by Kirby-Boer (Disc diffusion) and MIC. PCR-seconsing was performed to detect gyrB mutations in ciprofloxacin-resistant isolates. CLCmain workbench v3.5 software and Blast software (BLAST) were used to compare gyrB gene sequences in reference isolates resistant to isolates of PAO1 standard. In this study, 69 isolates, 33.33% were detected by disc diffusion method and 37.68% were diagnosed with ciprofloxacin-resistant MIC. The highest level of ciprofloxacin MIC was 1024 µg / ml 1024 in some isolates. The mutated N368S, I424L, L464I, S466F, E468D, M520L and I524V mutations were detected in gyrB gene in resistant isolates. These results suggest that mutation in the gyrB gene is one of the most important mechanisms of resistance to ciprofloxacin in clinical isolates of *Pseudomonas aeruginosa* in Guilan. The mutation in gyrB with several genes involved in the formation of resistance seems to increase resistance in different isolates. **Keywords:** Ciprofloxacin, gyrB, mutation, *Pseudomonas aeruginosa*, Sequencing

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## Sequencing

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