Species Pumilibacter intestinalis

Etymology

[in.tes.ti.na.lis] N.L. masc. adj. intestinalis, pertaining to the intestine

Nomenclatural type

Strain: ATCC TSD-350 = CLA-AA-M10 = JCM 35012

Description

The species has all features of the genus. Additional phylogenetic relatives based on 16S rRNA gene sequences are *Ruminiclostridium josui* (84.32%), *Ruminiclostridium cellulolyticum* (84.11%), and *Vallitalea guaymasensis* (83.95%). Assignment to *the genus Pumilibacter* was confirmed by a POCP value of 69.7% between the genome of the type strain and that of the type species of the genus, *Pumilibacter muris*. Cells are very small and coccoid with a diameter of ca. 0.4-0.6 μm when grown on YCFA or mGAM blood agar under anaerobic conditions for 7 days. In total, 155 CAZymes were identified within the genome and only starch was predicted to be utilised as a carbon source. KEGG analysis identified pathways for the production of acetate from acetyl-CoA (EC:2.3.1.8, 2.7.2.1), propionate from propanoyl-CoA (EC:2.3.1.8, 2.7.2.1), L-cysteine and acetate from sulfide and L-serine (EC:2.3.1.30, 2.5.1.47), and L-glutamate from ammonia via L-glutamine (EC:6.3.1.2, 1.4.1.-). Antibiotic resistance was predicted based on the detection of tetracycline-resistant ribosomal protection protein. Ecological analysis suggested that the species is most prevalent within amplicon datasets from the mouse gut (39.9%). The type strain is CLA-AA-M10T. Its G+C content of genomic DNA is 49.6%. It was isolated from a filtered (0.45 μm) caecal suspension of an SPF mouse.

Classification

Bacteria » Bacillota » Clostridia » Eubacteriales » Pumilibacteraceae » Pumilibacter » Pumilibacter intestinalis

References

Effective publication: Afrizal et al., 2022 [1]

Registry URL

https://segco.de/i:23520

References

1. Afrizal et al. (2022). Enhanced cultured diversity of the mouse gut microbiota enables custom-made synthetic communities. *Cell Host & Dol:10.1016/j.chom.2022.09.011*