

Species *Aquincolibacterium lacustre*

Etymology

[la.cus'tre] N.L. neut. adj. *lacustre*, belonging to the lake

Nomenclatural type

[NCBI Assembly: GCA_903856085.1](#)^{TS}

Description

Estimated genome sizes for the species are 2.27-2.36 Mb, with %GC content of 50.32-50.59 %. Sugar and amino acid transporters are encoded by genomes in this species. Only respiratory complexes I and V are encoded by genomes of the species, and no terminal electron acceptors can confidently be identified. A cytoplasmic group A3 [FeFe] electron bifurcating hydrogenase is encoded by genomes of the species. Due to the incompleteness of respiratory pathways in this species and no terminal electron acceptors being predicted from the genomes, a reversible acetyl-CoA synthetase encoded by genomes of this species coupled with the Group A3 [FeFe] hydrogenase may be indicative of acetogenesis in this species. Respiratory complex I may be providing oxidized NAD⁺ and maintain a proton gradient across the membrane, while the respiratory F-type ATPase (complex V) produces ATP. Genes for the production of a Type-4a pilus is also present, as well as the "symbiotic" F-type ATPase. Very large ORFs are encoded by members of this species. The nomenclatural type for the species is the genome GCA_903856085.1.

Classification

Bacteria » *Omnitrophota* » *Omnitrophia* » *Omnitrophales* » *Aquincolibacteriaceae* » *Aquincolibacterium* » *Aquincolibacterium lacustre*

References

Effective publication: Seymour et al., 2023 [1]

Registry URL

<https://seqco.de/i:23675>

References

1. Seymour et al. (2023). Hyperactive nanobacteria with host-dependent traits pervade Omnitrophota. *Nature Microbiology*. [DOI:10.1038/s41564-022-01319-1](https://doi.org/10.1038/s41564-022-01319-1)