

## عنوان مقاله:

Antibiotic Resistance Pattern and Evaluation of blaOXA-10, blaPER-1, blaVEB, blaSHV Genes in Clinical Isolates of *Pseudomonas aeruginosa* Isolated from Hospital in South of Iran in 2014-2015

## محل انتشار:

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## خلاصه مقاله:

Background: *Pseudomonas aeruginosa* is one of the main causes of nosocomial infections with a mortality rate up to 40-50%. Resistance to antibiotics is a global challenge in the treatment of infections caused by this bacterium. The Class A beta-lactamases genes, including blaSHV, blaPER, blaVEB, are the most common causes of resistance in this microorganism. This study was conducted to determine antibiotic resistance pattern and the presence of blaper, blaVEB, blaSHV and blaOXA-10 genes in clinical isolates of *P. aeruginosa* isolated from patients in a hospital in Bandar Abbas. Materials and Methods: This cross-sectional study was conducted on 72 *P. aeruginosa* clinical isolates. Antibiotic susceptibility testing was performed by disk diffusion method according to the clinical Laboratory Standard Institute. MIC (Minimum inhibitory concentration) of ceftazidime was performed by E-Test. Polymerase chain reaction (PCR) was performed to identify blaSHV, blaVEB-1, blaOXA-10, and blaPER-1 genes. Results: Most of the isolates were detected from intensive care unit and urine samples. The highest resistance rate which was observed to sulfamethoxazole and ceftazidime, were 68 (94.44%) and 44 (61.11%), respectively. About 27.8% of these isolates were multidrug resistant. Among 44 ceftazidime resistant isolates, 15 isolates (34%) showed MIC  $\geq 32$   $\mu\text{g.mL}$  in the E-test. The prevalence rates of genes were 4.16, 12.5, 8.33, and 1.38% for blaOXA-10, blaShv, blaVeb-1, and blaPer-1 genes, respectively. Conclusion: The ceftazidime resistance rate and the prevalence rate of resistance genes in the present study were lower than other Iranian studies. However, isolation of these genes is alarming that excessive use of antibiotics can lead to over expression of resistance genes and bacterial efflux pumps and the emergence of MDR phenotypes

## کلمات کلیدی:

*Pseudomonas aeruginosa*, Beta-Lactamase, Genes, Multidrug resistance

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