



Genome Announcement

Draft genome sequence of sulfur-reducing archaeon *Thermococcus thioeducens* DSM 14981^T



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ABSTRACT

Thermococcus thioeducens DSM 14981^T, a sulfur-reducing archaeon, was isolated from the rainbow hydrothermal vent site on the Mid-Atlantic Ridge. Herein, we report the draft genome sequence of *T. thioeducens* DSM 14981^T; we obtained 41 contigs with a genome size of 2,052,483 bp and G + C content of 53.5%. This genome sequence will not only help understand how the archaeon adapts to the deep-sea hydrothermal environment but also aid the development of enzymes that are highly stable under extreme conditions for industrial applications.

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Introduction

Thermococcus taxonomically belongs to the family Flavobacteriaceae and phylum Euryarchaeota.¹ Members of this genus are characterized by thermophilic anaerobiosis with sulfur-type respiration and sulfur stimulation for fermentation.² A decrease in S levels in the growth medium leads to the enhanced production of ethanol, butanol, H₂, and formate at the expense of H₂S and acetate production.³ The minimal growth temperature for most species is approximately 50 °C and the maximum is approximately 95–100 °C. Therefore, these microorganisms are generally good sources of enzymes for application in various biotechnological processes in the food, chemical, and pharmaceutical industries.⁴

A strain DSM 14981^T was isolated from “black smoker” chimney material from the rainbow hydrothermal vent site on the Mid-Atlantic Ridge. It is a hyperthermophilic, heterotrophic, sulfur-dependent, coccoid archaeon inhabiting a deep-sea hydrothermal system in the Mid-Atlantic Ridge (36.2° N, 33.9° W). The optimal growth conditions include a pH of 5.0–8.5, NaCl concentration of 1–5% (w/v), and temperature of 55–94 °C. A strain DSM 14981^T was identified by 16S rRNA gene sequence, was named as *Thermococcus thioeducens*. And, this strain is an obligate anaerobe and completely dependent upon elemental sulfur as the electron acceptor, but it does not reduce sulfate, sulfite, thiosulfate, Fe (III), or nitrate.⁵ In this communication, we present the draft genome sequence of *T. thioeducens* DSM 14981^T, with the aim to study the extreme adaptation of this archaeon in a hydrothermal environment.

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T. thioreducens DSM 14981^T was cultured in Bacto Marine broth with 0.5% (w/v) sulfur powder and incubated at 80 °C for 48 h. Genomic DNA was then extracted using the method reported by Ramakrishnan.⁶ Whole-genome sequencing of the strain was performed using the Ion Torrent PGM sequencer (400-bp library) and 316TM chip v2, according to the manufacturer's instructions (ThermoFisher Scientific, Germany).⁷ Sequencing generated 755,986 reads with an average read length of 290 bp. *De novo* assembly was performed using the MIRA assembler v4.0.2 and CLC Genomics Workbench v7.0 software. Forty-one contigs with N₅₀ contig length of 151,544 bp and a maximum contig size of 253,877 bp were obtained. The draft genome size was 2,052,483 bp, with a G + C content of 53.5% and no plasmids.

We used the Rapid Annotation using Subsystem Technology⁸ and National Centre for Biotechnology Information's Prokaryotic Genomes Annotation Pipeline v2.6 (http://www.ncbi.nlm.nih.gov/genome/annotation_prok) for gene prediction and annotation. Genes were predicted using the Glimmer 3.02 software.⁹ Forty-two tRNA genes were identified using tRNAscan-SE,¹⁰ and 5 rRNAs were identified using the RNAmmer 1.2 software.¹¹

Apart from encoding the archaeal-modified Embden-Meyerhof (EM) glycolysis pathway and protein and carbohydrate metabolism pathways,¹² the *T. thioreducens* DSM 14981 draft genome also encodes the archaeal RuBisCo to facilitate carbon fixation.¹³ In addition, this genome encodes genes involved in energy synthesis including a V-type ATP synthase gene cluster and NADH – ubiquinone oxidoreductase on the cell membrane. The genome also has a gene cluster for respiration, including membrane bound hydrogenase, sulfurhydrogenase II complex, and formate dehydrogenase H. In order to survive extreme conditions such as high temperature, pressure, and pH, the strain contains heat shock protein 60, a prefoldin protein, and a small heat shock protein.^{14,15} The important enzyme-encoding genes for potential use in commercial enzyme production,¹⁶ such as those encoding amylase, protease, pullulanase, glycosyltransferase, and alcohol dehydrogenase, were also found in its genome sequence. Further insights into the genome sequence of this archaeon should facilitate studying extreme environments in hydrothermal vents and aid the development of enzymes that are highly stable under extreme conditions for industrial applications.

Nucleotide sequence accession numbers

The whole genome sequence of *T. thioreducens* DSM 14981 has been deposited at DDBJ/EMBL/GenBank under the accession number LIXN00000000. The first version (LIXN00000000.1) has been described in this paper.

Conflicts of interest

The authors declare no conflicts of interest.

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