The Frequency of \textit{bla}_{PER}, \textit{bla}_{VEB} \textit{bla}_{CTX-M} \textit{tet}A and \textit{tet}B genes among \textit{Acinetobacter baumannii} strains isolated from hospitalized patients in Tehran

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Abstract

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

\textbf{Methods:} A total of 65 isolates of \textit{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 \textit{bla}_{OXA-51} \textit{tet}A, \textit{tet}B, \textit{bla}_{VEB}, \textit{bla}_{CTX} and \textit{bla}_{PER} were screened via the polymerase chain reaction (PCR).

\textbf{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 \textit{tet}A, \textit{tet}B, \textit{bla}_{VEB}, \textit{bla}_{CTX} and \textit{bla}_{PER} were detected in 75.3\%, 43\%, 35.3\%, 76.9\% and 61.5\% of isolates, respectively.

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

\textbf{Keywords:} \textit{Acinetobacter}, Antibiotic resistance, Beta-lactamase