

Species *Hydrogenophaga miladensis*

Etymology

[mi.la.den'sis] **N.L. fem. adj.** *miladensis*, pertaining to Lake Milada (Czechia), the isolation source of the type strain.

Nomenclatural type

[NCBI Assembly: GCA_965234585.1](#)^{Ts}

Reference Strain

[Strain sc|0038963](#): MiE-M28

Description

Type strain is *Hydrogenophaga miladensis* MiE-M28 (GCA_965234585.1), isolated from 5 m depth from Lake Milada, Czechia (date: 2019-10-15), *via* high-throughput dilution to extinction cultivation. MiE-M28 has a genome size of 2.4 Mbp with a genomic GC content of 60.6%, contains 6 rRNA genes and 43 tRNAs. The genome is complete, consisting of a circular chromosome. The genome contains genes encoding anoxygenic aerobic phototrophy (*pufABLM*) and the complete Calvin cycle for carbon fixation via RuBisCO. Genes for flagellar and pilus assembly were annotated. Pathways for thiosulfate oxidation (Sox pathway), glycolate and methane/alkanesulfonate oxidation and the biosynthesis of all amino acids were predicted. Further, pathways for thiamine, riboflavin, NAD, coenzyme A, pimeloyl-ACP, and heme biosynthesis were identified. The closest cultivated relative is *Hydrogenophaga intermedia* MER 62 (GCF_001571205.1), with an average nucleotide identity of 74.2%. Current GTDB classification (R220): d__Bacteria; p__Pseudomonadota; c__Gammaproteobacteria; o__Burkholderiales; f__Burkholderiaceae_B; g__Hydrogenophaga; s__Hydrogenophaga intermedia_C.

Classification

Bacteria » *Pseudomonadota* » *Betaproteobacteria* » *Burkholderiales* » *Comamonadaceae* » *Hydrogenophaga* » *Hydrogenophaga miladensis*

References

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

Registry URL

<https://seqco.de/i:48728>

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](https://doi.org/10.1038/s41467-025-63266-9)