

Species *Fervidibacter sacchari*^{TS}

Etymology

[sac'cha.ri] N.L. gen. n. *sacchari*, of sugar

Nomenclatural type

[NCBI Assembly: GCA_030520105.1](#)^{TS}

Reference Strain

PD1 = [JCM 39283](#) = [DSM 113467](#)

Description

Hyperthermophilic, microaerophilic, facultatively anaerobic, and grows chemoheterotrophically on monosaccharides and polysaccharides. Cells are ovoid- to rod-shaped, Gram-stain negative, and are 0.9-1.3 µm in width and 1.6-3.6 µm in length. Grows between 65 and 87.5 °C and an optimum temperature of 80 °C, and a pH range of 6.5-8.6 with an optimum pH of 7.5. Grows at an optimum O₂ concentration of 5-10%. Grows on D-arabinose, D-galactose, D-glucose, D-rhamnose, D-ribose, D-xylose, chondroitin sulfate, colloidal chitin, galactan, gellan gum, guar gum, karaya gum, locust bean gum, xanthan gum, xyloglucan, β-glucan, glycogen, starch, AFEX-pretreated corn stover, miscanthus, sugarcane bagasse, acetate and casamino acids. Grows weakly on xyloglucan under fermentation conditions. The major fatty acids (> 10%) are C16:0, C18:0 and/or cyclo-C17:0, and iso-C16:0. The major respiratory quinones (> 10%) are MK-8 and MK-9. The isolate and genomes of the species have been recovered from geothermal springs in the Great Basin, Nevada, USA. GC content of genomes range between 51-52%. Subunits for both the high-affinity and low-affinity terminal oxidases are encoded in the genomes. Genomes also encode a Group 3d [NiFe] hydrogenase, which produces hydrogen as an electron sink for NAD⁺ regeneration.

Classification

Bacteria » *Armatimonadota* » *Fervidibacteria* » *Fervidibacterales* » *Fervidibacteraceae* » *Fervidibacter* » *Fervidibacter sacchari*^{TS}

References

Effective publication: Nou et al., 2024 [1]
Assigned taxonomically: Rinke et al., 2013 [2]

Registry URL

<https://seqco.de/i:32165>

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
2. Rinke et al. (2013). Insights into the phylogeny and coding potential of microbial dark matter. *Nature*. DOI:10.1038/nature12352