

# Desulfosporosinus infrequens sp. nov.

Submitted by Loy, Alexander

Table 1: Complete list of names proposed in the current register list.

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Species <i>Desulfosporosinus infrequens</i>	[in.fre'quens] L. masc. adj. <i>infrequens</i> , infrequent	<p>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).</p> <p>The population genome of the low-abundance <i>Desulfosporosinus</i> species was obtained by coassembly and differential coverage binning of metagenomes obtained from native peat soil and <sup>13</sup>C-labeled fractions of a DNA-stable isotope probing experiment of the same peatland (see <a href="#">Fig. S1</a> 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 <i>Desulfosporosinus</i> 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 <i>rrn</i> operon copies, as is known from genomes of other <i>Desulfosporosinus</i> species (on average, 9.3 <i>rrn</i> operons; range, 8 to 11) (35).</p> <p>Based on its phylogenetic placement and novel ecophysiological behavior, we propose that <i>Desulfosporosinus</i> sp. MAG SbF1 represents a novel species with the proposed name <i>Desulfosporosinus infrequens</i> sp. nov. (in.fre'quens. L. adj. <i>infrequens</i>, rare, referring to its low relative abundance). Based on its genome-derived metabolic potential and support from metatranscriptomics, <i>Desulfosporosinus infrequens</i> 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).</p>	<i>Desulfosporosinus</i>	NCBI Assembly: GCA_900290375.1 T <sub>5</sub>	<a href="https://seqco.de/i:32296">seqco.de/i:32296</a>