TITLE: DISTINCT MOBILE RESISTOMES IN XDR *ACINETOBACTER BAUMANNII* PANDEMIC LINEAGES FROM AN OUTBREAK IN THE BRAZILIAN AMAZON BASIN

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ABSTRACT:

Multidrug resistant pathogens are frequently associated with high rates of morbidity and mortality outcomes, which reinforce the need of tracking and controlling the emergence and spread of antimicrobial resistance. Bacteria belonging to the ESKAPE group, such as Acinetobacter baumannii, present a remarkable multidrug resistance phenotype and have an increased ability in persisting, colonizing and causing epidemics. The aim of this study was to characterize extensively-drug resistant A. baumannii incriminated in a nosocomial outbreak occurred in the Brazilian Amazon region, and to determine their resistome/mobilome to assess the transmission dynamics of the antimicrobial resistance. PFGE and MLST analyses revealed two major pandemic lineages driving this outbreak belonging to the International clone I (IC-1/ST1) and V (IC-5/ST79). The complete genome sequence of one representative strain of each lineage was obtained and a global phylogenomic analysis was performed together with complete and draft publicly available A. baumannii genomes. The cgMLST revealed a cluster composed by IC-1/ST1 genomes from isolates recovered in the last three decades in several continents. The other cluster included ST79 and ST156 genomes from the Americas and Spain in the last ten years. In order to understand the evolution and spread of antimicrobial resistance, the resistome/mobilome was determined reveling a set of antibiotic resistance genes, all of them associated with insertion sequences embedded in a mobile genomic context. Four A. baumannii Resistance Genomic Islands (AbRGI) were identified AbRGI-1-4). The carbapenemase bla_{OXA-23} gene associated with ISAba1, was found in distinct AbRGIs in both IC-1 and Several genes involved with horizontal transfer, virulence and adaptation were IC-5 lineages. distributed among these AbRGIs. Genomic epidemiology analysis considering the mobilome indicated that the four AbRGIs were exclusive of these IC-1 and IC-5 Brazilian lineages. This study contributed to the understanding of A. baumannii evolution and demonstrated that, although phylogenetically stable, the accessory genome are shaping the microevolution of these pandemic lineages, since they harbour a particular arsenal of mobile genetic elements and resistance genes. This finding has significant implications for epidemiological tracking, hospital infection control and therapeutic strategies.

Keywords: International clone, Acinetobacter baumannii, XDR, mobilome, resistome

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