Species *Fontibacterium boreale*

Etymology

[bo.re.a'le] **L. neut. adj.** *boreale*, pertaining to the boreal region of the Northern hemisphere

Nomenclatural type

NCBI Assembly: GCA_903909545.1 ^{Ts}

Description

Type genome is *Fontibacterium boreale* Umea-bin-09620 (GCA_903909545.1), a metagenome-assembled genome (MAG) assembled from 1-5 m depth from Lake Bjarntjarnan, Sweden (date: 2018-01-01/07). Umea-bin-09620 has a genome size of 1 Mbp with a genomic GC content of 30.2% and contains 20 tRNAs. The genome is of high quality, consisting of 243 contigs, with a completeness of 96.4%, contamination of 0.1% and strain heterogeneity of 0% as assessed with checkM. The metagenome was assembled with Megahit (version 1.1.13) from short-read sequencing (Illumina MiSeq). Metagenomic fragment recruitment of >600 samples from five continents indicate that the species is present mainly in boreal lakes in Europe and North 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 82.49% and average nucleotide identity of 81.54 % and another newly proposed species, *Fontibacterium abundans* MiE-29 (GCA_965235095.1), with an AAI of 84.48% and an ANI of 83.54 %. 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 boreale*

References

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

Registry URL

https://seqco.de/i:49872

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