Species *Fontibacterium meridianamericanum*

Etymology

[me.ri.di.an.a.me.ri.ca'num] **L. masc. adj.** *meridianus*, Southerly, to the south; **N.L. neut. adj.** *americanum*, American; **L. neut. adj.** *meridianamericanum*, South American, referring to continent from the MAG was isolated

Nomenclatural type

NCBI Assembly: GCA_965235635.1 Ts

Description

Type genome is *Fontibacterium meridianamericanum* N-IMU-22jan24-050 (GCA_965235635.1), a metagenome-assembled genome (MAG) assembled from 0.5 m depth from Represa de India Muerta, a freshwater reservoir in Uruguay (date: 2024-01-22). N-IMU-22jan24-050 has a genome size of 1.0 Mbp with a genomic GC content of 29.3% and contains 30 tRNAs. The genome is of high quality, consisting of 4 contigs, with a completeness of 95.8%, contamination of 1.2% and strain heterogeneity of 100% as assessed with checkM. The metagenome was assembled with FLYE from combined long-and short-read sequencing (Oxford Nanopore and Illumina NovaSeq). Metagenomic fragment recruitment of >600 samples from five continents indicate that the species is present mainly in subtropical and tropical lakes in South America. The closest cultivated relatives are *Fontibacterium commune*, syn. '*Candidatus* Fonsibacter ubiquis' LSUCC0530 (GCF_002688585.1; later reclassified to '*Ca*. Allofontibacter communis'), with an average amino acid identity of 86.94% and average nucleotide identity of 84.39% and another newly proposed species, *Fontibacterium abundans* MiE-29 (GCA_965235095.1), with an AAI of 90.5% and an ANI of 88.11%. Current GTDB classification (R220): d__Bacteria; p__Pseudomonadota; c__Alphaproteobacteria; o__Pelagibacterales; f__Pelagibacteraceae; g__Fonsibacter; s__

Classification

Bacteria » *Pseudomonadota* » *Alphaproteobacteria* » *Pelagibacterales* » *Pelagibacteraceae* » *Fontibacterium* » *Fontibacterium meridianamericanum*

References

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

Registry URL

https://seqco.de/i:49882

References

1. Fernandes et al. (2025). Ecophysiology and global dispersal of the freshwater SAR11-IIIb genus Fontibacterium. *Nature Microbiology*. DOI:10.1038/s41564-025-02091-8