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GENOME ANNOUNCEMENT

Genome Sequence of *Acinetobacter baumannii* AC12, a Polymyxin-Resistant Strain Isolated from Terengganu, Malaysia

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***Acinetobacter baumannii* is a major cause of nosocomial infection worldwide. We report the draft genome sequence of *A. baumannii* AC12, a multidrug-resistant nosocomial strain with additional resistance to carbapenems and polymyxin. The genome data will provide insights into the genetic basis of antimicrobial resistance and its adaptive mechanism.**

The genus *Acinetobacter* consists of Gram-negative, strictly aerobic, nonfermenting, nonfastidious, nonmotile, catalase-positive, oxidase-negative coccobacilli. Members of the genus *Acinetobacter* are ubiquitous and can be found in soil and water (3). Given their natural competence and ubiquitous nature, recombinogenic *Acinetobacter* strains are now commonly found (2, 6, 9, 14). This is particularly true in a hospital setting where the constant bombardment of an armamentarium of antibiotics provides an excellent breeding ground for the emergence of multidrug-resistant *Acinetobacter* strains (6). *Acinetobacter baumannii* is notorious for its wide range of antibiotic resistance and implication in severe life-threatening infections (4, 12, 13).

A. baumannii AC12 was isolated from blood from a male patient in a tertiary hospital in Terengganu, Malaysia. Strain AC12 is resistant to multiple drugs, such as carbapenems, meropenem, imipenem, ceftoxitin, gentamicin, clindamycin, erythromycin, fusidic acid, oxacillin, penicillin, rifampin, vancomycin, tobramycin, trimethamycin, amikacin, kanamycin, chloramphenicol, neomycin, streptomycin, mupirocin, tetracycline, ciprofloxacin, teicoplanin, linezolid, and norfloxacin. Little genomic information is available for *A. baumannii* isolated from tropical countries such as Malaysia. In this study, the genome sequence of strain AC12 was determined to gain insight into the genetic basis of antibiotic resistance and virulence and host adaptation factors in the tropical strain of *A. baumannii*.

The genome sequencing of *A. baumannii* AC12 was performed using the Illumina genome analyzer IIx (100-bp paired-end reads). The paired-end reads were trimmed and assembled *de novo* using CLC genomics workbench 5.0 (CLC Bio, Denmark). Prodigal 2.60, tRNAscan-SE 1.3, and RNAmmer 1.2 (7, 10, 11) were used to predict open reading frames (ORFs), tRNAs, and rRNAs, respectively. Subsequent genome annotation was performed using Blast2GO 2.5.0 (5). A total of 86 contigs were produced from the *de novo* assembly with an accumulated length of 3,848,312 bp (245-fold coverage) and an average GC content of 38.93%. The contig N_{50} was 109,999 bp, and the largest assembled contig was 245,498 bp. A total of 3,643 ORFs, 42 tRNAs, and 3 rRNAs were predicted from the draft genome.

The draft genome of *A. baumannii* AC12 contains various genes involved in antibiotic resistance such as *adeABC*, bla_{TEM}, *tetA*, *aphA1*, and *uppP*. Notably, the *pmrCAB* operon is also present in the genome; the genes in this operon encode proteins that mediate resistance to colistin and other polymyxins which are usually reserved as the drugs of "last resort" (1). All the complete genes required for multilocus sequence typing (MLST) are present in the draft genome. On the basis of the sequence identity with the current entries in the MLST database for *A. baumannii* (8), strain AC12 was assigned to sequence type 159 in a cluster together with T25, M1, and K58-15 strains isolated in Thailand, Malaysia, and Norway, respectively.

Nucleotide sequence accession numbers. This Whole Genome Shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number ALAM00000000. The version described in this paper is the first version, ALAM01000000.

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