

Species *Faecalibacterium intestinale*

Etymology

[in.tes.ti.na'le] **N.L. neut. adj.** *intestinale*, pertaining to the intestine, from where the type strain was isolated

Nomenclatural type

Strain: CLA AA-H281 = DSM 116193 = LMG 33027

Description

The genome size is 2.97 Mbp, G+C percentage is 56.43%, with 100.0% completeness and 0.0% contamination. The isolate was determined to be related to *Faecalibacterium prausnitzii* (98.08%) based on 16S rRNA gene analysis. ANI comparison to *F. prausnitzii* was just below species level assignment (94.46%), and GTDB-Tk classification as '*Faecalibacterium prausnitzii*' recommended the creation of a novel species. Functional analysis showed the strain has 135 transporters, 18 secretion genes, and predicted utilization of starch and production of L-glutamate, riboflavin, and cobalamin. Production of butyrate (4.74 ± 0.30 mM) was confirmed for strain CLA-AA-H281 when grown in YCFA broth (DSMZ Medium No. 1611) in Hungate tubes for 48 hours at 37 °C. In total, 159 CAZymes were identified, with 27 different glycoside hydrolase families and 12 glycoside transferase families represented. The strain CLA-AA-H281 (phylum Bacillota, family Oscillospiraceae) was isolated from human faeces.

Classification

Bacteria » *Bacillota* » *Clostridia* » *Eubacteriales* » *Oscillospiraceae* » *Faecalibacterium* » *Faecalibacterium intestinale*

References

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

Registry URL

<https://seqco.de/i:48055>

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