

Planktophila gen. nov.

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Order *Nanopelagicales*

Etymology

[Na.no.pe.la.gi.ca'les] **N.L. masc. n.** *Nanopelagicus*, referring to the type genus *Nanopelagicus*; **-ales**, ending to denote an order; **N.L. fem. pl. n.** *Nanopelagicales*, the *Nanopelagicus* order

Nomenclatural type

Genus *Nanopelagicus*

Description

The order *Nanopelagicales* was proposed as *Candidatus* order by Neuenschwander et al. (2018, ISMEJ, doi: 10.1038/ismej.2017.156). It contains the family *Nanopelagicaceae* and two genera, *Nanopelagicus* and *Planktophila*, type strain for the order is *Nanopelagicus abundans* MMS-IIB-91 (GCF_002288305.1). Basis of the assignment is a phylogenetic tree of 48 conserved concatenated proteins of >100 complete genomes of all orders of Actinobacteria in Neuenschwander et al. (2018, ISMEJ, doi: 10.1038/ismej.2017.156). Aerobic chemoheterotrophs. Cells are tiny, non-motile, and inhabit the plankton of freshwaters. The order is also known as *acl* or *hgc1* (SILVA classification) from 16S rRNA based studies and is one of the most abundant microbes in freshwater lakes. *Nanopelagicaceae* can be recognized by the presence of the diagnostic oligonucleotide sequence 5'-AATGCGTTAGCTGCGTCGCA-3' in the 16S rRNA gene (positions 852-872, *E. coli* numbering). The initial pure cultures were lost after a few propagations to fresh medium, they were isolated in sterile lake water amended with minimal carbon medium, vitamins and amino acids, no growth was observed in rich medium or on agar plates. No growing culture of *Nanopelagicus* sp. is available, while some *Planktophila* sp. strains are actively growing in autoclaved lake water (Kim et al. 2019, ISMEJ, doi: 10.1038/s41396-019-0432-x) or artificial media (Salcher et al., in review). None of the isolated strains were yet submitted to a culture collection because these bacteria are hard to maintain, i.e., they are very slowly growing, reach low densities in liquid culture, and do not grow on agar plates.

Classification

Bacteria » *Actinomycetota* » *Actinomycetes* » *Nanopelagicales*

References

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

Registry URL

<https://seqco.de/i:23833>

Family *Nanopelagicaceae*

Etymology

[Na.no.pe.la.gi.ca'ce.ae] **N.L. masc. n.** *Nanopelagicus*, referring to the type genus *Nanopelagicus*; **-aceae**, ending to denote a family; **N.L. fem. pl. n.** *Nanopelagicaceae*, the *Nanopelagicus* family

Nomenclatural type

Genus *Nanopelagicus*

Description

The family *Nanopelagicaceae* and the order *Nanopelagicales* were proposed as *Candidatus* taxa by Neuenschwander et al. (2018, ISMEJ, doi: 10.1038/ismej.2017.156). It contains two genera, *Nanopelagicus* and *Planktophila*, type strain for the family is *Nanopelagicus abundans* MMS-IIB-91 (GCF_002288305.1). Basis of the assignment is a phylogenetic tree of 48 conserved concatenated proteins of >100 complete genomes of all orders of Actinobacteria in Neuenschwander et al. (2018, ISMEJ, doi: 10.1038/ismej.2017.156). Aerobic chemoheterotrophs. Cells are tiny, non-motile, and inhabit the plankton of freshwaters. The family is also known as *acl* or *hgc1* (SILVA classification) from 16S rRNA based studies and is one of the most abundant microbes in freshwater lakes. *Nanopelagicaceae* can be recognized by the presence of the diagnostic oligonucleotide sequence 5'-AATGCGTTAGCTGCGTCGCA-3' in the 16S rRNA gene (positions 852-872, *E. coli* numbering). The initial pure cultures were lost after a few propagations to fresh medium; no growing culture is available. The initial pure cultures were lost after a few propagations to fresh medium, they were isolated in sterile lake water amended with minimal carbon medium, vitamins and amino acids, no growth was observed in rich medium or on agar plates. No growing culture of *Nanopelagicus* sp. is available, while some *Planktophila* sp. strains are actively growing in autoclaved lake water (Kim et al. 2019, ISMEJ, doi: 10.1038/s41396-019-0432-x) or artificial media (Salcher et al., in review). None of the isolated strains were yet submitted to a culture collection because these bacteria are hard to maintain, i.e., they are very slowly growing, reach low densities in liquid culture, and do not grow on agar plates.

Classification

Bacteria » *Actinomycetota* » *Actinomycetes* » *Nanopelagicales* » *Nanopelagicaceae*

References

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

Registry URL

<https://seqco.de/i:23843>

Genus *Nanopelagicus*

Etymology

[Na.no.pe.la'gi.cus] **N.L. masc. adj.** *nano*, very small; **L. masc. adj.** *pelagicus*, belonging to the pelagial; **N.L. masc. n.** *Nanopelagicus*, very small pelagic; referring to the small cell and genome size and the pelagic habitat

Nomenclatural type

Species *Nanopelagicus abundans*^{TS}

Description

The genus *Nanopelagicus* as well as the family *Nanopelagicaceae* and order *Nanopelagicales* was proposed as *Candidatus* by Neuenschwander et al. (2018, ISMEJ, doi: 10.1038/ismej.2017.156). Three strains were isolated from Lake Zurich, Switzerland, that were proposed as *Nanopelagicus abundans*, *Nanopelagicus limnes* and *Nanopelagicus hibericus*, type strain for the genus is *Nanopelagicus abundans* MMS-IIB-91 (GCF_002288305.1). Basis of the assignment is a phylogenetic tree of 48 conserved concatenated proteins of >100 complete genomes of all orders of Actinobacteria in Neuenschwander et al. (2018, ISMEJ, doi: 10.1038/ismej.2017.156). The closest cultivated relatives are *Planktophilia* sp. with average amino acid identities of 62-63.9% and average nucleotide identities of 65.9-68.1%. Aerobic chemoheterotrophs. Cells are tiny, non-motile, and inhabit the plankton of freshwaters. The genus is also known as *aci-B1* or *hgc1* (SILVA classification) from 16S rRNA based studies and is one of the most abundant genera in freshwater lakes. Members of the genus *Nanopelagicus* can be recognized by the presence of the diagnostic oligonucleotide sequence 5'-ACAAGAGGTTCTCGTCCGTCC-3' in the 23S rRNA gene (positions 2669-2688, *E. coli* numbering). The initial pure cultures were lost after a few propagations to fresh medium; no growing culture is available. The initial cultures grew well in sterile lake water amended with minimal carbon medium, vitamins and amino acids.

Classification

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

References

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

Registry URL

<https://seqco.de/i:23834>

Genus *Planktophila*

Etymology

[Plan.kto.phi'la] **N.L. neut. n.** *plankton*, plankton; **N.L. fem. adj.** *phila*, friendly to; **N.L. fem. adj.** *Planktophila*, the friend fo plankton

Nomenclatural type

Species *Planktophila limnetica*^{Ts}

Description

The name *Planktophila* was initially proposed in Jezbera et al. 2009 based on a enrichment culture, with 'Ca. Planktophila limnetica' strain MWH-EgelM2-3.acl as type strain. Initial description: Represented by the aerobic strain MWH-EgelM2-3.acl, which was isolated from a small lake near Salzburg, Austria. Curved rods with lengths of 1.0–1.5 mm and diameters of 0.4–0.5 mm. No pure culture is available. Contained in a stable mixed culture together with 'Candidatus Limnoluna rubra' and a *Polynucleobacter necessarius* subsp. *asymbioticus* strain. The mixed culture grows well in liquid NSY medium. Supplementation of NSY medium with L-alanine results in an increase of the relative proportion of 'Ca. Planktophila limnetica' by more than one order of

magnitude. 'Ca. Planktophila limnetica' can be recognized by the presence of the diagnostic oligonucleotide sequence 5'-GAAACTTGGTGGCATCRCCG-3' in the 16S rRNA gene (positions 183–193, E. coli numbering). Phylogenetic analysis of the 16S rRNA gene sequence indicated the affiliation of the Candidatus taxon with the order Actinomycetales.

The genus description was later amended with the first genome-sequenced strains (Neuenschwander et al. 2018) and strain *Planktophila limnetica* MMS-VB-114 (GCF_002288365.1) as type strain.

Classification

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

References

Effective publication: Neuenschwander et al., 2018 [1]
Original (not valid) publication: Jezbera et al., 2009 [2]

Registry URL

<https://seqco.de/i:23847>

Species *Nanopelagicus abundans*^{Ts}

Etymology

[a.bun'dans] **L. masc. part. adj.** *abundans*, abundant; referring to high global abundances

Nomenclatural type

[NCBI Assembly: GCF_002288305.1](#)^{Ts}

Reference Strain

[Strain sc|0038983](#): MMS-IIB-91

Description

Type genome is *Nanopelagicus abundans* MMS-IIB-91 (GCF_002288305.1), which was isolated via dilution-to-extinction cultivation from Lake Zurich, Switzerland. Curved rods with lengths of 0.46 ± 0.47 μm and diameters of 0.26 ± 0.20 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 abundans MMS-IIB-91 has a genome size of 1.16 Mbp and a genomic GC content of 40.2%. The genome is complete, consisting of a circular chromosome and contains 3 rRNA genes and 39 tRNAs. It is auxotrophic for reduced sulfur sources, several amino acids (methionine, lysine, ornithine, histidine, betaine) and several vitamins (B1, B5, B7, B12) and possesses rhodopsins. Members of the genus *Nanopelagicus* can be recognized by the presence of the diagnostic oligonucleotide sequence 5'-ACAAGAGGTTCTCGTCCGTCC-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 hibericus* MMS-21-160 (GCF_002288005.1) with average amino acid identities of 81 and 80.7%, respectively, and average nucleotide identities of 77.1 and 76.2%, respectively.

Classification

Bacteria » *Actinomycetota* » *Actinomycetes* » *Nanopelagicales* » *Nanopelagicaceae* » *Nanopelagicus* » *Nanopelagicus abundans*^{Ts}

References

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

Registry URL

<https://seqco.de/i:23835>

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 $0.33 \pm 0.07 \mu\text{m}$ and diameters of $0.24 \pm 0.03 \mu\text{m}$. 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. *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>

Species *Nanopelagicus limnae*

Etymology

[lim'nae] **Gr. fem. n.** *limnê*, lake; **N.L. gen. fem. n.** *limnae*, of a lake, referring to the habitat

Nomenclatural type

[NCBI Assembly: GCF_002287885.2](#) ^{Ts}

Reference Strain

[Strain sc|0038985](#): MMS-21-122

Description

Type genome is *Nanopelagicus limnes* MMS-21-122 (GCF_002287885.2), which was isolated via dilution-to-extinction cultivation from Lake Zurich, Switzerland. Curved rods with lengths of $0.45 \pm 0.09 \mu\text{m}$ and diameters of $0.25 \pm 0.03 \mu\text{m}$. 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. *Nanopelagicus limnes* MMS-21-122 has a genome size of 1.24 Mbp and a genomic GC content of 41.5%. 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 (proline, 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'-ACAAGAGGTTTCGTCCGTCC-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 hibericus* MMS-21-160 (GCF_002288005.1) and *Nanopelagicus abundans* MMS-IIB-91 (GCF_002288305.1) with average amino acid identities of 84.5 and 81%, respectively, and average nucleotide identities of 78.6 and 77.1%, respectively.

Classification

Bacteria » *Actinomycetota* » *Actinomycetes* » *Nanopelagicales* » *Nanopelagicaceae* » *Nanopelagicus* » *Nanopelagicus limnae*

References

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

Corrigendum: Oren et al., 2020 [3] (from “*Nanopelagicus limnes*”)

Registry URL

<https://seqco.de/i:23844>

Species *Planktophila dulcis*

Etymology

[dul'cis] **L. fem. adj.** *dulcis*, sweet; referring to a high diversity of sugar transporters and metabolism

Nomenclatural type

[NCBI Assembly: GCF_002288225.1](#) ^{Ts}

Reference Strain

[Strain sc|0038989](#): MMS-IIA-65

Description

Type genome is *Planktophila dulcis* MMS-IIA-65 (GCF_002288225.1), which was isolated via dilution-to-extinction cultivation from Lake Zurich, Switzerland. Curved rods with lengths of $0.44 \pm 0.09 \mu\text{m}$ and diameters of $0.26 \pm 0.03 \mu\text{m}$. 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 dulcis* MMS-IIA-65 has a genome size of 1.35 Mbp and a genomic GC content of 48.0%. The genome is complete, consisting of a circular chromosome and contains 3 rRNA genes and 40 tRNAs. It is auxotrophic for reduced sulfur sources, betaine, and several vitamins (B1, B5, B7, B12) and possesses rhodopsins. 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 rubra* IMCC25003 (GCA_002284855) and *Planktophila sulfonica* MMS-IIA-56 (GCF_002288065.1) with average amino acid identities of 89.6 and 89.4%, respectively, and average nucleotide identities of 82.1 and 81.9%, respectively.

Classification

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

References

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

Registry URL

<https://seqco.de/i:42384>

Species *Planktophila lacus*

Etymology

[la'cus] **L. gen. n.** *lacus*, of a lake

Nomenclatural type

[NCBI Assembly: GCF_002287925.1](#) ^{Ts}

Reference Strain

[Strain sc|0038990](#): MMS-21-148

Description

Type genome is *Planktophila lacus*MMS-21-148 (GCF_002287925.1), which was isolated via dilution-to-extinction cultivation from Lake Zurich, Switzerland. Curved rods with lengths of $0.41 \pm 0.10 \mu\text{m}$ and diameters of $0.30 \pm 0.06 \mu\text{m}$. 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 lacus*MMS-21-148 has a genome size of 1.46 Mbp and a genomic GC content of 47.5%. The genome is complete, consisting of a circular chromosome and contains 3 rRNA genes and 41 tRNAs. It is auxotrophic for reduced sulfur sources, betaine, and several vitamins (B1, B5, B7, B12) and possesses rhodopsins. 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 aquatilis* IMCC26103 (GCA_002284875) and *Planktophila rubra* IMCC25003 (GCA_002284855) with average amino acid identities of 84.1 and 74.4%, respectively, and average nucleotide identities of 77.9 and 72.6%, respectively.

Classification

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

References

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

Registry URL

<https://seqco.de/i:42470>

Species *Planktophila limnetica*^{Ts}

Etymology

[lim.ne.ti'ca] **N.L. fem. adj.** *limnetica*, pertaining to lakes

Nomenclatural type

[NCBI Assembly: GCF_002288365.1](#)^{Ts}

Reference Strain

[Strain sc|0038937](#): MMS-VB-114

Description

We propose the genome of strain MMS-VB-114 (GCF_002288365.1) as type for *Planktophila limnetica* and as type of the genus *Planktophila* as the original strain was never genome-sequenced. According to the previous description of a mixed culture (MWH-EgelM2-3.acl) ([Jezbera et al., 2009](#)) that has a 100% identical 16S rRNA gene sequences with strain MMS-VB-114, we propose the name *Planktophila limnetica* for strain MMS-VB-114 and make an amended description based on a complete genome. Represented by strain MMS-VB-114, which was isolated from Lake Zurich, Switzerland. Curved rods with lengths of 0.38 ± 0.10 μm and diameters of 0.25 ± 0.06 μm (see Table S3, Figure S1 in Neuenschwander et al. 2018). 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 pyruvate, urea, vitamins, and amino acids. *P. limnetica* MMS-VB-114 has a genome size of 1.33 Mbp and a genomic GC content of 45.0 %. It is auxotrophic for reduced sulfur sources and vitamins (B1, B5, B7), and possesses rhodopsins (see Table S7 in Neuenschwander et al. 2018). A complete genome is available at Genbank (GCF_002288365.1). Phylogenetic analyses of 476 concatenated protein sequences, 16S rRNA, 23S rRNA, and rhodopsin genes, as well as average nucleotide identities and protein similarities indicated the affiliation of the taxon to the family *Nanopelagicaceae* and the order *Nanopelagicales*.

Classification

Bacteria » *Actinomycetota* » *Actinomycetes* » *Nanopelagicales* » *Nanopelagicaceae* » *Planktophila* » *Planktophila limnetica*^{Ts}

References

Effective publication: Neuenschwander et al., 2018 [1]
Original (not valid) publication: Jezbera et al., 2009 [2]

Registry URL

<https://seqco.de/i:164>

Species *Planktophila sulfonica*

Etymology

[sul.fo.ni'ca] **N.L. fem. adj.** *sulfonica*, pertaining to sulfonate; referring to sulfonate transporters

Nomenclatural type

[NCBI Assembly: GCF_002288065.1](#) ^{Ts}

Reference Strain

[Strain sc|0038987](#): MMS-IA-56

Description

Type genome is *Planktophila sulfonica* MMS-IA-56 (GCF_002288065.1), which was isolated via dilution-to-extinction cultivation from Lake Zurich, Switzerland. Curved rods with lengths of $0.50\pm 0.14\ \mu\text{m}$ and diameters of $0.28\pm 0.06\ \mu\text{m}$. 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 sulfonica* MMS-IA-56 has a genome size of 1.34 Mbp and a genomic GC content of 48.6%. The genome is complete, consisting of a circular chromosome and contains 3 rRNA genes and 39 tRNAs. It is auxotrophic for reduced sulfur sources, betaine, and several vitamins (B1, B5, B7, B12) and possesses rhodopsins. 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 rubra* IMCC25003 (GCA_002284855) and *Planktophila dulcis* MMS-IIA-65 (GCF_002288225.1) with average amino acid identities of 90.8 and 89.4%, respectively, and average nucleotide identities of 83.7 and 81.9%, respectively.

Classification

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

References

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

Registry URL

<https://seqco.de/i:43170>

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](#) ^{Ts}

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 ± 0.12 μm and diameters of 0.26 ± 0.05 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.

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>

Species *Planktophila versatilis*

Etymology

[ver.sa.ti'lis] **L. fem. adj.** *versatilis*, versatile; referring to high metabolic versatility

Nomenclatural type

[NCBI Assembly: GCF_002288105.1](#) ^{Ts}

Reference Strain

[Strain sc|0038988](#): MMS-IA-79

Description

Type genome is *Planktophila versatilis* MMS-IA-79 (GCF_002288105.1), which was isolated via dilution-to-extinction cultivation from Lake Zurich, Switzerland. Curved rods with lengths of 0.45 ± 0.10 μm and diameters of 0.27 ± 0.04 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.

Planktophila versatilis MMS-IA-79 has a genome size of 1.33 Mbp and a genomic GC content of 48.2%. The genome is complete, consisting of a circular chromosome and contains 3 rRNA genes and 38 tRNAs. It is auxotrophic for reduced sulfur sources, betaine, and several vitamins (B1, B5, B7, B12) and possesses rhodopsins. 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 dulcis* MMS-IIA-65 (GCF_002288225.1) and *Planktophila sulfonica* MMS-IA-56 (GCF_002288065.1) with average amino acid identities of 82.4 and 82.0%, respectively, and average nucleotide identities of 76.8 and 76.2%, respectively.

Classification

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

References

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

Registry URL

<https://seqco.de/i:42262>

References

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2. Jezbera et al. (2009). 'Candidatus Planktophila limnetica', an actinobacterium representing one of the most numerically important taxa in freshwater bacterioplankton. *INTERNATIONAL JOURNAL OF SYSTEMATIC AND EVOLUTIONARY MICROBIOLOGY*. DOI:10.1099/ijs.0.010199-0
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Register List Certificate of Validation

On behalf of the *Committee on the Systematics of Prokaryotes Described from Sequence Data* (SeqCode Committee), we hereby certify that the Register List **seqco.de/r:kv6gij82** submitted by **Salcher, Michaela M** and including 13 new names has been successfully validated.

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