Species *Fontibacterium universale*

Etymology

[u.ni.ver.sa'le] **L. neut. adj.** *universale*, universal, pertaining to the widespread distribution of the species

Nomenclatural type

NCBI Assembly: GCA_965236175.1 $^{\mathrm{Ts}}$

Description

Type genome is *Fontibacterium universale* N-InaE-25sep22-010 (GCA_965236175.1), a metagenome-assembled genome (MAG) assembled from 5 m depth from Lake Inawashiro, Japan (date: 2022-09-25). N-InaE-25sep22-010 has a genome size of 1.0 Mbp with a genomic GC content of 29.3% and contains 29 tRNAs. The genome is of high quality, consisting of 4 contigs, with a completeness of 98.8%, contamination of 0% and strain heterogeneity of 0% 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 in many lakes around the world. 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 87.08% and average nucleotide identity of 85.18% and another newly proposed species, *Fontibacterium abundans* MiE-29 (GCA_965235095.1), with an AAI of 92.44% and an ANI of 90.87%. Current GTDB classification (R220): d__Bacteria; p__Pseudomonadota; c__Alphaproteobacteria; o__Pelagibacterales; f__Pelagibacteraceae; g__Fonsibacter; s__Fonsibacter sp000371845.

Classification

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

References

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

Registry URL

https://seqco.de/i:49878

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