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EDITORIAL

An overview of *Acinetobacter baumannii*: deciphering this amazing pathogen

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The genus *Acinetobacter* comprises several groups of closely related species[1, 2], including the *Acinetobacter calcoaceticus-baumannii* complex that was initially proposed in 1991[3]. At that time, it had not yet been described what would become one of the most important multidrug-resistant pathogen, *Acinetobacter baumannii*[4]. In the following decades, *A. baumannii* became one of the most prevalent and well adapted pathogen to the nosocomial environment[5]. This adaptive ability is probably a consequence of its evolutionary exposure to selective pressure of antimicrobials, over a long period, in the complex and competitive environment[4, 5].

In the last 20 years, outbreaks caused by carbapenem-resistant *A. baumannii* isolates have become a major worldwide concern[4], and infections caused by such pathogen are associated with increased morbidity and mortality[6]. According to the SENTRY antimicrobial surveillance program for Latin America, carbapenem resistance rates increased almost 60% in just one decade among Brazilian *A. baumannii* isolates, from 12.6% between 1997 and 1999 to 71.4% between 2008 and 2010[7]. Due to the multidrug resistance phenotype frequently verified among the major *A. baumannii* clones (CC79, CC15, and CC1) disseminated in Brazil[8, 9], the therapeutic options to treat those infections are drastically limited[10]. Since the development of new drugs does not follow the speed and evolution of antimicrobial resistance expressed by Gram-negative bacilli, the polymyxins are generally the only clinically effective antimicrobials[10, 11], despite of toxicity, which have limited their use in the clinical practice[12, 13].

The production of carbapenem-hydrolyzing class D β-lactamase (CHDLs) is, by far, the most prevalent carbapenem resistance mechanism in *A. baumannii*[14, 15]. These enzymes weakly hydrolyze carbapenems and have no activity against the third-generation cephalosporins[14]. Thus, the presence of insertion sequences, which carry a strong promoter, are required to overexpress the vast majority of genes encoding for such group of β-lactamases[14], as well as the chromosomal encoded *ampC*[8]. Somehow, along its evolutionary course, *A. baumannii* uniquely developed insertion sequences into its genome in order to rearrange the expression of different genes according to need and, to a lesser extent, to the energy cost[16, 17]. The presence of multiple copies in the sequenced *A. baumannii* genomes confirms the importance of these mobile genetic elements for its adaptation and survival in the nosocomial environment[17, 18].

The spread of clones carrying $bla_{\text{OXA-23}}$ gene[8, 9] and, to a lesser extent, $bla_{\text{OXA-143}}$[19], has been considered the responsible for the high carbapenem resistance rates (77.4%) verified in *A. baumannii* isolates recovered from bloodstream infections among Brazilian intensive care units at 2015, according to the last bulletin of the Brazilian Health Surveillance Agency [Agência Nacional de Vigilância Sanitária (Anvisa)][20]. Recently, $bla_{\text{OXA-72}}$ has emerged as one the most frequent CHDL encoding gene found among carbapenem-resistant *A. baumannii* isolates retrieved in Brazilian hospitals[21], demonstrating the change in the epidemiology of carbapenem resistance in our country[22]. Considering the continental proportions of Brazil, which contributes with the diversity of carbapenemases encoding genes and clones found in our territory[8, 9, 19, 21, 22], epidemiological studies that aimed to characterize the antimicrobial resistance mechanisms of *Acinetobacter* spp. causing infections in hospitalized patients from distinct Brazilian regions are essential. One of the articles included in this edition evaluated the antimicrobial susceptibility profile and carbapenem-resistant determinants in a large collection of *A. baumannii* isolates retrieved from distinct Brazilian states. The authors described interesting and original results, as the inter-hospital spread of an emergent CHDL encoding gene across three Brazilian states, as well as the resistance to an important class of antimicrobial agents considered the optimal option to treat the infections caused by multidrug-resistant *A. baumannii* isolates. I hope you enjoy the reading.

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