Unraveling the Genomic Complexity of Resistome, Virulome, and Mobilome in Nosocomial *Acinetobacter baumannii*

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Abstract

Acinetobacter baumannii (*A. baumannii*) is a major multidrug-resistant pathogen that poses significant challenges in the clinical settings. This study presents a comprehensive genomic investigation of nosocomial A. baumannii genomes obtained from the NCBI Genome database. Multilocus sequence typing and capsule typing were used to assess clonal diversity. The genomes were analyzed to detect antimicrobial resistance genes (ARGs), virulence factors, and mobile genetic elements. Further, pangenome analysis was performed to explore the core and accessory genome composition of *A. baumannii*. Our dataset comprised of 609 genomes deposited from diverse geographic regions globally between 2004 and 2024. The dataset exhibited high clonal diversity, with sequence type ST2 observed as the predominant lineage. A total of 185 distinct ARGs were detected, most of which encode efflux pumps and β-lactamases. Over 25,000 IS elements were found, with IS4 family being the most common. Pangenome analysis revealed an open pangenome due to the presence of larger accessory genetic repertoire, indicating considerable genomic plasticity. These findings underscore *A. baumannii's* rapid evolutionary adaptability and resistance potential, highlighting the urgent need for the development of novel antimicrobial agents and alternative therapeutic options. Overall, continuous epidemiological surveillance, infection control, and antimicrobial stewardship are essential to curb this enduring healthcare threat.

Keywords: Antimicrobial resistance, Virulence, Mobile genetic elements, Pangenome, *A. baumannii*