Species *Lachnospira rogosae*

Etymology

[ro.go'sae] **N.L. gen. masc. n.** *rogosae*, of Rogosa, named after the American bacteriologist Morrison Rogosa

Nomenclatural type

Strain: CLA AA-H225 = CLA AA-H255 = DSM 118602 = LMG 33594

Description

Strain CLA-AA-H255 was determined to be similar to Lactobacillus rogosae (99.87%) based on 16S rRNA gene analysis. However, the lack of a genome for the type strain of the latter species, along with the lack of the type strain at any established culture collection prevented further comparison (Tindall, 2014). GTDB-Tk classification of CLA-AA-H255 as 'Lachnospira rogosae_A' suggested that it represents a species within a genus distantly related to Lactobacillus. This was reconfirmed by the same placement of a second strain, CLA-AA-H191, which was also assigned to the same placeholder by GTDB-Tk (ANI of 98.86% between our two isolates). Based on these results, we propose L. rogosae was previously misassigned as a member of the genus Lactobacillus. To provide a type strain, and correct its placement, we propose the creation of the species Lachnospira rogosae. Functional analysis showed that strain CLA-AA-H255 has 100 transporters, 25 secretion genes, and predicted utilization of starch, and production of L-glutamate, folate, and riboflavin. The prediction of motility and acetate production based on genomic analysis is consisting with the observed phenotype of motility in the original type strain of L. ragosae as stated by Holdeman and Moore (Holdeman and Moore, 1974). In total, 142 CAZymes were identified, including 20 different glycoside hydrolase families and 12 glycoside transferase families. Ecological analysis of 1,000 human gut 16S rRNA gene amplicon samples identified this strain in 1.20% of samples with a relative abundance of 0.43 ± 0.78%. The strain CLA-AA-H255 (phylum Bacillota, family Lachnospiraceae) was isolated from human faeces.

Classification

Bacteria » *Bacillota* » *Clostridia* » *Lachnospirales* » *Lachnospiraceae* » *Lachnospira* » *Lachnospira rogosae*

References

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

Registry URL

https://seqco.de/i:41617

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