Species *Fontibacterium subtropicum*

Etymology

[sub.tro'pi.cum] **N.L. neut. adj.** *subtropicum*, pertaining to subtropical zone, the isolation source of the MAG.

Nomenclatural type

NCBI Assembly: GCA_965235415.1 Ts

Description

Type genome is *Fontibacterium subtropicum* N-SamH-20apr23-026 (GCA_965235415.1), a metagenome-assembled genome (MAG) assembled from 15 m depth from Lake Samsonvale, Australia (date: 2023-04-20). N-SamH-20apr23-026 has a genome size of 1.15 Mbp with a genomic GC content of 29.3%, contains 3 rRNA genes and 34 tRNAs. The genome is of high quality, consisting of 100 contigs, with a completeness of 100%, 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 lakes. 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 88.13% and average nucleotide identity of 85.63% and another newly proposed species, *Fontibacterium medardicus* ME-17 (GCA_965235075.1), with an AAI of 90.92% and an ANI of 88.79%. Current GTDB classification (R220): d__Bacteria; p__Pseudomonadota; c__Alphaproteobacteria; o__Pelagibacterales; f__Pelagibacteraceae; g__Fonsibacter; s__Fonsibacter sp023257975.

Classification

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

References

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

Registry URL

https://seqco.de/i:49877

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