Species *Planktophila fontis*

Etymology
[fon'tis] **L. masc. gen. n.** *fontis*, of a spring

Nomenclatural type
Genome sc|0004096 Ts

Description
Etymology. It is named ‘fontis’ from the genitive singular Latin form of ‘fons’, meaning fresh water source.
Brief description. *Planktophila fontis* LanE-86 (ENA accession number GCA_965267645) was isolated from the epilimnion (5m depth) of Landštejn Reservoir, Czech Republic (date: 2020-07-30) and it is the representative genome for the species. The strain MRE-249 (GCA_965268255) belongs to the same species and it was isolated from the Římov Reservoir (Czech Republic) on 2021-11-01; these two strains share an average nucleotide identity of 96.87%. The circular genome of the representative isolate has 1,465,205 bp, a GC content of 47.7%, and a coding density of 96%. It encodes one rRNA operon and 41 tRNA genes. The closest cultivated species to is *Planktophila dulcis* Pe-89, with whom it shares an average nucleotide identity of 92%. Recruitment analysis indicates that *P. fontis* is relatively widespread and abundant in the environment, including the Delaware River and Bay (USA), Lake Stechlin, Tiefwaren and Breiter Luzin (Germany), Lake Inawashiro (Japan), Římov and Landštejn Reservoirs (Czech Republic), and boreal lakes such as Lake Botsford, Paradise, Simoncouche (Canada) and Lake Lomtjärnan and Odrolstjärnan (Sweden). It encodes for a complete pentose phosphate pathway, both an actinorhodopsin and a heliorhodopsin, and for the retinal biosynthesis pathway. The strains differ in their ability to synthesize amino acids. The Current GTDB classification (r220) is d__Bacteria;p__Actinomycetota;c__Actinomycetia;o__Nanopelagicales;f__Nanopelagicaceae; g__Planktophila; s__.

Classification
Bacteria » *Actinomycetota* » *Actinomycetes* » *Nanopelagicales* » *Nanopelagicaceae* » *Planktophila* » *Planktophila fontis*

References
Effective publication: Chiriac et al., 2025 [1]

Registry URL
https://seqco.de/i:51480

References

1. Chiriac et al. (2025). Ecological success in freshwater lakes: insights from novel cultivated lineages of the abundant Nanopelagicales order. *Microbiome*. DOI: 10.1186/s40168-025-02272-x