

## Species *Anaerotardibacter muris*

---

### Etymology

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

### Nomenclatural type

Strain: ATCC TSD-352 = CLA-AA-M13 = JCM 35014

### Description

The species shares all features of the genus. Cells are short rods (0.6-1.2 µm in length) when grown on YCFA or mGAM blood (5%) agar under anaerobic conditions for 1-3 weeks, as the bacterium is a slow grower. Very low DNA amount could be extracted when no enzymatic lysis was added during extraction. The total number of CAZymes identified in the genome was 73. No genes for carbon source utilisation were predicted. KEGG analysis identified pathways for the production of acetate from acetyl-CoA (EC:2.3.1.8, 2.7.2.1) and propionate from propanoyl-CoA (EC:2.3.1.8, 2.7.2.1). Ecological analysis suggested that the species is most prevalent within amplicon datasets from the human gut (17.3% of 1,000 samples positive), followed by wastewater (14.5%), and mouse gut (7.1%). The type strain is CLA-AA-M13T. No antibiotic resistance genes were detected in its

### Classification

*Bacteria* » *Actinomycetota* » *Coriobacteriia* » *Eggerthellales* » *Eggerthellaceae* » *Anaerotardibacter* » *Anaerotardibacter muris*

### References

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

### Registry URL

<https://seqco.de/i:23522>

## 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