

Species *Pumilibacter muris*^T

Etymology

[mu.ris] L. gen. n. *muris*, of a mouse

Nomenclatural type

Strain: ATCC TSD-349 = CLA-AA-M08 = JCM 35011

Description

The species has all features of the genus. Additional phylogenetic relatives based on 16S rRNA gene sequences are *Xylanivirga thermophila* (83.77%), *Ruminiclostridium josui* (83.68%), and *Hespellia porcina* (83.57%). Separation from the other novel species within this genus represented by strain CLA-AA-M10 (described below) was confirmed via an ANI value of 76.4% and GGDC value of 25% between the two genomes. Cells are very small and spherical (diameter: 0.3-0.5 µm) when grown on YCFA agar under anaerobic conditions for 7 days. In total, 121 CAZymes were identified within the genome of the type strain 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.-). No antibiotic resistance genes were identified within the genome. Ecological analysis suggested that the species is most prevalent within amplicon datasets from the mouse gut (32.8%). The type strain is **CLA-AA-M08^T**. Its G+C content of genomic DNA is 46.81%. It was isolated from a filtered (0.45 µm) caecal suspension of an SPF mouse.

Classification

Bacteria » *Bacillota* » *Clostridia* » *Eubacteriales* » *Pumilibacteraceae* » *Pumilibacter* » *Pumilibacter muris*^T

References

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

Registry URL

<https://seqco.de/i:23517>

References

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