The Frequency of \( \text{bla}_{\text{PER}}, \text{bla}_{\text{VEB}}, \text{bla}_{\text{CTX-M}} \) tetA and tetB genes among Acinetobacter baumannii strains isolated from hospitalizes 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 \( \text{bla}_{\text{PER}}, \text{bla}_{\text{VEB}} \) and \( \text{bla}_{\text{CTX-M}} \) 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 \( \text{bla}_{\text{OXA-51}} \) tetA, tetB, \( \text{bla}_{\text{VEB}}, \text{bla}_{\text{CTX}} \) and \( \text{bla}_{\text{PER}} \) 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, \( \text{bla}_{\text{VEB}}, \text{bla}_{\text{CTX}} \) and \( \text{bla}_{\text{PER}} \) 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