Data in Brief

Genome sequencing and annotation of Acinetobacter gyllenbergii strain MTCC 11365T

Nitin Kumar Singh, Indu Khatri, Srikrishna Subramanian, Shanmugam Mayilraj

A R T I C L E   I N F O

Article history:
Received 17 September 2013
Received in revised form 22 October 2013
Accepted 23 October 2013
Available online 28 November 2013

Keywords:
Acinetobacter gyllenbergii strain MTCC 11365T
Whole genome
Illumina-HiSeq 1000 technology
CLCbio wb6
Rapid annotations using subsystems technology (RAST)

A B S T R A C T

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 11365T. 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.

© 2013 The Authors. Published by Elsevier Inc. This is an open access article under the CC BY-NC-ND license (http://creativecommons.org/licenses/by-nc-nd/3.0/).

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 Ezube'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 11365T equivalent to DSM 22705T (= CCM 7267T = CCUG 51248T = NIPH 2150T).

A. gyllenbergii strain MTCC 11365T 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 11365T, 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 11365T 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 (N50, 212,525 bp) of 4,318,988 bp and average G + C content of 41.0%.
The functional annotation was carried out by RAST (rapid annotation using subsystem technology) [7]. Fig. 2 shows the subsystem distribution of strain A. gyllenbergii strain MTCC 11365T. 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 11365T relative to the type strains of the other species within the genus Acinetobacter.

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

Fig. 2. Sub-system distribution of strain A. gyllenbergii strain MTCC 11365T (based on RAST annotation server).
11365T 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 11365T whole genome shot gun (WGS) project has been deposited at DDBJ/EMBL/GenBank under the project accession ASHQ00000000 of the project (01) has the accession numbers ASHQ01000000 and consists of sequences ASHQ01000001–ASHQ01000048.

**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. and I.K. are supported by a University Grants Commission (UGC) fellowship. We thank the C-CAMP (http://www.ccamp.res.in/) next-generation genomics facility for help in obtaining the genome sequence. This is IMTECH communication number 0105/2013.

**References**

[1] J. Brisou, A.R. Prevot, Etudes de systematique bacterienne. X. Revision des especes reunies dans le genre Achromobacter. Ann. Inst. Pasteur 86 (1954) 722–728.
[2] A.Y. Peleg, H. Seifert, D.L. Paterson, *Acinetobacter baumanii*: emergence of a successful pathogen. Clin. Microbiol. Rev. 21 (2008) 538–582.
[3] A. Nemec, M. Musilek, M. Maixnerová, T.D. Baere, T.J.K. van der Reijden, M. Vaneechoutte, L. Dijkshoorn, Acinetobacter beijerinckii sp. nov. and Acinetobacter gyllenbergii sp. nov., haemolytic organisms isolated from humans. Int. J. Syst. Evol. Microbiol. 59 (2009) 118–124.
[4] S. Mayilraj, P. Saha, S. Korole, H.S. Saini, *Omnithinicrobium kibberense* sp. nov. isolated from the Himalayas, India. Int. J. Syst. Evol. Microbiol. 56 (2006) 1657–1661.
[5] O. Kim, Y.J. Cho, K. Lee, S.H. Yoon, M. Kim, H. Na, S.C. Park, Y.S. Jeon, J.H. Lee, H. Yi, S. Won, J. Chun, Introducing EzTaxon-e: a prokaryotic 16S rRNA gene sequence database with phylotypes that represent uncultured species. Int. J. Syst. Evol. Microbiol. 62 (2012) 716–721.
[6] K. Tamura, D. Peterson, N. Peterson, G. Stecher, M. Nei, S. Kumar, MEGAS: molecular evolutionary genetics analysis using maximum likelihood, evolutionary distance, and maximum parsimony methods. Mol. Biol. Evol. 28 (2011) 2731–2739.
[7] R.K. Aziz, D. Bartels, A.A. Best, M. DeJongh, T. Disz, R.A. Edwards, K. Formsma, S. Gerdes, E.M. Glass, M. Kubal, F. Meyer, G.J. Olsen, R. Olson, A.L. Osterman, R.A. Overbeek, L.K. McNeil, D. Paarmann, T. Paczian, B. Parrello, G.D. Pusch, C. Reich, R. Stevens, O. Vassieva, V. Vonstein, A. Wilke, O. Zagnitko, The RAST server: rapid annotations using subsystems technology. BMC Genomics 9 (2008) 75.
[8] T.M. Lowe, S.R. Eddy, tRNAscan-SE: a program for improved detection of transfer RNA genes in genomic sequence. Nucleic Acids Res. 25 (1997) 955–964.
[9] K. Lagesen, P. Hallin, E.A. Rudland, H.H. Staerfeldt, T. Rognes, D.W. Ussery, RNAmer: consistent annotation of rRNA genes in genomic sequences. Nucleic Acids Res. 35 (2007) 3100–3108.