Species *Pernthalerella lacunae*

Etymology
[la.cu'na.e] **L. fem. gen. n.** *lacunae*, of a ditch, pit, hole, pool, or pond, referring to the isolation source of the type from a freshwater lake.

Nomenclatural type
NCBI Assembly: GCA_965194545.1 [Ts]

Reference Strain
Strain scj0038789: MaE-M21

Description
Type species is *Pernthalerella lacuna* MaE-M21 (GCA_965194545.1), isolated from 5 m depth from Lake Maggiore, Italy (date: 2019-11-04), *via* high-throughput dilution to extinction cultivation. MaE-M21 has a genome size of 2.8 Mbp with a genomic GC content of 54.9%, contains 3 rRNA genes and 45 tRNAs. The genome is a high-quality draft consisting of 7 contigs. The genome contains genes encoding anoxygenic aerobic phototrophy (*pufABLM*). Genes for flagellar and pilus assembly were annotated. Pathways for benzene degradation, glycolate oxidation and the biosynthesis of all amino acids were predicted. Further, pathways for thiamine, riboflavin, NAD, pantothenate, coenzyme A, biotin, THF, and heme biosynthesis were identified. The closest cultivated relative is *Paucimonas lemoignei* DSM 7445 (GCF_004342585.1) with an average amino acid identity of 64.16% and average nucleotide identity of 70.49% and two other newly proposed species, *Pernthalerella aquatica* GE-M3 (GCA_965194445.1) and *Pernthalerella communis* MsE-6 (GCA_965194595.1), with AAI of 72.1-73.1% and ANI of 71.9-72.5%. Current GTDB classification (R220): d__Bacteria; p__Pseudomonadota; c__Gammaproteobacteria; o__Burkholderiales; f__Burkholderiaceae; g__SYFN01; s__SYFN01 sp021299035.

Classification
Bacteria » *Pseudomonadota* » *Betaproteobacteria* » *Burkholderiales* » *Burkholderiaceae* » *Pernthalerella* » *Pernthalerella lacunae*

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

Registry URL
https://seqco.de/i:49111

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