Register list for 40 new names including Acidimicrobilacustridaceae fam. nov.

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Family *Acidimicrobilacustridaceae*

Etymology

[A.ci.di.mi.cro.bi.la.cus.tri.da'ce.ae] **N.L. masc. n.** *Acidimicrobilacustris*, referring to the type genus Acidimicrobilacustris; *-aceae*, ending to denote a family; **N.L. fem. pl. n.** *Acidimicrobilacustridaceae*, the Acidimicrobilacustris family

Nomenclatural type

Genus *Acidimicrobilacustris*

Description

A family of *Acidimicrobiales* also known as “acIV-D Actinobacteria” or “uncultured Microtrichales” from 16S rRNA gene analyses and as f__UBA8139 in GTDB, that is commonly found in freshwater environments. Consisting of the genus *Acidimicrobilacustris* and two species, *Acidimicrobilacustris thunensis* (GCA_965194345.1) and *Acidimicrobilacustris europaeus* (GCA_965194515.1), both isolated from freshwater lakes. Type species is *Acidimicrobilacustris thunensis* TE-7 (GCA_965194345.1). The closest cultivated relative is *Rhabdothermincola salaria* (*Iamiaceae*, GCF_021246445.1), with an average amino acid identity of 66.55% and an average nucleotide identity of 71.1%. As this related taxon is also included in family UBA8139 in GTDB and not in *Iamiaceae*, we propose the new family *Acidimicrobilacustridaceae*. Current GTDB (R220) classification: d__Bacteria; p__Actinomycetota; c__Acidimicrobiia; o__Acidimicrobiales; f__UBA8139.

Classification

Bacteria » *Actinomycetota* » *Acidimicrobiia* » *Acidimicrobiales* » *Acidimicrobilacustridaceae*

References

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

Registry URL

https://seqco.de/i:48714

Family *Verrucolacustridaceae*

Etymology

[Ver.ru.co.la.cus.tri.da'ce.ae] **N.L. masc. n.** *Verrucolacustris*, referring to the type genus Verrucolacustris; *-aceae*, ending to denote a family; **N.L. fem. pl. n.** *Verrucolacustridaceae*, the Verrucolacustris family

Nomenclatural type

Genus *Verrucolacustris*

Description

Type strain is *Verrucolacustris abundans* MiH-22 (GCA_965194535.1). In contrast to other *Methylacidiphilales* including the only described genus *Methylacidimicrobium* (*Methylacidiphilaceae,* GCF_902143385.2), no genes for C1 metabolism were identified, therefore we suggest the establishment of a new family of non-methanotrophic *Methylacidiphilales*. The closest cultivated relative is *Methylacidimicrobium cyclopophantes* 3B_2 (GCF_902143385.2), with an average amino acid identity of 49.5% and average nucleotide identity of 62.8%. Current GTDB classification (R220): d__Bacteria; p__Verrucomicrobiota; c__Verrucomicrobiae; o__Methylacidiphilales; f__UBA3015.

Classification

Bacteria » *Verrucomicrobiota* » “Methylacidiphilae” » *Methylacidiphilales* » *Verrucolacustridaceae*

References

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

Registry URL

https://seqco.de/i:48695

Genus *Acidimicrobilacustris*

Etymology

[A.ci.di.mi.cro.bi.la.cus'tris] **N.L. neut. n.** *Acidimicrobium*, the genus Acidimicrobium, in reference to the order Acidimicrobiales; **L. masc. adj.** *lacustris*, of a lake, pond, pool; **N.L. masc. n.** *Acidimicrobilacustris*, a freshwater genus of Acidimicrobiales

Nomenclatural type

Species *Acidimicrobilacustris europaeus*^{Ts}

Description

Type genus of *Acidimicrobilacustridaceae* also known as “acIV-D Actinobacteria” or “uncultured Microtrichales” from 16S rRNA gene analyses and as g__F1-20-MAGs160 in GTDB, that is commonly found in freshwater environments. Consisting of two species, *Acidimicrobilacustris thunensis* (GCA_965194345.1) and *Acidimicrobilacustris europaeus* (GCA_965194515.1), both isolated from freshwater lakes. Type species is *Acidimicrobilacustris thunensis* TE-7 (GCA_965194345.1). The closest cultivated relative is *Rhabdothermincola salaria* (GCF_021246445.1), with an average amino acid identity of 66.55% and an average nucleotide identity of 71.1%. Current GTDB (R220) classification: d__Bacteria; p__Actinomycetota; c__Acidimicrobiia; o__Acidimicrobiales; f__UBA8139; g__F1-20-MAGs160.

Classification

Bacteria » *Actinomycetota* » *Acidimicrobiia* » *Acidimicrobiales* » *Acidimicrobilacustridaceae* » *Acidimicrobilacustris*

References

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

Registry URL

https://seqco.de/i:48715

Genus *Allorhodoferax*

Etymology

[A.llo.rho.do.fe'rax] **Gr. masc. pron.** *allos*, another, other, different; **N.L. masc. n.** *rhodoferax*, a bacterial genus name; **N.L. masc. n.** *Allorhodoferax*, another Rhodoferax.

Nomenclatural type

Species *Allorhodoferax aquaticus*^{Ts}

Description

The genus contains two species, *Allorhodoferax aquaticus* (GCA_965194715.1) and *Allorhodoferax lacus* (GCA_965194635.1), both isolated from freshwater lakes. Type species is *Allorhodoferax aquaticus* MsE-M22 (GCA_965194715.1). The genus is classified as d__Bacteria; p__Pseudomonadota; c__Gammaproteobacteria; o__Burkholderiales; f__Burkholderiaceae; Rhodoferax_C in GTDB (R220) and contains bacteria with various names such as *Curvibacter, Rhodoferax*, etc. The closest cultivated relative is *Curvibacter* sp. AEP1-3 (GCF_002163715.1), with average amino acid identities of 86.2-90.7% and average nucleotide identities of 81-9-86.6%. The type strain of the genus *Rhodoferax* (*Rhodoferax fermentans* JCM 7819; GCA_002017865.1) is classified as d__Bacteria; p__Pseudomonadota; c__Gammaproteobacteria; o__Burkholderiales; f__Burkholderiaceae; g__Rhodoferax; s__Rhodoferax fermentans, with AAIs of 66.0-66.8% and ANIs of 72.4-72.6%. We therefore suggest a reclassification of this genus (GTDB genus Rhodoferax_C) with the proposed name *Allorhodoferax*.

Classification

Bacteria » *Pseudomonadota* » *Betaproteobacteria* » *Burkholderiales* » *Comamonadaceae* » *Allorhodoferax*

References

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

Registry URL

https://seqco.de/i:49941

Genus *Allotabrizicola*

Etymology

[A.llo.ta.bri.zi'co.la] **Gr. masc. pron.** *allos*, another, other, different; **N.L. fem. n.** *Tabrizicola*, a bacterial genus; **N.L. fem. n.** *Allotabrizicola*, another Tabrizicola genus

Nomenclatural type

Species *Allotabrizicola aquatica*^{Ts}

Description

Type species is *Allotabrizicola aquatica* RE-M30 (GCA_965194375.1). The closest cultivated relative is *Tabrizicola oligotrophica* KMS-5 (GCF_011008935.1) with an average amino acid identity of 79.2% and average nucleotide identity of 79.5%. As the closest relative is classified as Tabrizicola_A in GTDB, we propose a new genus that encompasses both species. The type species of the genus *Tabrizicola* (*Tabrizicola aquatica*, GCF_002900975.1), has average amino acid identities of 68.4-69.2% and average nucleotide identities of 73.7-74.8% to *Tabrizicola oligotrophica* KMS-5 (GCF_011008935.1) and *Allotabrizicola aquatica* RE-M30. Current GTDB classification (R220): d__Bacteria; p__Pseudomonadota; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Tabrizicola_A.

Classification

Bacteria » *Pseudomonadota* » *Alphaproteobacteria* » *Rhodobacterales* » *Paracoccaceae* » *Allotabrizicola*

References

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

Registry URL

https://seqco.de/i:48698

Genus *Lacustribacter*

Etymology

[La.cus.tri.bac'ter] **N.L. masc. adj.** *lacustris*, belonging to a lake; **N.L. masc. n.** *bacter*, rod; **N.L. masc. n.** *Lacustribacter*, A rod-shaped bacterium living in freshwaters.

Nomenclatural type

Species *Lacustribacter communis*$^{\mathrm{Ts}}$

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. Type species is *Lacustribacter communis* MsE-M52 (GCA_965194335.1). The closest cultivated relatives are the undescribed *Burkholderiales* bacterium LSUCC0115 (GCA_009646425.1), with an average amino acid identity of 61.9% and average nucleotide identity of 67.9% and the newly established genus *Hahnella,* with 60.4-61.7% AAI and 67.2-67.9% ANI. The closest validly described relative is *Limnobacter thiooxidans* CS-K2 (GCF_036323495.1) with an AAI of 53.95% and an ANI of 66.33%. Current GTDB classification (R220): d__Bacteria; p__Pseudomonadota; c__Gammaproteobacteria; o__Burkholderiales; f__Burkholderiaceae; g__UBA954.

Classification

Bacteria » *Pseudomonadota* » *Betaproteobacteria* » *Burkholderiales* » *Burkholderiaceae* » *Lacustribacter*

References

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

Registry URL

https://seqco.de/i:48710

Genus *Novimethylotenera*

Etymology

[No.vi.me.thy.lo.te.ne'ra] **L. adj. masc.** *novus*, new; **N.L. fem. n.** *Methylotenera*, the bacterial genus Methylotenera; **N.L. fem. n.** *Novimethylotenera*, a new Methylotenera

Nomenclatural type

Species *Novimethylotenera aquatica*$^{\mathrm{Ts}}$

Description

Type species is *Novimethylotenera aquatica* ME-M6 (GCA_947054645.1). Although the closest cultivated relative (*Methylotenera versatilis* 7; GCF_000799165.1) has an average amino acid identity of 80.36% and average nucleotide identity of 76.56%, the genus *Methylotenera* is known to be polyphyletic in phylogenomic trees (e.g., Salcher et al. 2019; https://doi.org/10.1038/s41396-019-0471-3) and some strains that were previously termed *Methylotenera* should be reclassified. Current GTDB classification of the genus including the closest cultivated relative (GCF_000799165.1) is d__Bacteria; p__Pseudomonadota; c__Gammaproteobacteria; o__Burkholderiales; f__Methylophilaceae; g__Methylotenera_A. We propose a reclassification of the GTDB genus Methylotenera_A to *Novimethylotenera*, gen. nov.

Classification

Bacteria » *Pseudomonadota* » *Betaproteobacteria* » *Nitrosomonadales* » *Methylophilaceae* » *Novimethylotenera*

References

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

Registry URL

https://seqco.de/i:48702

Genus *Verrucolacustris*

Etymology

[Ver.ru.co.la.cus'tris] **N.L. pref.** *Verruco-*, derived from the bacterial phylum Verrucomicrobiota; **L. masc. adj.** *lacustris*, of a lake; **N.L. masc. n.** *Verrucolacustris*, a freshwater genus of Verrucomicrobiota

Nomenclatural type

Species *Verrucolacustris abundans*^{Ts}

Description

Type species is *Verrucolacustris abundans* MiH-22 (GCA_965194535.1). The closest cultivated relative is *Methylacidimicrobium cyclopophantes* 3B_2 (GCF_902143385.2), with an average amino acid identity of 49.5% and average nucleotide identity of 62.8%. Current GTDB classification (R220): d__Bacteria; p__Verrucomicrobiota; c__Verrucomicrobiae; o__Methylacidiphilales; f__UBA3015; g__UBA3015.

Classification

Bacteria » *Verrucomicrobiota* » “Methylacidiphilae” » *Methylacidiphilales* » *Verrucolacustridaceae* » *Verrucolacustris*

References

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

Registry URL

https://seqco.de/i:48696

Species *Acidimicrobilacustris europaeus*^{Ts}

Etymology

[e.u.ro.pae'us] **N.L. masc. adj.** *europaeus*, of/from Europe; named after the main occurrence in european lakes

Nomenclatural type

NCBI Assembly: GCA_965194515.1 ^{Ts}

Reference Strain

Strain sc|0040325: KE-4

Description

Type strain is *Acidimicrobilacustris europaeus* KE-4 (GCA_965194515.1), isolated from 5 m depth from Klíčava Reservoir, Czechia (date: 2019-04-25), *via* high-throughput dilution to extinction cultivation. KE-4 has a genome size of 2.35 Mbp with a genomic GC content of 58.2%, contains 3 rRNA genes and 44 tRNAs. The genome is complete, consisting of a circular chromosome. The genome contains genes encoding rhodopsins but lacks the biosynthetic pathway for retinal biosynthesis. No genes for flagella or pilus assembly and chemotaxis were annotated. Pathways for taurine degradation, assimilatory sulfate reduction and methane/alkanesulfonate oxidation and biosynthesis for all amino acids except histidine and threonine were predicted. Further, pathways for riboflavin, pyridoxal, NAD, coenzyme A, biotin and heme were identified. The closest cultivated relatives are *Rhabdothermincola salaria* (GCF_021246445.1) with an average amino acid identity of 64.98% and an average nucleotide identity of 69.8% and another newly proposed species, *Acidimicrobilacustris thunensis* TE-7 (GCA_965194345.1), with an AAI of 73.1% and an ANI of 72%. Current GTDB classification (R220): d__Bacteria; p__Actinomycetota; c__Acidimicrobiia; o__Acidimicrobiales; f__UBA8139; g__F1-20-MAGs160; s__F1-20-MAGs160 sp903827085.

Classification

Bacteria » *Actinomycetota* » *Acidimicrobiia* » *Acidimicrobiales* » *Acidimicrobilacustridaceae* » *Acidimicrobilacustris* » *Acidimicrobilacustris europaeus*^{Ts}

References

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

Registry URL

https://seqco.de/i:48713

Species *Acidimicrobilacustris thunensis*

Etymology

[thu.nen'sis] **N.L. masc. adj.** *thunensis*, of Thun, referring to Lake Thun, the isolation source of the type strain.

Nomenclatural type

NCBI Assembly: GCA_965194345.1 Ts

Reference Strain

Strain scj0040324: TE-7

Description

Type strain is *Acidimicrobilacustris thunensis* TE-7 (GCA_965194345.1), isolated from 5 m depth from Lake Thun, Switzerland (date: 2019-11-11), *via* high-throughput dilution to extinction cultivation. TE-7 has a genome size of 2.38 Mbp with a genomic GC content of 60.6%, contains 3 rRNA genes and 46 tRNAs. The genome is complete, consisting of a circular chromosome. The genome contains genes encoding rhodopsins but lacks the biosynthetic pathway for retinal biosynthesis. No genes for flagella or pilus assembly and chemotaxis were annotated. Pathways for taurine degradation, assimilatory sulfate reduction and methane/alkanesulfonate oxidation and biosynthesis for all amino acids except histidine were predicted. Further, pathways for riboflavin, pyridoxal, NAD, coenzyme A, biotin and heme were identified. The closest cultivated relatives are *Rhabdothermincola salaria* (GCF_021246445.1) with an average amino acid identity of 66.55% and an average nucleotide identity of 71.1% and another newly proposed species, *Acidimicrobilacustris europaeus* KE-4 (GCA_965194515.1), with an AAI of 73.1% and an ANI of 72%. Current GTDB (R220) classification: d__Bacteria; p__Actinomycetota; c__Acidimicrobiia; o__Acidimicrobiales; f__UBA8139; g__F1-20-MAGs160; s__F1-20-MAGs160 sp945878725.

Classification

Bacteria » *Actinomycetota* » *Acidimicrobiia* » *Acidimicrobiales* » *Acidimicrobilacustridaceae* » *Acidimicrobilacustris* » *Acidimicrobilacustris thunensis*

References

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

Registry URL

https://seqco.de/i:48740

Species *Allorhodoferax aquaticus*^{Ts}

Etymology

[a.qua'ti.cus] **L. masc. adj.** *aquaticus*, living, growing, or found in or by the water, aquatic

Nomenclatural type

NCBI Assembly: GCA_965194715.1 ^{Ts}

Reference Strain

Strain sc|0038967: MsE-M22

Description

Type strain is *Allorhodoferax aquaticus* MsE-M22 (GCA_965194715.1), isolated from 5 m depth from Lake Most, Czechia (date: 2019-07-30), *via* high-throughput dilution to extinction cultivation. MsE-M22 has a genome size of 3.7 Mbp with a genomic GC content of 59.3%, contains 6 rRNA genes and 47 tRNAs. The genome is complete, consisting of a circular chromosome. Genes for flagellar and pilus assembly were annotated. Pathways for nitrate reduction, cyanate and urea degradation, glycolate oxidation and the biosynthesis of all amino acids except for aspartate were predicted. Further, pathways for thiamine, riboflavin, NAD, coenzyme A, THF, cobalamin, and heme biosynthesis were identified. The closest cultivated relative is *Curvibacter* sp. AEP1-3 (GCF_002163715.1), with an average amino acid identity of 90.7% and average nucleotide identity of 86.6%. Current GTDB classification (R220): d__Bacteria; p__Pseudomonadota; c__Gammaproteobacteria; o__Burkholderiales; f__Burkholderiaceae; g__Rhodoferax_C; s__Rhodoferax_C sp027488985.

Classification

Bacteria » *Pseudomonadota* » *Betaproteobacteria* » *Burkholderiales* » *Comamonadaceae* » *Allorhodoferax* » *Allorhodoferax aquaticus*^{Ts}

References

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

Registry URL

https://seqco.de/i:48704

Species *Allorhodoferax lacus*

Etymology

[la'cus] **L. gen. n.** *lacus*, of a lake, referring to the habitat from which the type strain was isolated.

Nomenclatural type

NCBI Assembly: GCA_965194635.1 Ts

Reference Strain

Strain sc|0038966: ZE-M1

Description

Type strain is *Allorhodoferax lacus* ZE-M1 (GCA_965194635.1), isolated from 5 m depth from Lake Zurich, Switzerland (date: 2019-04-03), *via* high-throughput dilution to extinction cultivation. ZE-M1 has a genome size of 3.7 Mbp with a genomic GC content of 60.1%, contains 6 rRNA genes and 46 tRNAs. The genome is a high-quality draft consisting of 2 contigs. Genes for flagellar and pilus assembly were annotated. Pathways for cyanate and urea degradation, glycolate and methane/alkanesulfonate oxidation and the biosynthesis of all amino acids except for aspartate were predicted. Further, pathways for thiamine, riboflavin, NAD, coenzyme A, THF, cobalamin, and heme biosynthesis were identified. The closest cultivated relative is *Curvibacter* sp. AEP1-3 (GCF_002163715.1), with an average amino acid identity of 86.2% and average nucleotide identity of 81.9%. Current GTDB classification (R220): d__Bacteria; p__Pseudomonadota; c__Gammaproteobacteria; o__Burkholderiales; f__Burkholderiaceae; g__Rhodoferax_C; s__.

Classification

Bacteria » *Pseudomonadota* » *Betaproteobacteria* » *Burkholderiales* » *Comamonadaceae* » *Allorhodoferax* » *Allorhodoferax lacus*

References

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

Registry URL

https://seqco.de/i:48720

Species *Allotabrizicola aquatica*$^{\mathrm{Ts}}$

Etymology

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

Nomenclatural type

NCBI Assembly: GCA_965194375.1 $^{\mathrm{Ts}}$

Reference Strain

Strain sc|0038957: RE-M30

Description

Type strain is *Allotabrizicola aquatica* RE-M30 (GCA_965194375.1), isolated from 0.5 m depth from the Římov Reservoir, Czechia (date: 2019-08-05), *via* high-throughput dilution to extinction cultivation. RE-M30 has a genome size of 3.6 Mbp with a genomic GC content of 61.9%, contains 6 rRNA genes and 49 tRNAs. The genome is a high-quality draft consisting of 20 contigs. The genome contains genes encoding anoxygenic aerobic phototrophy (*pufABLM*). Genes for flagellar assembly were annotated in the genome. Pathways for urea and taurine degradation, glycolate oxidation and the biosynthesis of all amino acids were predicted. Further, pathways for riboflavin, pantothenate, coenzyme A, and heme biosynthesis were identified. The closest cultivated relative is *Tabrizicola oligotrophica* KMS-5 (GCF_011008935.1), with an average amino acid identity of 79.2% and average nucleotide identity of 79.5%. Current GTDB classification (R220): d__Bacteria; p__Pseudomonadota; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Tabrizicola_A; s__.

Classification

Bacteria » *Pseudomonadota* » *Alphaproteobacteria* » *Rhodobacterales* » *Paracoccaceae* » *Allotabrizicola* » *Allotabrizicola aquatica*$^{\mathrm{Ts}}$

References

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

Registry URL

https://seqco.de/i:48697

Species *Aquidulcibacter miladensis*

Etymology

[mi.la.den'sis] **N.L. masc. adj.** *miladensis*, pertaining to Lake Milada (Czechia), the isolation source of the type strain.

Nomenclatural type

NCBI Assembly: GCA_965234355.1 Ts

Reference Strain

Strain sc|0038952: MiH-15

Description

Type strain is *Aquidulcibacter miladensis* MiH-15 (GCA_965234355.1), isolated from 15 m depth from Lake Milada, Czechia (date: 2019-07-23), *via* high-throughput dilution to extinction cultivation. MiH-15 has a genome size of 3.2 Mbp with a genomic GC content of 55.7%, contains 3 rRNA genes and 41 tRNAs. The genome is a high-quality draft consisting of 8 contigs. The genome contains genes encoding anoxygenic aerobic phototrophy (*pufABLM*). Genes for flagellar assembly and chemotaxis were annotated in the genome. Pathways for taurine degradation, assimilatory sulfate reduction and methane/alkanesulfonate oxidation and the biosynthesis of all amino acids were predicted. Further, pathways for riboflavin, NAD, coenzyme A, pimeloyl-ACP, THF, and heme biosynthesis were identified. The closest cultivated relatives are *Aquidulcibacter paucihalophilus* TH1-2 (GCF_002105465.1) with an average amino acid identity of 87.1% and average nucleotide identity of 80.5% and another newly proposed species, *Aquidulcibacter rimovensis* RH-10 (GCA_965234525.1), with an AAI of 93.2% and an ANI of 89.4%. Current GTDB classification (R220): d__Bacteria; p__Pseudomonadota; c__Alphaproteobacteria; o__Caulobacterales; f__TH1-2; g__Aquidulcibacter; s__Aquidulcibacter sp945891505.

Classification

Bacteria » *Pseudomonadota* » *Alphaproteobacteria* » *Caulobacterales* » *Caulobacteraceae* » *Aquidulcibacter* » *Aquidulcibacter miladensis*

References

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

Registry URL

https://seqco.de/i:48727

Species *Aquidulcibacter rimovensis*

Etymology

[ri.mo.ven'sis] **N.L. masc. adj.** *rimovensis*, pertaining to the Římov Reservoir (Czechia), the isolation source of the type strain.

Nomenclatural type

NCBI Assembly: GCA_965234525.1 ^{Ts}

Reference Strain

Strain sc|0038951: RH-10

Description

Type strain is *Aquidulcibacter rimovensis* RH-10 (GCA_965234525.1), isolated from 30 m depth from Římov Reservoir, Czechia (date: 2019-08-05), *via* high-throughput dilution to extinction cultivation. RH-10 has a genome size of 3.3 Mbp with a genomic GC content of 55.4%, contains 3 rRNA genes and 42 tRNAs. The genome is a high-quality draft consisting of 2 contigs. The genome contains genes encoding anoxygenic aerobic phototrophy (*pufABLM*). Genes for flagellar assembly and chemotaxis were annotated in the genome. Pathways for taurine degradation, assimilatory sulfate reduction and methane/alkanesulfonate oxidation and the biosynthesis of all amino acids were predicted. Further, pathways for riboflavin, NAD, coenzyme A, pimeloyl-ACP, THF, and heme biosynthesis were identified. The closest cultivated relatives are *Aquidulcibacter paucihalophilus* TH1-2 (GCF_002105465.1) with an average amino acid identity of 87.3% and average nucleotide identity of 80.2% and another newly proposed species, *Aquidulcibacter miladensis* MiH-15 (GCA_965234355.1), with an AAI of 93.2% and an ANI of 89.4%. Current GTDB classification (R220): d__Bacteria; p__Pseudomonadota; c__Alphaproteobacteria; o__Caulobacterales; f__TH1-2; g__Aquidulcibacter; s__Aquidulcibacter sp027532555.

Classification

Bacteria » *Pseudomonadota* » *Alphaproteobacteria* » *Caulobacterales* » *Caulobacteraceae* » *Aquidulcibacter* » *Aquidulcibacter rimovensis*

References

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

Registry URL

https://seqco.de/i:48737

Species *Caulobacter lacus*

Etymology

[la'cus] **L. gen. n.** *lacus*, of a lake, referring to the habitat from which the type strain was isolated.

Nomenclatural type

NCBI Assembly: GCA_965234345.1 Ts

Reference Strain

Strain scl0038950: MiH-16

Description

Type strain is *Caulobacter lacus* MiH-16 (GCA_965234345.1), isolated from 15 m depth from Lake Milada, Czechia (date: 2019-07-23), *via* high-throughput dilution to extinction cultivation. MiH-16 has a genome size of 3.6 Mbp with a genomic GC content of 67.6%, contains 3 rRNA genes and 47 tRNAs. The genome is a high-quality draft consisting of 5 contigs. The genome contains genes encoding rhodopsins. Genes for flagellar assembly and chemotaxis were annotated in the genome. Pathways for taurine degradation, assimilatory sulfate reduction and methane/alkanesulfonate oxidation and the biosynthesis of all amino acids were predicted. Further, pathways for thiamine, riboflavin, NAD, coenzyme A, pimeloyl-ACP, THF, and heme biosynthesis were identified. The closest cultivated relative is *Caulobacter* sp. Root1455 (GCF_001426905.1), with an average amino acid identity of 64% and average nucleotide identity of 74.7%. Current GTDB classification (R220): d__Bacteria; p__Pseudomonadota; c__Alphaproteobacteria; o__Caulobacterales; f__Caulobacteraceae; g__Caulobacter; s__Caulobacter sp903858185.

Classification

Bacteria » *Pseudomonadota* » *Alphaproteobacteria* » *Caulobacterales* » *Caulobacteraceae* » *Caulobacter* » *Caulobacter lacus*

References

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

Registry URL

https://seqco.de/i:48721

Species *Flavobacterium neuenschwanderi*

Etymology

[ne.u.en.schwan.der'i] **L. masc. gen. n.** *neuenschwanderi*, of Neuenschwander, named after the Swiss scientist Stefan Neuenschwander, who studied freshwater Flavobacteria in Lake Zurich.

Nomenclatural type

NCBI Assembly: GCA_965234425.1 ^{Ts}

Reference Strain

Strain scl0038948: GE-10

Description

Type strain is *Flavobacterium neuenschwanderi* GE-10 (GCA_965234425.1), isolated from 5 m depth from Greifensee, Switzerland (date: 2019-04-03), *via* high-throughput dilution to extinction cultivation. GE-10 has a genome size of 3.56 Mbp with a genomic GC content of 33.1%, contains 4 rRNA genes and 38 tRNAs. The genome is a high-quality draft consisting of 44 contigs. The genome contains genes encoding rhodopsins. Genes for gliding motility (*gldBDHJKLMN*, *sprA*) were annotated in the genome. Pathways for assimilatory sulfate reduction and the biosynthesis of all amino acids were predicted. Further, pathways for riboflavin, NAD, coenzyme A, biotin, THF, menaquinone, and heme were identified. The closest cultivated relative is *Flavobacterium psychrotolerans* RB1R5 (GCF_003097635.1), with an average amino acid identity of 74.81% and average nucleotide identity of 74.37%. Current GTDB classification (R220): d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__Flavobacterium; s__.

Classification

Bacteria » *Bacteroidota* » *Flavobacteriia* » *Flavobacteriales* » *Flavobacteriaceae* » *Flavobacterium* » *Flavobacterium neuenschwanderi*

References

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

Registry URL

https://seqco.de/i:48730

Species *Flavobacterium rarum*

Etymology

[ra'rum] **L. neut. adj.** *rarum*, sporadic or uncommon, referring to the sporadic isolation and recovery from disparate sources of members of this species

Nomenclatural type

NCBI Assembly: GCA_965234445.1 Ts

Reference Strain

Strain sc|0038949: TH-M1

Description

Type strain is *Flavobacterium rarum* TH-M1 (GCA_965234445.1), isolated from 180 m from Lake Thun, Switzerland (date: 2019-04-08), *via* high-throughput dilution to extinction cultivation. TH-M1 has a genome size of 4.26 Mbp with a genomic GC content of 33.4%, contains 6 rRNA genes and 51 tRNAs. The genome is a high-quality draft consisting of 29 contigs. The genome contains genes encoding rhodopsins. Genes for gliding motility (*gldBDHJKLMN*, *sprA*) were annotated in the genome. Pathways for taurine degradation, assimilatory sulfate reduction and the biosynthesis of all amino acids were predicted. Further, pathways for thiamine, riboflavin, NAD, pantothenate, coenzyme A, biotin, THF, menaquinone, and heme were identified. The closest cultivated relative is *Flavobacterium praedii* IMCC34515 (GCF_026810365.1), with an average amino acid identity of 85.51% and average nucleotide identity of 83.7%. Current GTDB classification (R220): d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Flavobacteriales; f__Flavobacteriaceae; g__Flavobacterium; s__.

Classification

Bacteria » *Bacteroidota* » *Flavobacteriia* » *Flavobacteriales* » *Flavobacteriaceae* » *Flavobacterium* » *Flavobacterium rarum*

References

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

Registry URL

https://seqco.de/i:48736

Species *Fontibacterium abundans*

Etymology

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

Nomenclatural type

NCBI Assembly: GCA_965235095.1 Ts

Reference Strain

Strain sc|0038953: MiE-29

Description

Type strain is *Fontibacterium abundans* MiE-29 (GCA_965235095.1), isolated from 5 m depth from Lake Milada, Czechia (date: 2019-10-15), *via* high-throughput dilution to extinction cultivation. MiE-29 has a genome size of 1.1 Mbp with a genomic GC content of 29.4%, contains 3 rRNA genes and 31 tRNAs. The genome is a high-quality draft consisting of 2 contigs. The genome contains genes encoding rhodopsins and the biosynthetic pathway for retinal biosynthesis. No genes for flagella or pilus assembly and chemotaxis were annotated. Pathways for glycolate oxidation and the biosynthesis of 16 amino acids were predicted. Further, pathways for riboflavin, NAD, coenzyme A, and heme biosynthesis were identified. The closest cultivated relatives are *Fontibacterium commune*, syn. '*Candidatus* Fonsibacter ubiquis' LSUCC0530 (GCF_002688585.1; later reclassified to '*Ca*. Allofontibacter communis'), with an average amino acid identity of 86.5% and average nucleotide identity of 85.2% and another newly proposed species, *Fontibacterium medardicum* ME-17 (GCA_965235075.1), with an AAI of 92.7% and an ANI of 91.1%. Current GTDB classification (R220): d__Bacteria; p__Pseudomonadota; c__Alphaproteobacteria; o__Pelagibacterales; f__Pelagibacteraceae; g__Fonsibacter; s__.

Classification

Bacteria » *Pseudomonadota* » *Alphaproteobacteria* » "Pelagibacterales" » *Pelagibacteraceae* » *Fontibacterium* » *Fontibacterium abundans*

References

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

Registry URL

https://seqco.de/i:48693

Species *Fontibacterium medardense*

Etymology

[me.dar.den'se] **L. neut. adj.** *medardense*, pertaining to Lake Medard (Czechia), the isolation source of the type strain.

Nomenclatural type

NCBI Assembly: GCA_965235075.1 Ts

Reference Strain

Strain sc|0038954: ME-17

Description

Type strain is *Allofontibacter medardicus* ME-17 (GCA_965235075.1), isolated from 5 m depth from Lake Medard, Czechia (date: 2019-10-22), *via* high-throughput dilution to extinction cultivation. ME-17 has a genome size of 1.1 Mbp with a genomic GC content of 29.6%, contains 3 rRNA genes and 31 tRNAs. The genome is complete, consisting of a circular chromosome. The genome contains genes encoding rhodopsins and the biosynthetic pathway for retinal biosynthesis. No genes for flagella or pilus assembly and chemotaxis were annotated. Pathways for glycolate oxidation and the biosynthesis of 16 amino acids were predicted. Further, pathways for riboflavin, NAD, coenzyme A, and heme biosynthesis were identified. The closest cultivated relatives are ‘*Candidatus* Fonsibacter ubiquis’ LSUCC0530 (GCF_002688585.1; later reclassified to ‘*Ca*. Allofontibacter communis’), with an average amino acid identity of 87.2% and average nucleotide identity of 85.2% and another newly proposed species, *Allofontibacter abundans* MiE-29 (GCA_965235095.1), with an AAI of 92.7% and an ANI of 91.1%. Current GTDB classification (R220): d__Bacteria; p__Pseudomonadota; c__Alphaproteobacteria; o__Pelagibacterales; f__Pelagibacteraceae; g__Fonsibacter; s__Fonsibacter sp018882565.

Classification

Bacteria » *Pseudomonadota* » *Alphaproteobacteria* » “Pelagibacterales” » *Pelagibacteraceae* » *Fontibacterium* » *Fontibacterium medardense*

References

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

Registry URL

https://seqco.de/i:48726

Species *Hydrogenophaga miladensis*

Etymology

[mi.la.den'sis] **N.L. fem. adj.** *miladensis*, pertaining to Lake Milada (Czechia), the isolation source of the type strain.

Nomenclatural type

NCBI Assembly: GCA_965234585.1 ^{Ts}

Reference Strain

Strain sc|0038963: MiE-M28

Description

Type strain is *Hydrogenophaga miladensis* MiE-M28 (GCA_965234585.1), isolated from 5 m depth from Lake Milada, Czechia (date: 2019-10-15), *via* high-throughput dilution to extinction cultivation. MiE-M28 has a genome size of 2.4 Mbp with a genomic GC content of 60.6%, contains 6 rRNA genes and 43 tRNAs. 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 and pilus assembly were annotated. Pathways for thiosulfate oxidation (Sox pathway), glycolate and methane/alkanesulfonate oxidation and the biosynthesis of all amino acids were predicted. Further, pathways for thiamine, riboflavin, NAD, coenzyme A, pimeloyl-ACP, and heme biosynthesis were identified. The closest cultivated relative is *Hydrogenophaga intermedia* MER 62 (GCF_001571205.1), with an average nucleotide identity of 74.2%. Current GTDB classification (R220): d__Bacteria; p__Pseudomonadota; c__Gammaproteobacteria; o__Burkholderiales; f__Burkholderiaceae_B; g__Hydrogenophaga; s__Hydrogenophaga intermedia_C.

Classification

Bacteria » *Pseudomonadota* » *Betaproteobacteria* » *Burkholderiales* » *Comamonadaceae* » *Hydrogenophaga* » *Hydrogenophaga miladensis*

References

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

Registry URL

https://seqco.de/i:48728

Species *Lacustribacter communis*^{Ts}

Etymology

[com.mu'nis] **L. masc. adj.** *communis*, common; referring to a wide distribution in freshwater lakes.

Nomenclatural type

NCBI Assembly: GCA_965194335.1 ^{Ts}

Reference Strain

Strain sc|0038962: MsE-M52

Description

Type strain is *Lacustribacter communis* MsE-M52 (GCA_965194335.1), isolated from 5 m depth from Lake Most, Czechia (date: 2019-10-01), *via* high-throughput dilution to extinction cultivation. MsE-M52 has a genome size of 2.1 Mbp with a genomic GC content of 53.3%, contains 3 rRNA genes and 42 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 urea and taurine degradation, thiosulfate oxidation (Sox pathway), glycolate oxidation, and the biosynthesis of all amino acids except for aspartate 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 61.9% and average nucleotide identity of 67.9% and the newly established genus *Hahnella,* with 60.4-61.7% AAI and 67.2-67.9% ANI. The closest validly described relative is *Limnobacter thiooxidans* CS-K2 (GCF_036323495.1) with an AAI of 53.95% and an ANI of 66.33%. Current GTDB classification (R220): d__Bacteria; p__Pseudomonadota; c__Gammaproteobacteria; o__Burkholderiales; f__Burkholderiaceae; g__UBA954; s__UBA954 sp002293155.

Classification

Bacteria » *Pseudomonadota* » *Betaproteobacteria* » *Burkholderiales* » *Burkholderiaceae* » *Lacustribacter* » *Lacustribacter communis*^{Ts}

References

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

Registry URL

https://seqco.de/i:48709

Species *Leadbetterella lacustris*

Etymology

[la.cus'tris] **N.L. fem. adj.** *lacustris*, of a lake; referring to the habitat from where the strain was isolated.

Nomenclatural type

NCBI Assembly: GCA_965234335.1 ^{Ts}

Reference Strain

Strain scl0038947: RE-19

Description

Type strain is *Leadbetterella lacustris* RE-19 (GCA_965234335.1), isolated from 0.5 m depth from the Římov reservoir, Czechia (date: 2019-08-05), *via* high-throughput dilution to extinction cultivation. RE-19 has a genome size of 5 Mbp with a genomic GC content of 37.48 %, contains 9 rRNA genes and 36 tRNAs. The genome is a high-quality draft consisting of 36 contigs. The genome contains genes encoding rhodopsins. Genes for gliding motility (*gldBDHJKLMN*, *sprA*) were annotated in the genome. Pathways for assimilatory sulfate reduction, methane/alkanesulfonate oxidation and the biosynthesis of all amino acids were predicted. Further, pathways for riboflavin, NAD, coenzyme A, THF, menaquinone, and heme biosynthesis were identified. The closest cultivated relative is *Lacihabitans soyangensis* KCTC23259 (GCF_024343775.1), with an average amino acid identity of 85.5% and average nucleotide identity of 82.97%. *Lacihabitans* is grouped with the genus *Leadbetterella* in GTDB. Current GTDB classification (R220): d__Bacteria; p__Bacteroidota; c__Bacteroidia; o__Cytophagales; f__Spirosomaceae; g__Leadbetterella; s__Leadbetterella flu*via*le_A.

Classification

Bacteria » *Bacteroidota* » *Cytophagia* » *Cytophagales* » *Spirosomataceae* » *Leadbetterella* » *Leadbetterella lacustris*

References

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

Registry URL

https://seqco.de/i:48724

Species *Limnohabitans kasalickyi*

Etymology

[ka.sa.li.cky'i] **N.L. masc. gen. n.** *kasalickyi*, named after the Czech scientist Vojtěch (Vojta) Kasalický, who isolated many strains of the genus Limnohabitans and was involved in the description of the genus.

Nomenclatural type

NCBI Assembly: GCA_965234325.1 Ts

Reference Strain

Strain scl0038965: MaE-M4

Description

Type strain is *Limnohabitans kasalickyi* MaE-M4 (GCA_965234325.1), isolated from 5 m depth from Lake Maggiore, Italy (date: 2019-04-09), *via* high-throughput dilution to extinction cultivation. MaE-M4 has a genome size of 3.7 Mbp with a genomic GC content of 56.3%, contains 6 rRNA genes and 44 tRNAs. The genome is a high-quality draft consisting of 16 contigs. The genome contains genes encoding anoxygenic aerobic phototrophy (*pufABLM*). Genes for flagellar and pilus assembly were annotated. Pathways for cyanate, urea, and taurine degradation, thiosulfate oxidation (Sox pathway), methane/alkanesulfonate and glycolate oxidation, and the biosynthesis of all amino acids except for aspartate were predicted. Further, pathways for thiamine, riboflavin, pantothenate, coenzyme A, pimeloyl-ACP, THF, and heme biosynthesis were identified. The closest cultivated relative is *Limnohabitans* sp. Jir61 (GCF_003063545.1), with an average amino acid identity of 77.9% and average nucleotide identity of 80.1%. Current GTDB classification (R220): d__Bacteria; p__Pseudomonadota; c__Gammaproteobacteria; o__Burkholderiales; f__Burkholderiaceae_B; g__Limnohabitans; s__Limnohabitans sp002778325.

Classification

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

References

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

Registry URL

https://seqco.de/i:48719

Species *Limnohabitans rimovensis*

Etymology

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

Nomenclatural type

NCBI Assembly: GCA_965234775.1 Ts

Reference Strain

Strain scj0038964: RE-1

Description

Type strain is *Limnohabitans rimovensis* RE-1 (GCA_965234775.1), isolated from 0.5 m depth from the Římov Reservoir, Czechia (date: 2019-04-23), *via* high-throughput dilution to extinction cultivation. RE-1 has a genome size of 3.5 Mbp with a genomic GC content of 58.7%, contains 3 rRNA genes and 43 tRNAs. The genome is a high-quality draft consisting of 12 contigs. The genome contains genes encoding anoxygenic aerobic phototrophy (*pufABLM*). Genes for flagellar and pilus assembly were annotated. Pathways for urea degradation, thiosulfate oxidation (Sox pathway), methane/alkanesulfonate and glycolate oxidation, benzoate, salicylate, and phthalate degradation, and the biosynthesis of all amino acids except for aspartate were predicted. Further, pathways for thiamine, riboflavin, pantothenate, coenzyme A, THF, and heme biosynthesis were identified. The closest cultivated relative is *Limnohabitans* sp. JirII-31 (GCF_002778315.1), with an average amino acid identity of 65.1% and average nucleotide identity of 72.4%. Current GTDB classification (R220): d__Bacteria; p__Pseudomonadota; c__Gammaproteobacteria; o__Burkholderiales; f__Burkholderiaceae_B; g__Limnohabitans; s__.

Classification

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

References

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

Registry URL

https://seqco.de/i:48738

Species *Methylotenera 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

NCBI Assembly: GCA_965601845.1 Ts

Reference Strain

Strain sc|0038778: RH-M31

Description

Type strain is *Methylotenera hypolimnetica* RH-M31 (GCA_947054635.1), isolated from 30 m depth from the Římov Reservoir, Czechia (date: 15.08.2019), *via* high-throughput dilution to extinction cultivation. RH-M31 has a genome size of 1.8 Mbp with a genomic GC content of 49.2%, contains 6 rRNA genes and 38 tRNAs. The genome is complete, consisting of a circular chromosome. No genes for flagellar or pilus assembly and chemotaxis were annotated. Pathways for methanol oxidation (Xox), the RuMP and methylcitric acid (MCA) cycle for methylotrophy and the biosynthesis of all amino acids were predicted. Further, pathways for thiamine, riboflavin, NAD, coenzyme A, pimeloyl-ACP, biotin, THF, ubiquinone, and heme biosynthesis were identified. The closest cultivated relatives are *Methylotenera versatilis* 301 (GCF_000093025.1) with an average amino acid identity of 75.7% and average nucleotide identity of 72.6% and another newly proposed species, *Methylotenera profunda* RH-M32 (GCA_947054625.1), with an AAI of 94.2% and an ANI of 92%. Current GTDB classification (R220): d__Bacteria; p__Pseudomonadota; c__Gammaproteobacteria; o__Burkholderiales; f__Methylophilaceae; g__Methylotenera; s__Methylotenera sp903951385.

Classification

Bacteria » *Pseudomonadota* » *Betaproteobacteria* » *Nitrosomonadales* » *Methylophilaceae* » *Methylotenera* » *Methylotenera hypolimnetica*

References

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

Registry URL

https://seqco.de/i:48718

Species *Methylotenera profunda*

Etymology

[pro.fun'da] **L. fem. adj.** *profunda*, deep; referring to the deep zone of lakes where the species is common.

Nomenclatural type

NCBI Assembly: GCA_965601725.1 Ts

Reference Strain

Strain sc|0038971: RH-M32

Description

Type strain is *Methylotenera profunda* RH-M32 (GCA_947054625.1), isolated from 30 m depth from the Římov Reservoir, Czechia (date: 15.08.2019), *via* high-throughput dilution to extinction cultivation. RH-M32 has a genome size of 1.7 Mbp with a genomic GC content of 47.9%, contains 6 rRNA genes and 38 tRNAs. The genome is complete, consisting of a circular chromosome. The genome contains genes encoding rhodopsins and the biosynthetic pathway for retinal biosynthesis. No genes for flagellar or pilus assembly and chemotaxis were annotated. Pathways for methanol oxidation (Xox), the RuMP and methylcitric acid (MCA) cycle for methylotrophy and the biosynthesis of all amino acids were predicted. Further, pathways for thiamine, riboflavin, NAD, coenzyme A, pimeloyl-ACP, biotin, THF, ubiquinone, and heme biosynthesis were identified. The closest cultivated relatives are *Methylotenera versatilis* 301 (GCF_000093025.1) with an average amino acid identity of 75.9% and average nucleotide identity of 72.8% and another newly proposed species, *Methylotenera hypolimnetica* RH-M31 (GCA_947054635.1), with an AAI of 94.2% and an ANI of 92%. Current GTDB classification (R220): d__Bacteria; p__Pseudomonadota; c__Gammaproteobacteria; o__Burkholderiales; f__Methylophilaceae; g__Methylotenera; s__Methylotenera oryzisoli_A.

Classification

Bacteria » *Pseudomonadota* » *Betaproteobacteria* » *Nitrosomonadales* » *Methylophilaceae* » *Methylotenera* » *Methylotenera profunda*

References

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

Registry URL

https://seqco.de/i:48733

Species *Mycobacterium aquicola*

Etymology

[a.qui'co.la] **L. fem. n.** *aqua*, water; **L. masc. suff.** *-cola*, inhabitant; **N.L. masc. n.** *aquicola*, inhabitant of water, referring to the the isolation source from a freshwater lake.

Nomenclatural type

NCBI Assembly: GCA_965234515.1 Ts

Reference Strain

Strain scl0038945: MiE-22

Description

Type strain is *Mycobacterium aquicola* MiE-22 (GCA_965234515.1), isolated from 5 m depth from Lake Milada, Czechia (date: 2019-10-15), *via* high-throughput dilution to extinction cultivation. MiE-22 has a genome size of 3.4 Mbp with a genomic GC content of 66.3%, contains 3 rRNA genes and 57 tRNAs. The genome is a high-quality draft consisting of 3 contigs. The genome contains genes encoding rhodopsins. No genes for flagella or pilus assembly and chemotaxis were annotated. Pathways for taurine degradation, assimilatory sulfate reduction and the biosynthesis of all amino acids except for histidine and aspartate were predicted. Further, pathways for many vitamins and cofactors (riboflavin, pyridoxal, NAD, coenzyme A, biotin, tetrahydrofolate, heme, cobalamine and menaquinone) were identified. The closest cultivated relative is *Mycobacterium massilipolynesiensis* M26 (GCF_001494595.1), with an average amino acid identity of 71.31% and average nucleotide identity of 76.47%. Current GTDB classification (R220): d__Bacteria; p__Actinomycetota; c__Actinomycetia; o__Mycobacteriales; f__Mycobacteriaceae; g__Mycobacterium; s__Mycobacterium sp945897705.

Classification

Bacteria » *Actinomycetota* » *Actinomycetes* » *Mycobacteriales* » *Mycobacteriaceae* » *Mycobacterium* » *Mycobacterium aquicola*

References

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

Registry URL

https://seqco.de/i:48708

Species *Novimethylotenera aquatica*Ts

Etymology

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

Nomenclatural type

NCBI Assembly: GCA_965601485.1 Ts

Reference Strain

Strain sc|0038780: ME-M6

Description

Type strain is *Novamethylotenera aquatica* ME-M6 (GCA_947054645.1), isolated from 5 m depth from Lake Medard, Czechia (date: 09.07.2019), *via* high-throughput dilution to extinction cultivation. ME-M6 has a genome size of 2.1 Mbp with a genomic GC content of 41.7%, contains 6 rRNA genes and 37 tRNAs. The genome is complete, consisting of a circular chromosome. The genome contains genes encoding rhodopsins and the biosynthetic pathway for retinal biosynthesis. No genes for flagellar assembly and chemotaxis were annotated. Pathways for methanol oxidation (Xox), the RuMP and methylcitric acid (MCA) cycle for methylotrophy and the biosynthesis of all amino acids were predicted. Further, pathways for thiamine, riboflavin, NAD, coenzyme A, pimeloyl-ACP, biotin, THF, ubiquinone, and heme biosynthesis were identified. The closest cultivated relative is *Methylotenera versatilis* 7 (GCF_000799165.1) with an average amino acid identity of 80.36% and average nucleotide identity of 76.56%. Current GTDB classification (R220): d__Bacteria; p__Pseudomonadota; c__Gammaproteobacteria; o__Burkholderiales; f__Methylophilaceae; g__Methylotenera_A; s__Methylotenera_A oryzisoli_A.

Classification

Bacteria » *Pseudomonadota* » *Betaproteobacteria* » *Nitrosomonadales* » *Methylophilaceae* » *Novimethylotenera* » *Novimethylotenera aquatica*Ts

References

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

Registry URL

https://seqco.de/i:48701

Species *Planktophila warneckei*

Etymology

[war.ne.cke'i] **N.L. masc. gen. n.** *warneckei*, of Warnecke, named after the deceased German scientist Falk Warnecke, who intensively worked on the ecology of freshwater Planktophila

Nomenclatural type

NCBI Assembly: GCA_965234675.1 Ts

Reference Strain

Strain scj0038946: RE-8

Description

Type strain is *Planktophila warneckii* RE-8 (GCA_965234675.1), isolated from 0.5 m depth from the Římov reservoir, Czechia (date: 2019-04-23), *via* high-throughput dilution to extinction cultivation. RE-8 has a genome size of 1.4 Mbp with a genomic GC content of 46.2%, 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 the biosynthesis of all amino acids except for histidine were predicted. Further, pathways for riboflavin, pyridoxal, coenzyme A, and menaquinone biosynthesis were identified. The closest cultivated relative is Actinobacteria bacterium IMCC26103 (GCA_002284875.1), with an average amino acid identity of 72.2% and average nucleotide identity of 70.96%. 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 warneckei*

References

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

Registry URL

https://seqco.de/i:48741

Species *Polynucleobacter hahnii*

Etymology

[hah.ni'i] **L. masc. gen. n.** *hahnii*, of Hahn, named after the scientist Martin W. Hahn, who isolated and described many species of the genus Polynucleobacter.

Nomenclatural type

NCBI Assembly: GCA_965234415.1 Ts

Reference Strain

Strain sc|0038961: ZE-4

Description

Type strain is *Polynucleobacter hahnii* ZE-4 (GCA_965234415.1), isolated from 5 m depth from Lake Zurich, Switzerland (date: 2019-04-03), *via* high-throughput dilution to extinction cultivation. ZE-4 has a genome size of 2.3 Mbp with a genomic GC content of 43.7%, contains 3 rRNA genes and 38 tRNAs. The genome is complete, consisting of a circular chromosome. The genome contains genes encoding anoxygenic aerobic phototrophy (*pufABLM*). No genes for flagellar assembly and chemotaxis were annotated. Pathways for nitrate reduction, thiosulfate oxidation (Sox pathway), glycolate oxidation and the biosynthesis of all amino acids except for aspartate were predicted. Further, pathways for thiamine, riboflavin, NAD, pantothenate, coenzyme A, biotin, THF, ubiquinone, and heme biosynthesis were identified. The closest cultivated relative is *Polynucleobacter* sp. IMCC 30228 (GCF_021395205.1), with an average amino acid identity of 86.6% and average nucleotide identity of 82.8%. Current GTDB classification (R220): d__Bacteria; p__Pseudomonadota; c__Gammaproteobacteria; o__Burkholderiales; f__Burkholderiaceae; g__Polynucleobacter; s__Polynucleobacter sp903944725.

Classification

Bacteria » *Pseudomonadota* » *Betaproteobacteria* » *Burkholderiales* » *Burkholderiaceae* » *Polynucleobacter* » *Polynucleobacter hahnii*

References

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

Registry URL

https://seqco.de/i:48716

Species *Polynucleobacter hoetzingerianus*

Etymology

[hoet.zin.ge.ri.a'nus] **N.L. masc. adj.** *hoetzingerianus*, named after the Austrian scientist Mattias Hoetzinger, who characterized several species of the genus Polynucleobacter

Nomenclatural type

NCBI Assembly: GCA_965234555.1 Ts

Reference Strain

Strain sc|0038960: RE-M21

Description

Type strain is *Polynucleobacter hoetzingeranus* RE-M21 (GCA_965234555.1), isolated from 0.5 m depth from the Římov Reservoir, Czechia (date: 2019-08-05), *via* high-throughput dilution to extinction cultivation. RE-M21 has a genome size of 1.8 Mbp with a genomic GC content of 46.6%, contains 3 rRNA genes and 40 tRNAs. The genome is complete, consisting of a circular chromosome. The genome contains genes encoding anoxygenic aerobic phototrophy (*pufABLM*). No genes for flagellar assembly and chemotaxis were annotated. Pathways for cyanate degradation, thiosulfate oxidation (Sox pathway), glycolate oxidation and the biosynthesis of all amino acids except for aspartate were predicted. Further, pathways for thiamine, riboflavin, NAD, pantothenate, coenzyme A, biotin, THF, ubiquinone, and heme biosynthesis were identified. The closest cultivated relative is *Polynucleobacter sp.* MWH-UH24A (GCF_018687475.1), with an average amino acid identity of 82.7% and average nucleotide identity of 74.9%. Current GTDB classification (R220): d__Bacteria; p__Pseudomonadota; c__Gammaproteobacteria; o__Burkholderiales; f__Burkholderiaceae; g__Polynucleobacter; s__Polynucleobacter sp027486235.

Classification

Bacteria » *Pseudomonadota* » *Betaproteobacteria* » *Burkholderiales* » *Burkholderiaceae* » *Polynucleobacter* » *Polynucleobacter hoetzingerianus*

References

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

Registry URL

https://seqco.de/i:48717

Species *Rhabdaerophilum aquaticum*

Etymology

[a.qua.ti'cum] **L. neut. adj.** *aquaticum*, living or found in the water

Nomenclatural type

NCBI Assembly: GCA_965234495.1 Ts

Reference Strain

Strain sc|0038955: MsE-M23

Description

Type strain is *Rhabdoaerophilum aquaticum* MsE-M23 (GCA_965234495.1), isolated from 5 m depth from Lake Most, Czechia (date: 2019-07-30), *via* high-throughput dilution to extinction cultivation. MsE-M23 has a genome size of 34 Mbp with a genomic GC content of 58.6%, contains 3 rRNA genes and 46 tRNAs. The genome is complete, consisting of a circular chromosome and one circular plasmid. Genes for flagellar assembly and chemotaxis were annotated in the genome. Pathways for cyanate and urea degradation, thiosulfate oxidation (Sox pathway), glycolate oxidation and the biosynthesis of all amino acids were predicted. Further, pathways for thiamine, riboflavin, NAD, coenzyme A, THF, and heme biosynthesis were identified. The closest cultivated relative is *Rhabdaerophilum calidifontis* SYSU G02060 (GCF_008641065.1), with an average amino acid identity of 66.3% and average nucleotide identity of 70.3%. Current GTDB classification (R220): d__Bacteria; p__Pseudomonadota; c__Alphaproteobacteria; o__Rhizobiales; f__Beijerinckiaceae; g__Rhabdaerophilum; s__.

Classification

Bacteria » *Pseudomonadota* » *Alphaproteobacteria* » *Hyphomicrobiales* » *Rhabdaerophilaceae* » *Rhabdaerophilum* » *Rhabdaerophilum aquaticum*

References

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

Registry URL

https://seqco.de/i:48703

Species *Rhodoluna miladensis*

Etymology

[mi.la.den'sis] **N.L. fem. adj.** *miladensis*, pertaining to Lake Milada (Czechia), the isolation source of the type strain.

Nomenclatural type

NCBI Assembly: GCA_965234705.1 Ts

Reference Strain

Strain sc|0038944: MiE-23b

Description

Type strain is *Rhodoluna miladensis* MiE-23b (GCA_965234705.1), isolated from 5 m depth from Lake Milada, Czechia (date: 2019-10-15), *via* high-throughput dilution to extinction cultivation. MiE-23b has a genome size of 1.28 Mbp with a genomic GC content of 50.2%, contains 3 rRNA genes and 40 tRNAs. The genome is complete, consisting of a circular chromosome. The genome contains genes encoding rhodopsins but lacks the biosynthetic pathway for retinal biosynthesis. No genes for flagella or pilus assembly and chemotaxis were annotated. Pathways for the biosynthesis of all amino acids except for methionine and histidine were predicted. Further, pathways for riboflavin, pyridoxal, coenzyme A, and menaquinone were identified. The closest cultivated relative is *Rhodoluna lacicola* MWH-Ta8 (GCF_000699505), with an average amino acid identity of 65.06% and average nucleotide identity of 67.72%. Current GTDB classification (R220): d__Bacteria; p__Actinomycetota; c__Actinomycetia; o__Actinomycetales; f__Microbacteriaceae; g__Rhodoluna; s__.

Classification

Bacteria » *Actinomycetota* » *Actinomycetes* » *Micrococcales* » *Microbacteriaceae* » *Rhodoluna* » *Rhodoluna miladensis*

References

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

Registry URL

https://seqco.de/i:48729

Species *Sphingorhabdus communis*

Etymology

[com.mu'nis] **L. fem. adj.** *communis*, common, referring to a widespread distribution in freshwater lakes.

Nomenclatural type

NCBI Assembly: GCA_965234695.1 ^{Ts}

Reference Strain

Strain sc|0038959: GE-11

Description

Type strain is *Sphingorhabdus commune* GE-11 (GCA_965234695.1), isolated from 5 m depth from Lake Greifensee, Switzerland (date: 2019-04-03), *via* high-throughput dilution to extinction cultivation. GE-11 has a genome size of 2.4 Mbp with a genomic GC content of 54.9%, contains 3 rRNA genes and 42 tRNAs. The genome is complete, consisting of a circular chromosome. The genome contains genes encoding rhodopsins and the biosynthetic pathway for retinal biosynthesis. No genes for flagellar or pilus assembly and chemotaxis were annotated. Pathways for assimilatory sulfate reduction and methane/alkanesulfonate oxidation and the biosynthesis of all amino acids were predicted. Further, pathways for riboflavin, NAD, coenzyme A, THF, and heme biosynthesis were identified. The closest cultivated relative is *Sphingorhabdus wooponensis* 03SU3-P (GCF_003933235.1), with an average amino acid identity of 87.4% and average nucleotide identity of 80.5%. Current GTDB classification (R220): d__Bacteria; p__Pseudomonadota; c__Alphaproteobacteria; o__Sphingomonadales; f__Sphingomonadaceae; g__Sphingorhabdus_B; s__Sphingorhabdus_B sp903821685.

Classification

Bacteria » *Pseudomonadota* » *Alphaproteobacteria* » *Sphingomonadales* » *Sphingomonadaceae* » *Sphingorhabdus* » *Sphingorhabdus communis*

References

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

Registry URL

https://seqco.de/i:48711

Species *Sphingorhabdus rara*

Etymology

[ra'ra] **L. fem. adj.** *rara*, sporadic or uncommon, referring to the sporadic isolation and recovery from disparate sources of members of this species

Nomenclatural type

NCBI Assembly: GCA_965234565.1 Ts

Reference Strain

Strain sc|0038958: RE-M21a

Description

Type strain is *Sphingorhabdus rara* RE-M21a (GCA_965234565.1), isolated from 0.5 m depth from the Římov Reservoir, Czechia (date: 2019-08-05), *via* high-throughput dilution to extinction cultivation. RE-M21a has a genome size of 3.2 Mbp with a genomic GC content of 57.5%, contains 3 rRNA genes and 45 tRNAs. The genome is a high-quality draft consisting of 4 contigs. The genome contains genes encoding rhodopsins and the biosynthetic pathway for retinal biosynthesis. No genes for flagellar or pilus assembly and chemotaxis were annotated. Pathways for taurine degradation, assimilatory sulfate reduction and methane/alkanesulfonate oxidation and the biosynthesis of all amino acids were predicted. Further, pathways for thiamine, riboflavin, pantothenate, NAD, coenzyme A, THF, and heme biosynthesis were identified. The closest cultivated relative is *Sphingorhabdus pulchriflava* GY_G (GCF_003367235.1), with an average amino acid identity of 76.8% and average nucleotide identity of 75.4%. Current GTDB classification (R220): d__Bacteria; p__Pseudomonadota; c__Alphaproteobacteria; o__Sphingomonadales; f__Sphingomonadaceae; g__Sphingorhabdus_B; s__Sphingorhabdus_B sp021298455.

Classification

Bacteria » *Pseudomonadota* » *Alphaproteobacteria* » *Sphingomonadales* » *Sphingomonadaceae* » *Sphingorhabdus* » *Sphingorhabdus rara*

References

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

Registry URL

https://seqco.de/i:48734

Species *Tabrizicola rara*

Etymology

[ra'ra] **L. fem. adj.** *rara*, sporadic or uncommon, referring to the sporadic isolation and recovery from disparate sources of members of this species

Nomenclatural type

NCBI Assembly: GCA_965234505.1 Ts

Reference Strain

Strain scj0038956: LH-M10

Description

Type strain is *Tabrizicola rara* LH-M10 (GCA_965234505.1), isolated from 50 m depth from Lake Lugano, Switzerland (date: 2019-11-05), *via* high-throughput dilution to extinction cultivation. LH-M10 has a genome size of 4.2 Mbp with a genomic GC content of 62.8%, contains 4 rRNA genes and 48 tRNAs. The genome is a high-quality draft consisting of 22 contigs. The genome contains the complete Calvin cycle for carbon fixation via RuBisCO. Genes for flagellar assembly were annotated in the genome. Pathways for urea and taurine degradation, glycolate oxidation and the biosynthesis of all amino acids were predicted. Further, pathways for riboflavin, coenzyme A, cobalamin, and heme biosynthesis were identified. The closest cultivated relative is *Rhodobacter thermarum* YIM 73036 (GCF_003574395.1; Basonym: *Tabrizicola thermarum* Khan et al. 2019), with an average amino acid identity of 75.7% and average nucleotide identity of 77.1%. Current GTDB classification (R220): d__Bacteria; p__Pseudomonadota; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Tabrizicola; s__Tabrizicola sp903917595.

Classification

Bacteria » *Pseudomonadota* » *Alphaproteobacteria* » *Rhodobacterales* » *Paracoccaceae* » *Tabrizicola* » *Tabrizicola rara*

References

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

Registry URL

https://seqco.de/i:48735

Species *Verrucolacustris abundans*^Ts

Etymology

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

Nomenclatural type

NCBI Assembly: GCA_965194535.1 Ts

Reference Strain

Strain sc|0038970: MiH-22

Description

Type strain is *Verrucolacustris abundans* MiH-22 (GCA_965194535.1), isolated from 15 m depth from Lake Milada, Czechia (date: 2019-10-15), *via* high-throughput dilution to extinction cultivation. MiH-22 has a genome size of 2.0 Mbp with a genomic GC content of 52.8%, contains 3 rRNA genes and 46 tRNAs. The genome is complete, consisting of a circular chromosome. The genome contains genes encoding rhodopsins. No genes for flagellar assembly and chemotaxis were annotated. In contrast to other *Methylacidiphilales* members, no genes for C1 metabolism (methanotrophy) were identified. Pathways for assimilatory sulfate reduction and the biosynthesis of all amino acids except for methionine, histidine and tryptophan were predicted. Further, pathways for only three vitamins (thiamine, riboflavin, and biotin biosynthesis) were identified. The closest cultivated relative is *Methylacidimicrobium cyclopophantes* 3B_2 (GCF_902143385.2), with an average amino acid identity of 49.5% and average nucleotide identity of 62.8%. Current GTDB classification (R220): d__Bacteria; p__Verrucomicrobiota; c__Verrucomicrobiae; o__Methylacidiphilales; f__UBA3015; g__UBA3015; s__UBA3015 sp030054195.

Classification

Bacteria » *Verrucomicrobiota* » “Methylacidiphilae” » *Methylacidiphilales* » *Verrucolacustridaceae* » *Verrucolacustris* » *Verrucolacustris abundans*Ts

References

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

Registry URL

https://seqco.de/i:48694

Species *Zwartia lucis*

Etymology

[lu'cis] **L. fem. adj.** *lucis*, of light, referring to the presence of light driven proton pumps (rhodopsins) in the type strain.

Nomenclatural type

NCBI Assembly: GCA_965234455.1 Ts

Reference Strain

Strain sc|0038968: GE-14

Description

Type strain is *Zwartia lucis* GE-14 (GCA_965234455.1), isolated from 5 m depth from Greifensee, Switzerland (date: 2019-04-03), *via* high-throughput dilution to extinction cultivation. GE-14 has a genome size of 3.7 Mbp with a genomic GC content of 50.9%, contains 6 rRNA genes and 41 tRNAs. The genome is a high-quality draft consisting of 7 contigs. In contrast to other *Zwartia* sp., the genome contains genes encoding rhodopsins and the biosynthetic pathway for retinal biosynthesis. No genes for flagellar or pilus assembly and chemotaxis were annotated. Pathways for nitrate reduction, cyanate, urea and taurine degradation, thiosulfate oxidation (Sox pathway), glycolate and methane/alkanesulfonate oxidation, and the biosynthesis of all amino acids were predicted. Further, pathways for thiamine, riboflavin, pantothenate, coenzyme A, THF, ubiquinone, and heme biosynthesis were identified. The closest cultivated relative is *Zwartia panacis* strain KCTC42751 (GCF_030410395.1), with an average amino acid identity of 82.1% and average nucleotide identity of 77.6%. Current GTDB classification (R220): d__Bacteria; p__Pseudomonadota; c__Gammaproteobacteria; o__Burkholderiales; f__Burkholderiaceae; g__Zwartia; s__.

Classification

Bacteria » *Pseudomonadota* » *Betaproteobacteria* » *Burkholderiales* » *Alcaligenaceae* » *Zwartia* » *Zwartia lucis*

References

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

Registry URL

https://seqco.de/i:48725

Species *Zwartia planktonica*

Etymology
[plan.kto.ni'ca] **N.L. fem. adj.** *planktonica*, living in the plankton of lakes, planktonic; from Gr. masc. adj. planktos, wandering.

Nomenclatural type
NCBI Assembly: GCA_965234315.1 ^{Ts}

Reference Strain
Strain sc|0038969: RE-10

Description
Type strain is *Zwartia planktonica* RE-10 (GCA_965234315.1), isolated from 0.5 m depth from the Římov Reservoir, Czechia (date: 2019-04-23), *via* high-throughput dilution to extinction cultivation. RE-10 has a genome size of 4.5 Mbp with a genomic GC content of 52%, contains 6 rRNA genes and 44 tRNAs. The genome is complete, consisting of a circular chromosome. No genes for flagellar or pilus assembly and chemotaxis were annotated. Pathways for cyanate, urea and taurine degradation, 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, ubiquinone, and heme biosynthesis were identified. The closest cultivated relative is *Zwartia hollandica* LF4-65 (GCF_019923725.1), with an average amino acid identity of 71.2% and average nucleotide identity of 71.6%. Current GTDB classification (R220): d__Bacteria; p__Pseudomonadota; c__Gammaproteobacteria; o__Burkholderiales; f__Burkholderiaceae; g__Zwartia; s__Zwartia sp030832095.

Classification
Bacteria » *Pseudomonadota* » *Betaproteobacteria* » *Burkholderiales* » *Alcaligenaceae* » *Zwartia* » *Zwartia planktonica*

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

Registry URL
https://seqco.de/i:48732

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:opjv7zsc** submitted by **Layoun, Paul** and including 40 new names has been successfully validated.

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