Species *Novimethylotenera aquatica*^{Ts}

Etymology

[a.qua.ti'ca] **L. fem. adj.** *aquatica*, living or found in the water.

Nomenclatural type

NCBI Assembly: GCA_965601485.1 ^{Ts}

Reference Strain

Strain sc|0038780: ME-M6

Description

Type strain is *Novamethylotenera aquatica* ME-M6 (GCA_947054645.1), isolated from 5 m depth from Lake Medard, Czechia (date: 09.07.2019), *via* high-throughput dilution to extinction cultivation. ME-M6 has a genome size of 2.1 Mbp with a genomic GC content of 41.7%, contains 6 rRNA genes and 37 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 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 relative is *Methylotenera versatilis* 7 (GCF_000799165.1) with an average amino acid identity of 80.36% and average nucleotide identity of 76.56%. Current GTDB classification (R220): d__Bacteria; p__Pseudomonadota; c__Gammaproteobacteria; o__Burkholderiales; f__Methylophilaceae; g__Methylotenera_A; s__Methylotenera_A oryzisoli_A.

Classification

Bacteria » *Pseudomonadota* » *Betaproteobacteria* » *Nitrosomonadales* » *Methylophilaceae* » *Novimethylotenera* » *Novimethylotenera aquatica*^{Ts}

References

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

Registry URL

https://seqco.de/i:48701

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