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Data in Brief

Genome sequencing and annotation of *Acinetobacter guillouiae* strain MSP 4-18

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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 4.8 Mb genome of *Acinetobacter guillouiae* MSP 4-18, isolated from a mangrove soil sample from Parangipettai (11°30′N, 79°47′E), Tamil Nadu, India. The draft genome of *A. guillouiae* MSP 4-18 has a G + C content of 38.0% and includes 3 rRNA genes (5S, 23S, 16S) and 69 aminoacyl-tRNA synthetase genes.

Specifications	
Organism/cell line/tissue	*Acinetobacter guillouiae*
Strain(s)	MSP 4-18
Sequencer or array type	Sequencer; the Illumina-HiSeq 1000
Data format	Processed
Experimental factors	Microbial strain
Experimental features	Whole genome sequencing of *A. guillouiae* strain MSP 4-18, assembly and annotation
Consent	n/a

Direct link to the data

Direct link: http://www.ncbi.nlm.nih.gov/nuccore/ASQG00000000.

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 DNA G + C content of 39.0% to 47.0% [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 guillouiae* proposed by Nemec et al. [3] was isolated from sewage-containing gas-work effluent and shares characteristics corresponding to those of the genus *Acinetobacter*.

A. guillouiae strain MSP 4-18, isolated from a mangrove soil sample from Parangipettai (11°30′N, 79°47′E), Tamil Nadu, India, was 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. Amplification and sequencing of 16S rRNA was performed as described by Mayilraj et al. [4]. Identification was confirmed using 16S rRNA sequencing. To determine the phylogenetic relationship of strain MSP4-18, 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. guillouiae* MSP 4-18 was sequenced using the Illumina-HiSeq 1000 technology. Sequencing resulted in 26,685,818 paired-end reads (insert size of 350 bp) with a length of 101 bp. A total of 26,465,246 high-quality reads with approximately 550× coverage were assembled with CLCbio wb6 (word size 40 and bubble size 60) to obtain 94 contigs (N_{50}, 128,068 bp) of 4,848,959 bp and average

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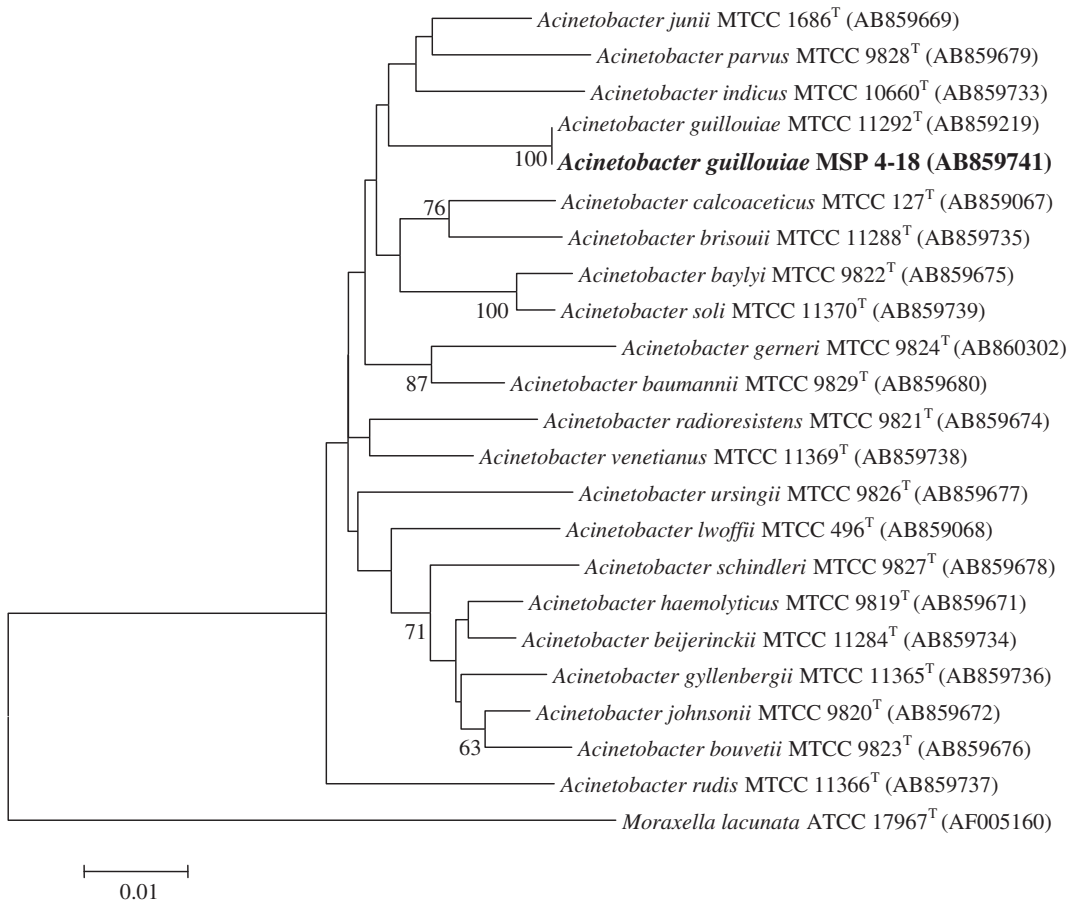

Fig. 1. Phylogenetic tree constructed using the neighbor-joining algorithm, shows the position of *A. guillouiae* MSP 4-18 relative to the type strains of the other species within the genus *Acinetobacter*.

G + C content of 38.0%. The functional annotation was carried out by RAST (Rapid Annotation using Subsystem Technology) [7], Fig. 2 shows the subsystem distribution of *A. guillouiae* strain MSP 4-18, 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 69 aminoacyl-tRNA synthetase genes. A total of 4543 coding regions (2294 genes transcribed from the positive strand and 2249 from the negative strand) were found in the genome, of which 3052 (67%) could be functionally annotated. The genome coding density is 83% with an average gene length of 883 bp. The annotated genome has 106 genes responsible for resistance to antibiotic and toxic compounds including 13 genes for MDR efflux pumps. One hundred and forty one genes code for membrane transport proteins. Sixty five genes are involved in oxidative stress, 12 in osmotic stress, 15 for heat shock and

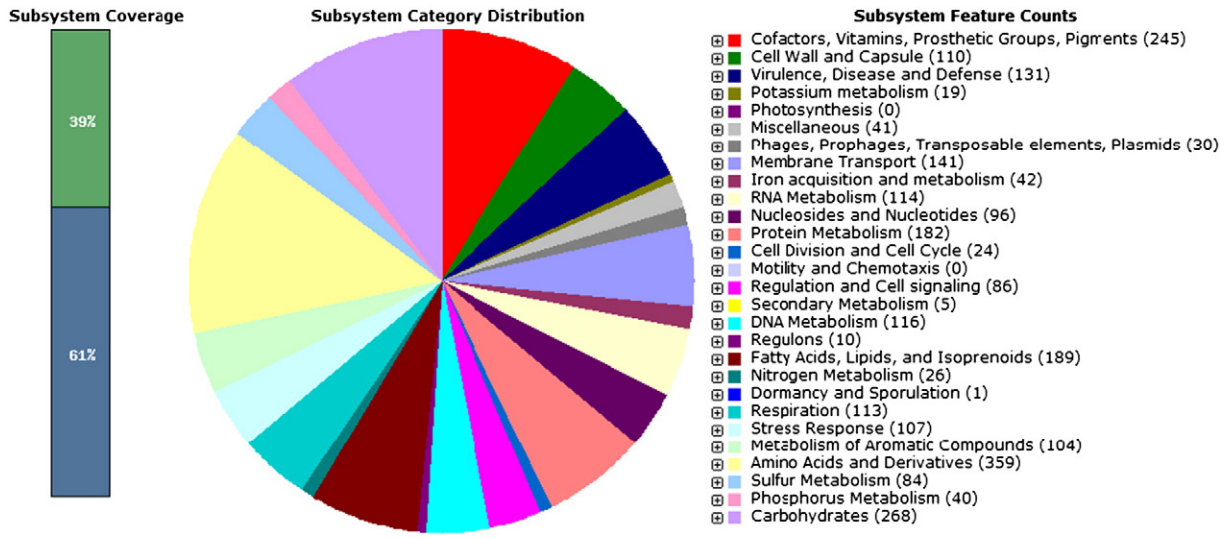

Fig. 2. Sub-system distribution of *A. guillouiae* strain MSP 4-18 (based on RAST annotation server).

several others for response to various other stresses, to make a total of 107 genes responsible for stress response in this organism.

The functional comparison of the genome sequences available on the RAST server revealed the closest neighbors of *A. guillouiae* MSP 4-18 as *Acinetobacter baumanii* AB0057 (score 502) followed by *A. baumanii* AYE (score 500), *Acinetobacter johnsonii* SH046 (score 494) and *A. baumanii* ACICU (score 494).

Nucleotide sequence accession number

The *A. guillouiae* MSP 4-18 whole genome shot gun (WGS) project which has been deposited at DDBJ/EMBL/GenBank under the project accession ASQG00000000 of the project (01) has the accession number ASQG01000000 and consists of sequences ASQG01000001ASQG01000094.

Conflict of interest

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

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