

Resistome profile of *Acinetobacter baumannii*

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Abstract

Acinetobacter baumannii is an important nosocomial pathogen. This Gram-negative bacterium causes several diseases, such as pneumonia, bacteremia, meningitis, osteomyelitis, and erysipelas. It is also a pathogen highly known for its resistance to antimicrobials and its ability to survive in intensive care units assisted ventilation devices. Its characteristics make this pathogen an essential model for studies of resistance to antimicrobials. Besides, in 2017 the World Health Organization announced that *A. baumannii* was a priority due to their exacerbated resistance to antimicrobials, mainly of the class of β -lactams. In this context, this work objective is to present the predicted resistance gene repertoire of *A. baumannii*. For this purpose, the public genomes of 206 strains of this species were selected and evaluated by Comprehensive Antibiotic Resistance, Antibacterial Biocide and Metal Resistance genes databases. These data are curated according to classes of antimicrobials. As main results, we obtained a robust resistome composed of 131 genes related to the enzymatic inactivation of the antimicrobial compound and 26 genes encoding putative efflux pumps. We emphasize that the highlighted genes *adeK*, *adeJ*, *adeI*, *adeF*, *adeG*, *adeL*, *adeN*, *abeM*, and *ampC* were identified in all *A. baumannii* strains. The drug resistance in hospital environments is associated with *AmpC* β -lactamases in this pathogen, requiring intensive monitoring. On average, each strain showed 26 resistance genes, except for the SDF strain, which presented 12 genes, and the AYE and 2008S11-069 strains that have 38 resistance genes. In conclusion, this pathogen can be used as a good model of bacterial resistance for directing future studies aimed at therapeutic targets.

Funding:

Link to Video: