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Data in Brief

Genome sequencing and annotation of *Acinetobacter junii* strain MTCC 11364

Indu Khatri [b,1], Nitin Kumar Singh [a,1], Srikrishna Subramanian [b,*], Shanmugam Mayilraj [a,*]

[a] Microbial Type Culture Collection and Gene Bank (MTCC), CSIR — Institute of Microbial Technology, Chandigarh 160036, India
[b] Protein Science and Engineering, CSIR — Institute of Microbial Technology, Chandigarh 160036, India

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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 3.5 Mb draft genome of the *Acinetobacter junii* strain MTCC 11364. The genome has a G + C content of 38.0% and includes 3 rRNA genes (5S, 23S, 16S) and 64 aminoacyl-tRNA synthetase genes.

Specifications	
Organism/cell line/tissue	*Acinetobacter junii*
Strain(s)	MTCC 11364
Sequencer or array type	Sequencer; the Illumina-HiSeq 1000
Data format	Processed
Experimental factors	Microbial strain
Experimental features	Whole genome sequencing of *A. junii* strain MTCC 11364, assembly and annotation
Consent	n/a

Direct link to the data

Direct link: http://www.ncbi.nlm.nih.gov/nuccore/ASYZ00000000.

Genus *Acinetobacter* was proposed by Brisou and Prévot in 1954 [1]. This genus comprises of 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. *Acinetobacter junii* was proposed by Bouvet and Grimont in 1986 [3]; it was isolated from human clinical specimens, with characteristics corresponding to those of the genus *Acinetobacter*. The organism in this study is *A. junii* strain MTCC 11364 equivalent to DSM 14968 (= CIP 107470) isolated from wastewater treatment plant. This organism was previously known as *Acinetobacter grimontii* [4], and was further re-classified as a later synonym of *A. junii* by Vaneechoutte et al. in 2008 [5].

A. junii strain MTCC 11364 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. in 2006 [6]. To determine the phylogenetic relationship of strain MTCC 11364, 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 [7] and aligned using mega version 5.0 [8]. 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. junii* MTCC 11364 was sequenced using the Illumina-HiSeq 1000 technology. Sequencing resulted in 29,216,732 paired-end reads (insert size of 350 bp) of length 101 bp. A total of 28,584,052 high-quality reads with approximately 810× coverage

* Corresponding authors at: CSIR — Institute of Microbial Technology (IMTECH), Sector 39-A, Chandigarh 160036, India. Tel.: +91 1726665483, +91 172 6665166; fax: +91 172 2695215.
E-mail addresses: krishna@imtech.res.in (S. Subramanian), mayil@imtech.res.in (S. Mayilraj).
[1] Both are first authors.

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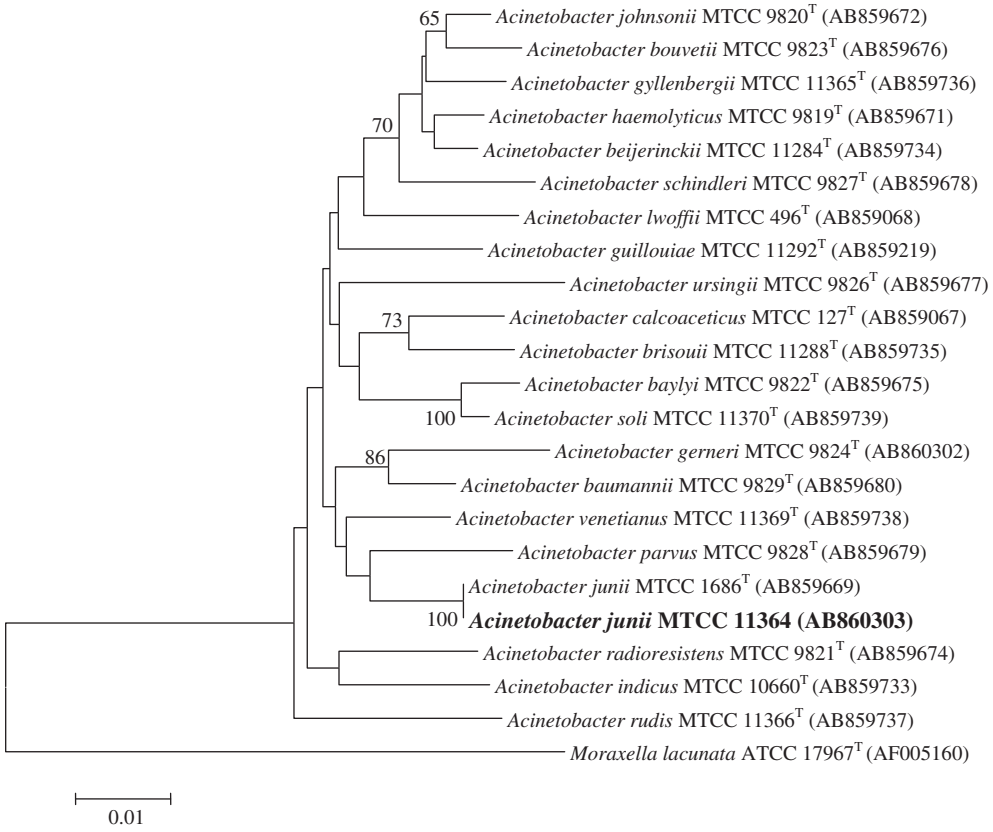

Fig. 1. Phylogenetic tree constructed using the neighbor-joining algorithm, shows the position of *A. junii* strain MTCC 11364 relative to the type strains of the other species within the genus *Acinetobacter*.

were assembled with CLCbio wb6 (word size 40 and bubble size 60) to obtain 248 contigs (N_{50}, 24,956 bp) with 3,549,566 bp and an average G + C content of 38.0%. The functional annotation was carried out by RAST (Rapid Annotation using Subsystem Technology) [9], Fig. 2 shows the subsystem distribution of strain *A. junii* strain MTCC 11364, tRNA was predicted by tRNAscan-SE 1.23 [10] and rRNA genes by RNAmmer 1.2 [11]. The genome includes 3 rRNA genes (5S, 23S, 16S) and 64 aminoacyl-tRNA synthetase genes.

A total of 3294 coding regions (1605 genes transcribed from the positive strand and 1689 from the negative strand) were found in the genome, of which 2332 (71%) could be functionally annotated. The genome coding density is 86% with an average gene length of 907 bp. The annotated genome has 77 genes responsible for resistance to antibiotic and toxic compounds including 10 genes for MDR efflux pumps. One hundred and one genes code for membrane transport proteins. Fifty one genes code for proteins that are involved in oxidative stress

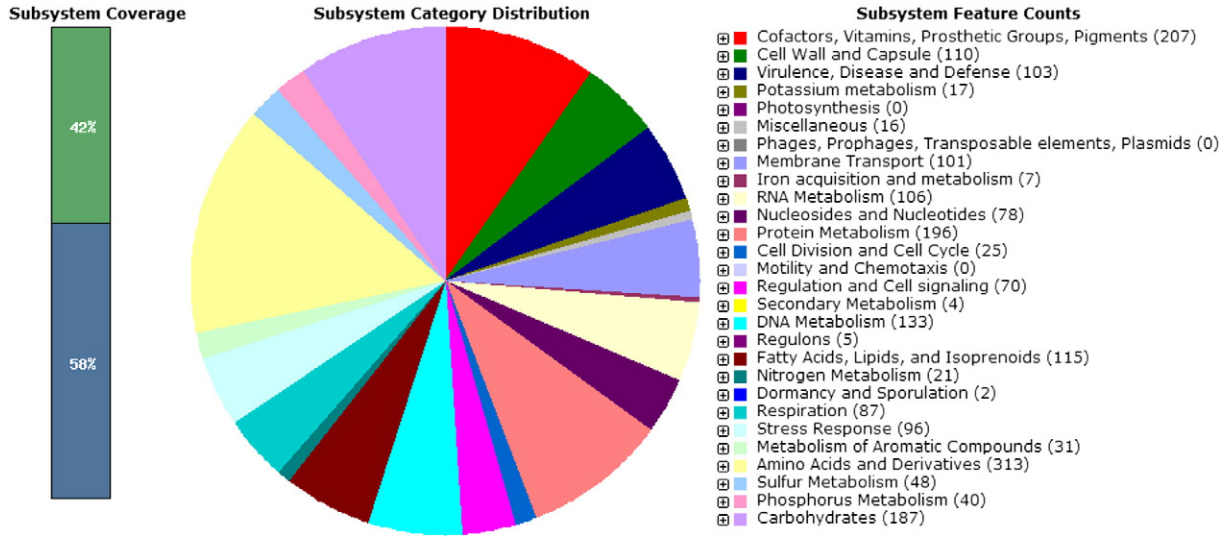

Fig. 2. Sub-system distribution of strain *A. junii* strain MTCC 11364 (based on RAST annotation server).

response, seven genes for osmotic stress response, fifteen genes for heat shock and several more genes for various other stress responses, to make a total of 96 genes involved in stress response.

The functional comparison of genome sequences available on the RAST server revealed the closest neighbors of *A. junii* MTCC 11364 as *A. junii* SH205 (score 512) followed by *Acinetobacter baumanii* ACICU (score 485), *Acinetobacter haemolyticus* ATCC 19194 (score 471) and *A. baumanii* AB0057 (score 465).

Nucleotide sequence accession number

The *A. junii* strain MTCC 11364 whole genome shot gun (WGS) project has been deposited at DDBJ/EMBL/GenBank under the project accession ASYZ00000000 of the project (01) that has the accession number ASYZ01000000 and consists of sequences ASYZ01000001-ASYZ01000248.

Conflict of interest

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

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