Species *Flavobacterium rarum*

Etymology

[ra'rum] **L. neut. adj.** *rarum*, sporadic or uncommon, referring to the sporadic isolation and recovery from disparate sources of members of this species

Nomenclatural type

NCBI Assembly: GCA_965234445.1 ^{Ts}

Reference Strain

Strain scJ0038949: TH-M1

Description

Type strain is *Flavobacterium rarum* TH-M1 (GCA_965234445.1), isolated from 180 m from Lake Thun, Switzerland (date: 2019-04-08), *via* high-throughput dilution to extinction cultivation. TH-M1 has a genome size of 4.26 Mbp with a genomic GC content of 33.4%, contains 6 rRNA genes and 51 tRNAs. The genome is a high-quality draft consisting of 29 contigs. The genome contains genes encoding rhodopsins. Genes for gliding motility (*gldBDHJKLMN*, *sprA*) were annotated in the genome. Pathways for taurine degradation, assimilatory sulfate reduction and the biosynthesis of all amino acids were predicted. Further, pathways for thiamine, riboflavin, NAD, pantothenate, coenzyme A, biotin, THF, menaquinone, and heme were identified. The closest cultivated relative is *Flavobacterium praedii* IMCC34515 (GCF_026810365.1), with an average amino acid identity of 85.51% and average nucleotide identity of 83.7%. Current GTDB classification (R220): d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__Flavobacterium; s__.

Classification

Bacteria » *Bacteroidota* » *Flavobacteriia* » *Flavobacteriales* » *Flavobacteriaceae* » *Flavobacterium* » *Flavobacterium rarum*

References

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

Registry URL

https://seqco.de/i:48736

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