

Complete Genome Sequence of an *Acinetobacter* Strain Harboring the NDM-1 Gene

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The NDM-1 gene is a significant public health concern. *Acinetobacter* is one of the most prevalent opportunistic pathogens causing recent nosocomial infections with NDM-1, and drug-resistant strains pose serious threats to public health worldwide. Herein, we present the genomic sequence of *Acinetobacter calcoaceticus* subsp. *anitratu*s XM1570, a multidrug-resistant isolate that carries the *bla*_{NDM-1} gene.

Received 30 October 2012 Accepted 13 March 2013 Published 18 April 2013

Citation Sun Y, Song Y, Song H, Liu J, Wang P, Qiu S, Chen S, Zhu L, Ji X, Wang Z, Liu N, Xia L, Chen W, Feng S. 2013. Complete genome sequence of an *Acinetobacter* strain harboring the NDM-1 gene. *Genome Announc.* 1(2):e00023-12. doi:10.1128/genomeA.00023-12.

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The NDM-1 gene (6) is present worldwide in diverse pathogens, including *Acinetobacter baumannii*, *Enterobacter cloacae*, *Escherichia coli*, *Klebsiella pneumoniae*, and *Pseudomonas aeruginosa* (2–5). Bacteria carrying the *bla*_{NDM-1} gene have been termed “superbugs” and have attracted worldwide research attention. The gene is usually present on a large plasmid (1, 3, 5).

Acinetobacter calcoaceticus subsp. *anitratu*s XM1570 was cultivated from a sputum sample of a lung cancer patient treated in a hospital in Xiamen, Fujian province, China, in 2010. The male patient was initially admitted because of cold symptoms. The patient was treated with clarithromycin, imipenem, and cilastatin sodium via injection, and he was then diagnosed with lung cancer, right pleural metastasis, and pneumonia. A sputum culture yielded a multidrug-resistant *Acinetobacter* strain that was resistant to beta-lactam antibiotics and carbapenems. The genome of this isolate, which harbors the *bla*_{NDM-1} gene, was completely sequenced. The total length of the assembled genome is 4,100,402 bp, and 3,959 coding sequences (CDSs) were identified. Further, a 47,274-bp plasmid carrying *bla*_{NDM-1} was identified. Our sequence data will be more valuable when further studies on the horizontal transfer of *bla*_{NDM-1} are conducted.

Our strain is very similar to *Acinetobacter calcoaceticus* PHEA-2. This drug-resistant strain, which has been identified in many Chinese hospitals, belongs to the *A. calcoaceticus*-*A. baumannii* (ACB) complex (7). This group includes *Acinetobacter* genomic species 3, *A. baumannii*, *Acinetobacter* genomic species 13TU, and *A. calcoaceticus*; it is difficult to phenotypically distinguish between these species (4). As is true of *A. baumannii*, *A. calcoaceticus* is a causative agent of both community-acquired and nosocomial infections (2). Intensive phylogenetic analysis has recently suggested that strain PHEA-2 is a novel species (termed *A. calcoaceticus*). Herein, we present the draft genomic sequence of the *bla*_{NDM-1}-bearing strain *Acinetobacter calcoaceticus* subsp. *anitratu*s XM1570.

Whole-genome sequencing was performed using the Illumina HiSeq 2000 method. Ultimately, 410 Mb and 210 Mb of high-quality data were generated from two libraries; the read lengths were both 90 bp. The paired-end reads were first assembled *de novo* using SOAPdenovo v1.05. *Acinetobacter oleivorans* DR1 and contigs were next manually connected with reference to paired-end relationships at the 2-kb level. After all sequence data were evaluated, we identified putative protein-encoding sequences using Glimmer 3.0 (3), and then used BLAST to identify homologies with publically available database data prior to functional annotation. rRNAs and tRNAs were identified using RNAmmer 1.2 and tRNAscan-SE 1.3.1, respectively; ultimately, 63 tRNAs and three rRNAs were found.

Finally, we obtained 95 contigs with a total length of 4,076,308 bp, including one 47.3-kb circular contig identified as a *bla*_{NDM-1}-bearing plasmid. A total of 3,959 CDSs were identified on the contigs. The *bla*_{NDM-1}-bearing plasmid differed from that reported previously in *E. coli* (5). The *bla*_{NDM-1} region in the plasmid is located in an island of medium G+C content (40.83%); the average G+C percentage of the strain is 38.82%. β -lactamase and 16S rRNA methylase genes were sought using PCR and specific sequencing protocols to check whether the sequencing data are accurate.

Nucleotide sequence accession numbers. The genome sequence of *Acinetobacter calcoaceticus* subsp. *anitratu*s XM1570 has been deposited at DDBJ/EMBL/GenBank under the accession no. [AMXH000000000](https://www.ncbi.nlm.nih.gov/nuccore/AMXH000000000). The version described in this paper is the first version, accession no. [AMXH010000000](https://www.ncbi.nlm.nih.gov/nuccore/AMXH010000000).

ACKNOWLEDGMENTS

This work was funded by the 863 of China (2012AA022006) and National Science & Technology Specific Projects (No. 2013ZX10004-217-002).

We thank Lizhi Xu for helping us analyze rRNA and tRNA genes and gene annotation and for critical comments on the manuscript.

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