Register list for 12 new names including Fontibacterium baikalense sp. nov.

Submitted by Salcher, Michaela M

Genus *Pelagilacustribacter*

Etymology

[Pe.la.gi.la.cus.tri.bac'ter] **L. neut. n.** *pelagus*, of the sea; **N.L. masc. adj.** *lacustris*, belonging to a lake; **N.L. masc. n.** *bacter*, a rod; **N.L. masc. n.** *Pelagilacustribacter*, a freshwater genus of otherwise marine Pelagibacterales

Nomenclatural type

Species *Pelagilacustribacter hypolimneticus*[Ts]

Description

Type species is *Pelagilacustribacter hypolimneticus* TrH-25oct19-165 (GCA_965235125.1), a metagenome-assembled genome (MAG) obtained from 150m depth from Traunsee, Austria. *Pelagilacustribacter* is a genus within marine SAR11-II (*Pelagibacterales*) that is found in deep freshwater lakes.

Classification

Bacteria » *Pseudomonadota* » *Alphaproteobacteria* » *Pelagibacterales* » *Pelagibacteraceae* » *Pelagilacustribacter*

References

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

Registry URL

https://seqco.de/i:49884

Species *Fontibacterium africanum*

Etymology

[a.fri.ca'num] **N.L. neut. adj.** *africanum*, pertaining to the isolation source of the MAG (Lake Malawi) and a prevalence in the African Great Lakes

Nomenclatural type

NCBI Assembly: GCA_965235885.1 [Ts]

Description

Type genome is *Fontibacterium africanum* N-Mw6-13nov23-081 (GCA_965235885.1), a metagenome-assembled genome (MAG) assembled from 50 m depth from Lake Malawi, Malawi (date: 2023-11-13). N-Mw6-13nov23-081 has a genome size of 1.1 Mbp with a genomic GC content of 30%, contains 1 rRNA gene (5S rRNA) and 28 tRNAs. The genome is of high quality, consisting of 7 contigs, with a completeness of 95.2%, contamination of 0% and strain heterogeneity of 0% as assessed with checkM. The metagenome was assembled with FLYE from combined long- and short-read sequencing (Oxford Nanopore and Illumina NovaSeq). Metagenomic fragment recruitment of >600 samples from five continents indicate that the species is present only in the African Great Lakes Malawi, Tanganyika, and Kivu. 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 68.64 % and average nucleotide identity of 71.78 % and another newly proposed species, *Fontibacterium abundans* MiE-29 (GCA_965235095.1), with an AAI of 68.51 % and an ANI of 71.6 %. Current GTDB classification (R220): d__Bacteria; p__Pseudomonadota; c__Alphaproteobacteria; o__Pelagibacterales; f__Pelagibacteraceae; g__Fonsibacter; s__Fonsibacter sp016882225.

Classification

Bacteria » *Pseudomonadota* » *Alphaproteobacteria* » *Pelagibacterales* » *Pelagibacteraceae* » *Fontibacterium* » *Fontibacterium africanum*

References

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

Registry URL

https://seqco.de/i:49874

Species *Fontibacterium baikalense*

Etymology

[ba.i.ka.len'se] **N.L. neut. adj.** *baikalense*, of Baikal, referring to Lake Baikal, where this organism was identified

Nomenclatural type

NCBI Assembly: GCA_009693745.1 [Ts]

Description

Type genome is *Fontibacterium baikalense* Baikal-deep-G36 (GCA_009693745.1), a metagenome-assembled genome (MAG) co-assembled from 1250 m and 1350 m depth from Lake Baikal, Russia (date: 2018-03-29). Baikal-deep-G36 has a genome size of 1 Mbp with a genomic GC content of 29.4%, contains 2 rRNA genes and 25 tRNAs. The genome is of high quality, consisting of 66 contigs, with a completeness of 95.2%, contamination of 3.9% and strain heterogeneity of 100% as assessed with checkM. The metagenome was assembled with IDBA-UD assembler from short-read sequencing (Illumina HiSeq 3000/4000). 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 85.75% and average nucleotide identity of 84.65% and another newly proposed species, *Fontibacterium medardicus* ME-17, with an AAI of 88.73% and an ANI of 87.93%. Current GTDB classification (R220): d__Bacteria; p__Pseudomonadota; c__Alphaproteobacteria; o__Pelagibacterales; f__Pelagibacteraceae; g__Fonsibacter; s__Fonsibacter sp009693745.

Classification

Bacteria » *Pseudomonadota* » *Alphaproteobacteria* » *Pelagibacterales* » *Pelagibacteraceae* » *Fontibacterium* » *Fontibacterium baikalense*

References

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

Registry URL

https://seqco.de/i:49754

Species *Fontibacterium boreale*

Etymology

[bo.re.a'le] **L. neut. adj.** *boreale*, pertaining to the boreal region of the Northern hemisphere

Nomenclatural type

NCBI Assembly: GCA_903909545.1 Ts

Description

Type genome is *Fontibacterium boreale* Umea-bin-09620 (GCA_903909545.1), a metagenome-assembled genome (MAG) assembled from 1-5 m depth from Lake Bjarntjarnan, Sweden (date: 2018-01-01/07). Umea-bin-09620 has a genome size of 1 Mbp with a genomic GC content of 30.2% and contains 20 tRNAs. The genome is of high quality, consisting of 243 contigs, with a completeness of 96.4%, contamination of 0.1% and strain heterogeneity of 0% as assessed with checkM. The metagenome was assembled with Megahit (version 1.1.13) from short-read sequencing (Illumina MiSeq). Metagenomic fragment recruitment of >600 samples from five continents indicate that the species is present mainly in boreal lakes in Europe and North America. 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 82.49% and average nucleotide identity of 81.54 % and another newly proposed species, *Fontibacterium abundans* MiE-29 (GCA_965235095.1), with an AAI of 84.48% and an ANI of 83.54 %. 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 boreale*

References

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

Registry URL

https://seqco.de/i:49872

Species *Fontibacterium meridianamericanum*

Etymology

[me.ri.di.an.a.me.ri.ca'num] **L. masc. adj.** *meridianus*, Southerly, to the south; **N.L. neut. adj.** *americanum*, American; **L. neut. adj.** *meridianamericanum*, South American, referring to continent from the MAG was isolated

Nomenclatural type

NCBI Assembly: GCA_965235635.1 Ts

Description

Type genome is *Fontibacterium meridianamericanum* N-IMU-22jan24-050 (GCA_965235635.1), a metagenome-assembled genome (MAG) assembled from 0.5 m depth from Represa de India Muerta, a freshwater reservoir in Uruguay (date: 2024-01-22). N-IMU-22jan24-050 has a genome size of 1.0 Mbp with a genomic GC content of 29.3% and contains 30 tRNAs. The genome is of high quality, consisting of 4 contigs, with a completeness of 95.8%, contamination of 1.2% and strain heterogeneity of 100% as assessed with checkM. The metagenome was assembled with FLYE from combined long-and short-read sequencing (Oxford Nanopore and Illumina NovaSeq). Metagenomic fragment recruitment of >600 samples from five continents indicate that the species is present mainly in subtropical and tropical lakes in South America. 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 86.94% and average nucleotide identity of 84.39% and another newly proposed species, *Fontibacterium abundans* MiE-29 (GCA_965235095.1), with an AAI of 90.5% and an ANI of 88.11%. 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 meridianamericanum*

References

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

Registry URL

https://seqco.de/i:49882

Species *Fontibacterium oligotrophicum*

Etymology

[o.li.go.tro'phi.cum] **Gr. masc. adj.** *oligo*, little; **Gr. masc. adj.** *trophikos*, nursing, tending; **N.L. neut. adj.** *oligotrophicum*, oligotrophic, referring to the low nutrient content of the isolation sites and the high abundance in oligotrophic lakes.

Nomenclatural type

NCBI Assembly: GCA_965235975.1 Ts

Description

Type genome is *Fontibacterium oligotrophicum* N-Balt2-05jul22-047 (GCA_965235975.1), a metagenome-assembled genome (MAG) assembled from 0.5 m depth from the slightly brackish part of Vistula Lagoon, Poland (date: 2022-07-05). N-Balt2-05jul22-047 has a genome size of 0.92 Mbp with a genomic GC content of 29.4% and contains 30 tRNAs. The genome is of high quality, consisting of 3 contigs, with a completeness of 96.4%, contamination of 0% and strain heterogeneity of 0% as assessed with checkM. The metagenome was assembled with FLYE from combined long- and short-read sequencing (Oxford Nanopore and Illumina NovaSeq). Metagenomic fragment recruitment of >600 samples from five continents indicate that the species is highly abundant in oligotrophic lakes in temperate and subtropical regions. 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 92.57% and average nucleotide identity of 90.07% and another newly proposed species, *Fontibacterium medardicus* ME-17 (GCA_965235075.1), with an AAI of 85.45% and an ANI of 88.16%. Current GTDB classification (R220): d__Bacteria; p__Pseudomonadota; c__Alphaproteobacteria; o__Pelagibacterales; f__Pelagibacteraceae; g__Fonsibacter; s__Fonsibacter sp947497305.

Classification

Bacteria » *Pseudomonadota* » *Alphaproteobacteria* » *Pelagibacterales* » *Pelagibacteraceae* » *Fontibacterium* » *Fontibacterium oligotrophicum*

References

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

Registry URL

https://seqco.de/i:49876

Species *Fontibacterium scandinaviense*

Etymology

[scan.di.na.vi.en'se] **N.L. neut. adj.** *scandinaviense*, pertaining to the Scandinavian region, the isolation source of the MAG and a main occurrence in Scandinavian lakes

Nomenclatural type

NCBI Assembly: GCA_903869725.1 [Ts]

Description

Type genome is *Fontibacterium scandinaviense* AM1_bin-0028 (GCA_903869725.1), a metagenome-assembled genome (MAG) assembled from 0.5 m depth from Lake Alinen Mustajärvi, Finland (date: 2015-08-8). AM1_bin-0028 has a genome size of 1.1 Mbp with a genomic GC content of 28.9%, contains 3 rRNA genes and 31 tRNAs. The genome is of high quality, consisting of 55 contigs, with a completeness of 100%, contamination of 0% and strain heterogeneity of 0% as assessed with checkM. The metagenome was assembled with Megahit (version 1.1.13) from short-read sequencing (Illumina MiSeq). Metagenomic fragment recruitment of >600 samples from five continents indicate that the species is mainly present in boreal lakes in Scandinavia. 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 72.71 % and average nucleotide identity of 75.18 % and another newly proposed species, *Fontibacterium abundans* MiE-29 (GCA_965235095.1), with an AAI of 73.3 % and an ANI of 75.56 %. Current GTDB classification (R220): d__Bacteria; p__Pseudomonadota; c__Alphaproteobacteria; o__Pelagibacterales; f__Pelagibacteraceae; g__Fonsibacter; s__Fonsibacter sp903869725.

Classification

Bacteria » *Pseudomonadota* » *Alphaproteobacteria* » *Pelagibacterales* » *Pelagibacteraceae* » *Fontibacterium* » *Fontibacterium scandinaviense*

References

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

Registry URL

https://seqco.de/i:49875

Species *Fontibacterium subtropicum*

Etymology

[sub.tro'pi.cum] **N.L. neut. adj.** *subtropicum*, pertaining to subtropical zone, the isolation source of the MAG.

Nomenclatural type

NCBI Assembly: GCA_965235415.1 [Ts]

Description

Type genome is *Fontibacterium subtropicum* N-SamH-20apr23-026 (GCA_965235415.1), a metagenome-assembled genome (MAG) assembled from 15 m depth from Lake Samsonvale, Australia (date: 2023-04-20). N-SamH-20apr23-026 has a genome size of 1.15 Mbp with a genomic GC content of 29.3%, contains 3 rRNA genes and 34 tRNAs. The genome is of high quality, consisting of 100 contigs, with a completeness of 100%, contamination of 1.2% and strain heterogeneity of 100% as assessed with checkM. The metagenome was assembled with FLYE from combined long-and short-read sequencing (Oxford Nanopore and Illumina NovaSeq). Metagenomic fragment recruitment of >600 samples from five continents indicate that the species is present mainly in subtropical lakes. 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 88.13% and average nucleotide identity of 85.63% and another newly proposed species, *Fontibacterium medardicus* ME-17 (GCA_965235075.1), with an AAI of 90.92% and an ANI of 88.79%. Current GTDB classification (R220): d__Bacteria; p__Pseudomonadota; c__Alphaproteobacteria; o__Pelagibacterales; f__Pelagibacteraceae; g__Fonsibacter; s__Fonsibacter sp023257975.

Classification

Bacteria » *Pseudomonadota* » *Alphaproteobacteria* » *Pelagibacterales* » *Pelagibacteraceae* » *Fontibacterium* » *Fontibacterium subtropicum*

References

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

Registry URL

https://seqco.de/i:49877

Species *Fontibacterium temperatum*

Etymology

[tem.pe.ra'tum] **L. neut. adj.** *temperatum*, referring to temperate climate, the species mainly occurs in lakes of the temperate region of the Northern Hemisphere

Nomenclatural type

NCBI Assembly: GCA_964203055.1 [Ts]

Description

Type genome is *Fontibacterium temperatum* ZE-03apr19-LR-3 (GCA_964203055.1), a metagenome-assembled genome (MAG) assembled from 5 m depth from Lake Zurich, Switzerland (date: 2019-04-03). ZE-03apr19-LR-3 has a genome size of 0.9 Mbp with a genomic GC content of 29.4% and contains 28 tRNAs. The genome is of high quality, consisting of 3 contigs, with a completeness of 94%, contamination of 0% and strain heterogeneity of 0% as assessed with checkM. The metagenome was assembled with FLYE from combined long-and short-read sequencing (Oxford Nanopore and Illumina NovaSeq). Metagenomic fragment recruitment of >600 samples from five continents indicate that the species is highly abundant in temperate lakes of the Northern Hemisphere. 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 87.44% and average nucleotide identity of 85.23% and another newly proposed species, *Fontibacterium abundans* MiE-29 (GCA_965235095.1), with an AAI of 93.82% and an ANI of 92.5%. Current GTDB classification (R220): d__Bacteria; p__Pseudomonadota; c__Alphaproteobacteria; o__Pelagibacterales; f__Pelagibacteraceae; g__Fonsibacter; s__Fonsibacter sp000510845.

Classification

Bacteria » *Pseudomonadota* » *Alphaproteobacteria* » *Pelagibacterales* » *Pelagibacteraceae* » *Fontibacterium* » *Fontibacterium temperatum*

References

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

Registry URL

https://seqco.de/i:49881

Species *Fontibacterium universale*

Etymology

[u.ni.ver.sa'le] **L. neut. adj.** *universale*, universal, pertaining to the widespread distribution of the species

Nomenclatural type

NCBI Assembly: GCA_965236175.1 [Ts]

Description

Type genome is *Fontibacterium universale* N-InaE-25sep22-010 (GCA_965236175.1), a metagenome-assembled genome (MAG) assembled from 5 m depth from Lake Inawashiro, Japan (date: 2022-09-25). N-InaE-25sep22-010 has a genome size of 1.0 Mbp with a genomic GC content of 29.3% and contains 29 tRNAs. The genome is of high quality, consisting of 4 contigs, with a completeness of 98.8%, contamination of 0% and strain heterogeneity of 0% as assessed with checkM. The metagenome was assembled with FLYE from combined long-and short-read sequencing (Oxford Nanopore and Illumina NovaSeq). Metagenomic fragment recruitment of >600 samples from five continents indicate that the species is present in many lakes around the world. 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 87.08% and average nucleotide identity of 85.18% and another newly proposed species, *Fontibacterium abundans* MiE-29 (GCA_965235095.1), with an AAI of 92.44% and an ANI of 90.87%. Current GTDB classification (R220): d__Bacteria; p__Pseudomonadota; c__Alphaproteobacteria; o__Pelagibacterales; f__Pelagibacteraceae; g__Fonsibacter; s__Fonsibacter sp000371845.

Classification

Bacteria » *Pseudomonadota* » *Alphaproteobacteria* » *Pelagibacterales* » *Pelagibacteraceae* » *Fontibacterium* » *Fontibacterium universale*

References

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

Registry URL

https://seqco.de/i:49878

Species *Pelagibacter malawiensis*

Etymology
[ma.la.wi.en'sis] **N.L. masc. adj.** *malawiensis*, pertaining to Lake Malawi, the origin of the metagenome-assembled genome

Nomenclatural type
NCBI Assembly: GCA_965235955.1 [Ts]

Description
Type genome is *Pelagibacter malawiensis* N-Mw13-23nov23-053 (GCA_965235955.1), a metagenome-assembled genome (MAG) assembled from 5 m depth from Lake Malawi, Malawi (date: 2023-11-23). N-Mw13-23nov23-053 has a genome size of 1 Mbp with a genomic GC content of 29.4%, contains 3 rRNA genes and 28 tRNAs. The genome is of high quality, consisting of 7 contigs, with a completeness of 99.5%, contamination of 0.5% and strain heterogeneity of 0% as assessed with checkM. The metagenome was assembled with FLYE from combined long-and short-read sequencing (Oxford Nanopore and Illumina NovaSeq). The closest cultivated relatives are '*Candidatus* Pelagibacter ubique SAR11 HTCC9022 (GCF_000472565.1), with an average amino acid identity of 75% and average nucleotide identity of 76.4% and '*Candidatus* Pelagibacter ubique SAR11 HTCC7211 (GCF_000155895.1), with an AAI of 74.2% and an ANI of 76.4%. Current GTDB classification (R220): d__Bacteria; p__Pseudomonadota; c__Alphaproteobacteria; o__Pelagibacterales; f__Pelagibacteraceae; g__Pelagibacter; s__Pelagibacter sp016870175.

Classification
Bacteria » *Pseudomonadota* » *Alphaproteobacteria* » *Pelagibacterales* » *Pelagibacteraceae* » *Pelagibacter* » *Pelagibacter malawiensis*

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

Registry URL
https://seqco.de/i:49883

Species *Pelagilacustribacter hypolimneticus*[Ts]

Etymology
[hy.po.lim.ne'ti.cus] **G.** *hypo*, below, under; **N.L. neut. adj.** *limneticus*, of a lake; **N.L. masc. adj.** *hypolimneticus*, referring to the deep zone of lakes, the hypolimnion

Nomenclatural type
NCBI Assembly: GCA_965235125.1 [Ts]

Description
Type genome is *Pelagilacustribacter hypolimneticus* TrH-25oct19-165 (GCA_965235125.1), a metagenome-assembled genome (MAG) assembled from 150 m depth from Traunsee, Austria (date: 2019-10-25). TrH-25oct19-165 has a genome size of 1 Mbp with a genomic GC content of 29.2% and contains 19 tRNAs. The genome is of high quality, consisting of 87 contigs, with a completeness of 93.4%, contamination of 4.8% and strain heterogeneity of 20% as assessed with checkM. The metagenome was assembled with megahit from short-read sequencing (Illumina NovaSeq). The closest cultivated relative is *Cosmipelagibacter malulaniensis* HIMB058 (GCA_000419545.1), with an average amino acid identity of 58.8% and average nucleotide identity of 68.1%. Current GTDB classification (R220): d__Bacteria; p__Pseudomonadota; c__Alphaproteobacteria; o__Pelagibacterales; f__Pelagibacteraceae; g__SYDM01; s__SYDM01 sp005801485.

Classification
Bacteria » *Pseudomonadota* » *Alphaproteobacteria* » *Pelagibacterales* » *Pelagibacteraceae* » *Pelagilacustribacter* » *Pelagilacustribacter hypolimneticus*[Ts]

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

Registry URL
https://seqco.de/i:49885

References

1. Fernandes et al. (2025). Ecophysiology and global dispersal of the freshwater SAR11-IIIb genus Fontibacterium. *Nature Microbiology*. DOI:10.1038/s41564-025-02091-8

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:gnukuc44** submitted by **Salcher, Michaela M** and including 12 new names has been successfully validated.

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