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GENOME ANNOUNCEMENT

Genome Sequence of *Acinetobacter baumannii* TYTH-1

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***Acinetobacter baumannii* has emerged recently as a major cause of health care-associated infections due to the extent of its antimicrobial resistance and its propensity to cause large nosocomial outbreaks. Here we report the genome sequence of *Acinetobacter baumannii* TYTH-1 isolated in Taiwan during 2008.**

Nowadays *Acinetobacter baumannii* has emerged as a leading nosocomial pathogen in Taiwan (3). The epidemic potential of *A. baumannii* is primarily related to this organism's ability to develop resistance to many commonly used antibiotics (7). In this paper, the TYTH-1 strain was isolated from a bacteremia patient at National Taiwan University Hospital (NTUH), Hsin-Chu Branch, Taiwan, and was found to be resistant to imipenem, penicillins, and the broad-spectrum cephalosporins. Additionally, this strain carried two OXA-type carbapenemase genes, $bla_{\text{oxa-23}}$ and $bla_{\text{oxa-66}}$, and was reported to be the predominant strain at NTUH, Hsin-Chu Branch, during the period from 2006 to 2007 (5). Strain typing showed that TYTH-1 belonged to multilocus strain typing (MLST) ST2, a molecular type that has been widespread in several countries (1).

The genome of *A. baumannii* strain TYTH-1 was sequenced using the Illumina/Solexa sequencing platform and generated 9,849,568 paired-end reads (492-fold coverage). One hundred sixty-five contigs were obtained by using the CLOVER software. The order of contigs was predicted from the chromosome sequences of *A. baumannii* TCDC-AB0715 (GenBank accession number CP002522), *A. baumannii* MDR-ZJ06 (accession no. CP001937), and *A. baumannii* MDR-TJ (accession no. CP003500) and confirmed by optical mapping (8) and PCR. The length of the draft sequence of the TYTH-1 circular chromosome is 3,957,368 bp. Gene prediction was performed using the Prodigal software program (2). The functional assignment of genes was predicted by homology comparison with the Cluster of Orthologous Groups (COG), the Kyoto Encyclopedia of Genes and Genomes (KEGG), and the NCBI Genome databases (http://ncbi.nlm.nih.gov). tRNA genes and 16S-23S-5S rRNA operons were predicted using the tRNAscan-SE tools (6) and the RNAmmer1.2 software program (4), respectively. The number of open reading frames in the TYTH-1 chromosome is 3,682. There are 75 tRNAs and 6 copies of 16S-23S-5S rRNA operons in this chromosome. The genome includes a 41.4-kb resistance island, and the GC content is 39%.

A comparative analysis of our isolate with those published *A. baumannii* genomes will be reported in the future.

Nucleotide sequence accession number. The draft genome sequence of *A. baumannii* TYTH-1 has been assigned GenBank accession number CP003856.

ACKNOWLEDGMENTS

The present work was partially supported by a grant (no. 99006) from Hsin-Chu General Hospital and the National Science Council (grants NSC100-2221-E-126-010-MY3).

REFERENCES

1. **Higgins PG, Dammhayn C, Hackel M, Seifert H.** 2010. Global spread of carbapenem-resistant *Acinetobacter baumannii*. J. Antimicrob. Chemother. **65**:233–238.
2. **Hyatt D, et al.** 2010. Prodigal: prokaryotic gene recognition and translation initiation site identification. BMC Bioinformatics **11**:119. doi:10.1186/1471-2105-11-119.
3. **Jean SS, Hsueh PR.** 2011. Antimicrobial drug resistance in Taiwan. J. Formos. Med. Assoc. **110**:4–13.
4. **Lagesen K, et al.** 2007. RNAmmer: consistent and rapid annotation of ribosomal RNA genes. Nucleic Acids Res. **35**:3100–3108.
5. **Lin MF, et al.** 2011. Emergence and dissemination of bla(OXA-23)-carrying imipenem-resistant *Acinetobacter* sp in a regional hospital in Taiwan. J. Microbiol. Immunol. Infect. **44**:39–44.
6. **Lowe TM, Eddy SR.** 1997. tRNAscan-SE: a program for improved detection of transfer RNA genes in genomic sequence. Nucleic Acids Res. **25**:955–964.
7. **Perez F, et al.** 2007. Global challenge of multidrug-resistant *Acinetobacter baumannii*. Antimicrob. Agents Chemother. **51**:3471–3484.
8. **Shukla SK, Kislow J, Briska A, Henkhaus J, Dykes C.** 2009. Optical mapping reveals a large genetic inversion between two methicillin-resistant *Staphylococcus aureus* strains. J. Bacteriol. **191**:5717–5723.

Received 27 September 2012 **Accepted** 3 October 2012

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doi:10.1128/JB.01860-12