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Data in Brief

Genome sequence of carboxylesterase, carboxylase and xylose isomerase producing alkaliphilic haloarchaeon *Haloterrigena turkmenica* WANU15

Samy Selim [a,b,*], Nashwa Hagagy [b]

[a] Department of Clinical Laboratory Sciences, College of Applied Medical Sciences, Aljouf University, Sakaka, P.O. 2014, Saudi Arabia
[b] Microbiology and Botany Department, Faculty of Science, Suez Canal University, Ismailia, P.O. 41522, Egypt

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ABSTRACT

We report draft genome sequence of *Haloterrigena turkmenica* strain WANU15, isolated from Soda Lake. The draft genome size is 2,950,899 bp with a G + C content of 64% and contains 49 RNA sequence. The genome sequence can be accessed at DDBJ/EMBL/GenBank under the accession no. LKCV00000000.

Specifications	
Organism	*Haloterrigena turkmenica*
Strain(s)	WANU15
Sequencer or array type	Sequencer; Roche 454
Data format	Processed
Experimental factors	Microbial strains
Experimental features	Draft genome sequence of *Haloterrigena turkmenica* WANU15 assembly and annotation
Consent	N/A
Sample source location	Soda Lake

1. Direct link to deposited data

http://www.ncbi.nlm.nih.gov/bioproject/?term=LKCV00000000

2. Introduction

Haloterrigena turkmenica (Zvyagintseva and Tarasov 1987) Ventosa et al. 1999, comb. nov. is the type species of the genus *Haloterrigena* in the euryarchaeal family *Halobacteriaceae.* It is of phylogenetic interest because of the yet unclear position of the genera *Haloterrigena* and *Natrinema* within the *Halobacteriaceae*, which created some taxonomic problems historically [1]. *H. turkmenica* WANU15 strain was isolated from sediment samples collected from Soda Lake. Here we describe the features of this organism, together with the complete genome sequence, and annotation.

2.1. Experimental design, materials and methods

H. turkmenica WANU15 strain was isolated on a complex medium described by Wallace (2008) [2] (Horikoshi medium) containing (gm/L^{-1}) glucose (10 g), peptone (5 g), yeast extract (5 g), K_2HPO_4 (1 g), $MgSO_4 \cdot 7H_2O$ (0.2 g), $NaCO_3$ (15 g) and NaCl (200 g). The pH was adjusted to 10 with 1 M NaOH. Solid medium was prepared by adding 2.0 (*w*/*v*) Bacto-agar (Difco). The incubation was at 37 °C for 7–21 days. A pure culture was obtained by repeated restreaking. Phenotypic tests were performed in accordance with the proposed minimal standards for the description of new taxa in the order *Halobacteriales* [3]. Cell morphology was examined using phase-contrast microscopy (Zeiss). Gram staining was performed as described by Dussault (1955) [4] and motility was examined on semi-solid agar. Optimal conditions for growth were determined in medium described by Tindall et al. (1980) [5], containing 0–30% (*w*/*v*) NaCl, and the pH range for growth was assayed with pH values of 5, 6, 7, 8, 8.5, 9, 9.5, 10, 11 and 12, and at different temperatures (4, 10, 20, 30, 40, 45, 50, 55 and 60 °C). Haloalkaliphilic minimal medium was used for all biochemical tests; this medium was developed by Mwatha and Grant (1993) [6], with the following composition, yeast extract, 1 g; KNO_3 1 g; KH_2PO_4, 1 g; $MgSO_4 \cdot 7H_2O$, 0.2 g; NaCl, 150 g; Na_2CO_3, 18 g; pH was adjusted to 9. Hydrolysis of starch, casein, gelatin, Tween 80; cellulose, nitrate reduction; production of indole and H_2S; catalase and oxidase activities; and utilization of sugars were evaluated. Genomic DNA was extracted

* Corresponding author at: Department of Clinical Laboratory Sciences, College of Applied Medical Sciences, Aljouf University, Sakaka, P.O. 2014, Saudi Arabia.
E-mail address: sadomm2003@yahoo.com (S. Selim).

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Table 1
Characteristics that distinguish strain WNU15 from species of the genus *Haloterrigena*. Strains: 1, strain WNU15; 2, *Htg. turkmenica* VKM B-1734 T (data from Ventosa et al., 1999); 3. *Htg. jeotgali* sp. nov. (Roh et al., 2009); 4, *Htg. limicola* (data from Cui et al., 2006); 5, *Htg. longa* (Cui et al., 2006); 6, *Htg. salina* (Gutie'rrez et al., 2008); 7, *Htg. hispanica* (Romano et al., 2007); 8, *Htg. saccharevitans* (Xu et al., 2005a); 9, *Htg. thermotolerans* (Montalvo-Rodri'guez et al., 2000).

Characteristics	1	2	3	4	5	6	7	8	9
Cell shape	Coccobacili	Coccoid	Rods	Rods	Rods	Coccoid	Coccoid	Rods/Coccoid	Rods
Cell size (um)	1.25–2.5	1.5–2.0	0.4–1.0	0.7–2.7	0.6–2.8	1.2–1.6	1.5–2.0	3-10 × 4-1	4-13 × 0.7–1
Motility	−	−	−	+	−	−	−	+	−
NaCl range (M)	2–4.5	›2	2–3.4	›1.7	1.7–5.1	2.5–5	2.2–4	›1.7	2–4.5
Temperature optimum (°C)	40	45	37–45	40–50	41–45	37	50	42–45	50
pH range for growth	8.5–11	7–7.5	7–7.5	7–7.5	7–7.5	7.0–8.0	7	7.5	
Carbohydrates used									
Glucose	+	+	−	−	+	+	−	−	−
Fructose	+	+	+	−	+	+	−	−	−
Sucrose	+	+	−	−	+	−	−	−	−
Ribose	+	+	NR	−	+	−	+	−	−
Mannose	+	+	NR	−	+	−	+	−	−
Formation of indole	+	−	+	−	+	−	+	−	−
Starch hydrolysis	−	−	−	−	−	−	−	−	−
Gelatin hydrolysis	−	−	−	−	−	−	−	−	+
Tween 80 hydrolysis	+	NR	+	+	−	+	NR	+	+
Casein hydrolysis	+	NR	+	NR	−	−	−	−	−
H_2S formation	−	−	NR	NR	+	NR	NR	+	NR
G + C content (mol%)	64%	59.80%	62.30%	61.90%	63.20%	67%	62%	66.60%	63.30%

+, Positive; −, negative; NR, not reported.

from pure culture of archaeal strain and subsequently sequenced using Roche 454 GS (FLX Titanium) pyrosequencing.

2.2. Results and discussion

H. turkmenica WANU15 is Gram-negative, coccobacilli or oval (1.5–2.0 mm in diameter) and non-motile. Colonies on complex agar medium with 3.4 M NaCl are red, elevated and circular. Growth occurs at NaCl concentrations of 2–4.5 M, with an optimum at 3.4 M, and pH values in the range 8.5–11, with an optimum at 9, and at temperatures of 30–60 °C, with an optimum at 40 °C. Oxidase and catalase are positive. Indole is produced. Nitrate reduction is reduced without production of gas. Gelatin and starch are not hydrolysed. Tweens 80, casein and cellulose are hydrolysed. The following substrates are utilized for growth: glycerol, sodium acetate, propionate and citrate. Acid is produced from glucose, mannose, fructose, sucrose, ribose and xylose. Other phenotypic characteristics that distinguish strain WNU15 from different species of the genus *Haloterrigena* are shown in Table 1.

All of the reads were assembled using GS De Novo Assembler version 2.9 (454 life science), which generated 574 contigs with *N*50 20,520 bp. The G + C content was calculated using the draft genome sequence. The G + C content for the draft genome is 64%. The genome contains 49 RNA genes predicted by Rapid Annotation using the Subsystems Technology (RAST) [7] server.

A total of 2959 protein coding sequences in 193 subsystems were functionally annotated by RAST (Fig. 1). Genome analysis revealed that the genome of *H. turkmenica* WANU15 contains various gene clusters for biosynthesis of secondary metabolites and peptides. The genome information displays several enzyme genes encoding carboxylesterase, carboxylase and xylose isomerase. There also exist in the genome multiple genes encoding cellulose and xylanase enzymes.

Functional comparison of genome sequences in the RAST server revealed the closest neighbors of *Halogeometricum borinquense DSM 11551* (score 515) followed by *Haloarcula marismortui* ATCC 43049(score 506), *Halomicrobium mukohataei DSM 12286* (score 501), *Halorhabdus utahensis DSM 12940* (score 497) and *Haloquadratum walsbyi DSM 16790* (score 488).

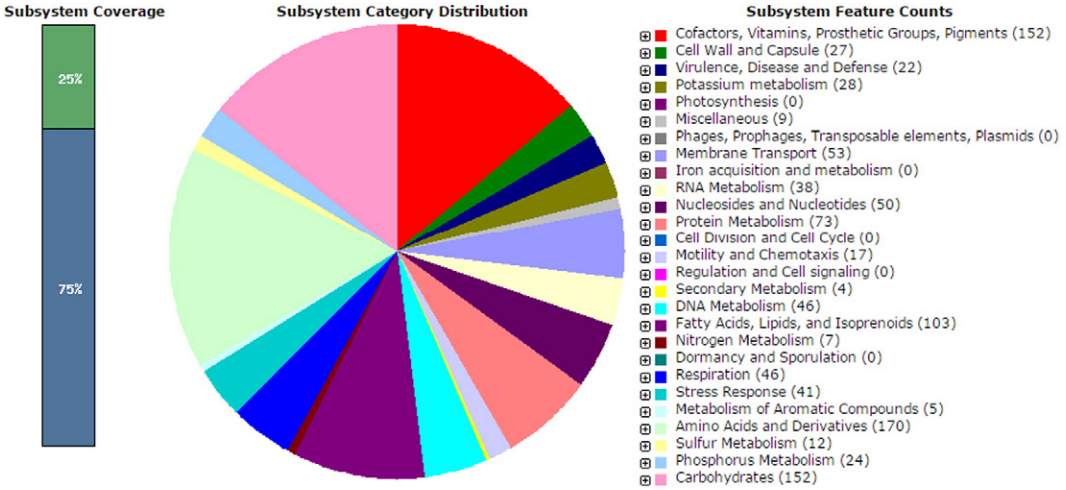

Fig 1. Subsystem distribution of *Haloterrigena turkmenica* strain WANU15 (based on RAST annotation server).

On the other hand, analysis of the complete 16S rRNA sequence in EzTaxonserver (http://www.ezbiocloud.net/eztaxon; [8]) under default settings (with matches only against cultured strains) identified *H. turkmenica*. Overall the various in silico results confirmed that the present environmental isolate is a member of the genus *Haloterrigena*, though further characterization work is required to determine its species.

2.3. Nucleotide sequence accession number

The *H. turkmenica* WANU15 whole genome shotgun project has been deposited in DDBJ/EMBL/GenBank under the accession no LKCV00000000.

Conflict of interest

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

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