Species *Limnohabitans kasalickyi*

Etymology

[ka.sa.li.cky'i] **N.L. masc. gen. n.** *kasalickyi*, named after the Czech scientist Vojtěch (Vojta) Kasalický, who isolated many strains of the genus Limnohabitans and was involved in the description of the genus.

Nomenclatural type

NCBI Assembly: GCA_965234325.1 Ts

Reference Strain

Strain sc|0038965: MaE-M4

Description

Type strain is *Limnohabitans kasalickyi* MaE-M4 (GCA_965234325.1), isolated from 5 m depth from Lake Maggiore, Italy (date: 2019-04-09), *via* high-throughput dilution to extinction cultivation. MaE-M4 has a genome size of 3.7 Mbp with a genomic GC content of 56.3%, contains 6 rRNA genes and 44 tRNAs. The genome is a high-quality draft consisting of 16 contigs. The genome contains genes encoding anoxygenic aerobic phototrophy (*pufABLM*). Genes for flagellar and pilus assembly were annotated. Pathways for cyanate, urea, and taurine degradation, thiosulfate oxidation (Sox pathway), methane/alkanesulfonate and glycolate oxidation, and the biosynthesis of all amino acids except for aspartate were predicted. Further, pathways for thiamine, riboflavin, pantothenate, coenzyme A, pimeloyl-ACP, THF, and heme biosynthesis were identified. The closest cultivated relative is *Limnohabitans* sp. Jir61 (GCF_003063545.1), with an average amino acid identity of 77.9% and average nucleotide identity of 80.1%. Current GTDB classification (R220): d__Bacteria; p__Pseudomonadota; c__Gammaproteobacteria; o__Burkholderiales; f__Burkholderiaceae_B; g__Limnohabitans; s__Limnohabitans sp002778325.

Classification

Bacteria » *Pseudomonadota* » *Betaproteobacteria* » *Burkholderiales* » *Comamonadaceae* » *Limnohabitans* » *Limnohabitans kasalickyi*

References

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

Registry URL

https://seqco.de/i:48719

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