

Desulfosporosinus infrequens sp. nov.

Submitted by Loy, Alexander

Species *Desulfosporosinus infrequens*

Etymology

[in.fre'quens] L. masc. adj. *infrequens*, infrequent

Nomenclatural type

[NCBI Assembly: GCA_900290375.1](#)^{TS}

Description

MAG SbF1 obtained from a wetland in Germany. A major driver of sulfate reduction in experimental microcosms established with acidic soil from the Schlöppnerbrunnen II fen (Bavaria, Germany).

The population genome of the low-abundance *Desulfosporosinus* species was obtained by coassembly and differential coverage binning of metagenomes obtained from native peat soil and ¹³C-labeled fractions of a DNA-stable isotope probing experiment of the same peatland (see [Fig. S1](#) in the supplemental material) (29). The high-quality metagenome-assembled genome (MAG) SbF1 had a size of 5.3 Mbp (on 971 scaffolds), a G+C content of 42.6%, a CheckM-estimated completeness of 98.0%, a potential residual contamination of 3.9%, and 10% strain heterogeneity. Besides 16S and 23S rRNA genes, SbF1 carried 6,440 protein-coding genes (CDS), five 5S rRNA gene copies, 59 tRNAs, and 37 other ncRNAs, making a total of 6,543 predicted genomic features. The genome size and G+C content were in the same range as observed for genomes of cultured *Desulfosporosinus* species (3.0 to 5.9 Mbp and 42 to 44%, respectively) (30–34). Scaffolds containing rRNA genes had a higher coverage than the average coverage of all scaffolds ([Fig. S1](#)), indicating multiple *rrn* operon copies, as is known from genomes of other *Desulfosporosinus* species (on average, 9.3 *rrn* operons; range, 8 to 11) (35).

Based on its phylogenetic placement and novel ecophysiological behavior, we propose that *Desulfosporosinus* sp. MAG SbF1 represents a novel species with the proposed name *Desulfosporosinus infrequens* sp. nov. (in.fre'quens. L. adj. *infrequens*, rare, referring to its low relative abundance). Based on its genome-derived metabolic potential and support from metatranscriptomics, *Desulfosporosinus infrequens* is capable of complete oxidation of acetate, propionate, and lactate with sulfate as the electron acceptor, with further potential for oxidation of molecular hydrogen ([Fig. 1](#)).

Classification

Bacteria » *Bacillota* » *Clostridia* » *Eubacteriales* » *Peptococcaceae* » *Desulfosporosinus* » *Desulfosporosinus infrequens*

References

Effective publication: Hausmann et al., 2019 [1]

Registry URL

<https://seqco.de/i:32296>

References

1. Hausmann et al. (2019). Long-Term Transcriptional Activity at Zero Growth of a Cosmopolitan Rare Biosphere Member. *mBio*. DOI:10.1128/mbio.02189-18

Register List Certificate of Validation

On behalf of the *Committee on the Systematics of Prokaryotes Described from Sequence Data* (SeqCode Committee), we hereby certify that the Register List seqco.de/r:zukezao3 submitted by **Loy, Alexander** and including 1 new name has been successfully validated.

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