



# Multidrug-resistant genes of aminoglycoside-modifying enzymes and 16S rRNA methylases in *Acinetobacter baumannii* strains

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**ABSTRACT.** We examined the distribution of genes of aminoglycoside-modifying enzymes and 16S rRNA methylases in multidrug-resistant *Acinetobacter baumannii* to explore the association of these genes with drug resistance. Strains isolated from clinical specimens were screened using an automatic microbial identification system, and 9 aminoglycoside-modifying enzyme and 6 16S rRNA methylase genes were analyzed using polymerase chain reaction and verified by DNA sequencing. Next, sequence alignment was carried out using the Chromas software and a susceptibility test was performed using the Kirby-Bauer disk diffusion method. Genes encoding aminoglycoside-modifying enzymes were detected in all 20 strains of multidrug-resistant *A. baumannii*. The positive rates of *aac(3')-I*, *aac(6')-Ib*, *ant(3'')-I*, and *aph(3')-I* were 90.0, 90.0, 85.0, and 35.0%, respectively. However, genes encoding 16S rRNA methylases were not positively detected in the 20 strains of multidrug-resistant *A. baumannii*. The resistance of multidrug-resistant *A. baumannii*

may be associated with aminoglycoside-modifying enzyme genes but not with 16S rRNA methylase genes.

**Key words:** *Acinetobacter baumannii*; 16S rRNA methylases; Aminoglycoside-modifying enzymes; Multidrug-resistant