Species *Fontibacterium oligotrophicum*

Etymology

[o.li.go.tro'phi.cum] **Gr. masc. adj.** *oligo*, little; **Gr. masc. adj.** *trophikos*, nursing, tending; **N.L. neut. adj.** *oligotrophicum*, oligotrophic, referring to the low nutrient content of the isolation sites and the high abundance in oligotrophic lakes.

Nomenclatural type

NCBI Assembly: GCA_965235975.1 Ts

Description

Type genome is *Fontibacterium oligotrophicum* N-Balt2-05jul22-047 (GCA_965235975.1), a metagenome-assembled genome (MAG) assembled from 0.5 m depth from the slightly brackish part of Vistula Lagoon, Poland (date: 2022-07-05). N-Balt2-05jul22-047 has a genome size of 0.92 Mbp with a genomic GC content of 29.4% and contains 30 tRNAs. The genome is of high quality, consisting of 3 contigs, with a completeness of 96.4%, 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 highly abundant in oligotrophic lakes in temperate and subtropical regions. 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 92.57% and average nucleotide identity of 90.07% and another newly proposed species, *Fontibacterium medardicus* ME-17 (GCA_965235075.1), with an AAI of 85.45% and an ANI of 88.16%. Current GTDB classification (R220): d__Bacteria; p__Pseudomonadota; c__Alphaproteobacteria; o__Pelagibacterales; f__Pelagibacteraceae; g__Fonsibacter; s__Fonsibacter sp947497305.

Classification

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

References

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

Registry URL

https://seqco.de/i:49876

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