

Genus *Thermosaccharophagus*

Etymology

[Ther.mo.sac.cha.ro.pha'gus] Gr. fem. adj. *therme*, heat; Gr. neut. n. *sakchar*, sugar; Gr. masc. adj. suff. *phagos*, eater; N.L. masc. n. *Thermosaccharophagus*, eater of sugar in high temperatures

Nomenclatural type

Species *Thermosaccharophagus gerlachensis*^{TS}

Description

Genomes belonging to the genus have been recovered from metagenomic sequence data from thermal environments in the USA and China. GC content range between 47% and 53%. ANI and AAI values among species are inconsistent, although all ANI values between species are below suggested species guidelines. Based on available genome data, the genus is strictly anaerobic. Between 64 and 105 glycoside hydrolases (GHs) are encoded by genomes of the genus, with > 25 GH families represented. Group 1a and 4b hydrogenases are conserved within the genus, suggesting hydrogen and formate metabolism in the genus. The core of the methyl-branch of the Wood-Ljungdahl pathway is conserved in the genus.

Classification

Bacteria » *Armatimonadota* » *Fervidibacteria* » *Fervidibacterales* » *Thermosaccharophagaceae* » *Thermosaccharophagus*

References

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

Registry URL

<https://seqco.de/i:44085>

References

1. Nou et al. (2024). Genome-guided isolation of the hyperthermophilic aerobic *Fervidibacter sacchari* reveals conserved polysaccharide metabolism in the Armatimonadota. *Nature Communications*. DOI:10.1038/s41467-024-53784-3