

## Species *Pumilibacter intestinalis*

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### 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://seqco.de/i:23520>

## 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