Register list for 26 new names including Aquilimus gen. nov.

Submitted by Layoun, Paul

Genus *Aquilimus*

Etymology

[A.qui.li'mus] **L. fem. n.** *aqua*, water; **L. masc. n.** *limus*, silt or alluvies; **N.L. masc. n.** *Aquilimus*, a microbe from alluvial or pelagial zones of freshwaters

Nomenclatural type

Species *Aquilimus communis*^{Ts}

Description

The isolates have streamlined circular genomes with sizes between 1.37 and 1.44 Mb, low GC content for *Actinomycetota*, ranging from 43.3 to 45%, and high coding densities ~95.6%. All isolates encode one rRNA operon and between 37 to 42 tRNA genes. They are auxotrophic for some amino acids and vitamins. They encode for actinorhodopsins, heliorhodopsins, and the biosynthesis pathway of the retinal. Recruitment analysis of 1720 metagenomes suggests that *Aquilimus* members are not particularly abundant, although some species are distributed on different continents and seem to be constantly recovered throughout the year, at least in the case of the Římov Reservoir (Czech Republic). The current GTDB classification (r220) is d__Bacteria;p__Actinomycetota; c__Actinomycetes;o__Nanopelagicales; f__Nanopelagicaceae;g__AAA044-D11.

Classification

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

References

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

Registry URL

https://seqco.de/i:51011

Species *Aquilimus communis*[Ts]

Etymology
[com.mu'nis] **L. masc. adj.** *communis*, common

Nomenclatural type
Genome sc|0003638 [Ts]

Description
Etymology. The species name ‘communis’ refers to the fact that the specie is found in a wide range of water environments, from rivers and bays to freshwater lakes.
Brief description. The genome of *A. communis* MZLE-42 (ENA accession number GCA_965268555) had a coding density of 96.78%, and the circular, complete genome has a size of 1,377,870 bp. The species has a GC content of 44.9%, which is similar to other representatives of this order. It possesses one rRNA operon and 39 tRNA genes. It was isolated from the epilimnion (0.5 m depth) of the Žlutice Reservoir, but recruitment analysis also show that it is present in the Římov Reservoir (Czech Republic), Lake Biwa (Japan), and in Delaware River and Bay (USA). It has an average nucleotide identity between 77 – 82% with other isolates on this genus, the closest one being *A. zluticensis* MZLE-12. Current GTDB classification (r220) is d__Bacteria;p__Actinomycetota;c__Actinomycetes;o__Nanopelagicales; f__Nanopelagicaceae; g__AAA044-D11;s__.

Classification
Bacteria » *Actinomycetota* » *Actinomycetes* » *Nanopelagicales* » *Nanopelagicaceae* » *Aquilimus* » *Aquilimus communis*[Ts]

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

Registry URL
https://seqco.de/i:51025

Species *Aquilimus klicavensis*

Etymology
[kli.ca.ven'sis] **N.L. masc. adj.** *klicavensis*, from the Klíčava Reservoir in the Czech Republic.

Nomenclatural type
Genome sc|0004102 [Ts]

Description
Etymology. The species name ‘klicavensis’ refers to the isolation source, the Klíčava Reservoir in the Czech Republic.
Brief description. The genome of *A. klicavensis* MKE-157 (ENA accession number GCA_965268275) is compact, with a complete genome size of 1,396,091 base pairs (bp). This species exhibits a CG content of 44.6%, which is typical of *Nanopelagicales* order. It possesses one rRNA operon and 37 tRNA genes. It is very rarely found in nature, a few examples being lake Breiter Luzin and Stechlin in Germany. Current GTDB classification (r220) is d__Bacteria;p__Actinomycetota;c__Actinomycetes;o__Nanopelagicales; f__Nanopelagicaceae; g__AAA044-D11;s__. The closest cultivated representative in this study is *A. parvus* MZLE-22, sharing an ANI of 77.9%.

Classification
Bacteria » *Actinomycetota* » *Actinomycetes* » *Nanopelagicales* » *Nanopelagicaceae* » *Aquilimus* » *Aquilimus klicavensis*

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

Registry URL
https://seqco.de/i:51012

Species *Aquilimus modestus*

Etymology
[mo.des'tus] **L. masc. adj.** *modestus*, modest, referring to modest or low abundance in which the species is present in the environment

Nomenclatural type
Genome sc|0004103 Ts

Description
Etymology. The name ‘parvus’ refers to the low abundance in which the species is present in the environment.
Brief description. The genome of *A. parvus* MZLE-22 (ENA accession number GCA_965268675) is relatively compact, with a complete genome size of 1,446,912 base pairs (bp). This species exhibits a CG content of 45%, which is typical of Nanopelagicales order. It possesses one rRNA operon and 42 tRNA genes. It is encountered throughout the year in the Římov reservoir in very low abundances, as well as in Žlutice Reservoir, Czech Republic. It has an average nucleotide identity of ~78% with *A. klicavensis, A. zluticensis* and *A. communis.* Current GTDB classification (r220) is d__Bacteria;p__Actinomycetota;c__Actinomycetes;o__Nanopelagicales; f__Nanopelagicaceae;g__AAA044-D11;s__.

Classification
Bacteria » *Actinomycetota* » *Actinomycetes* » *Nanopelagicales* » *Nanopelagicaceae* » *Aquilimus* » *Aquilimus modestus*

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

Registry URL
https://seqco.de/i:51024

Species *Aquilimus zluticensis*

Etymology
[zlu.ti.cen'sis] **L. masc. adj.** *zluticensis*, from the Žlutice Reservoir in the Czech Republic.

Nomenclatural type
Genome sc|0003654 Ts

Description
Etymology. The species name ‘zluticensis’ refers to the isolation source, the Žlutice Reservoir in the Czech Republic.
Brief description. The genome of *A. zluticensis* MZLE-12 (ENA accession number GCA_965268515) is compact, with a complete genome size of 1,398,358 base pairs (bp). This species exhibits a CG content of 44.3%, which is typical of *Nanopelagicales* order. It possesses one rRNA operon and 38 tRNA genes. Although not very abundant, it is encountered throughout the year in the Římov reservoir, Czech Republic. It has an average nucleotide identity of 78.81% with *A. klicavensis* MKE-157. Current GTDB classification (r220) is d__Bacteria;p__Actinomycetota;c__Actinomycetes;o__Nanopelagicales; f__Nanopelagicaceae; g__AAA044-D11;s__.

Classification
Bacteria » *Actinomycetota* » *Actinomycetes* » *Nanopelagicales* » *Nanopelagicaceae* » *Aquilimus* » *Aquilimus zluticensis*

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

Registry URL
https://seqco.de/i:51013

Species *Planktophila aestivalis*

Etymology
[aes.ti.va'lis] **N.L. fem. adj.** *aestivalis*, pertaining to summer

Nomenclatural type
Genome sc|0004081 Ts

Description
Planktophila aestivalis MRE-130 (ENA accession number GCA_965267825) was isolated from the epilimnion (0.5m depth) of Římov Reservoir, Czech Republic (date: 2021-07-19) and it is the only isolated representative of the species. It has a complete genome size of 1,384,434 bp with a GC content of 47.7% and coding density of 95.68%. It encodes for one rRNA operon and 38 tRNA genes. Recruitment analysis indicated that it prefers warmer waters due to its peak abundances in spring and summer in the surface water of the Římov Reservoir. The closest relative is *Planktophila primaveralis* MRE-185 with whom shares an average nucleotide identity of 86.8%. 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 aestivalis*

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

Registry URL
https://seqco.de/i:51252

Species *Planktophila alpina*

Etymology
[al.pi'na] **L. fem. adj.** *alpina*, of the Alps, Alpine

Nomenclatural type
Genome sc|0004104 Ts

Description
Etymology. It is named ‘alpinus’ after the isolation source of 2 strains of this species, Lake Gossenkollesee, a high alpine mountain lake in Austria.
Brief description. The type species is *Planktophila alpinus* PaE-42 (ENA accession number GCA_965267995), isolated from the epilimnion (5 m depth) of Lake Pavin, France (date: 2022-05-24) via high-throughput dilution to extinction cultivation. Other two strains were isolated in our laboratory from the epilimnion (5m depth) and hypolimnion (8m depth) of Lake Gossenkollesee, Austria. The genome size of the type strain PaE-42 is 1,467,434 bp and has a GC content of 41%, encoding for one rRNA operon and 41 tRNAs. The genome is complete, consisting of a circular chromosome. The genome contains genes encoding rhodopsins. No genes for flagella, pilus assembly or chemotaxis were annotated. The closest isolated relative of this species is *Planktophila aquatilis* IMCC26103, isolated from Lake Soyang (South Korea), with whom it shares an average nucleotide identity of 89.4%. 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 alpina*

References
Effective publication: Chiriac et al., 2025 [1]
Assigned taxonomically: Jezbera et al., 2009 [2]

Registry URL
https://seqco.de/i:51026

Species *Planktophila calida*

Etymology

[ca.li'da] **L. fem. adj.** *calida*, warm, hot, referring to the genome of this organism being recovered from a hot spring

Nomenclatural type

Genome sc|0004093 [Ts]

Description

Etymology. It is named after the Latin word ‘calidus’ or ‘calida’, meaning warm or hot; it refers to the preference of this species for warm waters and its maximum abundance during summer months.
Brief description. *Planktophila calida* RoE-11 (ENA accession number GCA_965267875) was isolated from the epilimnion (5m depth) of eutrophic Lake Roś, Poland (date: 2020-08-31) and it is the only isolated representative of the species. It has a complete circular genome with a size of 1,415,600 bp, a GC content of 48.9%, and a coding density of 95.9%. It encodes one rRNA operon and 38 tRNA genes. It distributed worldwide and in relatively high abundance, including the Delaware River and Bay (USA), Lake Breiter Luzin, Stechlin and Tiefwaren (Germany), Lake Micmac (Canada), Lake Loclat and Zurich (Switzerland) and well as in the Římov, Klíčava and Žlutice Reservoirs (Czech Republic). The closest isolated relative is *Planktophila thermolimna* MRE-226 with which it shared an average nucleotide identity of 89.53%. *Planktophila calida* RoE-11 encodes for a complete pentose phosphate pathway, both an actinorhodopsin and heliorhodopsin, and for the retinal biosynthesis pathway. It can synthesize all amino acids except asparagine. 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 calida*

References

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

Registry URL

https://seqco.de/i:51477

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

Species *Planktophila glycosidica*

Etymology

[gly.co.si.di'ca] **N.L. fem. adj.** *glycosidica*, named for the high number of carbohydrate active enzymes (CAZy) encoded by its genome

Nomenclatural type

Genome sc|0004105 Ts

Description

Etymology. It is named ‘glycosidica’ after the high number of carbohydrate active enzymes (CAZy) encoded by its genome.
Brief description. *Planktophila glycosidica* MKE-14 (ENA accession number GCA_965267915) was isolated from the epilimnion (0.5m depth) of the eutrophic Klíčava Reservoir, Czech Rebublic (date 2021-04-08). Recruitment analysis showed that even though is not very abundant in environment, it is present in various eutrophic lakes and reservoirs in Europe, including beside Klíčava Reservoir, Lake Loclat (Switzerland), Lake Tiefwaren, Stechlin and Breiter Luzin (Germany), Římov and Žlutice Reservoirs (Czech Republic). It has a circular genome of 1,436,726 bp and a GC content of 45.89%. It encodes one rRNA operon and 38 tRNAs, having a coding density of 95.52%. The genome encodes for rhodopsins and the retinal biosynthesis pathway. It can produce most amino acids, but it is auxotrophic for asparagine. The genome encodes for a total of 54 CAZy belonging to 36 different protein families. The closest cultivated relative is *Planktophila warneckii* RE-85 with who is shares an average nucleotide identity of 71.1%. 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 glycosidica*

References

Effective publication: Chiriac et al., 2025 [1]
Assigned taxonomically: Jezbera et al., 2009 [2]

Registry URL

https://seqco.de/i:51028

Species *Planktophila hypolimnetica*

Etymology

[hy.po.lim.ne.ti'ca] **Gr. prep.** *hypo*, below, under; **N.L. fem. adj.** *limnetica*, of a lake; **N.L. fem. adj.** *hypolimnetica*, from the hypolimnion of lakes

Nomenclatural type

Genome sc|0004092 Ts

Description

Etymology. It is named ‘hypolimnetica’ after the water layer from which it was isolated from Římov Reservoir, Czech Republic.
Brief description. *Planktophila hypolimnetica* MRH-37 (ENA accession number GCA_965268225) was isolated from the hypolimnion (30m depth) of Římov Reservoir, Czech Republic (date: 2021-04-06) and it is the only isolated representative of the species. It has a complete circular genome with a size of 1,381,774 bp, a GC content of 48.46%, and a coding density of 95.9%. It encodes one rRNA operon and 38 tRNA genes. It encodes for both actinorhodopsin and heliorhodopsin, as well as the capacity to *de novo* synthesize retinal. It encodes for both oxygenic and anoxygenic parts of the pentose phosphate pathway. Recruitment analysis showed that it is present both in the epilimnion and hypolimnion of Římov Reservoir. The closest cultivated species is *Planktophila grossartii* MRE-195, having an average nucleotide identity of 86.8%. 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 hypolimnetica*

References

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

Registry URL

https://seqco.de/i:51476

Species *Planktophila jirickensis*

Etymology

[ji.ri.cken'sis] **L. fem. adj.** *jirickensis*, of Jiricka, named for the dystrophic water body, Jiřická Pond, Czech Republic.

Nomenclatural type

Genome sc|0004106 [Ts]

Description

Etymology. It is named ‘jirickensis’ after the isolation source, a dystrophic water body, Jiřická Pond, Czech Republic.
Brief description. *Planktophila jirickensis* JirE-27 (ENA accession number GCA_965267775) is a very rare organism, isolated from the Jiřická Pond, Czech Republic (date 2020-06-03). Recruitment analysis showed that its presence is restricted to this dystrophic fishpond. Genome characteristics are very similar to those of other *Planktophila* species. It has a circular genome of 1,496,323 bp and a GC content of 48.9%. It encodes for one rRNA operon and 39 tRNAs, having a coding density of 95.57%. It can synthesize most amino acids, but it is auxotrophic for cysteine and asparagine. The genome contains genes encoding rhodopsins, but it is probably dependent on the exogenous retinal, as the last enzyme of the pathway (*blh* gene) is missing. No genes for flagella, pilus assembly or chemotaxis were annotated. The Current GTDB classification (r220) is d__Bacteria; p__Actinomycetota; c__Actinomycetia; o__Nanopelagicales; f__Nanopelagicaceae; g__Planktophila; s__. The closest cultivated representative is *Planktophila rimovensis* MRE-182, sharing an average nucleotide identity of 87.25%.

Classification

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

References

Effective publication: Chiriac et al., 2025 [1]
Assigned taxonomically: Jezbera et al., 2009 [2]

Registry URL

https://seqco.de/i:51027

Species *Planktophila landstejnensis*

Etymology

[lan.dstej.nen'sis] **N.L. fem. adj.** *landstejnensis*, of Landstejn, named for Landštejn Reservoir (Czech Republic), the place from which the representative strain was isolated

Nomenclatural type

Genome sc|0004097 Ts

Description

Etymology. It is named after Landštejn Reservoir (Czech Republic), the place from which the representative strain was isolated.
Brief description. The representative strain of *Planktophila landstejnensis* Bala-138 (ENA accession number GCA_965267445), was isolated from Vistula River, Poland (date: 2022-07-05). Other 15 isolates of the same species were obtained in our laboratory, most of them from Vistula River and Lagoon, and the coast of the Baltic Sea (date: 2022-07-05), as well as from the Landštejn Reservoir, Czech Republic (date: 2020-06-16). The closest isolated species is *Planktophila ubiquitis* MKE-26, with which it shares an average nucleotide identity of 93.2%. *Planktophila landstejnensis* strains shared 100% average nucleotide identity among themself. The circular genome of the Bala-138 strain has a size of 1,431,437 bp, a GC content of 46.5%, and a coding density of 95.8%. It encodes one rRNA operon and 38 tRNA genes. The oxidative part of the pentose phosphate pathway is not encoded by any strain of this species. The recruitment analysis indicates that the species is distributed worldwide in freshwaters, and sometimes in high abundances, including places such as Lake Loclat and Zurich (Switzerland), Torrens River (Australia), Lake Biwa (Japan), Římov, Žlutice and Klíčava Reservoirs (Czech Republic), Lake Michigan and Mendota, as well as the Delaware River and Bay (USA), and boreal lakes Bissett and Roche (Canada). 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 landstejnensis*

References

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

Registry URL

https://seqco.de/i:51481

Species *Planktophila maxigenoma*

Etymology

[ma.xi.ge.no'ma] **N.L. fem. adj.** *maxigenoma*, an arbitrarily formed name due to its genome size – it has the biggest genome of any Planktophila isolates at time of isolation

Nomenclatural type

Genome sc|0004110 Ts

Description

Etymology. It is named ‘maxigenoma’ due to its genome size – it has the biggest genome of any *Planktophila* isolates.
Brief description. *Planktophila maxigenoma* MRE-196 (ENA accession number GCA_965267625) was isolated from the epilimnion (0.5m depth) of Římov Reservoir, Czech Republic (date: 2021-11-01) and it is the only isolated representative of the species. It has a complete circular genome with a size of 1,500,077 bp, a GC content of 48.7%, and a coding density of 95.73%. It encodes one rRNA operon and 38 tRNA genes. It encodes for both actinorhodopsin and heliorhodopsin, as well as the capacity to *de novo* synthesize retinal. It encodes genes involved in pili assembly and maturation. The closest isolated species is *Planktophila jirickensis* JirE-27 with whom it shares an average nucleotide identity of 80.3%. Recruitment analysis showed that it is a very rare species, encountered only in the Římov Reservoir, and particularly in the hypolimnion (30m depth). 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 maxigenoma*

References

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

Registry URL

https://seqco.de/i:51472

Species *Planktophila ortensis*

Etymology

[or.ten'sis] **N.L. fem. adj.** *ortensis*, It is named after Lake Orta, Italy, the place from which the representative strain was isolated.

Nomenclatural type

Genome sc|0004099 Ts

Description

Etymology. It is named after Lake Orta, Italy, the place from which the representative strain was isolated.
Brief description. *Planktophila ortaensis* OrE-3 (ENA accession number GCA_965268165) was isolated from the epilimnion (5m depth) of the oligotrophic Lake Orta, Italy (date: 2021-07-12) and it is the only isolated representative of the species. It has a complete circular genome of 1,475,422 bp, a GC content of 47.6% and a coding density of 95.7%. The closest isolated species is *Planktophila lacus* MMS-21-148, with whom it shares an average nucleotide identity of 93.5%. It encodes one rRNA operon and 41 tRNA genes; additionally, it has both actinorhodopsin and heliorhodopsin, and the capacity for retinal biosynthesis. It lacks the oxidative part of the pentose phosphate pathway, as well as the capacity to synthesize asparagine. Recruitment analysis shows that this species is relatively abundant in freshwater environments and widespread, including Torrens River (Australia), Římov and Klíčava Reservoirs (Czech Republic), the German lakes Breiter Luzin, Stechlin, Tiefwaren, Lake Zurich and Loclat (Switzerland), Lake Michigan (USA), and Lake Micmac (Canada). 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 ortensis*

References

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

Registry URL

https://seqco.de/i:51483

Species *Planktophila perrara*

Etymology

[per'ra.ra] **N.L. fem. adj.** *perrara*, very rare, indicating its low abundance in the environment

Nomenclatural type

Genome sc|0004107 Ts

Description

Etymology. It is named ‘perrarus’, from Latin prefix ‘per-’ meaning very and ‘rarus’ meaning rare, indicating its low abundance in the environment.
Brief description. *Planktophila perrarus* MRE-203 (ENA accession number GCA_965268015) was isolated from the epilimnion (0.5m depth) of Římov Reservoir, Czech Republic (date: 2021-11-01) and it is the only isolated representative of the species. It has a complete circular genome with a size of 1,318,636 bp, a GC content of 48.28%, and a coding density of 95.4%. It encodes one rRNA operon and 38 tRNA genes. It encodes for both actinorhodopsin and heliorhodopsin, as well as the capacity to *de novo* synthesize retinal. It is extremely rare in the environment and in low abundances; recruitment analysis in >1700 metagenomes showed that it was never found with a coverage per Gb higher than 1. In low abundances, it was recovered from Lake Ontario (USA), the coast of the Baltic Sea and the hypolimnion of Římov Reservoir (Czech Republic). The closest relative is *Planktophila hypolimnetica* MRH-37, with whom shared an average nucleotide identity of 75.95%. 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 perrara*

References

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

Registry URL

https://seqco.de/i:51473

Species *Planktophila polyoliphila*

Etymology

[po.ly.o.li.phi'la] **N.L. neut. n.** *polyolum*, polyol, referring to the polyol-specific membrane transporters encoded by this species' genome; **N.L. fem. adj. suff.** *-phila*, loving; **N.L. fem. adj.** *polyoliphila*, a polyol-loving organism

Nomenclatural type

Genome sc|0004108 Ts

Description

Etymology. It is named ‘polyoliphila’ from the membrane transporters encoded by the genome of this isolate, specific for polyols.
Brief description. *Planktophila polyoliphila* MRE-193 (ENA accession number GCA_965267955) was isolated from the epilimnion (0.5m depth) of Římov Reservoir, Czech Republic (date: 2021-11-01) and it is the only isolated representative of the species. It has a circular genome of 1,347,427 bp, a GC content of 45% and a coding density of 96.16%. It encodes one rRNA operon and 40 tRNA genes. It encodes for both actinorhodopsin and heliorhodopsin, but it lacks the last gene involved in the biosynthesis of retinal, the *bhl* gene. It encodes membrane transporters for erythriol. It is a relatively abundant and widespread species, encountered in rives, reservoirs and lakes, including the Žlutice, Římov and Klíčava Reservoirs (Czech Republic), Lake Bissett (Canada), Lake Michigan (USA), Torrens River (Australia) etc. The closest cultivated relative to this species is *Planktophila limneticus* MMS-VB-114, sharing an average nucleotide identity of 81.9%. 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 polyoliphila*

References

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

Registry URL

https://seqco.de/i:51471

Species *Planktophila primivernalis*

Etymology

[pri.mi.ver.na'lis] **L. masc. adj.** *primus*, first or foremost; **L. fem. adj.** *vernalis*, of spring; **N.L. fem. adj.** *primivernalis*, of early spring, due to its occurrence in lakes during spring months

Nomenclatural type

Genome sc|0004084 Ts

Description

Etymology. It is named from ‘prima vera’, meaning early spring in Latin, due to its occurrence in lakes during spring months.
Brief description. *Planktophila primaveralis* MRE-185 (ENA accession number GCA_965267735) was isolated from the epilimnion (0.5m depth) of Římov Reservoir, Czech Republic (date: 2021-11-01) and it is the only isolated representative of the species. It has a circular genome with a size of 1,474,018 bp, a GC content of 47.25% and a coding density of 95.94%. It encodes for one rRNA operon and 37 tRNA genes. It encodes actinorhodopsin and heliorhodopsin, as well as the ability to *de novo* synthesize retinal. It can synthesize most amino acids, except asparagine. The closest relative is *Planktophila aestivalis* MRE-130 with whom it shares an average nucleotide identity of 86.8%. Recruitment analysis showed that it was present in Římov, Žlutice and Klíčava Reservoirs (Czech Republic) during the spring months, and at the coast of the Baltic Sea. It is usually present in the surface waters, but in Římov Reservoir it is also present in hypolimnion. 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 primivernalis*

References

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

Registry URL

https://seqco.de/i:51470

Species *Planktophila rara*

Etymology

[ra'ra] **L. fem. adj.** *rara*, rare, indicating its low abundance and distribution in the environment

Nomenclatural type

Genome sc|0004091 Ts

Description

Etymology. It is named ‘rarus’ from the Latin word meaning rare, indicating its low abundance and distribution in the environment.
Brief description. *Planktophila rarus* MRE-26 (ENA accession number GCA_965268205) was isolated from the epilimnion (0.5m depth) of Římov Reservoir, Czech Republic (date: 2021-04-06) and it is the only isolated representative of the species. It has a complete circular genome with a size of 1,468,350 bp, a GC content of 47.5%, and a coding density of 95.7%. It encodes one rRNA operon and 39 tRNA genes. It encodes for both actinorhodopsin and heliorhodopsin, as well as the capacity to *de novo* synthesize retinal. It encodes for both oxygenic and anoxygenic parts of the pentose phosphate pathway. It can synthesize most amino acids, being auxotrophic for asparagine. Recruitment analysis indicates a very restrictive distribution, specifically the epilimnetic waters of Římov Reservoir during spring. The closest cultivated species is *Planktophila aestivalis* MRE-130, having an average nucleotide identity of 86.5%. 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 rara*

References

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

Registry URL

https://seqco.de/i:51475

Species *Planktophila rimovensis*

Etymology
[ri.mo.ven'sis] **N.L. fem. adj.** *rimovensis*, of Rimov, pertaining to the Římov Reservoir, Czech Republic, the isolation source of the species

Nomenclatural type
Genome sc|0004109 Ts

Description
Etymology. It is named ‘rimovensis’ after the isolation source, the eutrophic Římov Reservoir, Czech Republic.
Brief description. *Planktophila rimovensis* MRE-182 (ENA accession number GCA_965267985) was isolated from the epilimnion (0.5m depth) of Římov Reservoir, Czech Republic (date: 2021-11-01) and it is the only isolated representative of the species. It has one circular genome with a size of 1,488,100 bp, a GC content of 48.8%, and a coding density of 95.67%. It encodes one rRNA operon and 37 tRNA genes. It encodes genes for actinorhodopsin and heliorhodopsin but is unable to synthesize retinal *de novo* due to the absence of the *bhl* gene. Also, it is auxotrophic for asparagine. Recruitment analysis showed that it was a very rare organism, occurring only in autumn in the Římov Reservoir. The closest relative is *Planktophila jirickensis* JirE-27 with which it shares an average nucleotide identity of 87.25%. 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 rimovensis*

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

Registry URL
https://seqco.de/i:51469

Species *Planktophila stagnalis*

Etymology
[stag.na'lis] **N.L. fem. adj.** *stagnalis*, of standing water, pond, or swamp

Nomenclatural type
Genome sc|0004095 Ts

Description
Etymology. The name ‘stagnalis’ comes from Latin, specifically from ‘stagnum’, which means standing water, pond, or swamp. The suffix -alis is a Latin adjectival ending meaning *related to*.
Brief description. *Planktophila stragnalis* MRE-20 (ENA accession number GCA_965267665) was isolated from the epilimnion (0.5m depth) of Římov Reservoir, Czech Republic (date: 2021-04-06) and it is the only isolated representative of the species. It has a complete circular genome with a size of 1,464,932 bp, a GC content of 47.6%, and a coding density of 96%. It encodes one rRNA operon and 42 tRNA genes. Recruitment analysis indicated its presence in the epilimnion (0.5m depth) of Římov Reservoir, and to a lower extent in the hypolimnion (30m depth). It encodes for a complete pentose phosphate pathway, both an actinorhodopsin and a heliorhodopsin, and for the retinal biosynthesis pathway. The closest isolated relative is *Planktophila lacus* MMS-IIB-60, with whom it shares an average nucleotide identity of 83.15%. 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 stagnalis*

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

Registry URL
https://seqco.de/i:51479

Species *Planktophila tarnitensis*

Etymology

[tar.ni.ten'sis] **N.L. fem. adj.** *tarnitensis*, of Tarnita, referring to Lake Tarnița, Romania, the place from which the representative strain was isolated

Nomenclatural type

Genome sc|0004098 Ts

Description

Etymology. It is named after Lake Tarnița, Romania, the place from which the representative strain was isolated.
Brief description. *Planktophila tarnitensis* TarE-7 (ENA accession number GCA_965267845) was isolated from the epilimnion (5m depth) of the mesotrophic Lake Tarnița, Romania (date: 2021-07-28) and it is the only isolated representative of the species. It has a complete circular genome of 1,347,384 bp, a GC content of 48.1% and a coding density of 95.3%. The closest isolated species is *Planktophila vernalis* MMS-IIB-142, with which it shares an average nucleotide identity of 92.3%. It lacks the oxidative part of the pentose phosphate pathway, as well as the capacity to synthesize asparagine. For *Planktophila*, it encodes a very low number of carbohydrate active enzymes (26 total enzymes belonging to 15 different families). It encodes one rRNA operon and 40 tRNA genes; additionally, it has both actinorhodopsin and heliorhodopsin, and the capacity for retinal biosynthesis. Recruitment analysis indicates that this species is not very abundant and widespread, but it is present in several freshwater environments, including Lake Paradise (Canada), and the German lakes Breiter Luzin, Stechlin and Tiefwaren. 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 tarnitensis*

References

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

Registry URL

https://seqco.de/i:51482

Species *Planktophila thermolimnae*

Etymology

[ther.mo.lim'na.e] **Gr. masc. adj.** *thermos*, hot; **Gr. fem. n.** *limne*, lake; **N.L. fem. adj.** *thermolimnae*, of a hot lake or standing body of water

Nomenclatural type

Genome sc|0004090 Ts

Description

Etymology. It is named ‘thermolimna’ after the Greek words ‘thermo’ meaning heat or warm, and ‘limna’, referring to a lake or standing water.
Bried description. *Planktophila thermolimna* MRE-226 (ENA accession number GCA_965267965) was isolated from the epilimnion (0.5m depth) of Římov Reservoir, Czech Republic (date: 2021-11-01) and it is the only isolated representative of the species. It has a complete circular genome with a size of 1,436,178 bp, a GC content of 48.89%, and a coding density of 96%. It encodes for one rRNA operon and 39 tRNA genes. It encodes for both actinorhodopsin and heliorhodopsin, as well as the capacity to *de novo* synthesize retinal. It encodes for both oxygenic and anoxygenic parts of the pentose phosphate pathway. It can synthesize most amino acids, being auxotrophic for asparagine. Recruitment analysis indicates that the species prefers warm, epilimnetic waters, being present in spring and summer in Římov, Žlutice and Klíčava Reservoirs. The closest isolated relative is *Planktophila calida* RoE-11, with whom shared an average nucleotide identity of 89.53%. 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 thermolimnae*

References

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

Registry URL

https://seqco.de/i:51474

Species *Planktophila toyensis*

Etymology

[to.y.en'sis] **N.L. fem. adj.** *toyensis*, of Toya, named for the lake from which the organism was isolated, Lake Toya, Japan

Nomenclatural type

Genome sc|0004094 Ts

Description

Etymology. It is named ‘toyensis’ after the lake from which it was isolated, Lake Toya, Japan. Bried description. *Planktophila toyensis* ToyE-15 (ENA accession number GCA_965267865) was isolated from the epilimnion (5m depth) of the oligotrophic Lake Toya, Japan (date: 2022-09-29) and it is the only isolated representative of the species. It has a complete circular genome with a size of 1,367,129 bp, a GC content of 47.8%, and a coding density of 95.9%. It encodes one rRNA operon and 38 tRNA genes. It is distributed worldwide and in relatively high abundance, including the Delaware River and Bay (USA), Lake Toya and Inawashiro (Japan), Římov Reservoir (Czech Republic), Lake Zurich (Switzerland), and especially in boreal lakes such as Lake Eden, Paradise, Montjoie, and Nukko (Canada), Lake Odrolstjärnen and Lomtjärnam (Sweden), and Lake Lovojärvi (Finland). The closest isolated relative is *Planktophila landstejnensis* MRE-249 with which it shared an average nucleotide identity of 91.4%. It encodes for a complete pentose phosphate pathway, both an actinorhodopsin and a heliorhodopsin, and for the retinal biosynthesis pathway. It can synthesize all amino acids except asparagine. It can produce a range of vitamins, including riboflavin (B2). 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 toyensis*

References

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

Registry URL

https://seqco.de/i:51478

Species *Planktophila vulgaris*

Etymology

[vul.ga'ris] **L. fem. adj.** *vulgaris*, common, referring to the occurrence of this species in a wide range of water environments and in high abundance

Nomenclatural type

Genome sc|0004101 Ts

Description

Etymology. It is named ‘ubiquitis’ after the occurrence of this species in a wide range of water environments and in high abundance.
Brief description. *Planktophila ubiquitis* MKE-26 (ENA accession number GCA_965267815) was isolated from the epilimnion (0.5m depth) of Klíčava Reservoir, Czech Republic (date: 2021-04-08) and it is the representative genome for the species. Strain MKE-27 (GCA_965267675) belongs to the same species and was isolated from the same place, and on the same date; these two strains share an average nucleotide identity of 96.11%. *P. ubiquitis* MKE-26 has a complete, circular genome with a size of 1,335,437 bp, a GC content of 46.8%, and a coding density of 95.76%. It encodes one rRNA operon and 38 tRNAs. The oxidative part of the pentose phosphate pathway is missing. The two strains differ in their ability to synthesize amino acids; the MKE-27 strain can synthesize all of them, while MKE-26 is auxotrophic for asparagine. The closest cultivated relative of this species is *Planktophila landstejnensis* Bala-34 with whom it shares an average nucleotide identity of 93.23%. The species is found in high abundance all over the world and in different water bodies, such as Torrens River (Australia), Delaware River and Bay (USA), Lake Tiefwaren (Germany), Lake Ikeda (Japan), Lake Michigan (USA), Římov and Klíčava Reservoirs (Czech Republic), and boreal lakes in Canada. 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 vulgaris*

References

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

Registry URL

https://seqco.de/i:51468

Species *Planktophila zluticensis*

Etymology
[z.lu.ti.cen'sis] **L. fem. adj.** *zluticensis*, from the Žlutice Reservoir in the Czech Republic.

Nomenclatural type
Genome sc|0004100 Ts

Description
Etymology. It is named after the Žlutice Reservoir, Czech Republic, the place from which the representative strain was isolated.
Brief description. *Planktophila zlutica* MZLE-14 (ENA accession number GCA_965268005) was isolated from the epilimnion (5m depth) of the eutrophic Žlutice Reservoir, Czech Republic (date: 2021-04-07) and it is the only isolated representative of the species. It has a complete circular genome of 1,406,539 bp, a GC content of 46.1% and a coding density of 95.9%. The closest isolated species is *Planktophila warneckii* RE-8, with which it shares an average nucleotide identity of 87.8%. It encodes one rRNA operon and 39 tRNA genes; additionally, it has both actinorhodopsin and heliorhodopsin but lacks the capacity for retinal biosynthesis. Also, it lacks the oxidative part of the pentose phosphate pathway but can synthesize all amino acids. It has a limited distribution and low abundance, being recovered in the recruitment analysis only from the Žlutice and Římov Reservoirs in Czech Republic. 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 zluticensis*

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

Registry URL
https://seqco.de/i:51484

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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:pdwftyg3** submitted by **Layoun, Paul** and including 26 new names has been successfully validated.

Date of Priority: 2026-09-15 04:32 UTC
DOI: 10.57973/seqcode.r:pdwftyg3