genomeA
Journals.ASM.org

Draft Genome Sequence of *Thermus scotoductus* Strain K1, Isolated from a Geothermal Spring in Karvachar, Nagorno Karabakh

Ani Saghatelyan,[a] Lianna Poghosyan,[b] Hovik Panosyan,[a] Nils-Kåre Birkeland[b]

Department of Microbiology, Plants and Microbes Biotechnology, Yerevan State University, Yerevan, Armenia[a]; Department of Biology and Centre for Geobiology, University of Bergen, Bergen, Norway[b]

The 2,379,636-bp draft genome sequence of *Thermus scotoductus* strain K1, isolated from geothermal spring outlet located in the Karvachar region in Nagorno Karabakh is presented. Strain K1 shares about 80% genome sequence similarity with *T. scotoductus* strain SA-01, recovered from a deep gold mine in South Africa.

Received 29 September 2015 **Accepted** 30 September 2015 **Published** 12 November 2015

Citation Saghatelyan A, Poghosyan L, Panosyan H, Birkeland N-K. 2015. Draft genome sequence of *Thermus scotoductus* strain K1, isolated from a geothermal spring in Karvachar, Nagorno Karabakh. Genome Announc 3(6):e01346-15. doi:10.1128/genomeA.01346-15.

Address correspondence to Hovik Panosyan, hpanosyan@ysu.am, or Nils-Kåre Birkeland, nils.birkeland@uib.no.

Bacteria belonging to the extremely thermophilic genus, *Thermus,* have been isolated from geothermal environments and compost with temperatures ranging from 55°C to 75°C (1). These microorganisms are of biotechnological interest due to their production of thermostable enzymes (2) and carotenoid antioxidants (3). They also serve as biological models for elucidating the mechanisms for biological adaptation to high temperatures (4). Although major advances have been made in the last decade, our knowledge of the physiology, geographic distribution, enzymology, and genetics of this group of organisms is still limited. Fifteen species belonging to this genus have been validly described, with *Thermus aquaticus* as the type species (5). Two strains belonging to the species *Thermus scotoductus* have been described; type strain SE-1, isolated from hot tap water in Iceland (6), and strain SA-01, isolated from fissure water with a temperature of about 60°C collected from a South African gold mine 3.2 km below surface (7). Only *T. scotoductus* strain SA-01 has been fully sequenced (8).

We have recently isolated a novel strain of *T. scotoductus* (designated K1) from sludge samples of a neutral 70°C geothermal spring outlet located in the Karvachar region of Nagorno Karabakh (40°17′41″ N, 46°27′50″ E). The strain was isolated on nutrient agar medium containing 0.1% tryptone and 0.1% yeast extract and subsequently cultivated in liquid medium containing 0.1% tryptone and 0.5% yeast extract. It grows optimally around 65°C and pH 8, is catalase and oxidase positive, and can grow anaerobically using nitrate respiration. Strain K1 shares $>99\%$ 16S rRNA sequence identity with strain SA-01. The draft genome of strain K1 was sequenced and assembled with PacBio RS technology and Celera Assembler, respectively, at GATC Biotech, Germany (http://www.gatc-biotech.com). A total of 110,643 reads, accounting for 303,436 kb of sequenced bases were obtained and assembled into 55 contigs comprising a total of 2,379,636 bp, which is slightly larger than the 2,346,803-bp genome of its closest relative, strain SA-01. The G+C content is 65.2%. Average nucleotide identity (ANI) analysis using the online ANI calculator (http://enve-omics.ce.gatech.edu/ani/index) and DNA:DNA hybridization analysis using the Genome-to-Genome Distance Calculator (http://ggdc.dsmz.de/distcalc2.php) revealed a two-way ANI value of 97.55% and 80.70% overall genome homology, respectively, between the K1and SA-01 strains, supporting their affiliation to the same species.

Gene prediction carried out with the NCBI Prokaryotic Genome Annotation Pipeline (9), as well as the RAST server (http://rast.nmpdr.org/rast.cgi), identified a total of 2,529 genes, including 2,104 coding DNA sequences, 3 sets of rRNA genes, 48 tRNA genes, and 2 ncRNA genes. The rRNA genes are unlinked, and located in separate 16S and 23/5S rRNA genes/operons, as is generally the case in *Thermus* spp. (10, 11). Two CRISPR arrays were identified. Genome-based knowledge of thermophilic microbes is of great importance and interest for assessing the diversity of enzymes of biotechnological importance and revealing their adaptation mechanisms to extreme conditions.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number LJJR00000000. The version described in this paper is the first version, LJJR01000000.

ACKNOWLEDGMENT

The work was funded by the Norwegian Centre for International Cooperation in Education (grant no. CPEALA-2014/10068; Cooperation in environmental microbiology between Armenia and Norway), within the framework of the Norwegian Cooperation Programme in Higher Education with Eurasia.

REFERENCES

1. **Da Costa MS, Rainey FA, Nobre MF**. 2006. The genus *Thermus* and relatives, p 797–812. *In* Dworkin M, Falkow S, Rosenberg E, Schleifer KH, Stackebrandt E (ed), The prokaryotes: a handbook on the biology of bacteria, vol 7, 3rd ed., vol 7. Springer, New York, NY.
2. **Bruins ME, Janssen AEM, Boom RM**. 2001. Thermozymes and their applications. Appl Biochem Biotechnol **90:**155–186. http://dx.doi.org/10.1385/abab:90:2:155.
3. **Mandelli F, Miranda VS, Rodrigues E, Mercadante AZ**. 2012. Identification of carotenoids with high antioxidant capacity produced by extremophile microorganisms. World J Microbiol Biotechnol **28:**1781–1790. http://dx.doi.org/10.1007/s11274-011-0993-y.

4. **Cava F, Hidalgo A, Berenguer J.** 2009. *Thermus thermophilus* as biological model. Extremophiles **13:**213–231. http://dx.doi.org/10.1007/s00792-009-0226-6.
5. **Brock TD, Freeze H.** 1969. *Thermus aquaticus* gen. n. and sp. n., a nonsporulating extreme thermophile. J Bacteriol **98:**289–297.
6. **Kristjánsson JK, Hjörleifsdóttir S, Marteinsson VT, Alfredsson GA.** 1994. *Thermus scotoductus*, sp. nov., a pigment-producing thermophilic bacterium from hot tap water in Iceland and including *Thermus* sp. X-1. Syst Appl Microbiol **17:**44–50. http://dx.doi.org/10.1016/S0723-2020(11)80030-5.
7. **Kieft TL, Fredrickson JK, Onstott TC, Gorby YA, Kostandarithes HM, Bailey TJ, Kennedy DW, Li SW, Plymale AE, Spadoni CM, Gray MS.** 1999. Dissimilatory reduction of Fe(III) and other electron acceptors by a *Thermus* isolate. Appl Environ Microbiol **65:**1214–1221.
8. **Gounder K, Brzuszkiewicz E, Liesegang H, Wollherr A, Daniel R, Gottschalk G, Reva O, Kumwenda B, Srivastava M, Bricio C, Berenguer J, van Heerden E, Litthauer D.** 2011. Sequence of the hyperplastic genome of the naturally competent *Thermus scotoductus* SA-01. BMC Genomics **12:**577. http://dx.doi.org/10.1186/1471-2164-12-577.
9. **Tatusova T, DiCuccio M, Badretdin A, Chetvernin V, Ciufo S, Li W.** 2013. Prokaryotic genome annotation pipeline. *In* Beck J, Benson D, Coleman J, Hoeppner M, Johnson M, Maglott D, Mizrachi I, Morris R, Ostell J, Pruitt K, Rubinstein W, Sayers E, Sirotkin K, Tatusova T (ed), The NCBI handbook, 2nd ed. National Center for Biotechnology Information, Bethesda, MD.
10. **Hartmann RK, Ulbrich N, Erdmann VA.** 1987. An unusual rRNA operon constellation: in *Thermus thermophilus* HB8 the 23S/5S rRNA operon is a separate entity from the 16S rRNA operon. Biochimie **69:**1097–1104. http://dx.doi.org/10.1016/0300-9084(87)90009-5.
11. **Menke MAOH, Liesack W, Stackebrandt E.** 1991. Ribotyping of 16S and 23S rRNA genes and organization of rrn operons in members of the bacterial genera *Gemmata, Planctomyces, Thermotoga, Thermus*, and *Verrucomicrobium*. Arch Microbiol **155:**263–271. http://dx.doi.org/10.1007/BF00252210.