Species *Rhabdaerophilum aquaticum*

Etymology
[a.qua.ti'cum] **L. neut. adj.** *aquaticum*, living or found in the water

Nomenclatural type
Genome sc|0003595 Ts

Reference Strain
Strain sc|0038955: MsE-M23

Description
Type strain is *Rhabdoaerophilum aquaticum* MsE-M23 (GCA_965234495.1), isolated from 5 m depth from Lake Most, Czechia (date: 2019-07-30), *via* high-throughput dilution to extinction cultivation. MsE-M23 has a genome size of 34 Mbp with a genomic GC content of 58.6%, contains 3 rRNA genes and 46 tRNAs. The genome is complete, consisting of a circular chromosome and one circular plasmid. Genes for flagellar assembly and chemotaxis were annotated in the genome. Pathways for cyanate and urea degradation, thiosulfate oxidation (Sox pathway), glycolate oxidation and the biosynthesis of all amino acids were predicted. Further, pathways for thiamine, riboflavin, NAD, coenzyme A, THF, and heme biosynthesis were identified. The closest cultivated relative is *Rhabdaerophilum calidifontis* SYSU G02060 (GCF_008641065.1), with an average amino acid identity of 66.3% and average nucleotide identity of 70.3%. Current GTDB classification (R220): d__Bacteria; p__Pseudomonadota; c__Alphaproteobacteria; o__Rhizobiales; f__Beijerinckiaceae; g__Rhabdaerophilum; s__.

Classification
Bacteria » *Pseudomonadota* » *Alphaproteobacteria* » *Hyphomicrobiales* » *Rhabdaerophilaceae* » *Rhabdaerophilum* » *Rhabdaerophilum aquaticum*

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

Registry URL
https://seqco.de/i:48703

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