Species *Solibaculum 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-H44 = DSM 114601 = LMG 33034

Description
The genome size is 2.81 Mbp, G+C percentage is 54.62 %, with 97.99% completeness and 0.67% contamination. The isolate was determined to be a new species based on 16S rRNA gene analysis, with the closest validly named match being Solibaculum mannosilyticum (94.93%). Placement within Solibaculum was confirmed with POCP values above 50% to S. mannosilyticum (55.7%), the type species, and only member of this genus. ANI comparison confirmed the isolate represents a novel species, as no ANI values were above 80%. Functional analysis showed the strain has 82 transporters, 16 secretion genes, and predicted utilization of starch, and production of acetate, propionate, and L-glutamate. In total, 169 CAZymes were identified, with 20 different glycoside hydrolase families and 15 glycoside transferase families represented. The strain CLA-JM-H44 (phylum Bacillota, family Oscillospiraceae) was isolated from human faeces.

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

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

Registry URL
https://seqco.de/i:48069

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