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Comparative Analysis of Resistance Genes between Lab-Induced and Clinically Resistant *Acinetobacter baumannii*

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Structured Abstract

Background: Antibiotic resistance poses a significant global health threat, with *Acinetobacter baumannii* emerging as a prominent multidrug-resistant pathogen. Its ability to persist in hospital environments and rapidly acquire resistance genes complicates treatment strategies, highlighting the urgent need for effective antimicrobial solutions. This study addresses the challenges posed by *A. baumannii*'s adaptability and resistance mechanisms through comprehensive research aimed at understanding its genetic evolution and response to antibiotic pressure in clinical and laboratory settings.

Methods: This study compares resistance gene profiles between *Acinetobacter baumannii* strain PR07 and clinically resistant ESKAPE pathogens. PR07's resistance genes were retrieved and edited to include specific mutations. Whole-genome sequencing data for 120 clinically resistant strains were screened using CARD and ResFinder tools. MAUVE alignment and manual extraction identified target resistance genes, followed by multiple sequence alignment (MSA) to analyze mutation patterns. Phylogenetic tree construction visualized evolutionary relationships among genes, emphasizing genetic diversity and resistance mechanisms.

Results: Analysis revealed genetic conservation of *gyrA*, *mexB*, *ftsI*, and *atpD* genes across strains, with notable variability in resistance gene distribution among clinical isolates. MSA identified specific mutation positions in key resistance genes, highlighting unique genetic signatures within clinical isolates compared to strain PR07. Phylogenetic analysis constructed from MAUVE alignment data delineated distinct clades among ESKAPE pathogens. These findings suggest that lab-induced strains can serve as reliable models for studying antibiotic resistance mechanisms observed in clinical scenarios.

Conclusion: This study successfully achieved its objectives by comparing mutations in antimicrobial resistance (AMR) genes between laboratory-induced and clinical strains of *Acinetobacter baumannii* and assessing the phylogenetic clustering of these genes across both settings. The findings indicate that both lab-induced and clinical strains exhibited similar and unique mutations in AMR genes. Despite being developed in controlled environments, lab-induced strains did not significantly diverge evolutionarily, remaining within their own clade and species. This suggests that lab-induced strains are relevant models for clinical studies to understand the evolution of AMR, as they mirror clinical strains closely in genetic characteristics.

Keywords: Antibiotic resistance, Acinetobacter baumannii, resistance genes, multi-drug resistance, laboratory strain, clinical isolates, bioinformatic tools.

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