

Species *Pelagibacter malawiensis*

Etymology

[ma.la.wi.en'sis] **N.L. masc. adj.** *malawiensis*, pertaining to Lake Malawi, the origin of the metagenome-assembled genome

Nomenclatural type

[NCBI Assembly: GCA_965235955.1](#) ^{Ts}

Description

Type genome is *Pelagibacter malawiensis* N-Mw13-23nov23-053 (GCA_965235955.1), a metagenome-assembled genome (MAG) assembled from 5 m depth from Lake Malawi, Malawi (date: 2023-11-23). N-Mw13-23nov23-053 has a genome size of 1 Mbp with a genomic GC content of 29.4%, contains 3 rRNA genes and 28 tRNAs. The genome is of high quality, consisting of 7 contigs, with a completeness of 99.5%, contamination of 0.5% 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). The closest cultivated relatives are '*Candidatus Pelagibacter ubique* SAR11 HTCC9022 (GCF_000472565.1), with an average amino acid identity of 75% and average nucleotide identity of 76.4% and '*Candidatus Pelagibacter ubique* SAR11 HTCC7211 (GCF_000155895.1), with an AAI of 74.2% and an ANI of 76.4%. Current GTDB classification (R220): d__Bacteria; p__Pseudomonadota; c__Alphaproteobacteria; o__Pelagibacterales; f__Pelagibacteraceae; g__Pelagibacter; s__Pelagibacter sp016870175.

Classification

Bacteria » *Pseudomonadota* » *Alphaproteobacteria* » *Pelagibacterales* » *Pelagibacteraceae* » *Pelagibacter* » *Pelagibacter malawiensis*

References

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

Registry URL

<https://seqco.de/i:49883>

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