

Species *Pernthalerella communis*

Etymology

[com.mu'nis] **L. fem. adj.** *communis*, common

Nomenclatural type

[NCBI Assembly: GCA_965194595.1](#) ^{Ts}

Reference Strain

[Strain sc|0038790](#): MsE-6

Description

Type species is *Pernthalerella communis* MsE-6 (GCA_965194595.1), isolated from 5 m depth from Lake Most, Czechia (date: 2019-04-30), *via* high-throughput dilution to extinction cultivation. MsE-6 has a genome size of 3 Mbp with a genomic GC content of 47.7%, contains 3 rRNA genes and 37 tRNAs. The genome is a high-quality draft consisting of 27 contigs. The genome contains genes encoding anoxygenic aerobic phototrophy (*pufABLM*) and the complete Calvin cycle for carbon fixation via RuBisCO. Genes for flagellar and pilus assembly were annotated. Pathways for salicylate 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 64.02% and average nucleotide identity of 69.11% and two other newly proposed species, *Pernthalerella lacuna* MaE-M21 (GCA_965194545.1) and *Pernthalerella aquatica* GE-M3 (GCA_965194445.1), 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 sp903846425.

Classification

Bacteria » *Pseudomonadota* » *Betaproteobacteria* » *Burkholderiales* » *Burkholderiaceae* » *Pernthalerella* » *Pernthalerella communis*

References

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

Registry URL

<https://seqco.de/i:49112>

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)