Species *Eutrophocola salsuginis*[Ts]

Etymology

[sal.su'gi.nis] **L. gen. n.** *salsuginis*, of the brackish water

Nomenclatural type

NCBI Assembly: GCA_038147195.1 [Ts]

Description

Inferred to break down a Chitin and Pectin, as well as carries genes for rTCA cycle to fix inorganic carbon (korABCD). Carries genes for nitrate uptake (NRT2) and anaerobic dissimilatory nitrate reduction (nirBD). Capable of sulfate assimilation (cys), phosphorus uptake and regulation (pho, pst) and polyphosphate accumulation (ppk1). Likely performing osmoregulation using trk1 (K+ transporter) and proXV (Glycine betaine) and inferred to be motile (fliGMN, motAB gene). Based on the genome reporting standards for MAGs , the estimated completeness was 93.58%, contamination 1.79%, and the presence of the 5S (106bp), 16S (1,551 bp), and 23S (2,877 bp) rRNA gene and 42 tRNAs. Type genome is defined as “high-quality” draft MAG,with genome size of 3Mbps.

Classification

Bacteria » *Pseudomonadota* » *Gammaproteobacteria* » *Pseudomonadales* » *Pseudohongiellaceae* » *Eutrophocola* » *Eutrophocola salsuginis*[Ts]

References

Effective publication: Prabhu et al., 2024 [1]

Registry URL

https://seqco.de/i:46744

References

1. Prabhu et al. (2024). Machine learning and metagenomics identifies uncharacterized taxa inferred to drive biogeochemical cycles in a subtropical hypereutrophic estuary. *ISME Communications*. DOI:10.1093/ismeco/ycae067