Species *Ruminococcoides 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 JM-H38 = DSM 118486 = LMG 33604

Description
The genome size is 2.32 Mbp, G+C percentage is 40.88%, with 99.33% completeness and 1.01% contamination. The isolate was determined to be similar to Ruminococcus bromii (98.91%) and more distantly related to Ruminococcoides bili (96.76%) based on 16S rRNA gene analysis. While POCP comparison of strain CLA-JM-H38 to R. bromii was 59.79%, and 53.56% to Ruminococcus bovis, suggesting they belong to the same genus, all other comparisons to Ruminococcus species were below 50%, including to the type species, Ruminococcus flavefaciens (27.58%). POCP to R. bili, the type species of the genus Ruminococcoides, was 64.44%. GTDB-Tk classified strain CLA-JM-H38 as “Ruminococcus_E bromii_B”, confirming it is not a member of the genus Ruminococcus. These results support GTDB assignment that both R. bovis and R. bromii should be reclassified as members of the genus Ruminococcoides. Strain CLA-JM-H38 was confirmed to represent a novel species as all ANI comparisons to close relatives were below 95%, and it represents a distinct novel species from Ruminococcoides intestinihominis described in this work (78.33%). Functional analysis showed the strain has 81 transporters, 15 secretion genes, and predicted utilization of starch, and production of L-glutamate. In total, 108 CAZymes were identified, with 15 different glycoside hydrolase families and 12 glycoside transferase families represented. Ecological analysis based on 16S rRNA gene amplicons identified this species in 55.20% of 1,000 human gut samples with a relative abundance of 1.50 ± 2.49%. The strain CLA-JM-H38 (phylum Bacillota, family Oscillospiraceae) was isolated from human faeces.

Classification
Bacteria » *Bacillota* » *Clostridia* » *Eubacteriales* » *Oscillospiraceae* » *Ruminococcoides* » *Ruminococcoides intestinale*

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

Registry URL
https://seqco.de/i:48067

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