# Species *Verrucolacustris abundans*Ts

**Etymology**

[a.bun'dans] **L. masc. part. adj.** *abundans*, abundant; referring to high global abundances

**Nomenclatural type**

NCBI Assembly: GCA_965194535.1 Ts

**Reference Strain**

Strain sc|0038970: MiH-22

**Description**

Type strain is *Verrucolacustris abundans* MiH-22 (GCA_965194535.1), isolated from 15 m depth from Lake Milada, Czechia (date: 2019-10-15), *via* high-throughput dilution to extinction cultivation. MiH-22 has a genome size of 2.0 Mbp with a genomic GC content of 52.8%, contains 3 rRNA genes and 46 tRNAs. The genome is complete, consisting of a circular chromosome. The genome contains genes encoding rhodopsins. No genes for flagellar assembly and chemotaxis were annotated. In contrast to other *Methylacidiphilales* members, no genes for C1 metabolism (methanotrophy) were identified. Pathways for assimilatory sulfate reduction and the biosynthesis of all amino acids except for methionine, histidine and tryptophan were predicted. Further, pathways for only three vitamins (thiamine, riboflavin, and biotin biosynthesis) were identified. The closest cultivated relative is *Methylacidimicrobium cyclopophantes* 3B_2 (GCF_902143385.2), with an average amino acid identity of 49.5% and average nucleotide identity of 62.8%. Current GTDB classification (R220): d__Bacteria; p__Verrucomicrobiota; c__Verrucomicrobiae; o__Methylacidiphilales; f__UBA3015; g__UBA3015; s__UBA3015 sp030054195.

**Classification**

*Bacteria* » *Verrucomicrobiota* » “Methylacidiphilae” » *Methylacidiphilales* » *Verrucolacustridaceae* » *Verrucolacustris* » *Verrucolacustris abundans*Ts

**References**

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

**Registry URL**

https://seqco.de/i:48694

# 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