# Species *Pumilibacter muris*<sup>T</sup>

# 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 X ylanivirga 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-M08T. 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<sup>T</sup>

#### 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 & Dol:10.1016/j.chom.2022.09.011*