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Data in Brief

Genome sequencing and annotation of *Acinetobacter gerneri* strain MTCC 9824^T☆

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ABSTRACT

The genus *Acinetobacter* consists of 31 validly published species ubiquitously distributed in nature and primarily associated with nosocomial infection. We report the 4.4 Mb genome of *Acinetobacter gerneri* strain MTCC 9824^T. The genome has a G + C content of 38.0% and includes 3 rRNA genes (5S, 23S16S) and 64 aminoacyl-tRNA synthetase genes.

Specifications	
Organism/cell line/tissue	*Acinetobacter gerneri*
Strain(s)	MTCC 9824^T
Sequencer or array type	Sequencer; the Illumina-HiSeq 1000
Data format	Processed
Experimental factors	Microbial strain
Experimental features	Whole genome sequencing of *A. gerneri* strain MTCC 9824^T, assembly and annotation
Consent	n/a

Direct link to the data

Direct link: http://www.ncbi.nlm.nih.gov/nuccore/ASYY00000000.

Genus *Acinetobacter* was proposed by Brisou and Pre'vot in 1954 [1]. This genus comprises Gram-negative, strictly-aerobic, non-fermenting, non-fastidious, non-motile, catalase-positive, oxidase-negative bacteria with a DNA G + C content of 39% to 47% [2]. According to Euzeby's list of prokaryotic names with standing in nomenclature (http://www.bacterio.cict.fr/a/acinetobacter.html) the genus *Acinetobacter* consists of 31 validly published species. *A. gerneri* was proposed by Carr et al. [3] and it was isolated from activated sludge, with characteristics corresponding to those of the genus *Acinetobacter*. The organism in this study is *Acinetobacter gerneri* strain MTCC 9824^T equivalent to DSM 14967^T (= CIP 107464^T).

A. gerneri strain MTCC 9824^T was obtained from MTCC and grown on tryptic soya agar medium (TSA; HiMedia) at 30 °C. Genomic DNA was extracted from 36 hour old culture using ZR Fungal/Bacterial DNA MiniPrep™ as per manufacturer's instructions. Identification was reconfirmed using 16S rRNA sequencing. Amplification and sequencing of 16S rRNA were performed as described by Mayilraj et al. [4]. To determine the phylogenetic relationship of strain MTCC 9824^T, the 16S rRNA sequence consisting of 1502 bp was compared with that of type strains of species of related genera and identification of phylogenetic neighbors and the calculation of pairwise 16S rRNA gene sequence similarities were achieved using the EzTaxon server [5] and aligned using mega version 5.0 [6]. Phylogenetic trees were constructed using the neighbor-joining algorithm. Bootstrap analysis was performed to assess the confidence limits of the branching (Fig. 1).

The genome of *A. gerneri* MTCC 9824^T was sequenced using the Illumina-HiSeq 1000 technology. Sequencing resulted in 29,584,672 paired-end reads (insert size of 350 bp) of length 101 bp. A total of 29,337,619 high-quality reads with approximately 670× coverage were assembled with CLCbio wb6 (word size 55 and bubble size 65)

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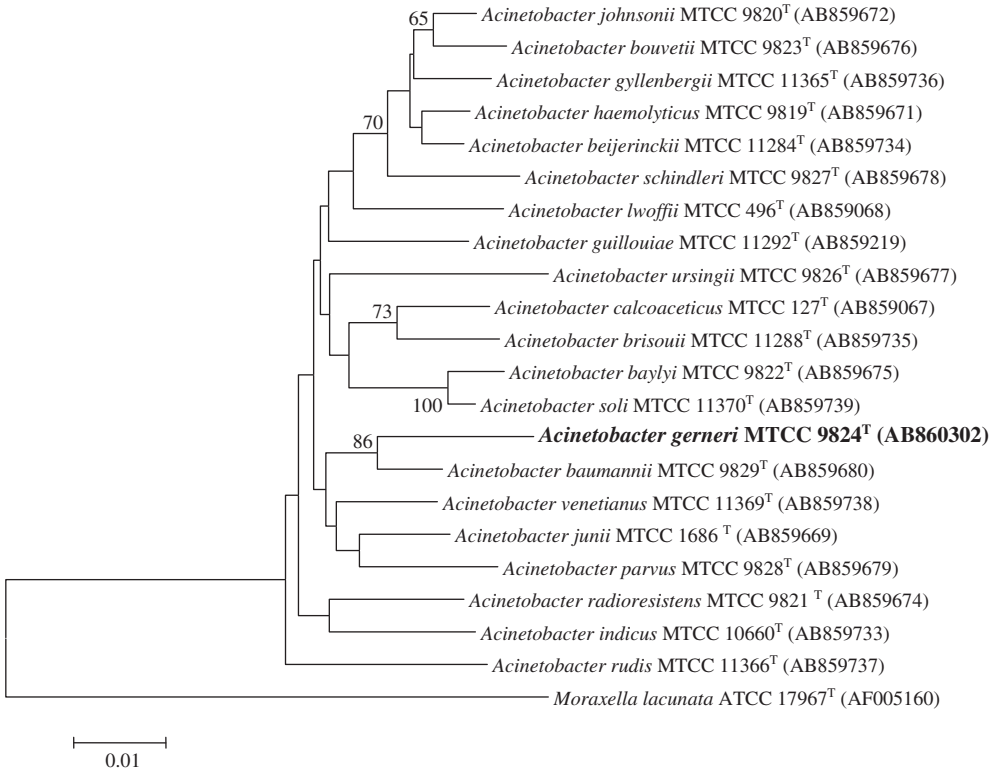

Fig. 1. Phylogenetic tree constructed using the neighbor-joining algorithm shows the position of *A. gerneri* MTCC 9824^T relative to the type strains of the other species within the genus *Acinetobacter*.

and to obtain 167 contigs (N_{50}, 64,311 bp) of 4,420,969 bp with an average GC content of 38%.

The functional annotation was carried out by RAST (Rapid Annotation using Subsystem Technology) [7]. Fig. 2 shows the subsystem distribution of strain *A. gerneri* MTCC 9824^T, tRNA was predicted by tRNAscan-SE 1.23 [8] and rRNA genes by RNAmmer 1.2 [9]. The genome contains 3 rRNA genes (5S, 23S, 16S) and 64 aminoacyl-tRNA synthetase genes. A total of 4110 coding regions (2079 transcribed from the positive strand and 2031 from the negative strand) were found in the genome, of which 2805 (68%) could be functionally annotated. The genome coding density is 83% with an average gene length of 890 bp. The annotated genome has 49 genes responsible for resistance to antibiotic and toxic compounds including 12 genes for MDR efflux pumps. One hundred and twenty nine genes code for membrane transport proteins. Fifty four genes are involved in response to oxidative stress, 6 for osmotic stress response and 15 genes for heat shock and many more stress responses, all summed up to 102 genes for stress response are present.

The functional comparison of genome sequences available on the RAST server revealed the closest neighbors of *A. gerneri* MTCC 9824^T as *Acinetobacter baumannii* 1656-2 (score 686) followed by *Acinetobacter baumannii* 3990 (score 651), *Acinetobacter baumannii* ACICU (score 459) and *Acinetobacter baumannii* AB0057 (score 456).

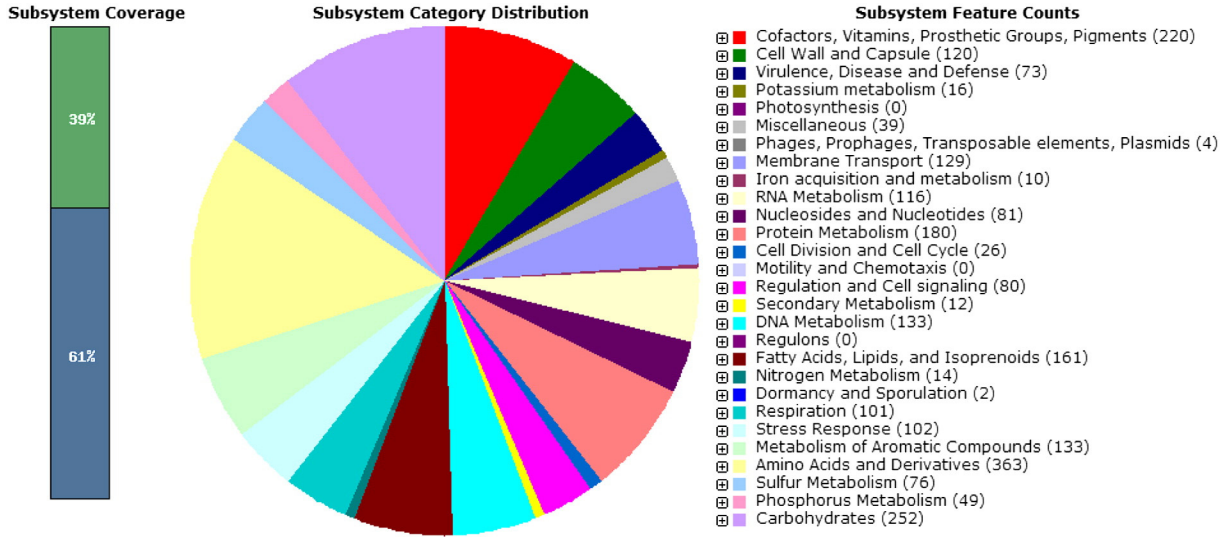

Fig. 2. Sub-system distribution of strain *A. gerneri* strain MTCC 9824^T (based on RAST annotation server).

Nucleotide sequence accession number

The *A. gerneri* strain MTCC 9824^T whole genome shot gun (WGS) project has been deposited at DDBJ/EMBL/GenBank under the project accession ASYY00000000 of the project (01), has the accession numbers ASYY01000000 and consists of sequences ASYY01000001–ASYY01000167.

Conflict of interest

The authors declare that there is no conflict of interest on any work published in this paper.

Acknowledgments

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