

Species *Waltera hominis*

Etymology

[ho.mi'nis] **L. gen. n.** *hominis*, of a human being, pertaining to the human gut habitat, from where the type strain was isolated

Nomenclatural type

Strain: CLA AA-H183 = DSM 114684 = LMG 33586

Description

The genome size is 3.88 Mbp, G+C percentage is 45.72%, with 99.52% completeness and 2.13% contamination. The isolate was assigned to the species *Waltera intestinalis* (100.0%) based on 16S rRNA gene analysis. However, ANI comparison identified strain CLA-AA-H183 as a novel species within the genus *Waltera*, with an ANI value of 91.97% against the type species *Waltera intestinalis*. GTDB-Tk currently lacks the inclusion of *Waltera*, causing misclassification as 'Acetatifactor sp003447295', however this confirmed the proposition of a novel species. Separation of *Waltera* from *Acetatifactor* was revalidated via both phylogenomic analysis, which shows both genera form separate monophyletic groups, and POCP analysis, which shows clear similarity within each genus (*Waltera*: 68.86%, *Acetatifactor*: 59.25%), and separation between the genera (39.94 ± 1.63 %). Functional analysis showed the strain has 141 transporters, 36 secretion genes, and predicted utilization of starch, cellulose, and production of butyrate, propionate, acetate, and folate. In total, 228 CAZymes were identified, with 38 different glycoside hydrolase families and 14 glycoside transferase families represented. The strain CLA-AA-H183 (phylum Bacillota, family Lachnospiraceae) was isolated from human faeces.

Classification

Bacteria » *Bacillota* » *Clostridia* » *Lachnospirales* » *Lachnospiraceae* » *Waltera* » *Waltera hominis*

References

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

Registry URL

<https://seqco.de/i:48070>

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