Syntrophosphaera thermopropionivorans gen. nov. sp. nov.

Submitted by Nguyen, Huong

Genus *Syntrophosphaera*

Etymology

[Syn.tro.pho.sphae'ra] **Gr. prep.** *syn*, together; **Gr. fem. n.** *trophos*, one who feeds; **L. fem. n.** *sphaera*, a sphere; **N.L. fem. n.** *Syntrophosphaera*, a syntrophic sphere

Nomenclatural type

Species *Syntrophosphaera thermopropionivorans*[Ts]

Description

Syntrophosphaera belongs to the candidate phylum Cloacimonetes. It forms a monophyletic cluster with uncultured bacteria of the *Cloacimonadaceae* W5 in 16S rRNA gene phylogeny. It's closest related completely sequenced bacterium, *Cloacimonas acidaminovorans*, displays 86.4% 16S rRNA gene identity and 78.92% ANI. Members are proposed to be syntrophic propionate-oxidising bacteria and likely include meso- and thermophilic representatives. The genus is associated in particular with mesophilic anaerobic digestion systems. 16S rRNA gene amplicon sequencing and a novel genus-specific quantitative PCR assay showed that it outnumbered other syntrophic propionate-oxidising bacteria, such as *Pelotomaculum*, *Smithella* and *Syntrophobacter*, in 9 of 12 full-scale biogas reactors (Dyksma and Gallert, 2019)

Classification

Bacteria » *Cloacimonadota* » *Cloacimonadia* » *Cloacimonadales* » *Cloacimonadaceae* » *Syntrophosphaera*

References

Effective publication: Dyksma, Gallert, 2019 [1]

Registry URL

https://seqco.de/i:39377

Species *Syntrophosphaera thermopropionivorans*[Ts]

Etymology

[ther.mo.pro.pi.o.ni.vo'rans] **Gr. masc. adj.** *thermos*, hot; **N.L. pref.** *propioni-*, pertaining to propionic acid or propionate; **L. pres. part.** *vorans*, devouring; **N.L. fem. part. adj.** *thermopropionivorans*, devouring propionate at high temperature

Nomenclatural type

Genome sc|0006306 [Ts]

Description

The species is represented by a draft metagenome assembled genome (SMOG01000000) recovered from a propionate-degrading enrichment culture, inoculated from a thermophilic biogas reactor (PFR1)-treating biowaste. The draft genome is 1,753,479 bp with a GC content of 36.6%, 1,463 predicted genes, an estimated completeness of 95.6% and 2.2% contamination. In enrichment culture, methane was produced from propionate, and *S. thermopropionivorans* was the dominant organism. The genome encodes genes for propionate oxidation via methylmalonyl-CoA and for a syntrophic, fermentative lifestyle (Dyksma and Gallert, 2019)

Classification

Bacteria » *Cloacimonadota* » *Cloacimonadia* » *Cloacimonadales* » *Cloacimonadaceae* » *Syntrophosphaera* » *Syntrophosphaera thermopropionivorans*[Ts]

References

Effective publication: Dyksma, Gallert, 2019 [1]

Registry URL

https://seqco.de/i:271

References

1. Dyksma, Gallert (2019). *Candidatus* Syntrophosphaera thermopropionivorans: a novel player in syntrophic propionate oxidation during anaerobic digestion. *Environmental Microbiology Reports*. DOI: 10.1111/1758-2229.12759

Register List Certificate of Validation

On behalf of the *Committee on the Systematics of Prokaryotes Described from Sequence Data* (SeqCode Committee), we hereby certify that the Register List **seqco.de/r:ljw7z7qb** submitted by **Nguyen, Huong** and including 2 new names has been successfully validated.

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