Species *Methylotenera hypolimnetica*

Etymology
[hy.po.lim.ne.ti'ca] **Gr. prep.** *hypo*, below, under; **N.L. fem. adj.** *limnetica*, of a lake; **N.L. fem. adj.** *hypolimnetica*, from the hypolimnion of lakes.

Nomenclatural type
NCBI Assembly: GCA_965601845.1 [Ts]

Reference Strain
Strain sc|0038778: RH-M31

Description
Type strain is *Methylotenera hypolimnetica* RH-M31 (GCA_947054635.1), isolated from 30 m depth from the Římov Reservoir, Czechia (date: 15.08.2019), *via* high-throughput dilution to extinction cultivation. RH-M31 has a genome size of 1.8 Mbp with a genomic GC content of 49.2%, contains 6 rRNA genes and 38 tRNAs. The genome is complete, consisting of a circular chromosome. No genes for flagellar or pilus assembly and chemotaxis were annotated. Pathways for methanol oxidation (Xox), the RuMP and methylcitric acid (MCA) cycle for methylotrophy and the biosynthesis of all amino acids were predicted. Further, pathways for thiamine, riboflavin, NAD, coenzyme A, pimeloyl-ACP, biotin, THF, ubiquinone, and heme biosynthesis were identified. The closest cultivated relatives are *Methylotenera versatilis* 301 (GCF_000093025.1) with an average amino acid identity of 75.7% and average nucleotide identity of 72.6% and another newly proposed species, *Methylotenera profunda* RH-M32 (GCA_947054625.1), with an AAI of 94.2% and an ANI of 92%. Current GTDB classification (R220): d__Bacteria; p__Pseudomonadota; c__Gammaproteobacteria; o__Burkholderiales; f__Methylophilaceae; g__Methylotenera; s__Methylotenera sp903951385.

Classification
Bacteria » *Pseudomonadota* » *Betaproteobacteria* » *Nitrosomonadales* » *Methylophilaceae* » *Methylotenera* » *Methylotenera hypolimnetica*

References
Effective publication: Salcher et al., 2025 [1]

Registry URL
https://seqco.de/i:48718

References

1. Salcher et al. (2025). Bringing the uncultivated microbial majority of freshwater ecosystems into culture. *Nature Communications*. DOI:10.1038/s41467-025-63266-9