

Genome Sequence of *Desulfosporosinus* sp. OT, an Acidophilic Sulfate-Reducing Bacterium from Copper Mining Waste in Norilsk, Northern Siberia

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We have sequenced the genome of *Desulfosporosinus* sp. OT, a Gram-positive, acidophilic sulfate-reducing Firmicute isolated from copper tailing sediment in the Norilsk mining-smelting area in Northern Siberia, Russia. This represents the first sequenced genome of a *Desulfosporosinus* species. The genome has a size of 5.7 Mb and encodes 6,222 putative proteins.

Members of the genus *Desulfosporosinus* are sulfate-reducing bacteria, often found in microbial communities associated with mining environments and involved in the bioremediation of metal-contaminated water and sediments (1, 5–8, 12). In these environments, enriched with SO_4^{2-} , sulfate reduction contributes to precipitation of metal sulfides and thereby the immobilization of toxic metals. Recently, *Desulfosporosinus* bacteria were identified as key players in microbial sulfate reduction in a low-sulfate peatland (13). Here we announce the first draft genome of a member of the genus *Desulfosporosinus*. *Desulfosporosinus* sp. OT was isolated from acidic sediment (sample T9) of a copper-mining waste site in Norilsk, Russia (10).

Genomic DNA was isolated by alkaline lysis (4). Sequencing was carried out by pyrosequencing, using an FLX genome sequencer (Roche). A total of 357,734 reads with an average read length of 400 bp resulted in 142,885,740 sequenced bases. Sequence assembly was performed with GS De Novo Assembler version 2.3 software with default settings, yielding 304 contigs with an average size of 22,674 nucleotides and an average of 42% GC content. The number of the bases in all contigs totaled 5,705,508, corresponding to 25-fold sequencing coverage. Identification of open reading frames and annotation were performed by the annotation service for microbial genomes of the Institute for Genome Sciences (IGS), School of Medicine, University of Maryland. The annotation yielded 6,222 open reading frames for proteins, 74 tRNA genes, and 3 rRNA genes. The 16S RNA sequence of *Desulfosporosinus* sp. OT is 99.4% and 98.1% identical with those of *Desulfosporosinus* sp. 5apy (GenBank accession no. AF159120) and *Desulfosporosinus lacus* (GenBank accession no. AJ582757) (14), respectively, which are the most closely related microbial isolates.

Desulfosporosinus sp. OT withstands copper concentrations of up to 236 mM, which is severalfold higher than the concen-

trations so far reported for other sulfate-reducing bacteria such as *Desulfovibrio* sp. A2 (genome announcement submitted for publication) or *Desulfovibrio* sp. R2, also isolated from metal-contaminated habitats (9, 11). *Desulfosporosinus* sp. OT harbors two CopA-like CPx-type ATPases (see reference 16 for a review), DOT_2451 and DOT_2536, and a polyphosphate kinase-phosphatase couple, DOT_3559 and DOT_4690, as present in *Acidithiobacillus ferrooxidans*. These systems appear to play a key role in copper tolerance (2). As would be expected for a Gram-positive organism, no CueO-like multicopper oxidase system or *cus*-like copper efflux system, both of which serve in the control of periplasmic copper in *Escherichia coli* and other Gram-negative bacteria, is present (15). Also, neither a CopC-like periplasmic copper-binding protein nor a CopD-like integral membrane protein could be found in the genome of *Desulfosporosinus* sp. OT. These two proteins were first identified as copper resistance determinants carried on a plasmid of *Pseudomonas syringae* but are also found in the genomes of Gram-negative as well as Gram-positive organisms (3). Based on the genomic information, investigations of the exceptional copper resistance of *Desulfosporosinus* sp. OT can now be tackled experimentally. Work along these lines in our laboratory is currently proceeding.

Nucleotide sequence accession numbers. The sequence from the Whole Genome Shotgun project investigating *Desulfosporosinus* sp. OT has been deposited at DDBJ, EMBL, and GenBank under accession number AGAF00000000. The version described in this paper is the first version, AGAF01000000.

We thank Sean Daugherty and Michelle Giglio at the IGS annotation service of the University of Maryland and Galina Stykon for technical support.

This work was supported by a grant from the Swiss State Secretary for Education & Research, by the Russian Ministry of Education and Science (FCP program), and by the Russian Fund for Fundamental Research (RFBR).

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