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Acinetobacter baumannii clonal lineages I and II harboring different carbapenem-hydrolyzing-β-lactamase genes are widespread among hospitalized burn patients in Tehran

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Summary The aim of this study was to analyze antimicrobial resistance patterns and their encoding genes and genotypic diversity of *Acinetobacter baumannii* isolated from burn patients in Tehran, Iran. The presence of extended-spectrum beta-lactamase- and bla_{OXA}-encoding genes among 37 multidrug resistant (MDR) *A. baumannii* strains isolated from patients hospitalized in a teaching hospital in Tehran was evaluated. Susceptibility to 7 antibiotics was tested by disk agar diffusion and to polymyxin B and colistin was tested by E-test, according to CLSI guidelines. All isolates were then analyzed by PCR for the presence of bla_{IMP}, bla_{VIM}, bla_{SIM} $bla_{OXA\text{-}23}$,

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bla$_{OXA\text{-}24}$, and *bla*$_{OXA\text{-}58}$-like carbapenemase genes, and *bla*$_{OXA\text{-}51}$-like, *bla*$_{TEM}$, *bla*$_{SHV}$, *bla*$_{PER}$, *bla*$_{VEB}$, and *bla*$_{GIM}$ genes. Genotyping of *A. baumannii* strains was performed by repetitive sequence-based (REP)-PCR and cluster analysis of REP-PCR profiles. *A. baumannii* isolates were assigned to international clones by multiplex PCR sequence group analysis. Twenty-five *A. baumannii* isolates were classified as MDR, and 12 were classified as extensively drug resistant. All isolates were susceptible to colistin and polymyxin B. Eighty-one percent of the isolates was resistant to imipenem or meropenem and harbored at least one or both of the *bla*$_{OXA\text{-}23}$-like or *bla*$_{OXA\text{-}24}$-like carbapenemase genes. Co-existence of different resistance genes was found among carbapenem-resistant isolates. Multiplex PCR sequence group analysis most commonly assigned *A. baumannii* isolates to international clones I (18/37; 48.6%) and II (18/37; 48.6%). An alarming increase in resistance to carbapenems and the spread of *bla*$_{OXA\text{-}23}$-like and/or *bla*$_{OXA\text{-}24}$-like carbapenemase genes was observed among *A. baumannii* strains belonging to clonal lineages I and II, isolated from burn patients in Tehran.

Introduction

Acinetobacter baumannii is a gram-negative bacterium causing hospital-acquired infections in critically ill patients [1]. The spread of a restricted number of clonal lineages that have been selected because of their multiple drug resistance has been reported worldwide [1—4].

Antimicrobial resistance owing to enzymatic degradation, modification of targets, and active efflux of drugs, together with persistence of the bacterium in contaminated environments are responsible for epidemics of *A. baumannii* in hospital settings [1,2,5,6]. Carbapenems are considered the first-line drugs for treatment of *A. baumannii* infections in Iran; however, resistance to these drugs is increasing owing to the overexpression of efflux pumps and to the ability of the bacterium to produce different carbapenemases, in particular class D carbapenemases [1,2,5,6]. *A. baumannii* is increasingly causing infections in burn units worldwide including Iran [7—9]. In addition, *A. baumannii* strains resistant to different classes of antibiotics including carbapenems have reportedly been isolated from burn patients in Iran [8,9]. The alarming increase in resistance to carbapenems in Iranian burn units from 2001 to 2009 [8,9] prompted us to analyze whether carbapenem resistance in *A. baumannii* strains isolated from burn patients was caused by horizontal gene transfer or selection of carbapenem-resistant epidemic clones, which has not been investigated to date. Previous studies in different clinical settings have shown the spread of *A. baumannii* isolates belonging to different repetitive sequence-based (REP)-PCR profiles and international clones I and II in Iran [10—12]. The aim of this study was to analyze the antimicrobial resistance patterns, β-lactamase gene content, genotypic diversity, and clonal lineage distribution of *A. baumannii* isolates in a burn ward of a university teaching hospital in Tehran, Iran.

Material and methods

Study population

In total, 37 non-replicate *A. baumannii* isolates associated with infection in patients admitted to the burn ward of a teaching hospital in Tehran were selected for this study. The Motahari Burn and Reconstruction Center is one of the few large, highly equipped, tertiary burn centers in Iran, providing care to severely burned patients from the province of Tehran and to those with complications that have been referred from other centers across the country. All patients were admitted immediately after burn injuries, except for referral cases.

Available epidemiological data from these isolates were retrospectively collected from patient charts and diagnostic microbiological laboratory culture reports. We used the criteria for diagnosis of infections in burn units described by Santucci and colleagues [13]. In addition, the following criteria were adopted to define wound infection or colonization: bacteria in the wound and wound eschar