Genomics Data 2 (2014) 10–12

Contents lists available at ScienceDirect

Genomics Data

journal homepage: http://www.journals.elsevier.com/genomics-data/

Data in Brief

Genome sequencing and annotation of *Acinetobacter haemolyticus* strain MTCC 9819^T

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ARTICLE INFO

Article history:
Received 17 September 2013
Received in revised form 23 October 2013
Accepted 23 October 2013
Available online 27 November 2013

Keywords:
Acinetobacter haemolyticus strain MTCC 9819^T
Whole genome
Illumina-HiSeq 1000 technology
CLCbio wb6
Rapid annotations using subsystems technology (RAST)

ABSTRACT

The genus *Acinetobacter* consists of 31 validly published species ubiquitously distributed in nature and primarily associated with nosocomial infection. We report the 3.4 Mb genome of *Acinetobacter haemolyticus* strain MTCC 9819^T. The genome has a G + C content of 40.0% and includes 3 rRNA genes (5S, 23S, 16S) and 65 aminoacyl-tRNA synthetase genes.

Specifications	
Organism/cell line/tissue	*Acinetobacter haemolyticus*
Strain(s)	MTCC 9819^T
Sequencer or array type	Sequencer; the Illumina-HiSeq 1000
Data format	Processed
Experimental factors	Microbial strain
Experimental features	Whole genome sequencing of *A. haemolyticus* strain MTCC 9819^T, assembly and annotation
Consent	n/a

Direct link to the data

Direct link: http://www.ncbi.nlm.nih.gov/nuccore/ASYX00000000.

Genus *Acinetobacter* was proposed by Brisou and Pre'vot in 1954 [1]. This genus comprises Gram-negative, strictly aerobic, nonfermenting, nonfastidious, nonmotile, 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 haemolyticus* was proposed by Bouvet and Grimont 1986 [3]; it was isolated from human clinical specimens and environment, with characteristics corresponding to those of the genus *Acinetobacter*. The organism in this study is *Acinetobacter haemolyticus* strain MTCC 9819^T equivalent to DSM 6962 (=ATCC 17906, CIP 64.3, NCTC 10305).

A. haemolyticus strain MTCC 9819^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 was performed as described by Mayilraj et al. 2006 [4]. To determine the phylogenetic relationship of strain MTCC 9819^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. haemolyticus* strain MTCC 9819^T was sequenced using Illumina-HiSeq 1000 technology. Sequencing resulted in 5,755,416 paired-end reads (insert size of 350 bp) of length 101 bp. A total of 5,580,067 high-quality reads with approximately 166× coverage were assembled with CLCbio wb6 (word size = 50 and bubble size = 100) and to obtain 182 contigs (N_{50}, 57,666 bp) of 3,384,229 bp with an average GC content of 40%. The functional annotation was carried out by RAST

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http://dx.doi.org/10.1016/j.gdata.2013.10.004

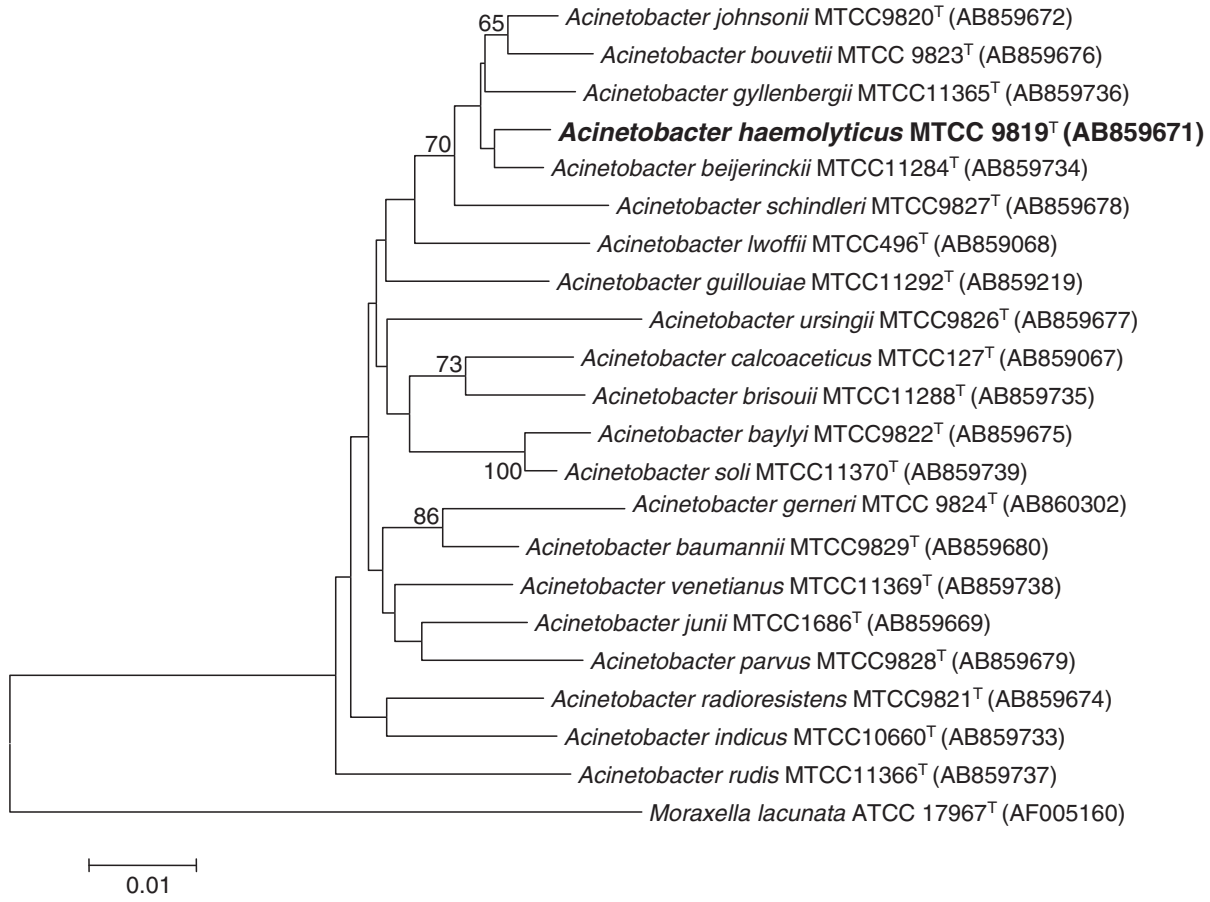

Fig. 1. Phylogenetic tree constructed using the neighbor-joining algorithm, shows the position of *A. haemolyticus* strain MTCC 9819^T relative to the type strains of the other species within the genus *Acinetobacter*.

(rapid annotation using subsystem technology) [7], Fig. 2 shows the subsystem distribution of strain *A. haemolyticus* strain MTCC 9819^T, and 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 65 aminoacyl-tRNA synthetase genes. A total of 3122 coding regions (1546 transcribed from the positive strand and 1576 from the negative strand) were found in the genome, of which 2298 (74%) could be functionally annotated. The genome coding density is 87% with an average gene length of 911 bp. The annotated genome has 65 genes responsible for resistance to antibiotic and toxic compounds including 13 genes for MDR efflux pumps. One hundred and six genes code for membrane transport proteins. Forty four genes are involved in response to

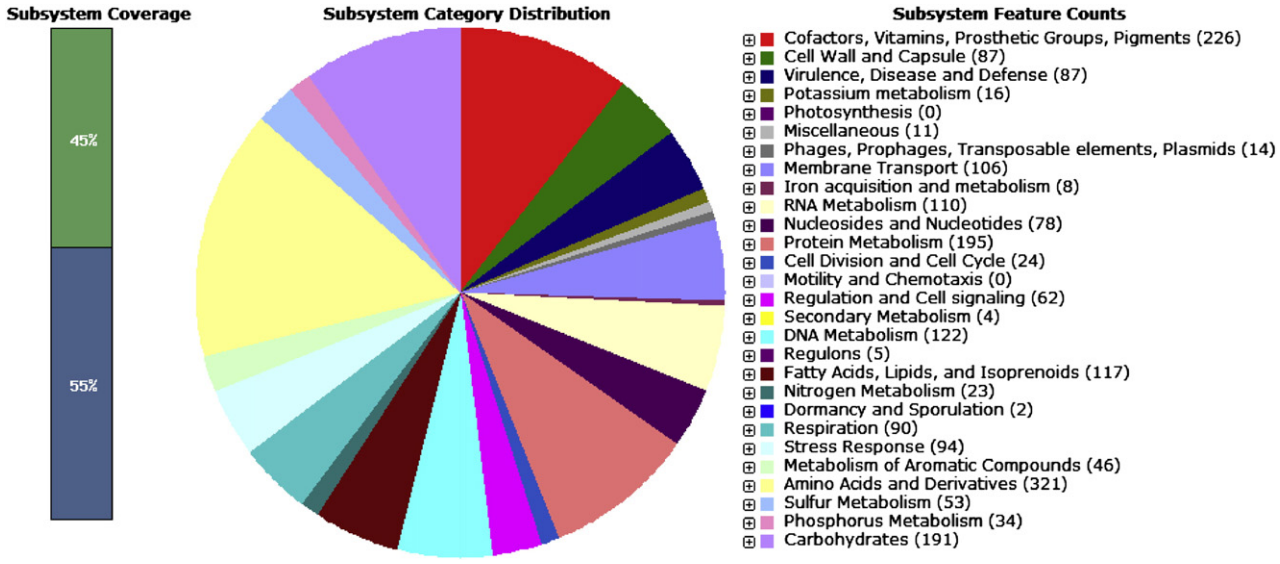

Fig. 2. Sub-system distribution of strain *A. haemolyticus* strain MTCC 9819^T (based on RAST annotation server).

oxidative stress, 10 for osmotic stress response and 16 genes for heat shock and many more stress responses, all summed up to 94 genes for stress response are present.

The functional comparison of genome sequences available on the RAST server revealed the closest neighbors of *A. haemolyticus* strain MTCC 9819^T as *Acinetobacter junii* SH205 (score 503) followed by *Acinetobacter baumanii* ACICU (score 489), *Acinetobacter haemolyticus* ATCC 19194 (score 476) and *Acinetobacter baumanii* AB0057 (score 453).

Nucleotide sequence accession number

The *A. haemolyticus* strain MTCC 9819^T whole genome shot gun (WGS) project has been deposited at DDBJ/EMBL/GenBank under the project accession ASYX00000000 of project (01) which has the accession numbers ASYX01000000 and consists of sequences ASYX01000001 ASYX01000182.

Conflict of interest

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

Acknowledgments

This work was funded by CSIR-IMTECH. N.K.S. is supported by a University Grant Commission (UGC) fellowship, and I.K. is supported by a research fellowship from CSIR. We thank the Sandor next-generation genomics facility for the help in obtaining the genome sequence. This is IMTECH communication number 0107/2013.

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