Species *Nanopelagicus hibericus*

Etymology
[hi.be'ri.cus] **L. masc. adj.** *hibericus*, Spanish; referring to a high abundance in two Spanish reservoirs

Nomenclatural type
NCBI Assembly: GCF_002288005.1 [Ts]

Reference Strain
Strain sc|0038984: MMS-21-160

Description
Type genome is *Nanopelagicus hibericus* MMS-21-160 (GCF_002288005.1), which was isolated via dilution-to-extinction cultivation from Lake Zurich, Switzerland. Curved rods with lengths of 0.33±0.07 µm and diameters of 0.24±0.03 µm. 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. *Nanopelagicus hibericus* MMS-21-160 has a genome size of 1.22 Mbp and a genomic GC content of 42.4%. The genome is complete, consisting of a circular chromosome and contains 3 rRNA genes and 38 tRNAs. It is auxotrophic for reduced sulfur sources, several amino acids (ornithine, histidine, betaine) and several vitamins (B1, B2, B5, B7, B12) and possesses rhodopsins. Members of the genus *Nanopelagicus* can be recognized by the presence of the diagnostic oligonucleotide sequence 5'-ACAAGAGGTTCGTCCGTCC-3' in the 23S rRNA gene (positions 2669-2688, *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 *Nanopelagicus limnes* MMS-21-122 (GCF_002287885.2) and *Nanopelagicus abundans* MMS-IIB-91 (GCF_002288305.1) with average amino acid identities of 84.5 and 80.7%, respectively, and average nucleotide identities of 78.6 and 76.2%, respectively.

Classification
Bacteria » *Actinomycetota* » *Actinomycetes* » *Nanopelagicales* » *Nanopelagicaceae* » *Nanopelagicus* » *Nanopelagicus hibericus*

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

Registry URL
https://seqco.de/i:23845

References

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