

Trends of AMR genes of *Acinetobacter baumannii* in Malaysia

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Structured Abstract

Background: *Acinetobacter baumannii*, a gram-negative, nonmotile, glucose non-fermenting, oxidase-negative coccobacillus. This opportunistic pathogen is often linked with nosocomial infections. Recent studies have shown a rise in antimicrobial resistance (AMR) in this pathogen towards sulfonamides, cephalosporins and even carbapenems, which were once considered a class of strong antibiotics for *A. baumannii* infection treatment. This study utilized the use of the National Centre for Biotechnology Information (NCBI) for data mining of whole genome sequences (WGS) of *A. baumannii* in Malaysia between 2014 to 2024. The purpose of this study is to acquire *A. baumannii* WGS in Malaysia and screen using Comprehensive Antibiotic Resistance Database (CARD) to create a timeline of acquired AMR-genes by this pathogen.

Methods: NCBI database was accessed and *A. baumannii* WGS were obtained in FASTA format and compiled into Microsoft Excel. These data were chosen based on the WGS quality, year of report and geographical location. CARD was then used to screen the raw data for AMR-related genes. The screened genes were then compiled into Microsoft Excel. By further categorizing and grouping the obtained data, construction of graphs, figures and tables were made possible.

Results: This study managed to construct invaluable data such as chart of gene abundance, AMR-genes timeline, table relating to genes along with associated drug resistance and heat map of the distribution of reported AMR-related *A. baumannii* throughout the states of Malaysia. Resistance genes found prevalent in *A. baumannii* were ANT(3'')-IIa, LpsB, mphE, msrE, ADC-73 and OXA-66. However, there was a skew in data suggesting disparities in the surveillance and reports among the states of Malaysia. Some states such as Perlis, Pulau Pinang, Sabah, Kedah and Melaka did not report any *A. baumannii* WGS in a timespan of 10 years, while some states reported sporadically and inconsistently.

Conclusion: In conclusion, the findings of this study indicated that there exists a knowledge gap regarding *A. baumannii* AMR-genes in Malaysia. This urges the necessity of a large-scale WGS project for a better understanding of the mechanisms of *A. baumannii* in developing drug resistance.

Keywords: *Acinetobacter baumannii*, Antimicrobial Resistance, Drug Resistance, Trends, Malaysia

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