Genomics Data 11 (2017) 1–2

Contents lists available at ScienceDirect

Genomics Data

journal homepage: www.elsevier.com/locate/gdata

Draft genome sequence of *Thermoactinomyces sp.* Gus2-1 isolated from the hot-spring Gusikha in Bargusin Valley (Baikal Rift Zone, Russia)

Aleksey S. Rozanov *, Alla V. Bryanskaya, Anastasia V. Kotenko, Sergey E. Peltek

Federal Research Center "Institute of Cytology and Genetics of the Siberian Branch of the RAS", Novosibirsk, Russia

ARTICLE INFO

Article history:
Received 24 October 2016
Received in revised form 3 November 2016
Accepted 9 November 2016
Available online 14 November 2016

ABSTRACT

The *Thermoactinomyces* sp. strain Gus2-1 was isolated from hot-spring sediments sample from the hot-spring Gusikha in Bargusin Valley (Baikal Rift Zone, Russia). The sequenced and annotated genome is 2,623,309 bp and encodes 2513 genes. The draft genome sequence of the *Thermoactinomyces* sp. strain Gus2-1 has been deposited at DDBJ/EMBL/GenBank under the accession JPZM01000000 and the sequences could be found at the site https://www.ncbi.nlm.nih.gov/nuccore/JPZM01000000.

Specifications	
Organism/cell line/tissue	*Thermoactinomyces sp.* Gus2–1
Sex	–
Sequencer or array type	Ion PGM™ Template OT2 400 kits
Data format	Processed
Experimental factors	Bacteria
Experimental features	Whole genome sequence of *N. lepida*, assembly and annotation
Consent	Level of consent allowed for reuse if applicable
Sample source location	The hot-spring Gusikha (60 °C) in Bargusin Valley (Baikal Rift Zone, Russia)

1. Direct link to deposited data

https://www.ncbi.nlm.nih.gov/nuccore/JPZM01000000.

2. Introduction

The genus *Thermoactinomyces* is one of the earliest known Actinomycete taxa, and the type species of this genus is *Thermoactinomyces vulgaris* [1]. The members of this genus are aerobic, endospore-forming, Gram-positive bacteria belonging to the order *Bacillales* [2]. They produce endospores that are formed endogenously inside the aerial and substrate hyphae of the bacteria [3]. Currently, researchers are finding new species belonging to this genus [4].

3. Strain isolation

The strain Gus2-1 was isolated from sediments sample from the hot-spring Gusikha (60 °C) in Bargusin Valley (Baikal Rift Zone, Russia). *Thermoactinomyces sp.* Gus2-1 culture was cultivated in liquid medium containing 1% trypton, 0.5% yeast extract, and 3.5 M of NaCl. Eight ml of cell culture were pelleted by centrifugation and resuspended in 75 μl of H_2O by intense pipetting.

4. DNA isolation and sequencing

DNA was isolated using the DNA Purification Kit (Fermentas). Ion PGM™ Template OT2 400 and Ion PGM™ Template OT2 400 kits were used to create libraries for genome sequencing. Genome sequencing was performed on an IonTorrent platform (Applied Biosistems) using Ion PGM™ Sequencing 400 Kit in the SBRAS Sequencing Center.

5. Genome assembly and annotation

De novo assembly of short reads into contigs was performed using MIRA v. 4. Contigs shorter than 1000 bp were deleted. A total of 92 contigs yielded a genome sequence 2,623,309 bp long, and the G + C content is 48.01%. ORF prediction and automatic annotation was performed using NCBI PGAAP (http://www.ncbi.nlm.nih.gov/genome/annotation_prok). The complete genome sequence contained 2513 genes, 2315 CDS, 14 rRNAs (5S, 16S, 23S), 76 tRNAs, one ncRNA.

6. Phylogenetic analysis

Phylogenetic analysis was performed using 16S rRNA sequences with the UPGMA algorithm implemented in MEGA v.6. 16S rRNA

* Corresponding author at: Federal Research Center "Institute of Cytology and Genetics of the Siberian Branch of the RAS", Lavrentieva Ave., 10, Novosibirsk 630090, Russia.
E-mail address: sibiryak.n@gmail.com (A.S. Rozanov).

http://dx.doi.org/10.1016/j.gdata.2016.11.014

sequences of *Thermoactinomyces* type strains were found using the StrainInfo (www.straininfo.net) and GenBank (www.ncbi.nlm.nih.gov/nucleotide) databases. According to phylogenetic analysis, the *Thermoactinomyces* sp. strain Gus2-1 is most closely related to *Thermoactinomyces vulgaris*.

7. Nucleotide sequence accession numbers

The draft genome sequence for *Thermoactinomyces* sp. strain Gus2-1 has been deposited in DDBJ/EMBL/Genbank under the accession no. JPZM01000000. The 92 contigs have been deposited under accession no. JPZM01000001-JPZM01000092.

Conflict of interest

The authors declare that there is no conflict of interests with respect to the work published in this paper.

Acknowledgments

This work was supported by the Federal Agency of Scientific Organizations *via* the Institute of Cytology and Genetics SB RAS (project # 0324-2016-0004).

References

[1] P. Tsiklinsky, Sur les mucedinees thermophiles. Ann. Inst. Pasteur 13 (1899) 500–505.
[2] S.A. Waksman, C.T. Corke, Thermoactinomyces tsiklinsky, a genus of thermophilic actinomycetes. J. Bacteriol. 66 (4) (1953) 377.
[3] J.C. Ensign, Formation, properties, and germination of actinomycete spores. Annu. Rev. Microbiol. 32 (1) (1978) 185–219.
[4] S. Yao, Y. Liu, M. Zhang, X. Zhang, H. Li, T. Zhao, C. Xin, L. Xu, B. Zhang, C. Chi, Thermoactinomyces daqus sp. nov., a thermophilic bacterium isolated from high-temperature Daqu. Int. J. Syst. Evol. Microbiol. 64 (1) (2014) 206–210.