Species *Megasphaera 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-H81 = DSM 118069 = LMG 33597

Description
The genome size is 2.38 Mbp, G+C percentage is 53.59%, with 100.00% completeness and 0.0% contamination. The closest relative to strain CLA-AA-H81 was Megasphaera indica (99.09%) based on 16S rRNA gene analysis. ANI comparison to all close relatives were below species assignment threshold (highest to Megasphaera elsdenii, 90.78%). GTDB-Tk classification as ‘Megasphaera sp000417505’ supports the creation of a novel species. Functional analysis showed the strain has 133 transporters, 16 secretion genes, and predicted utilization of starch, and production of butyrate, propionate, L-glutamate, folate, riboflavin, and cobalamin. Ecological analysis identified 152 matching (MASH distance < 0.05) MAGs, of which 124 originate from the human gut, suggesting this species is most commonly observed within this environment. This is supported by ecological analysis using 16S rRNA gene amplicon datasets which identified it within 19.0% of 1,000 human gut samples, with a relative abundance of 2.14 ± 5.23%. The strain CLA-AA-H81 (phylum Bacillota, family Veillonellaceae) was isolated from human faeces.

Classification
Bacteria » *Bacillota* » *Negativicutes* » *Veillonellales* » *Veillonellaceae* » *Megasphaera* » *Megasphaera intestinihominis*

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

Registry URL
https://seqco.de/i:48062

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