Species *Allorhodoferax aquaticus*^{Ts}

Etymology

[a.qua'ti.cus] **L. masc. adj.** *aquaticus*, living, growing, or found in or by the water, aquatic

Nomenclatural type

NCBI Assembly: GCA_965194715.1 ^{Ts}

Reference Strain

Strain sc|0038967: MsE-M22

Description

Type strain is *Allorhodoferax aquaticus* MsE-M22 (GCA_965194715.1), isolated from 5 m depth from Lake Most, Czechia (date: 2019-07-30), *via* high-throughput dilution to extinction cultivation. MsE-M22 has a genome size of 3.7 Mbp with a genomic GC content of 59.3%, contains 6 rRNA genes and 47 tRNAs. The genome is complete, consisting of a circular chromosome. Genes for flagellar and pilus assembly were annotated. Pathways for nitrate reduction, cyanate and urea degradation, glycolate oxidation and the biosynthesis of all amino acids except for aspartate were predicted. Further, pathways for thiamine, riboflavin, NAD, coenzyme A, THF, cobalamin, and heme biosynthesis were identified. The closest cultivated relative is *Curvibacter* sp. AEP1-3 (GCF_002163715.1), with an average amino acid identity of 90.7% and average nucleotide identity of 86.6%. Current GTDB classification (R220): d__Bacteria; p__Pseudomonadota; c__Gammaproteobacteria; o__Burkholderiales; f__Burkholderiaceae; g__Rhodoferax_C; s__Rhodoferax_C sp027488985.

Classification

Bacteria » *Pseudomonadota* » *Betaproteobacteria* » *Burkholderiales* » *Comamonadaceae* » *Allorhodoferax* » *Allorhodoferax aquaticus*^{Ts}

References

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

Registry URL

https://seqco.de/i:48704

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