

## RESUMO - GENÉTICA DE MICRORGANISMOS

### **IDENTIFICATION OF ACINETOBACTER BAUMANNII ISOLATES USING MATRIX-ASSISTED LASER DESORPTION/IONIZATION TIME-OF-FLIGHT MASS SPECTROMETRY (MALDI-TOF MS)**

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Acinetobacter baumannii is a critically prioritized nosocomial pathogen, frequently associated with severe infections and widely recognized for its extensive antimicrobial resistance. Accurate identification of clinical microorganisms is essential for infection control and for selecting appropriate antimicrobial therapies. Automated systems such as BD Phoenix® are widely used due to their reliability and cost-effectiveness. However, alternative methods like matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF-MS) have gained prominence for their speed and higher accuracy in microbial identification. This study aimed to reassess clinical isolates previously identified as A. baumannii by the BD Phoenix® automated system, using MALDI-TOF-MS. A total of 112 strains from hospitalized patients

were analyzed by the MALDI-TOF-MS. Results were interpreted based on score values:  $\geq 2.00$  indicated reliable species-level identification; between 1.70 and 1.99, genus-level identification; and  $< 1.70$ , unreliable identification. Among the isolates, 94.6% ( $n = 106$ ) were reliably identified as *A. baumannii* at the species level, 4.4% ( $n = 5$ ) at the genus level, and 0.9% ( $n = 1$ ) yielded unreliable identification. The isolates are currently undergoing whole-genome sequencing (WGS) to map genes associated with antimicrobial resistance. The high concordance between MALDI-TOF-MS and the automated system reinforces the effectiveness of both approaches. MALDI-TOF-MS stands out for its rapidity, representing a strategic tool to expedite therapeutic decisions in clinical settings.

Palavras-chave: antimicrobial resistance; carbapenems; bacterial identification; epidemiological surveillance.