Register list for 12 new names including Hahnella lacustris sp. nov.

Submitted by Salcher, Michaela M

Genus *Fimbriicoccus*

Etymology

[Fim.bri.i.coc'cus] **L. fem. n.** *fimbria*, fibres, threads, fringe, and in biology, fimbriae; **N.L. masc. n.** *coccus*, coccus; **N.L. masc. n.** *Fimbriicoccus*, a coccus with fimbriae

Nomenclatural type

Species *Fimbriicoccus planktonicus*$^{\mathrm{Ts}}$

Description

Genus of *Fimbriimonadaceae* that is commonly found in freshwater environments. Type species is *Fimbriicoccus planktonicus* MsE-15 (GCA_965234685.1). The closest cultivated relative is *Fimbriimonas ginsengisoli* Gsoil 348 (GCF_000724625.1), with an average amino acid identity of 55.26% and an average nucleotide identity of 66.05%. Current GTDB classification (R220): d__Bacteria; p__Armatimonadota; c__Fimbriimonadia; o__Fimbriimonadales; f__Fimbriimonadaceae; g__Fimbriimonas.

Classification

Bacteria » *Armatimonadota* » *Fimbriimonadia* » *Fimbriimonadales* » *Fimbriimonadaceae* » *Fimbriicoccus*

References

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

Registry URL

https://seqco.de/i:49105

Genus *Hahnella*

Etymology

[Hah.ne'lla] **N.L. fem. dim. n.** *Hahnella*, named after the scientist Martin W. Hahn, a pioneer in cultivating important freshwater bacteria; he also isolated the first strains of this genus (MWH-UniP1) and closely related taxa.

Nomenclatural type

Species *Hahnella aquatica*^{Ts}

Description

Description: A genus of abundant freshwater bacteria, commonly known from metagenomic and 16S rRNA amplicon studies, often referred to MWH-UniP1 group or betaVI in 16S rRNA based studies (PMCID: PMC3063352, 31919153). It contains two species: *Hahnella aquatica* (MiE-11, GCA_965194505.1) and *Hahnella lacustris* (MsE-M47, GCA_965194655.1), both isolated from freshwater lakes. Type species is *Hahnella aquatica* MiE-11 (GCA_965194505.1). The closest cultivated relative is the undescribed *Burkholderiales* bacterium LSUCC0115 (GCA_009646425.1), with an average amino acid identity of 67-67.3% and average nucleotide identity of 70.6-71.7%. The closest validly described relative is *Limnobacter thiooxidans* CS-K2 (GCF_036323495.1), with AAIs of 53.6-54.4% and ANIs of 66.4-66.9%. Current GTDB classification (R220): d__Bacteria; p__Pseudomonadota; c__Gammaproteobacteria; o__Burkholderiales; f__Burkholderiaceae_A; g__UBA2463.

Classification

Bacteria » *Pseudomonadota* » *Betaproteobacteria* » *Burkholderiales* » *Burkholderiaceae* » *Hahnella*

References

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

Registry URL

https://seqco.de/i:49113

Genus *Pernthalerella*

Etymology

[Pern.tha.le.re'lla] **N.L. fem. dim. n.** *Pernthalerella*, Named after Austrian scientist Jakob Pernthaler, who greatly contributed to the field of aquatic microbial ecology.

Nomenclatural type

Species *Pernthalerella aquatica*^{Ts}

Description

The genus contains three species, *Pernthalerella aquatica* (GCA_965194445.1), *Pernthalerella lacuna* (GCA_965194545.1), and *Pernthalerella communis* (GCA_965194595.1) that were isolated from freshwater lakes. Type species is *Pernthalerella aquatica* GE-M3 (GCA_965194445.1). The closest cultivated relative is *Paucimonas lemoignei* DSM 7445 (GCF_004342585.1) with average amino acid identities of 64-64.5% and average nucleotide identities of 69.1-71%. SILVA classification of 16S rRNA genes is Bacteria/Proteobacteria/Gammaproteobacteria/Burkholderiales/Oxalobacteraceae/Noviherbaspirillum_3. Current GTDB classification (R220): d__Bacteria; p__Pseudomonadota; c__Gammaproteobacteria; o__Burkholderiales; f__Burkholderiaceae; g__SYFN01.

Classification

Bacteria » *Pseudomonadota* » *Betaproteobacteria* » *Burkholderiales* » *Burkholderiaceae* » *Pernthalerella*

References

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

Registry URL

https://seqco.de/i:49109

Species *Fimbriicoccus planktonicus*Ts

Etymology

[plan.kto'ni.cus] **N.L. masc. adj.** *planktonicus*, living in the plankton, planktonic; from Gr. masc. adj. planktos, wandering

Nomenclatural type

NCBI Assembly: GCA_965234685.1 Ts

Reference Strain

Strain scJ0038787: MsE-15

Description

Type species is *Fimbriicoccus planktonicus* MsE-15 (GCA_965234685.1), isolated from 5 m depth from Lake Most, Czechia (date: 2019-07-30), *via* high-throughput dilution to extinction cultivation. MsE-15 has a genome size of 3.29 Mbp with a genomic GC content of 56.5 %, contains 3 rRNA genes and 48 tRNAs. The genome is complete, consisting of a circular chromosome. No genes for flagella assembly and chemotaxis were annotated. Pathways for the biosynthesis of all amino acids except for alanine, proline, and histidine were predicted. Further, pathways for riboflavin, pyridoxal, NAD, coenzyme A, THF, and menaquinone biosynthesis were identified. The closest cultivated relative is *Fimbriimonas ginsengisoli* Gsoil 348 (GCF_000724625.1) with an average amino acid identity of 55.26% and an average nucleotide identity of 66.05%. Current GTDB classification (R220): d__Bacteria; p__Armatimonadota; c__Fimbriimonadia; o__Fimbriimonadales; f__Fimbriimonadaceae; g__Fimbriimonas; s__Fimbriimonas sp945882415.

Classification

Bacteria » *Armatimonadota* » *Fimbriimonadia* » *Fimbriimonadales* » *Fimbriimonadaceae* » *Fimbriicoccus* » *Fimbriicoccus planktonicus*Ts

References

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

Registry URL

https://seqco.de/i:49104

Species *Hahnella aquatica*Ts

Etymology

[a.qua.ti'ca] **L. fem. adj.** *aquatica*, living or found in the water.

Nomenclatural type

NCBI Assembly: GCA_965194505.1 Ts

Reference Strain

Strain sc|0040315: MiE-11

Description

Type species is *Hahnella aquatica* MiE-11 (GCA_965194505.1), isolated from 5 m depth from Lake Milada, Czechia (date: 2019-07-23), *via* high-throughput dilution to extinction cultivation. MiE-11 has a genome size of 1.8 Mbp with a genomic GC content of 61.8%, contains 3 rRNA genes and 43 tRNAs. The genome is complete, consisting of a circular chromosome. The genome contains genes encoding anoxygenic aerobic phototrophy (*pufABLM*). Genes for flagellar assembly were annotated. Pathways for thiosulfate oxidation (Sox pathway), glycolate oxidation, and the biosynthesis of all amino acids were predicted. Further, pathways for thiamine, riboflavin, NAD, pantothenate, coenzyme A, THF, and heme biosynthesis were identified. The closest cultivated relatives are the undescribed *Burkholderiales* bacterium LSUCC0115 (GCA_009646425.1), with an average amino acid identity of 67.3% and average nucleotide identity of 71.7% and another newly proposed species, *Hahnella lacustris* MsE-M47 (GCA_965194655.1), with an AAI of 65.8% and an ANI of 70.4%. The closest validly described relative is *Limnobacter thiooxidans* CS-K2 (GCF_036323495.1) with an AAI of 54.41% and an ANI of 66.9%. Current GTDB classification (R220): d__Bacteria; p__Pseudomonadota; c__Gammaproteobacteria; o__Burkholderiales; f__Burkholderiaceae_A; g__UBA2463; s__.

Classification

Bacteria » *Pseudomonadota* » *Betaproteobacteria* » *Burkholderiales* » *Burkholderiaceae* » *Hahnella* » *Hahnella aquatica*Ts

References

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

Registry URL

https://seqco.de/i:49114

Species *Hahnella lacustris*

Etymology

[la.cus'tris] **N.L. fem. adj.** *lacustris*, pertaining to a lake

Nomenclatural type

NCBI Assembly: GCA_965194655.1 ^{Ts}

Reference Strain

Strain sc|0038792: MsE-M47

Description

Type species is *Hahnella lacustris* MsE-M47 (GCA_965194655.1), isolated from 5 m depth from Lake Most, Czechia (date: 2019-10-01), *via* high-throughput dilution to extinction cultivation. MsE-M47 has a genome size of 2.2 Mbp with a genomic GC content of 59.2%, contains 3 rRNA genes and 42 tRNAs. The genome is complete, consisting of a circular chromosome. The genome is complete, consisting of a circular chromosome. The genome contains genes encoding anoxygenic aerobic phototrophy (*pufABLM*) and the complete Calvin cycle for carbon fixation via RuBisCO. Genes for flagellar assembly and chemotaxis were annotated. Pathways for taurine degradation, thiosulfate oxidation (Sox pathway), glycolate oxidation, and the biosynthesis of all amino acids were predicted. Further, pathways for riboflavin, NAD, pantothenate, coenzyme A, biotin, THF, and heme biosynthesis were identified. The closest cultivated relative is the undescribed *Burkholderiales* bacterium LSUCC0115 (GCA_009646425.1), with an average amino acid identity of 67% and average nucleotide identity of 70.6% and another newly proposed species, *Hahnella aquatica* MiE-11 (GCA_965194505.1), with an AAI of 65.8% and an ANI of 70.4%. The closest validly described relative is *Limnobacter thiooxidans* CS-K2 (GCF_036323495.1) with an AAI of 53.55% and an ANI of 66.44%. Current GTDB classification (R220): d__Bacteria; p__Pseudomonadota; c__Gammaproteobacteria; o__Burkholderiales; f__Burkholderiaceae_A; g__UBA2463; s__UBA2463 sp945862985.

Classification

Bacteria » *Pseudomonadota* » *Betaproteobacteria* » *Burkholderiales* » *Burkholderiaceae* » *Hahnella* » *Hahnella lacustris*

References

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

Registry URL

https://seqco.de/i:49117

Species *Limnohabitans simekii*

Etymology

[si.me.ki'i] **N.L. masc. gen. n.** *simekii*, From Simek, named after the Czech scientist Karel Šimek, who first recognized the importance of the genus Limnohabitans and was involved in the description of the genus.

Nomenclatural type

NCBI Assembly: GCA_965234735.1 Ts

Reference Strain

Strain sc|0038785: MiE-M12

Description

Type strain is *Limnohabitans simekii* MiE-M12 (GCA_965234735.1), isolated from 5 m depth from Lake Milada, Czechia (date: 2019-04-16), *via* high-throughput dilution to extinction cultivation. MiE-M12 has a genome size of 2.7 Mbp with a genomic GC content of 55.8 %, contains 3 rRNA genes and 37 tRNAs. The genome is a high-quality draft consisting of 9 contigs. The genome contains genes encoding anoxygenic aerobic phototrophy (*pufABLM*) and the complete Calvin cycle for carbon fixation via RuBisCO. Genes for flagellar and pilus assembly were annotated. Pathways for urea degradation, thiosulfate oxidation (Sox pathway), glycolate oxidation, and the biosynthesis of all amino acids were predicted. Further, pathways for thiamine, riboflavin, coenzyme A, biotin, THF, and heme biosynthesis were identified. The closest cultivated relative is *Limnohabitans* sp. Jir61 (GCF_003063545.1) with an average amino acid identity of 66.2% and average nucleotide identity of 72.6%. Current GTDB classification (R220): d__Bacteria; p__Pseudomonadota; c__Gammaproteobacteria; o__Burkholderiales; f__Burkholderiaceae_B; g__Limnohabitans; s__Limnohabitans sp937891045.

Classification

Bacteria » *Pseudomonadota* » *Betaproteobacteria* » *Burkholderiales* » *Comamonadaceae* » *Limnohabitans* » *Limnohabitans simekii*

References

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

Registry URL

https://seqco.de/i:44274

Species *Pernthalerella aquatica*^{Ts}

Etymology

[a.qua.ti'ca] **L. fem. adj.** *aquatica*, living or found in the water.

Nomenclatural type

NCBI Assembly: GCA_965194445.1 ^{Ts}

Reference Strain

Strain sc|0038788: GE-M3

Description

Type species is *Pernthalerella aquatica* GE-M3 (GCA_965194445.1), isolated from 5 m depth from Greifensee, Switzerland (date: 2019-04-03), *via* high-throughput dilution to extinction cultivation. GE-M3 has a genome size of 3.1 Mbp with a genomic GC content of 53.8%, contains 3 rRNA genes and 41 tRNAs. The genome is a high-quality draft consisting of 7 contigs. The genome contains genes encoding anoxygenic aerobic phototrophy (*pufABLM*) and the complete Calvin cycle for carbon fixation via RuBisCO. Genes for flagellar and pilus assembly were annotated. Pathways for urea degradation, glycolate oxidation and the biosynthesis of all amino acids were predicted. Further, pathways for thiamine, riboflavin, NAD, pantothenate, coenzyme A, biotin, THF, and heme biosynthesis were identified. The closest cultivated relative is *Paucimonas lemoignei* DSM 7445 (GCF_004342585.1) with an average amino acid identity of 64.5% and average nucleotide identity of 71.1% and two other newly proposed species, *Pernthalerella lacuna* MaE-M21 (GCA_965194545.1) and *Pernthalerella communis* MsE-6 (GCA_965194595.1), with AAI of 72.1-73.1% and ANI of 71.9-72.5%. Current GTDB classification (R220): d__Bacteria; p__Pseudomonadota; c__Gammaproteobacteria; o__Burkholderiales; f__Burkholderiaceae; g__SYFN01; s__.

Classification

Bacteria » *Pseudomonadota* » *Betaproteobacteria* » *Burkholderiales* » *Burkholderiaceae* » *Pernthalerella* » *Pernthalerella aquatica*^{Ts}

References

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

Registry URL

https://seqco.de/i:49110

Species *Pernthalerella communis*

Etymology

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

Nomenclatural type

NCBI Assembly: GCA_965194595.1 Ts

Reference Strain

Strain sc|0038790: MsE-6

Description

Type species is *Pernthalerella communis* MsE-6 (GCA_965194595.1), isolated from 5 m depth from Lake Most, Czechia (date: 2019-04-30), *via* high-throughput dilution to extinction cultivation. MsE-6 has a genome size of 3 Mbp with a genomic GC content of 47.7%, contains 3 rRNA genes and 37 tRNAs. The genome is a high-quality draft consisting of 27 contigs. The genome contains genes encoding anoxygenic aerobic phototrophy (*pufABLM*) and the complete Calvin cycle for carbon fixation via RuBisCO. Genes for flagellar and pilus assembly were annotated. Pathways for salicylate degradation, glycolate oxidation and the biosynthesis of all amino acids were predicted. Further, pathways for thiamine, riboflavin, NAD, pantothenate, coenzyme A, biotin, THF, and heme biosynthesis were identified. The closest cultivated relative is *Paucimonas lemoignei* DSM 7445 (GCF_004342585.1) with an average amino acid identity of 64.02% and average nucleotide identity of 69.11% and two other newly proposed species, *Pernthalerella lacuna* MaE-M21 (GCA_965194545.1) and *Pernthalerella aquatica* GE-M3 (GCA_965194445.1), with AAI of 72.1-73.1% and ANI of 71.9-72.5%. Current GTDB classification (R220): d__Bacteria; p__Pseudomonadota; c__Gammaproteobacteria; o__Burkholderiales; f__Burkholderiaceae; g__SYFN01; s__SYFN01 sp903846425.

Classification

Bacteria » *Pseudomonadota* » *Betaproteobacteria* » *Burkholderiales* » *Burkholderiaceae* » *Pernthalerella* » *Pernthalerella communis*

References

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

Registry URL

https://seqco.de/i:49112

Species *Pernthalerella lacunae*

Etymology

[la.cu'na.e] **L. fem. gen. n.** *lacunae*, of a ditch, pit, hole, pool, or pond, referring to the isolation source of the type from a freshwater lake.

Nomenclatural type

NCBI Assembly: GCA_965194545.1 Ts

Reference Strain

Strain scJ0038789: MaE-M21

Description

Type species is *Pernthalerella lacuna* MaE-M21 (GCA_965194545.1), isolated from 5 m depth from Lake Maggiore, Italy (date: 2019-11-04), *via* high-throughput dilution to extinction cultivation. MaE-M21 has a genome size of 2.8 Mbp with a genomic GC content of 54.9%, contains 3 rRNA genes and 45 tRNAs. The genome is a high-quality draft consisting of 7 contigs. The genome contains genes encoding anoxygenic aerobic phototrophy (*pufABLM*). Genes for flagellar and pilus assembly were annotated. Pathways for benzene degradation, glycolate oxidation and the biosynthesis of all amino acids were predicted. Further, pathways for thiamine, riboflavin, NAD, pantothenate, coenzyme A, biotin, THF, and heme biosynthesis were identified. The closest cultivated relative is *Paucimonas lemoignei* DSM 7445 (GCF_004342585.1) with an average amino acid identity of 64.16% and average nucleotide identity of 70.49% and two other newly proposed species, *Pernthalerella aquatica* GE-M3 (GCA_965194445.1) and *Pernthalerella communis* MsE-6 (GCA_965194595.1), with AAI of 72.1-73.1% and ANI of 71.9-72.5%. Current GTDB classification (R220): d__Bacteria; p__Pseudomonadota; c__Gammaproteobacteria; o__Burkholderiales; f__Burkholderiaceae; g__SYFN01; s__SYFN01 sp021299035.

Classification

Bacteria » *Pseudomonadota* » *Betaproteobacteria* » *Burkholderiales* » *Burkholderiaceae* » *Pernthalerella* » *Pernthalerella lacunae*

References

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

Registry URL

https://seqco.de/i:49111

Species *Planktophila grossartii*

Etymology

[gros.sar.ti'i] **N.L. masc. gen. n.** *grossartii*, named after the German scientist Hans-Peter Grossart, who greatly contributed to the ecological characterization of freshwater Actinomycetota.

Nomenclatural type

NCBI Assembly: GCA_965234365.1 Ts

Reference Strain

Strain scJ0038786: RE-3

Description

Type species is *Planktophila grossartii* RE-3 (GCA_965234365.1), isolated from 0.5 m depth from the Římov reservoir, Czechia (date: 2019-04-23), *via* high-throughput dilution to extinction cultivation. RE-3 has a genome size of 1.4 Mbp with a genomic GC content of 48.8 %, contains 3 rRNA genes and 38 tRNAs. The genome is complete, consisting of a circular chromosome. The genome contains genes encoding rhodopsins. No genes for flagella or pilus assembly and chemotaxis were annotated. Pathways for taurine degradation and the biosynthesis of all amino acids except for histidine were predicted. Further, pathways for riboflavin, pyridoxal, coenzyme A, NAD, and menaquinone biosynthesis were identified. The closest cultivated relative is Actinobacteria bacterium IMCC25003 (GCA_002284855.1) with an average nucleotide identity of 90.33%. Current GTDB classification (R220): d__Bacteria; p__Actinomycetota; c__Actinomycetia; o__Nanopelagicales; f__Nanopelagicaceae; g__Planktophila; s__Planktophila sp009701085.

Classification

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

References

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

Registry URL

https://seqco.de/i:49103

Species *Planktophila turicensis*

Etymology

[tu.ri.cen'sis] **N.L. neut. n.** *Turicum*, the Latin name of Zurich; **N.L. fem. adj.** *turicensis*, referring to Turicum, the latin name of Zurich, pertaining to Lake Zurich, the isolation source of the type strain

Nomenclatural type

NCBI Assembly: GCA_965234405.1 Ts

Reference Strain

Strain sc|0038793: ZE-9

Description

Type species is *Planktophila turicensis* ZE-9 (GCA_965234405.1), isolated from 5 m depth from Lake Zurich, Switzerland (date: 2019-11-13), *via* high-throughput dilution to extinction cultivation. ZE-9 has a genome size of 1.4 Mbp with a genomic GC content of 48.5%, contains 3 rRNA genes and 39 tRNAs. The genome is complete, consisting of a circular chromosome. The genome contains genes encoding rhodopsins. No genes for flagella or pilus assembly and chemotaxis were annotated. Pathways for taurine degradation and the biosynthesis of all amino acids except for histidine were predicted. Further, pathways for riboflavin, pyridoxal, coenzyme A, NAD, and menaquinone biosynthesis were identified. The closest cultivated relative is '*Candidatus* Planktophila sulfonica' MMS-IA-56 (GCF_002288185.1), with an average nucleotide identity of 94.22%. Current GTDB classification (R220): d__Bacteria; p__Actinomycetota; c__Actinomycetia; o__Nanopelagicales; f__Nanopelagicaceae; g__Planktophila; s__.

Classification

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

References

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

Registry URL

https://seqco.de/i:49118

References

1. Salcher et al. (2025). Bringing the uncultivated microbial majority of freshwater ecosystems into culture. *Nature Communications*. DOI:10.1038/s41467-025-63266-9

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:o5wsiwof** submitted by **Salcher, Michaela M** and including 12 new names has been successfully validated.

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