

Species *Coprococcus intestinihominis*

Etymology

[in.tes.ti.ni.ho.mi'nis] **L. neut. n.** *intestinum*, the intestine; **L. masc. n.** *homo*, a human being; **N.L. gen. n.** *intestinihominis*, of the human gut

Nomenclatural type

Strain: CLA AA-H190 = DSM 114688 = LMG 33015

Description

The genome size is 3.6 Mbp, G+C percentage is 43.29%, with 98.43% completeness and 2.52% contamination. A single plasmid of 20,255 bp was detected. The closest relative to strain CLA-AA-H190 was *Coprococcus catus* (96.76%) based on 16S rRNA gene analysis. ANI comparison identified CLA-AA-H190 as a novel species within the genus *Coprococcus*, with an ANI value of 90.25% against the closest relative *C. catus*. GTDB-Tk classification as 'Coprococcus_A catus_A' confirmed the proposition of a novel species, but also suggests that separation of *Coprococcus* into multiple genera could occur in future. Functional analysis showed the strain has 119 transporters, 18 secretion genes, and predicted utilization of starch and production of propionate, butyrate, acetate, cobalamin, and folate. In total, 122 CAZymes were identified, with 19 different glycoside hydrolase families and 13 glycoside transferase families represented. The strain CLA-AA-H190 (phylum *Bacillota*, family *Lachnospiraceae*) was isolated from human faeces.

Classification

Bacteria » *Bacillota* » *Clostridia* » *Lachnospirales* » *Lachnospiraceae* » *Coprococcus* » *Coprococcus intestinihominis*

References

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

Registry URL

<https://seqco.de/i:48046>

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](https://doi.org/10.1038/s41467-025-59229-9)