Species *Electrothrix gahaiensis*

Etymology

[ga.ha.i.en'sis] **N.L. fem. adj.** *gahaiensis*, of Gahai, name of a salt lake located in Qinghai-Tibet Plateau in China.

Nomenclatural type

NCBI Assembly: GCA_052785085.1 [Ts]

Description

Cells are multicellular filaments, up to several centimeters in length. Gram-negative. The species live in hypersaline water sediments with a salinity of 69.1-89.2 g/L and a pH of 7.8-8.1. The genomes of the species have been recovered from salt lakes on the Qinghai-Tibet Plateau in China. GC content of the genomes range between 47.2-47.6%. Genomes encode the enzymes for Long-distance electron transfer from sulfide-oxidizing to oxygen-reducing. Genomes encode the enzymes for CO2 fixation via the Wood-Ljungdahl pathway. Genomes encode [NiFe] hydrogenases of Groups 3c, 3d and 4a, which are involved in the consumption or production of hydrogen. Genomes encode monovalent cation/proton antiporter system Mrp, cation:H+ antiporter YrbG, potassium/proton antiporter CPA2 and potassium uptake protein Trk, which is involved in the “salt-in” strategy to maintain the osmotic balance of cells. Genomes also encode glycine betaine/proline transport system (ProVWX) and choline/glycine/proline betaine transport protein (BetT) for glycine betaine derived directly from the environment, as well as glycine/sarcosine N-methyltransferase (GSMT) and sarcosine/dimethylglycine N-methyltransferase (SDMT) for glycine betaine synthesis, which is involved in the “compatible solute” strategy to maintain the osmotic balance of cells. Nomenclatural type, NCBI Assembly: JALAAI000000000 (MAG XCD06.Bin23) is a metagenome-assembled genome derived from a salt lake sediment sample (Biosample: SAMN25126231). The assembly is of high quality with a completeness of 98.8% and 0.89% contamination and contains 43 tRNA.

Classification

Bacteria » *Desulfobacterota* » *Desulfobulbia* » *Desulfobales* » *Desulfobulbaceae* » *Electrothrix* » *Electrothrix gahaiensis*

References

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

Registry URL

https://seqco.de/i:49758

References

1. Hu et al. (2025). Insights on adaptive strategies and evolution of cable bacteria in saline lakes. *Limnology and Oceanography*. DOI:10.1002/lno.70262