Register list for 4 new names including Acaudatibacter gen. nov.

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Genus *Acaudatibacter*

Etymology

[A.cau.da.ti.bac'ter] **Gr. pref.** *a-*, not, without [inseparable prefix]; **L. masc. adj.** *caudatus*, tailed or having a tail; **N.L. masc. n.** *bacter*, rod; **N.L. masc. n.** *Acaudatibacter*, tailless rod

Nomenclatural type

Species *Acaudatibacter aquilonius*$^{\mathrm{Ts}}$

Description

Members of this genus have been identified in freshwater, wastewater, and in soils from permafrost active layers, of glacier regions, and of rhizospheres of *Barbacenia macrantha* and *Vellozia epidendroides*. ANI values among genomes representing separate species within the genus range between < 76.6% and 81.0%. AAI values among genomes representing separate species within the genus range between 65.4% and 78.8%. Genomes of this genus notably contain genes for the Entner-Doudoroff Pathway, for aerobic respiration using an NADH-quinone oxidoreductase, a ubiquinol-cytochrome *c* reductase, and a cytochrome *c* oxidase, an F-type ATPase, and for biosynthesis of polyphosphate and polyhydroxybutyrate. Some members have the genetic potential to produce bacteriochlorophyll and/or carotenoid pigments. Most members encode genes for type IV tight adhesion pili, with some members further encoding genes for flagellar motility, chemotaxis, and holdfast formation, with genetic potential similar to members of the *Caulobacteraceae* family with obligate dimorphic lifecycles. However, most members likely have a monomorphic cell developmental program, as inferred from their lack genes for flagella, chemotaxis, and polar holdfast adhesin, as well as absence of a large number (> 20) of cell cycle regulation and polar morphogenesis genes present in related dimorphic taxa. The genus includes genomes with chemoheterotrophic, photoheterotrophic, and photoautotrophic genetic potentials. The taxon is supported as a genus-level group by phylogenomics and AAI, and corresponds to the GTDB taxonomy (R220) genus “g__Palsa-881”.

The nomenclatural type for the genus is *Acaudatibacter aquilonius*.

Classification

Bacteria » *Pseudomonadota* » *Alphaproteobacteria* » *Caulobacterales* » *Caulobacteraceae* » *Acaudatibacter*

References

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

Registry URL

https://seqco.de/i:49710

Species *Acaudatibacter aquilonius*^{Ts}

Etymology

[a.qui.lo'ni.us] **L. masc. adj.** *aquilonius*, northern, northerly, referring to the recovery of genomes of the organism from northern freshwater bodies

Nomenclatural type

NCBI Assembly: GCA_903872075.1 ^{Ts}

Description

Twelve metagenome-assembled genomes representing this species were assembled from sequence data obtained from samples taken from lakes Björntjärnen (Sweden), Alinen Mustajärvi (Finland), Keskinen Rajajärvi (Finland), and Valkea Kotinen (Finland). Completeness estimates for genomes, as determined by CheckM (v1.1.3; 'lineage_wf'), are 69.50–97.53%, with 1.62–4.21% estimated contamination. Genome assemblies range between 3.06–4.56 Mbp in size, comprising 100–973 contigs, with a G+C content of 67.37%–67.58%. Estimated complete genome sizes from CheckM range between 4.40–4.68 Mbp. ANI and AAI values between these genomes are 97.8%–100% and 99.3–100%, respectively, while such pairwise comparisons to closely related taxa are below 81.0% and 78.8%, respectively. Phylogenomic analysis of 72 concatenated conserved alphaproteobacterial single-copy genes places this species in the genus *Acaudatibacter*, in the family *Caulobacteraceae*. The species corresponds to GTDB taxonomy (R220) species "Palsa-881 sp903872075".

Genomes lack multiple genes for flagellar motility, chemotaxis, holdfast adhesin production, and for the caulobacterial obligate dimorphic cell developmental program. Genomes contain genes for type IV tight-adhesion pili; for carotenoid pigment production; for complete biosynthesis pathways of all standard amino acids; for aerobic respiration using cytochrome *c* oxidases cytochrome *aa*3 (*coxABC*) and cytochrome *cbb*3 (*ccoNOPQ*); for thiosulfate oxidation using thiosulfate dehydrogenase TsdA; for biosynthesis and degradation of polyphosphate and polyhydroxybutyrate; and for high-affinity PstABCS phosphate and PhnDEC phosphonate transporters. In addition, they have genetic potential for photoautotrophy, containing genes for bacteriochlorophyll synthesis, type II anoxygenic photosynthesis using a light-harvesting II (LH2) complex and a reaction center–light-harvesting I supercomplex (RC–LH1), as well as carbon fixation using the Calvin-Benson-Bassham (CBB) cycle, including the accessory genes for red-type RuBisCO activase (*cbbX*) and XuBP phosphatase (*cbbY*). The species has been detected in both oxic and anoxic strata of stratified freshwater bodies in Finland and Sweden. Likely a psychrophilic/mesophilic facultative anaerobe, based on its genetic repertoire and environmental distribution.

The proposed nomenclatural type for the species is the genome Umea_bin-04329^Ts, available under the NCBI WGS assembly accession number GCA_903872075.1^Ts (BioProject ID PRJEB38681), recovered as a metagenome coassembly from samples taken in autumn of 2018 from the stratified lakes Björntjärnen (lat. 64.12, long. 18.78) and Nästjärnen (lat. 64.15, long. 18.80), both in Umeå, Sweden (metagenomes ERS4600559–565 and ERS4600568–570). It comprises 100 contigs with a total of 4,361,582 bp, and has an estimated completeness of 95.32% and contamination of 1.62%.

Classification

Bacteria » *Pseudomonadota* » *Alphaproteobacteria* » *Caulobacterales* » *Caulobacteraceae* » *Acaudatibacter* » *Acaudatibacter aquilonius*^{Ts}

References

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

Registry URL

https://seqco.de/i:49709

Species *Acaudatibacter boreus*

Etymology

[bo're.us] **L. masc. adj.** *boreus*, northern, referring to the recovery of genomes of the organism from northern freshwater bodies

Nomenclatural type

NCBI Assembly: GCA_903870555.1 ^{Ts}

Description

Four metagenome-assembled genomes representing this species were assembled from sequence data obtained from samples taken from anoxic strata of a lake in Kiruna (Sweden), referred to as Ki1. Completeness estimates for genomes, as determined by CheckM (v1.1.3; ‘lineage_wf’), are 93.45%–94.46%, with 2.03–3.83% estimated contamination. Genome assemblies range between 4.23 Mbp–4.36 Mbp, comprising 576–699 contigs, with a G+C content of 67.46%–67.60%. Estimated complete genome sizes from CheckM range between 4.52–4.62 Mbp. ANI and AAI values between these genomes are 99.2%–100% and 99.6–100%, respectively, while such pairwise comparisons to closely related taxa are below 80.9% and 77.9%, respectively. Phylogenomic analysis of 72 conserved alphaproteobacterial single-copy genes places this species in the genus *Acaudatibacter*, in the family *Caulobacteraceae*. The species corresponds to GTDB taxonomy (R220) species “Palsa-881 sp903870555”.

Genomes lack multiple genes for flagellar motility, chemotaxis, holdfast adhesin production, and for the caulobacterial obligate dimorphic cell developmental program. Genomes contain genes for type IV tight-adhesion pili; for carotenoid pigment production; for complete biosynthesis pathways of all standard amino acids; for aerobic respiration using cytochrome *c* oxidases cytochrome *aa*3 (*coxABC*) and cytochrome *cbb*3 (*ccoNOPQ*), and ubiquinol oxidase cytochrome *bd* (*cydABX*); for thiosulfate oxidation using the thiosulfate dehydrogenase TsdA; for sulfide oxidation using the Sqr sulfide:quinone oxidoreductase; for biosynthesis and degradation of polyphosphate, polyhydroxybutyrate, and starch/glycogen; and for the high-affinity PstABCS phosphate, PhnDEC phosphonate, and SsuABC sulfonate transporters. In addition, they have partial genetic potential for photoautotrophy, containing genes for type II anoxygenic photosynthesis using a light-harvesting II (LH2) complex and a reaction center–light-harvesting I supercomplex (RC–LH1), as well as partial genetic potential for carbon fixation using the Calvin-Benson-Bassham (CBB) cycle. The species has been detected in both oxic and anoxic strata of stratified freshwater bodies in Canada, Finland, and Sweden. Likely a psychrophilic/mesophilic facultative anaerobe, based on its genetic repertoire and environmental distribution.

The proposed nomenclatural type for the species is the genome Ki1-2-2m_bin-386^Ts, available under the NCBI WGS assembly accession number GCA_903870555.1^Ts (BioProject ID PRJEB38681), recovered 24 July 2018 from a stratified lake in Kiruna, Sweden (lat. 67.93, long. 20.36; from the metagenome ERS4600419). It comprises 692 contigs with a total of 4,349,168 bp, and has an estimated completeness of 94.45% and contamination of 2.03%.

Classification

Bacteria » *Pseudomonadota* » *Alphaproteobacteria* » *Caulobacterales* » *Caulobacteraceae* » *Acaudatibacter* » *Acaudatibacter boreus*

References

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

Registry URL

https://seqco.de/i:49711

Species *Acaudatibacter lapponiensis*

Etymology

[lap.po.ni.en'sis] **N.L. masc. adj.** *lapponiensis*, pertaining to Lapponia, the Latin name for Lapland, the geographical region from which genomes of the organism were recovered

Nomenclatural type

NCBI Assembly: GCA_903923135.1 ^{Ts}

Description

Four metagenome-assembled genomes representing this species were assembled from sequence data obtained from samples taken from a lake in Kiruna (Sweden), referred to as Ki2, Swedish lake code: 754378-169136. Completeness estimates for genomes, as determined by CheckM (v1.1.3; 'lineage_wf'), are 94.86%–96.97%, with 1.94%–4.47% estimated contamination. Genomes assemblies range between 4.57–4.64 Mbp, comprising 279–357 contigs, with a G+C content of 68.83%–68.84%. Estimated complete genome sizes from CheckM range between 4.73–4.81 bp. ANI and AAI values between these genomes are 99.9%–100% and 99.9–100%, respectively, while such pairwise comparisons to closely related taxa are below 81.0% and 78.8%, respectively. Phylogenomic analysis of 72 conserved alphaproteobacterial single-copy genes places this species in the genus *Acaudatibacter*, in the family *Caulobacteraceae*. The species corresponds to GTDB taxonomy (R220) species "Palsa-881 sp903923135".

Genomes lack multiple genes for flagellar motility, chemotaxis, holdfast adhesin production, and for the caulobacterial obligate dimorphic cell developmental program. Genomes contain genes for type IV tight-adhesion pili; for carotenoid pigment production; for complete biosynthesis pathways of all standard amino acids; for aerobic respiration using cytochrome *c* oxidases cytochrome *aa*3 (*coxABC*) and cytochrome *cbb*3 (*ccoNOPQ*), and for ubiquinol oxidase cytochrome *bd* (*cydA*; partial genetic potential); for biosynthesis and degradation of polyphosphate, polyhydroxybutyrate, and starch/glycogen; for the high-affinity PstABCS phosphate, PhnDEC phosphonate, and SsuABC sulfonate transporters. In addition, they have genetic potential for photoautotrophy, containing genes for type II anoxygenic photosynthesis using a light-harvesting II (LH2) complex and a reaction center–light-harvesting I supercomplex (RC–LH1), as well as carbon fixation using the Calvin-Benson-Bassham (CBB) cycle, including the accessory genes for red-type RuBisCO activase (*cbbX*) and XuBP phosphatase (*cbbY*). The species has been detected in both oxic and anoxic strata of stratified freshwater bodies in Finland and Sweden. Likely a psychrophilic/mesophilic facultative anaerobe, based on its genetic repertoire and environmental distribution.

The proposed nomenclatural type for the species is the genome Kiruna2_bin-0871^Ts, available under the NCBI WGS assembly accession number GCA_903923135.1^Ts (BioProject ID PRJEB38681), recovered as a coassembly from samples taken 27 July 2018 from a stratified lake in Kiruna, Sweden (lat. 67.92, long. 20.37; from the metagenomes ERS4600421–424). It comprises 279 contigs with a total of 4,636,946 bp, and has an estimated completeness of 96.47% and contamination of 2.20%.

Classification

Bacteria » *Pseudomonadota* » *Alphaproteobacteria* » *Caulobacterales* » *Caulobacteraceae* » *Acaudatibacter* » *Acaudatibacter lapponiensis*

References

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

Registry URL

https://seqco.de/i:49712

References

1. Hallgren et al. (2025). Widespread potential for phototrophy and convergent reduction of lifecycle complexity in the dimorphic order Caulobacterales. *Nature Communications*. DOI:10.1038/s41467-025-65642-x

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:9aocwnme** submitted by **Hallgren, Joel** and including 4 new names has been successfully validated.

Date of Priority: 2026-05-11 05:58 UTC
DOI: 10.57973/seqcode.r:9aocwnme