Species *Fontibacterium baikalense*

Etymology

[ba.i.ka.len'se] **N.L. neut. adj.** *baikalense*, of Baikal, referring to Lake Baikal, where this organism was identified

Nomenclatural type

NCBI Assembly: GCA_009693745.1 ^{Ts}

Description

Type genome is *Fontibacterium baikalense* Baikal-deep-G36 (GCA_009693745.1), a metagenome-assembled genome (MAG) co-assembled from 1250 m and 1350 m depth from Lake Baikal, Russia (date: 2018-03-29). Baikal-deep-G36 has a genome size of 1 Mbp with a genomic GC content of 29.4%, contains 2 rRNA genes and 25 tRNAs. The genome is of high quality, consisting of 66 contigs, with a completeness of 95.2%, contamination of 3.9% and strain heterogeneity of 100% as assessed with checkM. The metagenome was assembled with IDBA-UD assembler from short-read sequencing (Illumina HiSeq 3000/4000). 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 85.75% and average nucleotide identity of 84.65% and another newly proposed species, *Fontibacterium medardicus* ME-17, with an AAI of 88.73% and an ANI of 87.93%. Current GTDB classification (R220): d__Bacteria; p__Pseudomonadota; c__Alphaproteobacteria; o__Pelagibacterales; f__Pelagibacteraceae; g__Fonsibacter; s__Fonsibacter sp009693745.

Classification

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

References

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

Registry URL

https://seqco.de/i:49754

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