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Data in Brief

Genome sequencing and annotation of *Acinetobacter gyllenbergii* strain MTCC 11365^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 4.3 Mb genome of the *Acinetobacter gyllenbergii* strain MTCC 11365^T. The draft genome of *A. gyllenbergii* has a G + C content of 41.0% and includes 3 rRNA genes (5S, 23S, 16S) and 67 aminoacyl-tRNA synthetase genes.

Specifications	
Organism/cell line/tissue	*Acinetobacter gyllenbergii*
Strain(s)	MTCC 11365^T
Sequencer or array type	Sequencer; the Illumina-HiSeq 1000
Data format	Processed
Experimental factors	Microbial strain
Experimental features	Whole Genome Sequencing of *A. gyllenbergii* strain MTCC 11365^T, Assembly and Annotation.
Consent	n/a

Direct link to the data

Direct link: http://www.ncbi.nlm.nih.gov/nuccore/ASQH00000000.

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 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. gyllenbergii* proposed by Nemec et al., 2009 [3] was isolated from the urine of a patient in Leiden University Hospital, The Netherlands, and shares characteristics corresponding to those of the genus *Acinetobacter*. The organism in this study is *A. gyllenbergii* strain MTCC 11365^T equivalent to DSM 22705^T (=CCM 7267^T = CCUG 51248^T = NIPH 2150^T).

A. gyllenbergii strain MTCC 11365^T was obtained from MTCC and grown on tryptic soya agar medium (TSA; HiMedia) at 30 °C. Genomic DNA was extracted from 36 h 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 11365^T, the 16S rRNA sequence consisting of 1502 bp was compared with those 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. gyllenbergii* MTCC 11365^T was sequenced using the Illumina-HiSeq 1000 technology. Sequencing resulted in 20,678,502 paired-end reads (insert size of 350 bp) of length 101 bp. A total of 20,483,505 high-quality reads with approximately 690× coverage were assembled with CLCbio wb6 (word size 40 and bubble size 50) and to obtain 48 contigs (N_{50}, 212,525 bp) of 4,318,988 bp and average G + C content of 41.0%.

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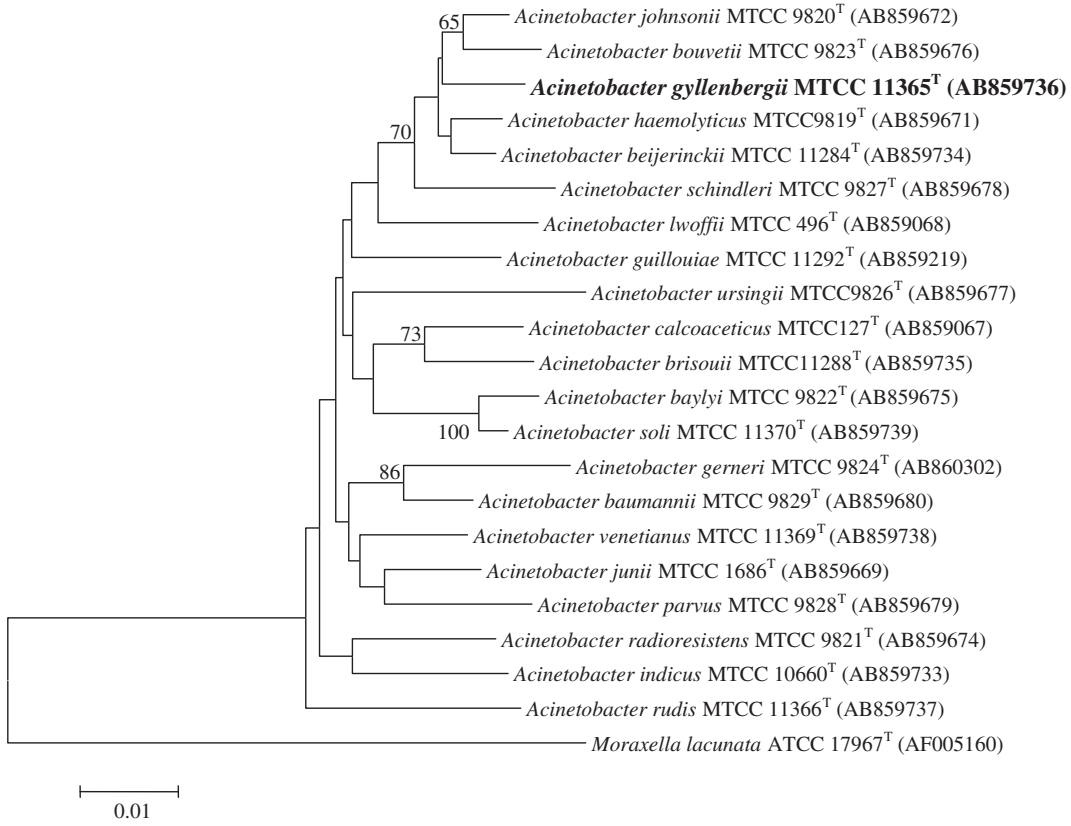

Fig. 1. Phylogenetic tree constructed using the neighbor-joining algorithm, shows the position of *A. gyllenbergii* MTCC 11365^T relative to the type strains of the other species within the genus *Acinetobacter*.

The functional annotation was carried out by RAST (rapid annotation using subsystem technology) [7], Fig. 2 shows the subsystem distribution of strain *A. gylenbergii* strain MTCC 11365^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 67 aminoacyl-tRNA synthetase genes. A total of 4019 coding regions (2188 genes transcribed from the positive strand and 1831 from the negative strand) were found in the genome, of which 2827 (70%) could be functionally annotated. The genome coding density is 86% with an average gene length of 915 bp. The annotated genome has 82 genes responsible for resistance to antibiotic and toxic compounds including 18 genes for MDR efflux pumps. One hundred and twenty nine genes contribute to the membrane transport proteins. Sixty five genes in response to oxidative stress, 17 osmotic stress responsive genes, 16 genes for heat shock and many more stress responses, all summed up to 122 genes for stress response are present.

The functional comparison of genome sequences available on the RAST server revealed the closest neighbors of *A. gyllenbergii* MTCC

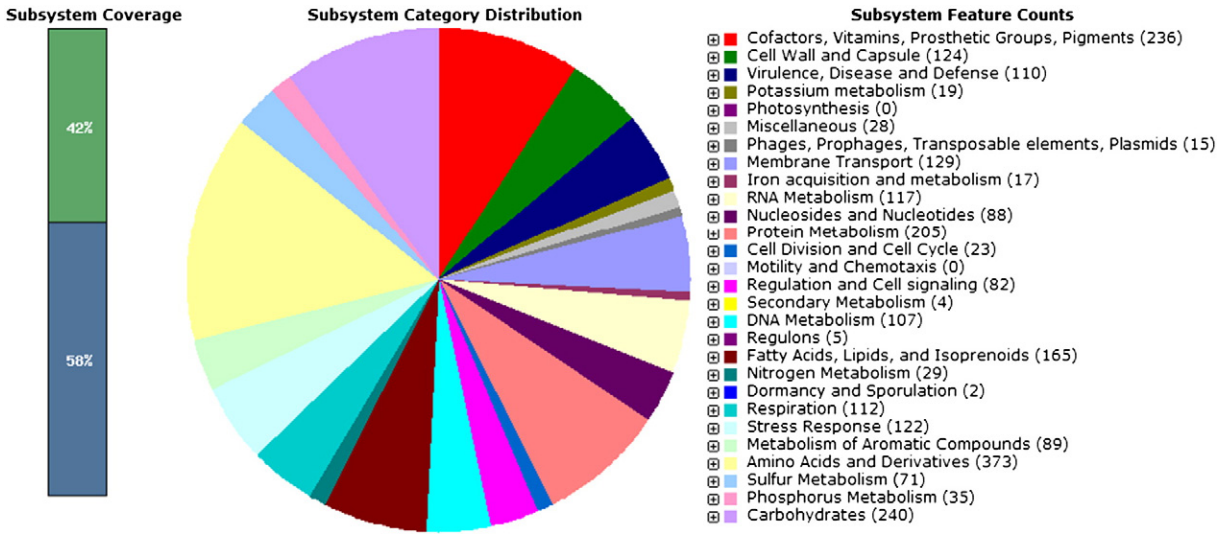

Fig. 2. Sub-system distribution of strain *A. gyllenbergii* strain MTCC 11365^T (based on RAST annotation server).

11365^T as *Acinetobacter junii* SH205 (score 510) followed by *Acinetobacter baumanii* ACICU (score 483), *Acinetobacter baumanii* AB0057 (score 453) and *Acinetobacter* sp. DR1 (score 451).

Nucleotide sequence accession number

The *A. gyllenbergii* strain MTCC 11365^T whole genome shot gun (WGS) project has been deposited at DDBJ/EMBL/GenBank under the project accession ASQH00000000 of the project (01) has the accession numbers ASHQ01000000 and consists of sequences ASQH01000001–ASQH01000048.

Conflict of interest

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

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