Species *Allotabrizicola aquatica*^Ts

Etymology

[a.qua.ti'ca] **L. fem. adj.** *aquatica*, living or found in the water.

Nomenclatural type

NCBI Assembly: GCA_965194375.1 Ts

Reference Strain

Strain sc|0038957: RE-M30

Description

Type strain is *Allotabrizicola aquatica* RE-M30 (GCA_965194375.1), isolated from 0.5 m depth from the Římov Reservoir, Czechia (date: 2019-08-05), *via* high-throughput dilution to extinction cultivation. RE-M30 has a genome size of 3.6 Mbp with a genomic GC content of 61.9%, contains 6 rRNA genes and 49 tRNAs. The genome is a high-quality draft consisting of 20 contigs. The genome contains genes encoding anoxygenic aerobic phototrophy (*pufABLM*). 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, pantothenate, coenzyme A, and heme biosynthesis were identified. The closest cultivated relative is *Tabrizicola oligotrophica* KMS-5 (GCF_011008935.1), with an average amino acid identity of 79.2% and average nucleotide identity of 79.5%. Current GTDB classification (R220): d__Bacteria; p__Pseudomonadota; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Tabrizicola_A; s__.

Classification

Bacteria » *Pseudomonadota* » *Alphaproteobacteria* » *Rhodobacterales* » *Paracoccaceae* » *Allotabrizicola* » *Allotabrizicola aquatica*^Ts

References

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

Registry URL

https://seqco.de/i:48697

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