



# Draft Genome Sequence of *Methylovulum psychrotolerans* Sph1<sup>T</sup>, an Obligate Methanotroph from Low-Temperature Environments

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**ABSTRACT** *Methylovulum psychrotolerans* Sph1<sup>T</sup> is an aerobic, obligate methanotroph, which was isolated from cold methane seeps in West Siberia. This bacterium possesses only a particulate methane monooxygenase and is widely distributed in low-temperature environments. Strain Sph1<sup>T</sup> has the genomic potential for biosynthesis of hopanoids required for the maintenance of intracytoplasmic membranes.

*Methylovulum psychrotolerans* Sph1<sup>T</sup> is a neutrophilic aerobic methanotroph of the class *Gammaproteobacteria*, family *Methylococcaceae*. It was isolated from a cold methane seep in the Irtysh basin, West Siberia (1). This methanotroph grows well at low temperatures and is commonly detected in various low-temperature environments, such as arctic lakes, glaciers, and northern peatlands (2–4). Cells of *M. psychrotolerans* Sph1<sup>T</sup> are Gram-negative, nonmotile, encapsulated, large cocci that multiply by binary fission and utilize methane and methanol.

For the genome sequencing of strain Sph1<sup>T</sup>, a combination of fragment and mate-paired library approaches was used. Both libraries were sequenced with the Illumina MiSeq platform using 2 × 250-bp paired-end sequencing reagents. Mate-paired reads were treated with the NextClip tool (5), resulting in 1,082,354 read pairs with a mean insert size of 3,183 bp. Paired-end reads were filtered and trimmed by quality with CLC Genomics Workbench (Qiagen, Germany) using recommended parameters, resulting in 431,801 read pairs. *De novo* assembly was performed with the SPAdes version 3.11.0 assembler (6). The total length of the final assembly was 5,189,806 bp; it consisted of 97 genomic scaffolds with an  $N_{50}$  value of 334,445 bp. Final genome coverage was 40× for the mate-paired library and 23× for the paired-end library. The estimated size of the *M. psychrotolerans* Sph1<sup>T</sup> genome is 5.2 Mb (coverage, 63×), with an average G+C content of 50.8%. In total, 4,577 predicted protein-coding genes were identified.

The average nucleotide identity between the genomes of *M. psychrotolerans* Sph1<sup>T</sup> and another described member of this genus, *M. miyakonense* HT12<sup>T</sup> (7), is only 79%, which confirms their classification as two different species. The genome of *M. psychrotolerans* Sph1<sup>T</sup> contains a single *pmoCAB* operon for particulate methane monooxygenase (MMO). The presence of the homologous *pxmABC* operon, which is characteristic of many gammaproteobacterial methanotrophs (7, 8), was not detected. In contrast to *M. miyakonense* HT12<sup>T</sup>, an operon encoding soluble MMO (*mmoXYBZDC*) is lacking in *M. psychrotolerans* Sph1<sup>T</sup>. The ability to grow on methanol is explained by the presence of the gene operons encoding MxaFI- and XoxF-methanol dehydrogenases (9). Genes involved in tetrahydromethanopterin (H<sub>4</sub>MTP), tetrahydrofolate (H<sub>4</sub>-folate)-linked C1 transfer, and formate oxidation were

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identified. A complete set of genes encoding formaldehyde assimilation in the ribulose monophosphate pathway was present, while the serine cycle was incomplete.

The genome includes all genes required for glycogen biosynthesis (*glgA*, *glgB*, and *glgC*) (10) and nitrogen metabolism, including genes for nitrate/nitrite reduction, ammonium and urea uptake and assimilation, as well as key genes for nitrogen fixation.

Strain Sph1<sup>T</sup> has the genomic potential for the biosynthesis of hopanoids, which is required for the maintenance of intracytoplasmic membranes (11). A complete set of genes for the nonmevalonate pathway and the *ispA* gene encoding farnesyl diphosphate synthase were identified. The genes responsible for squalene synthesis (12), two copies of the *shc* gene encoding the enzyme responsible for the cyclization of squalene into diploptene (13), as well as the *hpnH* and *hpnG* genes involved in the conversion of diploptene to bacteriohopanetetrol (14) were also present.

**Accession number(s).** The *M. psychrotolerans* Sph1<sup>T</sup> genome sequence was deposited in GenBank under the accession no. [PGFZ00000000](https://doi.org/10.1128/genomeA.00515-15).

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