Species *Sphingorhabdus rara*

Etymology

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

Nomenclatural type

NCBI Assembly: GCA_965234565.1 Ts

Reference Strain

Strain sc|0038958: RE-M21a

Description

Type strain is *Sphingorhabdus rara* RE-M21a (GCA_965234565.1), isolated from 0.5 m depth from the Římov Reservoir, Czechia (date: 2019-08-05), *via* high-throughput dilution to extinction cultivation. RE-M21a has a genome size of 3.2 Mbp with a genomic GC content of 57.5%, contains 3 rRNA genes and 45 tRNAs. The genome is a high-quality draft consisting of 4 contigs. The genome contains genes encoding rhodopsins and the biosynthetic pathway for retinal biosynthesis. No genes for flagellar or pilus assembly and chemotaxis were annotated. Pathways for taurine degradation, assimilatory sulfate reduction and methane/alkanesulfonate oxidation and the biosynthesis of all amino acids were predicted. Further, pathways for thiamine, riboflavin, pantothenate, NAD, coenzyme A, THF, and heme biosynthesis were identified. The closest cultivated relative is *Sphingorhabdus pulchriflava* GY_G (GCF_003367235.1), with an average amino acid identity of 76.8% and average nucleotide identity of 75.4%. Current GTDB classification (R220): d__Bacteria; p__Pseudomonadota; c__Alphaproteobacteria; o__Sphingomonadales; f__Sphingomonadaceae; g__Sphingorhabdus_B; s__Sphingorhabdus_B sp021298455.

Classification

Bacteria » *Pseudomonadota* » *Alphaproteobacteria* » *Sphingomonadales* » *Sphingomonadaceae* » *Sphingorhabdus* » *Sphingorhabdus rara*

References

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

Registry URL

https://seqco.de/i:48734

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