Species *Leadbetterella lacustris*

Etymology

[la.cus'tris] **N.L. fem. adj.** *lacustris*, of a lake; referring to the habitat from where the strain was isolated.

Nomenclatural type

NCBI Assembly: GCA_965234335.1 ^{Ts}

Reference Strain

Strain scJ0038947: RE-19

Description

Type strain is *Leadbetterella lacustris* RE-19 (GCA_965234335.1), isolated from 0.5 m depth from the Římov reservoir, Czechia (date: 2019-08-05), *via* high-throughput dilution to extinction cultivation. RE-19 has a genome size of 5 Mbp with a genomic GC content of 37.48 %, contains 9 rRNA genes and 36 tRNAs. The genome is a high-quality draft consisting of 36 contigs. The genome contains genes encoding rhodopsins. Genes for gliding motility (*gldBDHJKLMN*, *sprA*) were annotated in the genome. Pathways for assimilatory sulfate reduction, methane/alkanesulfonate oxidation and the biosynthesis of all amino acids were predicted. Further, pathways for riboflavin, NAD, coenzyme A, THF, menaquinone, and heme biosynthesis were identified. The closest cultivated relative is *Lacihabitans soyangensis* KCTC23259 (GCF_024343775.1), with an average amino acid identity of 85.5% and average nucleotide identity of 82.97%. *Lacihabitans* is grouped with the genus *Leadbetterella* in GTDB. Current GTDB classification (R220): d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Cytophagales; f__Spirosomaceae; g__Leadbetterella; s__Leadbetterella flu*via*le_A.

Classification

Bacteria » *Bacteroidota* » *Cytophagia* » *Cytophagales* » *Spirosomataceae* » *Leadbetterella* » *Leadbetterella lacustris*

References

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

Registry URL

https://seqco.de/i:48724

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