Genome Sequence of a Dominant, Multidrug-Resistant *Acinetobacter baumannii* Strain, TCDC-AB0715[▽]

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***Acinetobacter baumannii* has emerged as a significant nosocomial pathogen worldwide. The increasing trend of carbapenem and fluoroquinolone resistance in *A. baumannii* severely limits the usage of therapeutic antimicrobial agents. Here we report the genome sequence of a multidrug-resistant *A. baumannii* strain, TCDC-AB0715, harboring both *bla*_{OXA-23} and *bla*_{OXA-66}.**

Among the 135 isolates collected from *Acinetobacter baumannii* complex bacteremia patients during January 2007 and July 2009, the clinical *A. baumannii* (genospecies 2) strain TCDC-AB0715 was one of the isolates exhibiting high resistance to carbapenems (e.g., imipenem and meropenem MICs of >16 mg/liter), fluoroquinolones (e.g., ciprofloxacin, >4 mg/liter, and levofloxacin, >8 mg/liter), and cephalosporins (ceftriaxone, >64 mg/liter, and cefepime, 32 mg/liter) (2, 7, 8). Additionally, this strain had two carbapenemase genes, *bla*_{OXA-23} and *bla*_{OXA-66}, which was a difference from other clinical isolates. TCDC-AB0715 belonged to multilocus sequence type (MLST) ST2, a molecular type previously reported in Europe (5).

The genome of TCDC-AB0715 was sequenced using the Illumina/Solexa sequencing platform (720× coverage rate), and the automated DNA sequencing chromatograms were analyzed by the CLC bio software package. In particular, the order of 141 contigs was predicted by comparison with the chromosome sequences of *A. baumannii* ACICU (GenBank accession number CP000863) (5) and AB0057 (accession no. CP001182) (1) and then confirmed by optical mapping (10) and PCR. The length of the draft sequence of the TCDC-AB0715 circular chromosome is 4,130,792 bp more than 80 kb larger than those of seven other completely sequenced *A. baumannii* isolates, AB0057 (4.05 Mb), ATCC 17978 (3.98 Mb) (11), 1656-2 (3.94 Mb), AYE (3.94 Mb) (4), ACICU (3.90 Mb), AB307-0294 (3.76 Mb) (1), and SDF (3.42 Mb) (1). We also isolated two circular plasmids, p1ABTDC0715 (8,731 bp) and p2ABTDC0715 (70,894 bp). Then, we performed open reading frame (ORF) prediction and functional assignment of genes by using the GLIMMER3 (3), BLAST, and BioNumerics 6.5 (Applied Maths) software programs. The numbers of predicted ORFs in the TCDC-AB0715 chromosome, p1ABTDC0715, and p2ABTDC0715 are 3,844, 10, and 95, respectively. There are 42 tRNAs and four copies of

16S-23S-5S rRNA operons in the chromosome. The overall chromosome sequence identity to ACICU is 90.3%, and that to AB0057 is 79.2% (determined by the MUMmer software program) (6). The G+C content of the genome is 38.9%, near that of ACICU (38.9%) and AB0057 (39.2%).

Several antibiotic resistance islands (i.e., AbaR regions) have been identified in *A. baumannii* (9). The TCDC-AB0715 chromosome has a 40-kb resistance island which was similar to AbaR3 of the highly resistant strain AB0057. In particular, p1ABTDC0715 in TCDC-AB0715 has 100% identity to the plasmid pAB0057 in AB0057 (8,729 bp; accession no. CP001183). p2ABTDC0715 was 99% similar to plasmid pACICU2 of strain ACICU (64,366 bp; accession no. CP000865) but was interwoven with insertion sequences (in total, 6,528 bp).

A detailed report of our isolate will be included in a future publication, with the results of a full comparative analysis between these published *A. baumannii* genomes.

Nucleotide sequence accession numbers. The draft genome sequence of *A. baumannii* TCDC-AB0715 has been assigned GenBank accession numbers CP002522 (chromosome), CP002523 (p1ABTDC0715), and CP002524 (p2ABTDC0715).

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