

The Frequency of bla_{PER}, bla_{VEB}, bla_{CTX-M}, tetA and tetB genes among Acinetobacter baumannii strains isolated from hospitalized patients in Tehran

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Abstract

Background & Aim: Infections and outbreaks caused by multidrug-resistant *Acinetobacter baumannii* are prevalent and have been reported worldwide over the past twenty or more years. Beta-lactamase genes including *bla_{PER}*, *bla_{VEB}* and *bla_{CTX-M}* confer resistance to beta-lactam antibiotics and *tetA* and *tetB* are responsible for resistance to tetracycline in such bacteria.

Methods: A total of 65 isolates of *A. Baumannii* from clinical samples were collected. Antimicrobial susceptibility testing was performed by the disk diffusion method according to the CLSI guideline and the presence of *bla_{OXA-51}*, *tetA*, *tetB*, *bla_{VEB}*, *bla_{CTX}* and *bla_{PER}* were screened via the polymerase chain reaction (PCR).

Results: The isolates were 100% resistant to gentamicin, ciprofloxacin, piperacillin, cefotaxime, ceftazidime and tetracycline. Resistance to minocycline and imipenem stood at 89% and 85%, respectively. All isolates were identified as multi-drug resistant (MDR). The genes *tetA*, *tetB*, *bla_{VEB}*, *bla_{CTX}* and *bla_{PER}* were detected in 75.3%, 43%, 35.3%, 76.9% and 61.5% of isolates, respectively.

Conclusion: This study revealed the high prevalence of antimicrobial resistance genes amongst *Acinetobacter baumannii* and thus confirms the need for isolating and identifying them in clinical laboratory and hospital settings.

Keywords: *Acinetobacter*, Antibiotic resistance, Beta-lactamase