Genomic surveillance of Acinetobacter baumannii in Brazil: temporal dynamics and dissemination of high-risk clones

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Acinetobacter *baumannii* is an opportunistic pathogen of clinical relevance, commonly associated with healthcare-associated infections, particularly in critically ill patients. Its ability to persist on inanimate surfaces under adverse conditions contributes to survival in hospital environments and facilitates transmission between patients. In addition, this species has resistance mechanisms to multiple classes of antimicrobials, including β-lactams, aminoglycosides, and fluoroquinolones. The dissemination of high-risk clonal complexes plays an important role in its epidemiology, contributing to outbreaks and the persistence of lineages across different regions. In Brazil, the population structure of *A. baumannii* remains little explored at the genomic level. This study aimed to evaluate the population structure of Brazilian isolates available in a public database, based on the identification of $bla_{\text{OXA-51-like}}$ variants, inference of clonal complexes, and phylogenetic analysis. Genomes deposited in PubMLST until April 2026 and identified as originating from Brazil were analyzed. Clonal complex classification was inferred based on $bla_{\text{OXA-51-like}}$ (variants). Metadata on year and location of isolation were used to assess the temporal and geographic distribution of clones. Analyses were performed using the Galaxy Europe platform. Genomes were annotated with Prokka, and the pangenome was determined using Roary to identify the core genome. From this alignment, single nucleotide polymorphisms (SNPs) were extracted using SNP-sites and used to construct a maximum likelihood phylogenetic tree with RAxML. Visualization and integration of phylogenetic and epidemiological data were performed using Microreact. This study used ChatGPT (OpenAI, GPT-5.3) to assist in improving the clarity of writing and the organization of ideas in the manuscript. The authors reviewed and edited all generated content to ensure accuracy and scientific integrity. A total of 282 Brazilian genomas were collected, isolated from at least eight different states. Between 2005 and 2020, diversity was observed, with co-circulation of CC1, CC15, CC25, and CC79 across different regions. From 2021 onwards, the emergence and predominance of CC2 among more recent isolates were observed, suggesting clonal replacement, mainly due to isolates from São Paulo state. Resistance profiles indicated a high frequency of determinants associated with resistance to carbapenems and multiple antimicrobial classes, with no reduction over time. The $bla_{\text{OXA-143}}$ gene was detected mainly in isolates belonging to CC15 and CC25, the $bla_{\text{OXA-24}}$ was strongly associated with CC79 (50.7%), and co-production of OXA-23 and OXA-24 was observed predominantly in isolates from CC25, whereas $bla_{\text{OXA-23}}$ remained the most widespread gene across all clones analyzed. Phylogenetic analysis showed clustering consistent with clonal complexes and temporal distribution. These findings indicate the continuous circulation of *A. baumannii* lineages in Brazil, with periods of co-circulation and clonal replacement. The integration of publicly available genomic data with temporal analysis supports the

identification of patterns of persistence, emergence, and lineage replacement, improving the understanding of population dynamics and informing epidemiological surveillance and control strategies in healthcare settings.

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