

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

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### Etymology

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

### Nomenclatural type

Strain: ATCC TSD-351 = CLA-AA-M11 = JCM 35013

### Description

Cells are rods (length: 1.2-2.7  $\mu\text{m}$ , diameter ca. 0,5 $\mu\text{m}$ ) when grown on YCFA or mGAM Blood agar under anaerobic conditions for 2-4 weeks. In total, 93 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.-). 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 (16.3%). The type strain is **CLA-AA-M11T**. Its G+C content of genomic DNA is 50.3 mol%. It was isolated from a filtered (0.45  $\mu\text{m}$ ) faecal suspension of an SPF, Fsp27<sup>-/-</sup> mouse.

### Classification

*Bacteria* » *Bacillota* » *Clostridia* » *Eubacteriales* » *Pumilibacteraceae* » *Anaerocaecibacter* » *Anaerocaecibacter muris*<sup>T</sup>

### References

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

### Registry URL

<https://seqco.de/i:23524>

## 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