High Frequency of OXA-253-Producing Acinetobacter baumannii in Different Hospitals in Recife, Brazil

Felipe Lira de Sá Cavalcanti,a,b Carina Lucena Mendes-Marques,b Chrísllane Rafaelé dos Santos Vasconcelos,b Túlio de Lima Campos,b Antonio Mauro Rezende,b Danilo Elias Xavier,b Nilma Cintra Leal,b Osvaldo Pompilio de-Melo-Neto,b Marcia Maria Camargo de Morais,a Tereza Cristina Leal-Balbinob

Laboratório de Resistência Microbiana, Instituto de Ciências Biológicas, Universidade de Pernambuco, Recife, Brazil; Centro de Pesquisas Aggeu Magalhães/Fiocruz, Recife, Pernambuco, Brazil; Departamento de Genética, Universidade Federal de Pernambuco, Recife, Brazil

ABSTRACT Here, we report the isolation of 31 Acinetobacter baumannii strains producing OXA-253 in a single large Brazilian city. These strains belonged to five different sequence types (STs), including 4 STs not previously associated with blaOXA-253. In all strains, the blaOXA-253 gene was located in a plasmid within a genetic environment similar to what was found previously in Brazil and Italy. The reported data emphasize the successful transmission of the blaOXA-253 gene through a large area and the tendency for this resistance determinant to remain in the A. baumannii population.

KEYWORDS Acinetobacter, MLST, antibiotic resistance, genome analysis, oxacillinase

Acinetobacter baumannii is an opportunistic Gram-negative pathogen responsible for a large number of outbreaks of hospital-acquired infections. This bacterium has been linked with serious infections affecting mainly debilitated patients in intensive care units (1), and it can become resistant to a wide range of antibiotics, leading to serious impediments to treatment. Carbapenems, such as imipenem and meropenem, have been often used as drugs of last resort, but outbreaks of carbapenem-resistant A. baumannii have been reported in several countries, including Brazil (2).

Resistance to carbapenems in A. baumannii may be due to various mechanisms, including the loss of outer membrane protein (OMP), overexpression of efflux pumps, or through alterations in the penicillin-binding protein (3). An increase in reported carbapenem resistance by A. baumannii isolates, however, has been mostly attributed to yet another mechanism, the production of carbapenemases, such as those belonging to the class D OXA type (4).

Here, we report OXA-253-producing A. baumannii strains isolated from different hospitals localized within the city of Recife, state of Pernambuco, in northeastern Brazil. This variant of the OXA-143-like carbapenemase belongs to the Ambler class D of β-lactamases (5), which has previously been the subject of studies discussing its incidence in Brazil. So far, however, the blaOXA-143 gene has only been reported for samples from the states of São Paulo and Rio de Janeiro, over 1,800 km to the south of Recife (2, 6–8).

Identification of the OXA-253-producing strains occurred after sequencing of the genomes of 45 A. baumannii strains displaying an extensively drug-resistant (XDR) phenotype and isolated from different individual hospitalized patients in five public hospitals in Recife between 2010 and 2014. These strains were considered resistant to the two carbapenems tested (imipenem and meropenem) according to the Brazilian Committee

January 2017 Volume 61 Issue 1 e01309-16 Antimicrobial Agents and Chemotherapy aac.asm.org
on Antimicrobial Susceptibility Testing (BRCAST) guidelines, using the broth microdilution method. A detailed report of the whole-genomic data analysis, in the context of resistance and virulence characteristics, will be provided in future publications. Analysis of the sequencing data led to identification in 31 strains of the recently described class D β-lactamase blaOXA-253 (9). According to a multilocus sequence typing (MLST) analysis based on the sequenced genes, these strains were assigned to five different STs (ST 1, ST 15, ST 25, ST 79, and ST 113). So far, the only report of blaOXA-253 in Brazil (9) is from a single A. baumannii strain from the city of Belo Horizonte. This strain belongs to ST 113, the same ST associated with 12 of the blaOXA-253-positive strains from Recife. Considering that the two cities are geographically far apart (~2,000 km), the evidence indicates a large distribution of both the ST and the resistance gene in Brazil. Nevertheless, since 19 strains producing OXA-253 in Recife are distributed between the four other STs (ST 1, ST 15, ST 25, and ST 79), and to our knowledge, this is the first report of multiple STs related to strains carrying the blaOXA-253 gene and distinct from ST 113, the data highlight the potential for this gene to spread further.

To confirm the plasmid localization of the blaOXA-253 gene, and in order to minimize assembly errors due to lower sequence coverage in some strains, two different approaches were carried out in order to assemble plasmid-derived DNA. For the first approach, the whole set of sequenced reads was used for a de novo assembly of the blaOXA-253 gene and neighboring sequences. For the second approach, the reads used for the de novo assembly were only those which were first seen to map to plasmid-derived DNA sequences deposited at the European Nucleotide Archive. The two approaches yielded similar results, although the second approach sometimes resulted in shorter contigs. Within the different genomes, the resulting contigs harboring the blaOXA-253 gene also varied in size, depending on the strain and the sequence coverage. Nevertheless, multiple strains (from various STs) yielded large contigs, which represented up to 91% identity and 97% coverage of the previously described plasmid pABVA01, found in two OXA-24-producing A. baumannii strains in Italy (10). Manual inspection of smaller contigs and reads matching to the plasmid pABVA01 also led to the identification, for most strains, of overlapping contigs covering nearly all of the plasmid and compatible with circular DNA elements 9 to 10 kb in length. The genetic environment surrounding the blaOXA-253 gene was also investigated and, in general, the genetic organization seen was similar to what was found in A. baumannii isolates producing OXA-253 and OXA-24 in Brazil and Italy, respectively (9, 10). In almost all isolates, the blaOXA-253 gene was found to be flanked by conserved elements, including genes coding for hypothetical proteins, a membrane protein, and a TonB-dependent receptor gene.

Overall, the data presented confirm the plasmid localization of the blaOXA-253 gene for most, if not all, strains studied here, suggesting a constant and efficient dispersion of the blaOXA-253 gene between different A. baumannii isolates. This report then draws attention to the highly successful transmission of OXA-253-producing A. baumannii in Brazil and the tendency of the blaOXA-253 gene to remain in the bacterial population over the years, reinforcing the potential for this gene to expand further.

ACKNOWLEDGMENTS

This work was supported by the Brazilian Funding Agencies CNPq, CAPES, and FACEPE.

We thank the Núcleo de Plataformas Tecnológicas (NPT) from Centro de Pesquisas Aggeu Magalhães (CPqAM/Fiocruz) for use of the sequencing platform.

REFERENCES


tant mechanisms and risk factors for infection. Epidemiol Infect 140: 137–145.

Downloaded from http://aac.asm.org/ on November 12, 2017 by guest