Species *Fredricksoniimonas aquilentivivens*^{Ts}

Etymology

[a.qui.len.ti.vi'vens] **L. fem. n.** *aqua*, water; **L. masc. adj.** *lentus*, slow; **L. pres. part.** *vivens*, living; **N.L. part. adj.** *aquilentivivens*, living in slow water

Nomenclatural type

NCBI Assembly: GCA_903860135.1 Ts

Description

This species is the type for the genus *Fredricksoniimonas.* In addition to genus characteristics, the estimated genome size for this species is 2 Mb. The %GC for the genome is 50.78 %. Coupled with a Group A3 [FeFe] hydrogenase encoded by the genome of this species, a reversible acetyl-CoA synthetase indicates likely acetogenesis in this species, through the production of acetate from acetyl-CoA by the fermentation of glucose and nucleotides. Respiratory complex I is present in the genome of this species, and can provide oxidized NAD+ and maintain a proton gradient across the membrane. A respiratory F-type ATPase (complex V) is also present in the genome, and can produce ATP. A metal-reducing cytochrome is present in the genome. Additionally, a "symbiotic" F-type ATPase is also encoded by this genome, along with all genes required for the tight-adherence complex and a Type-4a pilus. A very large ORF is also encoded by this genome. The assembly was recovered from a metagenomic sample of lake water from Nästjärnen, Sweden. The nomenclatural type for the species is the genome GCA_903860135.1.

Classification

Bacteria » *Omnitrophota* » “Velamenicoccia” » “Zapsychrales” » *Fredricksoniimonadaceae* » *Fredricksoniimonas* » *Fredricksoniimonas aquilentivivens*Ts

References

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

Registry URL

https://seqco.de/i:23752

References

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