

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 *aa3* (*coxABC*) and cytochrome *ccb3* (*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](https://doi.org/10.1038/s41467-025-65642-x)