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Genome Sequence of *Acinetobacter baumannii* MDR-TJ▽

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***Acinetobacter baumannii* is a pathogenic species of bacteria, identified as an aerobic Gram-negative bacterium, that is resistant to most antibiotics. In this study, the MDR-TJ strain was isolated at the Second Hospital of Tianjin Medical University, China, and was found to be resistant to penicillin, cephalosporins, aminoglycosides, quinolones, and also imipenem. The genome sequence of *Acinetobacter baumannii* strain MDR-TJ was determined by using a combination of 454 pyrosequencing and paired-end sequencing performed with the Roche Genome Sequencer FLX system to generate a scaffolded assembly.**

Acinetobacter baumannii is a pathogenic species of bacteria, identified as an aerobic Gram-negative bacterium, that is resistant to most antibiotics (4, 9). As an important opportunistic pathogen, *A. baumannii* strains are an increasing cause of concern because of various reported nosocomial infections, which are often severe (11). In this paper, the MDR-TJ strain was isolated at the Second Hospital of Tianjin Medical University, China, and was found to be resistant to penicillin, cephalosporins, aminoglycosides, quinolones, and also imipenem.

The genome sequence of *Acinetobacter baumannii* strain MDR-TJ was determined by using a combination of 400- to 500-base shotgun reads and multispan paired-end reads (3 kb and 8 kb) performed with the Roche genome sequencer FLX Titanium system (454 Life Sciences, Branford, CT). During the first run, shotgun sequencing randomly shears genomic DNA into small pieces. Although 727,217 reads and 285,166,509 bases were obtained, the number of contigs was far above 100 after sustained efforts for the optimization of assembly. Therefore, genomic libraries containing 3-kb and 8-kb inserts were constructed afterwards, in which 159,601 and 257,488 paired-end reads were generated successively. The three rounds provided genome coverages of 69×, 20×, and 31×, respectively. In total, more than 1.78 million reads were generated, to reach a depth of 120-fold coverage, and assembled into 43 scaffolds by using the 454 Newbler assembler software (Roche). The average size of the scaffolds was 692,977 bp, while the largest one was 3,958,653 bp. The gaps between scaffolds were then filled by sequencing PCR products by using an ABI 3730 capillary sequencer apparatus.

Currently, the draft genome, excluding gaps, has a total of 3,943,262 bp distributed in four contigs, with an average G+C content of 39.1%, and the sizes of the four contigs are 2,932,185 bp, 3,572 bp, 1,004,857 bp, and 2,648 bp. The origin of replication (*oriC*) and nine putative DnaA boxes were identified by using Ori-Finder (6). The regions with abnormal G+C contents in the genomic sequence were obtained by using the GC-Profile program (5) to identify the genomic resistance islands. Protein-coding genes were predicted by using three *ab initio* gene-finding programs: Glimmer v3.02 (3), GeneMark (2), and ZCURVE v2.0 (7). Seventeen rRNA genes (five 5S rRNAs, six 16S rRNAs, and six 23S rRNAs) of the draft assembly were identified by using RNAmmer (8). Seventy-four tRNA genes for all 20 amino acids were predicted by using tRNAscan-SE (10). Automatic functional annotation results and subsystems represented in the genome were obtained by using the Rapid Annotation using Subsystem Technology (RAST) server (1). Consequently, 78 subsystem features predicted by the RAST server were relevant to resistance to antibiotics and toxic compounds, which will be helpful for revealing the mechanisms of *Acinetobacter baumannii* strain MDR-TJ's high resistance to almost all antibiotics.

Nucleotide sequence accession numbers. The information reported here from the Whole Genome Shotgun project has been deposited with DDBJ/EMBL/GenBank under the accession number AEOE00000000. The version described in this paper is the first version and has been assigned accession number AEOE01000000.

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