Species *Fontibacterium abundans*

Etymology

[a.bun'dans] **L. neut. part. adj.** *abundans*, abundant, referring to high global abundances.

Nomenclatural type

NCBI Assembly: GCA_965235095.1 Ts

Reference Strain

Strain sc|0038953: MiE-29

Description

Type strain is *Fontibacterium abundans* MiE-29 (GCA_965235095.1), isolated from 5 m depth from Lake Milada, Czechia (date: 2019-10-15), *via* high-throughput dilution to extinction cultivation. MiE-29 has a genome size of 1.1 Mbp with a genomic GC content of 29.4%, contains 3 rRNA genes and 31 tRNAs. The genome is a high-quality draft consisting of 2 contigs. The genome contains genes encoding rhodopsins and the biosynthetic pathway for retinal biosynthesis. No genes for flagella or pilus assembly and chemotaxis were annotated. Pathways for glycolate oxidation and the biosynthesis of 16 amino acids were predicted. Further, pathways for riboflavin, NAD, coenzyme A, and heme biosynthesis were identified. 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 86.5% and average nucleotide identity of 85.2% and another newly proposed species, *Fontibacterium medardicum* ME-17 (GCA_965235075.1), with an AAI of 92.7% and an ANI of 91.1%. 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 abundans*

References

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

Registry URL

https://seqco.de/i:48693

References

1. Salcher et al. (2025). Bringing the uncultivated microbial majority of freshwater ecosystems into culture. *Nature Communications*. DOI:10.1038/s41467-025-63266-9