

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 *aa3* (*coxABC*) and cytochrome *cbb3* (*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>

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)

