Species *Methylotenera profunda*

Etymology

[pro.fun'da] **L. fem. adj.** *profunda*, deep; referring to the deep zone of lakes where the species is common.

Nomenclatural type

NCBI Assembly: GCA_965601725.1 ^{Ts}

Reference Strain

Strain sc|0038971: RH-M32

Description

Type strain is *Methylotenera profunda* RH-M32 (GCA_947054625.1), isolated from 30 m depth from the Římov Reservoir, Czechia (date: 15.08.2019), *via* high-throughput dilution to extinction cultivation. RH-M32 has a genome size of 1.7 Mbp with a genomic GC content of 47.9%, contains 6 rRNA genes and 38 tRNAs. The genome is complete, consisting of a circular chromosome. The genome contains genes encoding rhodopsins and the biosynthetic pathway for retinal biosynthesis. 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 75.9% and average nucleotide identity of 72.8% and another newly proposed species, *Methylotenera hypolimnetica* RH-M31 (GCA_947054635.1), 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 oryzisoli_A.

Classification

Bacteria » *Pseudomonadota* » *Betaproteobacteria* » *Nitrosomonadales* » *Methylophilaceae* » *Methylotenera* » *Methylotenera profunda*

References

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

Registry URL

https://seqco.de/i:48733

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