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Genome Sequence of a Sulfate-Reducing Thermophilic Bacterium, *Thermodesulfobacterium commune* DSM 2178^T (Phylum *Thermodesulfobacteria*)

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Here, we present the complete genome sequence of *Thermodesulfobacterium commune* DSM 2178^T of the phylum *Thermodesulfobacteria*.

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Thermodesulfobacterium commune is the type species of genus *Thermodesulfobacterium* contained within the small class *Thermodesulfobacteria*, and first isolated from Ink Pot spring in Yellowstone National Park, WY, in 1980. It is a sulfate-reducing obligate anaerobic thermophile with an optimum growth temperature of 70°C and a growth temperature range of 45°C to 80°C. This Gram-negative bacterium has nonmotile, non-cyst-forming, nonsporulating, straight, rod-shaped (0.3 × 0.9 μm) cells (1). It can metabolize lactate and pyruvate as energy sources using sulfate and thiosulfate as electron acceptors (1). *T. commune* contains cytochrome c3 but lacks desulfoviridin-type bisulfate reductase (2). It was sequenced as part of the "Assembling the Tree of Life" project at The Institute of Genomic Research (TIGR). It was chosen as a representative of the phylum *Thermodesulfobacteria*, which had no sequenced members during the starting phase of the project (2002).

The type strain of *T. commune* (DSM 2178^T) was obtained from the Leibniz Institute DSMZ-German Collection of Microorganisms and Cell Cultures and grown under 95% N_2/5% CO_2 atmosphere at 70°C using DSMZ medium 206. DNA was obtained by solubilizing cells with N-lauryl sulfate and sodium dodecyl sulfate followed by incubation with proteinase K. The lysate was extracted with Tris-EDTA-saturated phenol, chloroform/isoamyl alcohol, and was precipitated from the aqueous phase with 95% ethanol. It was resolubilized, incubated with DNase-free RNase and further purified by cesium-chloride gradient centrifugation and visualized using 365-nm UV light (3). Pulse-field gel electrophoresis was used to confirm the size and uniformity of the DNA preparation. Genome sequencing was performed as for the other genomes from the Tree of Life project (4). It included insert libraries of three different sizes: small (2 to 3 kb), medium (4 to 5 kb), and large (8 to 10 kb), which were sequenced with Sanger sequencing and assembled as previously described (5–7); assemblies were edited and gaps were closed by clone walking and targeted PCR and sequencing. Finishing was completed by (i) generating additional coverage in low coverage regions, (ii) verification of repeats, and (iii) resolution of ambiguities (8). The final assembly had ~9× coverage for the 1,764,045-bp genome with a GC content of 36.97%.

The origin of replication was identified using GC skew and colocalization of origin-associated genes (9). All the universal single-copy bacterial marker genes (10) were found in the sequenced genome using Phylosift (11). The genome was annotated using NCBI Prokaryotic Genome Annotation Pipeline version 2.6 (revision 438450) (12, 13). Of the 1,532 genes identified, 1,453 were protein-coding sequences (CDS), 29 were pseudogenes, and 50 were noncoding RNA genes. The 50 RNA genes comprise 1 noncoding RNA (ncRNA), 3 rRNAs (5S, 16S, and 23S), and 46 tRNAs. Additionally, two clustered regularly interspaced short palindromic repeat (CRISPR) arrays were identified in the genome.

Nucleotide sequence accession number. The genome sequence has been deposited at GenBank under the accession no. CP008796.

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Sanger sequencing was performed at The Institute for Genomic Research (TIGR), in Rockville, MD.

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