Species Aquidulcibacter miladensis

Etymology

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

Nomenclatural type

NCBI Assembly: GCA 965234355.1 Ts

Reference Strain

Strain sc|0038952: MiH-15

Description

Type strain is *Aquidulcibacter miladensis* MiH-15 (GCA_965234355.1), isolated from 15 m depth from Lake Milada, Czechia (date: 2019-07-23), *via* high-throughput dilution to extinction cultivation. MiH-15 has a genome size of 3.2 Mbp with a genomic GC content of 55.7%, contains 3 rRNA genes and 41 tRNAs. The genome is a high-quality draft consisting of 8 contigs. The genome contains genes encoding anoxygenic aerobic phototrophy (*pufABLM*). Genes for flagellar assembly and chemotaxis were annotated in the genome. Pathways for taurine degradation, assimilatory sulfate reduction and methane/alkanesulfonate oxidation and the biosynthesis of all amino acids were predicted. Further, pathways for riboflavin, NAD, coenzyme A, pimeloyl-ACP, THF, and heme biosynthesis were identified. The closest cultivated relatives are *Aquidulcibacter paucihalophilus* TH1-2 (GCF_002105465.1) with an average amino acid identity of 87.1% and average nucleotide identity of 80.5% and another newly proposed species, *Aquidulcibacter rimovensis* RH-10 (GCA_965234525.1), with an AAI of 93.2% and an ANI of 89.4%. Current GTDB classification (R220): d_Bacteria; p_Pseudomonadota; c_Alphaproteobacteria; o_Caulobacterales; f_TH1-2; g_Aquidulcibacter; s_Aquidulcibacter sp945891505.

Classification

Bacteria » Pseudomonadota » Alphaproteobacteria » Caulobacterales » Caulobacteraceae » Aquidulcibacter » Aquidulcibacter miladensis

References

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

Registry URL

https://seqco.de/i:48727

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