

## Species *Planktophila vernalis*

### Etymology

[ver.na'lis] **L. fem. adj.** *vernalis*, belonging to spring; referring to high abundances in spring

### Nomenclatural type

[NCBI Assembly: GCA\\_002288185.1](#) <sup>Ts</sup>

### Reference Strain

[Strain sc|0038986](#): MMS-IIA-15

### Description

Type genome is *Planktophila vernalis* MMS-IIA-15 (GCF\_002288185.1), which was isolated via dilution-to-extinction cultivation from Lake Zurich, Switzerland. Curved rods with lengths of  $0.43 \pm 0.12$   $\mu\text{m}$  and diameters of  $0.26 \pm 0.05$   $\mu\text{m}$ . The initial pure culture was lost after a few propagations to fresh medium; no growing culture is available. The initial culture grew well in sterile lake water amended with minimal carbon medium, vitamins and amino acids.

*Planktophila vernalis* MMS-IIA-15 has a genome size of 1.36 Mbp and a genomic GC content of 45.7%. The genome is complete, consisting of a circular chromosome and contains 3 rRNA genes and 39 tRNAs. It is auxotrophic for reduced sulfur sources, serine, and several vitamins (B1, B5, B7, B12) and possesses rhodopsins. *Planktophila vernalis* can be recognized by the presence of the diagnostic oligonucleotide sequence 5'-AACTACTACCACACCGGTTTCG-3' in the 23S rRNA gene (positions 1420-1441, E. coli numbering). Basis for the assignment is a phylogenomic tree of 476 concatenated protein sequences, phylogenetic analysis of 16S rRNA, 23S rRNA, and rhodopsin genes, as well as average nucleotide and amino acid identities presented in Neuenschwander et al. (2018, ISMEJ, doi: 10.1038/ismej.2017.156). The closest cultivate relatives are *Planktophila* sp. IMCC19121 (GCA\_002284895) and *Planktophila limnetica* MMS-VB-114 (GCF\_002288365.1) with average amino acid identities of 93.1 and 72.1%, respectively, and average nucleotide identities of 89.7 and 71.3%, respectively.

### Classification

*Bacteria* » *Actinomycetota* » *Actinomycetes* » *Nanopelagicales* » *Nanopelagicaceae* » *Planktophila* » *Planktophila vernalis*

### References

Effective publication: Neuenschwander et al., 2018 [1]

### Registry URL

<https://seqco.de/i:23846>

## References

1. Neuenschwander et al. (2018). Microdiversification in genome-streamlined ubiquitous freshwater Actinobacteria. *The ISME Journal*. DOI:10.1038/ismej.2017.156