Species *Mycobacterium aquicola*

Etymology

[a.qui'co.la] **L. fem. n.** *aqua*, water; **L. masc. suff.** *-cola*, inhabitant; **N.L. masc. n.** *aquicola*, inhabitant of water, referring to the the isolation source from a freshwater lake.

Nomenclatural type

NCBI Assembly: GCA_965234515.1 Ts

Reference Strain

Strain scJ0038945: MiE-22

Description

Type strain is *Mycobacterium aquicola* MiE-22 (GCA_965234515.1), isolated from 5 m depth from Lake Milada, Czechia (date: 2019-10-15), *via* high-throughput dilution to extinction cultivation. MiE-22 has a genome size of 3.4 Mbp with a genomic GC content of 66.3%, contains 3 rRNA genes and 57 tRNAs. The genome is a high-quality draft consisting of 3 contigs. The genome contains genes encoding rhodopsins. No genes for flagella or pilus assembly and chemotaxis were annotated. Pathways for taurine degradation, assimilatory sulfate reduction and the biosynthesis of all amino acids except for histidine and aspartate were predicted. Further, pathways for many vitamins and cofactors (riboflavin, pyridoxal, NAD, coenzyme A, biotin, tetrahydrofolate, heme, cobalamine and menaquinone) were identified. The closest cultivated relative is *Mycobacterium massilipolynesiensis* M26 (GCF_001494595.1), with an average amino acid identity of 71.31% and average nucleotide identity of 76.47%. Current GTDB classification (R220): d__Bacteria; p__Actinomycetota; c__Actinomycetia; o__Mycobacteriales; f__Mycobacteriaceae; g__Mycobacterium; s__Mycobacterium sp945897705.

Classification

Bacteria » *Actinomycetota* » *Actinomycetes* » *Mycobacteriales* » *Mycobacteriaceae* » *Mycobacterium* » *Mycobacterium aquicola*

References

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

Registry URL

https://seqco.de/i:48708

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