

Species *Tabrizicola 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_965234505.1](#) ^{Ts}

Reference Strain

[Strain sc|0038956](#): LH-M10

Description

Type strain is *Tabrizicola rara* LH-M10 (GCA_965234505.1), isolated from 50 m depth from Lake Lugano, Switzerland (date: 2019-11-05), *via* high-throughput dilution to extinction cultivation. LH-M10 has a genome size of 4.2 Mbp with a genomic GC content of 62.8%, contains 4 rRNA genes and 48 tRNAs. The genome is a high-quality draft consisting of 22 contigs. The genome contains the complete Calvin cycle for carbon fixation via RuBisCO. Genes for flagellar assembly were annotated in the genome. Pathways for urea and taurine degradation, glycolate oxidation and the biosynthesis of all amino acids were predicted. Further, pathways for riboflavin, coenzyme A, cobalamin, and heme biosynthesis were identified. The closest cultivated relative is *Rhodobacter thermarum* YIM 73036 (GCF_003574395.1; Basonym: *Tabrizicola thermarum* Khan et al. 2019), with an average amino acid identity of 75.7% and average nucleotide identity of 77.1%. Current GTDB classification (R220): d__Bacteria; p__Pseudomonadota; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Tabrizicola; s__Tabrizicola sp903917595.

Classification

Bacteria » *Pseudomonadota* » *Alphaproteobacteria* » *Rhodobacterales* » *Paracoccaceae* » *Tabrizicola* » *Tabrizicola rara*

References

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

Registry URL

<https://seqco.de/i:48735>

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)