

Genome Sequence of *Acinetobacter baumannii* Strain 10441_14 Belonging to ST451, Isolated from India

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***Acinetobacter baumannii* resistance to carbapenems is of global concern. Here, we report the 3.9 Mb draft genome of a cerebrospinal fluid isolate of *A. baumannii* strain 10441_14 which is carbapenem resistant and belongs to ST451. This genome will further help in the understanding of the drug resistance mechanism, epidemiology, and pathology of this bacterium.**

Received 23 September 2015 Accepted 25 September 2015 Published 5 November 2015

Citation Kumar S, Patil PP, Midha S, Ray P, Patil PB, Gautam V. 2015. Genome sequence of *Acinetobacter baumannii* strain 10441_14 belonging to ST451, isolated from India. *Genome Announc* 3(6):e01322-15. doi:10.1128/genomeA.01322-15.

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Acinetobacter baumannii is one of the leading causes of nosocomial infections worldwide (1, 2). Multidrug resistance is a major public health concern, and is even more so in *A. baumannii* as it has the ability to develop resistance against almost all available antimicrobials (3). Carbapenems are widely being used as a treatment option for infections of *A. baumannii*. However, carbapenem-resistant *A. baumannii* has emerged as a serious challenge to health care systems globally as few treatment options are available (4).

Here, we present the genome sequence of the *A. baumannii* strain 10441_14, isolated from the cerebrospinal fluid of patient admitted into the neurosurgery ward of the Post Graduate Institute of Medical Education and Research (PGIMER), Chandigarh, a tertiary care hospital in northern part of India. Multilocus sequence typing by scheme defined by Bartual et al. (5) shows that isolate 10441_14 belongs to ST451. ST451 belongs to clonal complex 92 (CC92), which corresponds to the international clone lineage II that is commonly observed among carbapenem-resistant *A. baumannii* in hospitals worldwide (6, 7).

For whole-genome sequencing, genomic DNA was isolated using a ZR Fungal/Bacterial DNA miniprep Kit (Zymo Research). The quality of DNA was assessed using NanoDrop (Thermo Scientific, Wilmington, MA, USA) and agarose gel electrophoresis and concentration were estimated using a Qubit 2.0 Fluorometer (Life Technologies). An Illumina sequencing library of genomic DNA was prepared using a Nextera XT sample preparation kit (Illumina, Inc., San Diego, CA, USA) with dual indexing adapters. The Illumina sequencing library was sequenced on an in-house Illumina Miseq (Illumina, Inc., San Diego, CA, USA) platform using the 2 × 250 bp paired-end configuration. Sequencing of the DNA generated 2,521,072 reads, accounting for 365,553,621 bp. Raw reads were assembled using CLC Genomics Workbench v7.5 (CLC bio, Aarhus, Denmark) into 136 contigs with a genome size of 3,909,844 bp and average coverage 92.78×. N_{50} for the assembly is 61,813 bp and the genome has an average G+C content of 38.93%. The genome was annotated using the NCBI Prokaryotic

Genome Annotation Pipeline (http://www.ncbi.nlm.nih.gov/genome/annotation_prok/), which predicted 3,775 genes, 63 tRNAs, and 3 rRNAs.

A complete 16S rRNA gene sequence was retrieved from the genome by using RNAmmer v1.2 (8) and the average nucleotide identity (ANI) was calculated using Jspecies v1.2.1 (9). The *A. baumannii* strain 10441_14 has 16S rRNA identities of 99.97% and 97.7% ANI with the type strain *A. baumannii* ATCC 19606^T.

The genome information of *A. baumannii* 10441_14 will accelerate our understanding of the whole-genome-based phylogenetic and the comparative analysis of this globally important nosocomial pathogen.

Nucleotide sequence accession numbers. The draft genome sequence of *Acinetobacter baumannii* 10441_14 is available in DDBJ/EMBL/GenBank under accession no. **LGYW00000000**. The version described in this paper is the first version, **LGYW01000000**.

ACKNOWLEDGMENT

S.K. is working as a senior research fellow supported by the Department of Biotechnology (DBT). P.P.P. and S.M. are supported by fellowships from the University Grant Commission (UGC) and Council of Scientific and Industrial Research (CSIR), respectively.

This study was supported by a grant received from the Department of Biotechnology of India (102/IPD/SAN/497/2014-2015).

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