Species *Lachnospira intestinalis*

Etymology
[in.tes.ti.na'lis] **N.L. fem. adj.** *intestinalis*, pertaining to the intestines, from where the type strain was isolated

Nomenclatural type
Strain sc|0042870 T

Description
The genome size is 3.1 Mbp, G+C percentage is 41.75%, with 99.33% completeness and 0.0% contamination. Strain CLA-AA-H89B was determined to represent a separate species to its closest relative, Lachnospira pectinoschiza (97.48%), based on 16S rRNA gene analysis. This was confirmed based on ANI comparison to all close relatives which were below the species threshold. GTDB-Tk classification of strain CLA-AA-H89B as 'Lachnospira sp000437735' confirmed that this isolate represents a novel species. Functional analysis showed the strain has 112 transporters, 29 secretion genes, and predicted utilization of starch and cellulose, along with production of L-glutamate, folate, acetate, propionate, and riboflavin. Motility was predicted based on the presence of the following genes: FlhA, FlhB, FlgB, FlgC, FlgD, FlgE, FlgF, FlgJ, FlgK, FlgL, FliC, FliD, FliE, FliF, FliG, FliK, FliM, FliN, MotA, MotB. In total, 162 CAZymes were identified, with 21 different glycoside hydrolase families and 11 glycoside transferase families represented. The strain CLA-AA-H89B (phylum Bacillota, family Lachnospiraceae) was isolated from human faeces.

Classification
Bacteria » *Bacillota* » *Clostridia* » *Lachnospirales* » *Lachnospiraceae* » *Lachnospira* » *Lachnospira intestinalis*

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

Registry URL
https://seqco.de/i:48060

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