Species *Faecalibacterium tardum*

Etymology
[tar'dum] **L. neut. adj.** *tardum*, slow, pertaining to its slow growth

Nomenclatural type
Strain sc|0042703 T

Description
The genome size is 3.04 Mbp, G+C percentage is 56.28%, with 99.32% completeness and 0.0% contamination. It contains one plasmid of 14,735 bp in size, which encodes for vancomycin resistance via the vanY gene. The isolate was determined to be closely related to Faecalibacterium prausnitzii (98.7%) based on 16S rRNA gene analysis. ANI comparison to F. prausnitzii was on the border of species level assignment (95.05%), however, GTDB-Tk classification as 'Faecalibacterium prausnitzii_A' recommended the creation of a novel species. Strain CLA-AA-H175 was confirmed to represent a distinct species to Faecalibacterium intestinale (CLA-AA-H281) (ANI: 94.39%) and Faecalibacterium faecis (CLA-JM-H7B) (ANI: 86.46%), also described in this paper. Functional analysis showed the strain has 116 transporters, 18 secretion genes, and predicted utilization of starch, and production of L-glutamate. Production of butyrate (0.81 ± 0.16 mM) was confirmed for strain CLA-AA-H175 when grown in YCFA broth (DSMZ Medium No. 1611) in Hungate tubes for 48 hours at 37 °C. In total, 177 CAZymes were identified, with 28 different glycoside hydrolase families and 12 glycoside transferase families represented. The strain CLA-AA-H175 (phylum Bacillota, family Oscillospiraceae) was isolated from human faeces.

Classification
Bacteria » *Bacillota* » *Clostridia* » *Eubacteriales* » *Oscillospiraceae* » *Faecalibacterium* » *Faecalibacterium tardum*

References
Effective publication: Hitch et al., 2025 [1]

Registry URL
https://seqco.de/i:48056

References

1. Hitch et al. (2025). HiBC: a publicly available collection of bacterial strains isolated from the human gut. *Nature Communications*. DOI: 10.1038/s41467-025-59229-9