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

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Table 1: Complete list of names proposed in the current register list.

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Family *Acidimicrobilacustridaceae*	[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	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.	*Acidimicrobiales*	*Acidimicrobilacustris*	seqco.de/i:48714
		Type strain is *Verrucolacustris*			

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Family *Verrucolacustridaceae*	[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	Type strain is *Verrucolacustris abundans* MH-21 (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.	*Methylacidiphilales*	*Verrucolacustris*	seqco.de/i:48695
Genus *Acidimicrobilacustris*	[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	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	*Acidimicrobilacustridaceae*	*Acidimicrobilacustris europaeus*^{Ts}	seqco.de/i:48715

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		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.			
Genus *Allorhodoferax*	[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.	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	*Comamonadaceae*	*Allorhodoferax aquaticus*^{Ts}	seqco.de/i:49941

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
		reclassification of this genus (GTDB genus Rhodoferax_C) with the proposed name *Allorhodoferax*.			
Genus *Allotabrizicola*	[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	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.	*Paracoccaceae*	*Allotabrizicola aquatica*^{Ts}	seqco.de/i:48698
	[La.cus.tri.bac'ter] **N.L. masc.**	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_000646435.1) with			

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Genus *Lacustribacter*	[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.	(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.	*Burkholderiaceae*	*Lacustribacter communis*^{Ts}	seqco.de/i:48710
Genus *Novimethylotenera*	[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	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	*Methylophilaceae*	*Novimethylotenera aquatica*^{Ts}	seqco.de/i:48702

Novimethylotenera, gen. nov.

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Genus *Verrucolacustris*	[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	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.	*Verrucolacustridaceae*	*Verrucolacustris abundans*^{Ts}	seqco.de/i:48696
Species *Acidimicrobilacustris europaeus*^{Ts}	[e.u.ro.pae'us] **N.L. masc. adj.** *europaeus*, of/from Europe; named after the main occurrence in european lakes	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	*Acidimicrobilacustris*	NCBI Assembly: GCA_965194515.1 ^{Ts}	seqco.de/i:48713

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		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.			
Species *Acidimicrobilacustris thunensis*	[thu.nen'sis] **N.L. masc. adj.** *thunensis*, of Thun, referring to Lake Thun, the isolation source of the type strain.	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,	*Acidimicrobilacustris*	NCBI Assembly: GCA_965194345.1 $^{\mathrm{Ts}}$	seqco.de/i:48740

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		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.			
Species *Allorhodoferax aquaticus*^{Ts}	[a.qua'ti.cus] **L. masc. adj.** *aquaticus*, living, growing, or found in or by the water, aquatic	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	*Allorhodoferax*	NCBI Assembly: GCA_965194715.1 ^{Ts}	seqco.de/i:48704

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		(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.			
Species *Allorhodoferax lacus*	[la'cus] **L. gen. n.** *lacus*, of a lake, referring to the habitat from which the type strain was isolated.	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;	*Allorhodoferax*	NCBI Assembly: GCA_965194635.1 ^{Ts}	seqco.de/i:48720

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		f__Burkholderiaceae; g__Rhodoferax_C; s__.			
Species *Allotabrizicola aquatica*^{Ts}	[a.qua.ti'ca] **L. fem. adj.** *aquatica*, living or found in the water.	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__.	*Allotabrizicola*	NCBI Assembly: GCA_965194375.1 ^{Ts}	seqco.de/i:48697
		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			

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Species *Aquidulcibacter miladensis*	[mi.la.den'sis] **N.L. masc. adj.** *miladensis*, pertaining to Lake Milada (Czechia), the isolation source of the type strain.	dilution to extinction cultivation. MH-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.	*Aquidulcibacter*	NCBI Assembly: GCA_965234355.1 ^{Ts}	seqco.de/i:48727
		Type strain is *Aquidulcibacter rimovensis* RH-10 (GCA_965234525.1), isolated from 30 m depth from Římov Reservoir, Czechia (date: 2019-			

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Species *Aquidulcibacter rimovensis*	[ri.mo.ven'sis] **N.L. masc. adj.** *rimovensis*, pertaining to the Římov Reservoir (Czechia), the isolation source of the type strain.	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.	*Aquidulcibacter*	NCBI Assembly: GCA_965234525.1 $^{\mathrm{Ts}}$	seqco.de/i:48737
		Type strain is *Caulobacter lacus* MiH-16 (GCA_965234345.1), isolated from 15 m depth from Lake			

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Species *Caulobacter lacus*	[la'cus] **L. gen. n.** *lacus*, of a lake, referring to the habitat from which the type strain was isolated.	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.	*Caulobacter*	NCBI Assembly: GCA_965234345.1 Ts	seqco.de/i:48721
		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			

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Species *Flavobacterium neuenschwanderi*	[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.	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__.	*Flavobacterium*	NCBI Assembly: GCA_965234425.1 ^{Ts}	seqco.de/i:48730
	[ra'rum] **L. neut. adj.** *rarum*	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			

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Species *Flavobacterium rarum*	[ra'rum] **L. neut. adj.** *rarum*, sporadic or uncommon, referring to the sporadic isolation and recovery from disparate sources of members of this species	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__.	*Flavobacterium*	NCBI Assembly: GCA_965234445.1 ^{Ts}	seqco.de/i:48736
Species *Fontibacterium abundans*	[a.bun'dans] **L. neut. part. adj.** *abundans*, abundant, referring to high global abundances	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	*Fontibacterium*	NCBI Assembly: GCA_965235095.1 ^{Ts}	seqco.de/i:48693

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
	high global abundances.	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__.			
Species *Fontibacterium medardense*	[me.dar.den'se] **L. neut. adj.** *medardense*, pertaining to Lake Medard (Czechia), the isolation source of the type strain	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	*Fontibacterium*	NCBI Assembly: GCA_965235075.1 ^{Ts}	seqco.de/i:48726

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
	source of the type strain.	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.			
Species *Hydrogenophaga miladensis*	[mi.la.den'sis] **N.L. fem. adj.** *miladensis*, pertaining to Lake Milada (Czechia), the isolation source of the type strain.	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	*Hydrogenophaga*	NCBI Assembly: GCA_965234585.1 ^{Ts}	seqco.de/i:48728

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
		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.			
Species *Lacustribacter communis*^{Ts}	[com.mu'nis] **L. masc. adj.** *communis*, common; referring to a wide distribution in freshwater lakes.	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	*Lacustribacter*	NCBI Assembly: GCA_965194335.1 ^{Ts}	seqco.de/i:48709

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
		biosynthesis were identified. The closest described 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.			
Species *Leadbetterella lacustris*	[la.cus'tris] **N.L. fem. adj.** *lacustris*, of a lake; referring to the habitat from where the strain was isolated.	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	*Leadbetterella*	NCBI Assembly: GCA_965234335.1 Ts	seqco.de/i:48724

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
		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.			
Species *Limnohabitans kasalickyi*	[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.	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,	*Limnohabitans*	NCBI Assembly: GCA_965234325.1 ^{Ts}	seqco.de/i:48719

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
		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.			
Species *Limnohabitans rimovensis*	[ri.mo.ven'sis] **N.L. masc. adj.** *rimovensis*, pertaining to the Římov Reservoir, Czech Republic, the isolation source of the species.	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*	NCBI Assembly: GCA_965234775.1 $^{\mathrm{Ts}}$	seqco.de/i:48738

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
		cultivated relative is *Limnohabitans* sp. Jin-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__.			
Species *Methylotenera hypolimnetica*	[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.	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	*Methylotenera*	NCBI Assembly: GCA_965601845.1 Ts	seqco.de/i:48718

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
		(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.			
Species *Methylotenera profunda*	[pro.fun'da] **L. fem. adj.** *profunda*, deep; referring to the deep zone of lakes where the species is common.	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%	*Methylotenera*	NCBI Assembly: GCA_965601725.1 $^{\mathrm{Ts}}$	seqco.de/i:48733

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
		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.			
Species *Mycobacterium aquicola*	[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.	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	*Mycobacterium*	NCBI Assembly: GCA_965234515.1 Ts	seqco.de/i:48708

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
		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.			
Species *Novimethylotenera aquatica*^{Ts}	[a.qua.ti'ca] **L. fem. adj.** *aquatica*, living or found in the water.	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;	*Novimethylotenera*	NCBI Assembly: GCA_965601485.1 ^{Ts}	seqco.de/i:48701

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
		p__Pseudomonadota; c__Gammaproteobacteria; o__Burkholderiales; f__Methylophilaceae; g__Methylotenera_A; s__Methylotenera_A oryzisoli_A.			
Species *Planktophila warneckei*	[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	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__.	*Planktophila*	NCBI Assembly: GCA_965234675.1 $^{\mathrm{Ts}}$	seqco.de/i:48741
		Type strain is *Polynucleobacter hahnii* ZE-4			

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Species *Polynucleobacter hahnii*	[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.	(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.	*Polynucleobacter*	NCBI Assembly: GCA_965234415.1 ^{Ts}	seqco.de/i:48716
		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			

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Species *Polynucleobacter hoetzingerianus*	[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	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.	*Polynucleobacter*	NCBI Assembly: GCA_965234555.1 ^{Ts}	seqco.de/i:48717
		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			

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Species *Rhabdaerophilum aquaticum*	[a.qua.ti'cum] **L. neut. adj.** *aquaticum*, living or found in the water	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__.	*Rhabdaerophilum*	NCBI Assembly: GCA_965234495.1 ^{Ts}	seqco.de/i:48703
		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			

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
Species *Rhodoluna miladensis*	[mi.la.den'sis] **N.L. fem. adj.** *miladensis*, pertaining to Lake Milada (Czechia), the isolation source of the type strain.	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__.	*Rhodoluna*	NCBI Assembly: GCA_965234705.1 $^{\mathrm{Ts}}$	seqco.de/i:48729
Species *Sphingorhabdus communis*	[com.mu'nis] **L. fem. adj.** *communis*, common, referring to a widespread distribution in freshwater lakes.	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	*Sphingorhabdus*	NCBI Assembly: GCA_965234695.1 $^{\mathrm{Ts}}$	seqco.de/i:48711

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
		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.			
Species *Sphingorhabdus rara*	[ra'ra] **L. fem. adj.** *rara*, sporadic or uncommon, referring to the sporadic isolation and recovery from disparate sources of members of this species	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	*Sphingorhabdus*	NCBI Assembly: GCA_965234565.1 ^{Ts}	seqco.de/i:48734

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
		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.			
Species *Tabrizicola rara*	[ra'ra] **L. fem. adj.** *rara*, sporadic or uncommon, referring to the sporadic isolation and recovery from disparate sources of members of this species	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%.	*Tabrizicola*	NCBI Assembly: GCA_965234505.1 ^{Ts}	seqco.de/i:48735

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
		Current GTDB classification (R220): d__Bacteria; p__Pseudomonadota; c__Alphaproteobacteria; o__Rhodobacterales; f__Rhodobacteraceae; g__Tabrizicola; s__Tabrizicola sp903917595.			
Species *Verrucolacustris abundans*^{Ts}	[a.bun'dans] **L. masc. part. adj.** *abundans*, abundant; referring to high global abundances	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):	*Verrucolacustris*	NCBI Assembly: GCA_965194535.1 ^{Ts}	seqco.de/i:48694

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
		d__Bacteria; p__Verrucomicrobiota; c__Verrucomicrobiae; o__Methylacidiphilales; f__UBA3015; g__UBA3015; s__UBA3015 sp030054195.			
Species *Zwartia lucis*	[lu'cis] **L. fem. adj.** *lucis*, of light, referring to the presence of light driven proton pumps (rhodopsins) in the type strain.	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;	*Zwartia*	NCBI Assembly: GCA_965234455.1 $^{\mathrm{Ts}}$	seqco.de/i:48725

Proposed Taxon	Etymology	Description	Parent Taxon	Type	Registry URL
		c__Gammaproteobacteria; o__Burkholderiales; f__Burkholderiaceae; g__Zwartia; s__.			
Species *Zwartia planktonica*	[plan.kto.ni'ca] **N.L. fem. adj.** *planktonica*, living in the plankton of lakes, planktonic; from Gr. masc. adj. planktos, wandering.	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.	*Zwartia*	NCBI Assembly: GCA_965234315.1 $^{\mathrm{Ts}}$	seqco.de/i:48732