

# Clinical Microbiology Congress

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### Genomic features, novel antibiotic resistance genes and pan-genome analysis of clinical multidrug-resistant *Acinetobacter baumannii* strains in Vietnam hospital

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**Background:** *Acinetobacter baumannii* is an important nosocomial pathogen that can develop multidrug resistance. In this study, we sought to explore the genomic properties, phylogenetic relationships and comparative genomics of this pathogen through strain DMS06669 and DMS06670 (isolated from the sputum of two male patients with hospital-acquired pneumonia).

**Methods:** Whole genome analysis of *A. baumannii* DMS0669 and DMS06670 included *de novo* assembly; gene prediction; functional annotation to public databases; phylogenetic tree construction by average nucleotide identity; pan-genome analysis and antibiotics resistance genes identification. Antibiotics resistance genes *in-vitro* were isolated by PCR and re-confirmed by improved Sanger method.

**Results:** The data showed that a total of 19 possible antibiotic resistance genes, conferring resistance to eight distinct classes of antibiotics, were identified in two strains. Nine of these genes have not previously been reported to occur in *A. baumannii*. Comparative analysis of 23 available genomes of *A. baumannii* revealed an open pan-genome consisting of 15,883 genes. All antibiotics resistance genes were isolated.

**Conclusions:** Our results provide important information regarding mechanisms that may contribute to antibiotic resistance in the DMS06669 and DMS06670 strain and have implications for treatment of patients infected with *A. baumannii*.

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