Draft Genome Sequence of a Multidrug-Resistant *bla*_{NDM-1}-Producing *Acinetobacter soli* Isolate in China

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Abstract *Acinetobacter* spp. are one of the most prevalent opportunistic pathogens causing nosocomial infections and have become a major clinical and public health threat. In this study, we presented the first draft genome sequence of *A. soli* TCM341, a multidrug resistant isolate that carried the *bla*_{NDM-1} gene in China. Genome sequencing of *A. soli* TCM341 was carried out in Illumina Hiseq 2000 next-generation sequencer. The data obtained revealed 74 contigs with genome size of 3.49 Mb and G+C content of 41.37 %.

Keywords *Acinetobacter soli* · *bla*_{NDM-1} · Genome sequence · Multidrug-resistant

In recent years, carbapenem resistance in species of the genus *Acinetobacter*, which is involved in outbreaks of nosocomial infections, has been raised as an important public-health concern and currently reported to be a worldwide menace [1–4]. Recently, the emergence and worldwide dissemination of a new carbapenemase NDM-1 encoded by *bla*_{NDM-1} gene in diverse pathogens has been

reported in several countries and bacteria carrying this gene have been termed as “superbugs”. *Acinetobacter soli* was first isolated from the forest soil in Korea, 2007. Since then, the bloodstream infection outbreak caused by this species in neonatal intensive care unit (ICU) has also been reported in Korea, 2011 and the first carbapenem-resistant isolates were detected in Japan, 2012 [5–7]. However, carbapenem-resistant and *bla*_{NDM-1} producing *A. soli* has not yet been reported in China.

Acinetobacter soli TCM341 was cultivated from a sputum sample of a male patient treated in our hospital at Hangzhou, Zhejiang province, China, in 2013. A sputum culture yielded a multidrug-resistant *Acinetobacter* strain that was resistant to β -lactam antibiotics and carbapenems. The strain was grown overnight at 37 °C in Mueller–Hinton broth (Oxoid, Hampshire, United Kingdom). Genomic DNA was extracted using a QIAamp DNA minikit (Qiagen, Valencia, CA) according to the protocol recommended by manufacturers. The quality and quantity of genomic DNA were determined by an agarose gel electrophoresis and a NanoDrop spectrophotometer. The 300-bp library for Illumina paired-end sequencing was constructed from 5 μ g DNA using a paired-end DNA sample prep kit (Illumina Inc., Cambridge, United Kingdom). The genome of TCM341 were sequenced via the Illumina Hiseq 2000 (398 $\times$). In total, 39 million 100-bp paired-end reads were generated for TCM341. Draft genome sequence was assembled using Velvet 1.2.09 tool, at a *k*-mer value of 63 [8], and automatically annotated by the Rapid Annotation using Subsystems Technology (RAST) server [9]. Besides, rRNAs and tRNAs were identified using RNAmmer 1.2 and tRNAscan-SE 1.3.1, respectively [10, 11].

The draft genome sequences of *A. soli* TCM341 consisted of 74 contigs and the *N*₅₀ size was 151,748 bp, which comprised 3,498,905 bases, and RAST server predicted a

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Table 1 *Acinetobacter soli* TCM341 genome features

Attributes	Value
Genome size (bp)	3,498,905
Total number of contigs	74
GC content (%)	41.37 %
rRNA operons	3
tRNA operons	68
Total predicted ORFs	3,355

total of 3,355 protein-coding sequences. The overall G+C content of this strain amounted to 41.37 %. In total, 68 tRNAs and 3 rRNA were identified respectively. Genome features of *A. soli* TCM341 were listed in Table 1.

Since the *bla*_{NDM-1} gene was first reported in 2008, it has disseminated around the world [12, 13]. In China, *bla*_{NDM-1} gene could be detected in different bacteria species, such as *Acinetobacter baumannii*, *Enterobacter cloacae*, *Escherichia coli*, *Klebsiella pneumoniae*, and *Pseudomonas aeruginosa* [14–17]. However, carbapenem-resistant *A. soli* isolate carried *bla*_{NDM-1} gene has been detected in our study, which indicated that it could disseminate more widely and promptly than we anticipated, and its prevalence should be monitored with care.

Further studies on the *bla*_{NDM-1}-producing *A. soli* and other nosocomial multidrug-resistant bacterial isolates obtained from patients in China are currently on the way. These data may shed important light on the molecular mechanisms contributing to bacterial drug resistance dissemination and help guide preventive measures for hospital transmission. To the best of our knowledge, this is the first draft genome sequence report of this species in China.

Nucleotide Sequence Accession Number

This Whole Genome Shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession JAPY000000000. The version described in this paper is the first version, NZ_JAPY000000000.1. Bioproject registered under accession: PRJNA231561 ID: 231561.

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