

Family *Verrucolacustridaceae*

Etymology

[Ver.ru.co.la.cus.tri.da'ce.ae] **N.L. masc. n.** *Verrucolacustris*, referring to the type genus *Verrucolacustris*; **-aceae**, ending to denote a family; **N.L. fem. pl. n.** *Verrucolacustridaceae*, the *Verrucolacustris* family

Nomenclatural type

Genus *Verrucolacustris*

Description

Type strain is *Verrucolacustris abundans* MiH-22 (GCA_965194535.1). In contrast to other *Methylacidiphilales* including the only described genus *Methylacidimicrobium* (*Methylacidiphilaceae*, GCF_902143385.2), no genes for C1 metabolism were identified, therefore we suggest the establishment of a new family of non-methanotrophic *Methylacidiphilales*. 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.

Classification

Bacteria » *Verrucomicrobiota* » “*Methylacidiphilae*” » *Methylacidiphilales* » *Verrucolacustridaceae*

References

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

Registry URL

<https://seqco.de/i:48695>

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)