

## Species *Faecalibacterium hominis*

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### Etymology

[ho.mi.nis] *hominis*

### Nomenclatural type

Strain: 4 P-15 = CGMCC 1.5250 = JCM 39347

### Description

The strain CLA-AA-H223, CLA-AA-H254, and CLA-AA-H283 had the highest 16S rRNA gene sequence similarities to *Faecalibacterium prausnitzii* (98.04–98.38%). The highest ANI value was to *F. prausnitzii* (85.6–85.8%). GTDB-Tk placed the genome under the genus *Faecalibacterium*, and species 'Faecalibacterium\_prausnitzii\_C'. The highest POCP values were 71.2–74.1% to *F. prausnitzii*. The isolates were also grouped together with *F. prausnitzii* based on the genome tree analysis. These analyses confirmed the classification of the isolates as a novel species within the genus *Faecalibacterium*. The isolates were found to represent the same species as 'Faecalibacterium hominis' (Liu et al., 2021), with ANI and GGDC values of 96.5–96.9% and 72.5–73.7%, respectively. However, this species has not yet been validated. Cells are long rods to string like on modified Gifu Anaerobic Medium under anaerobic conditions. Genome analysis predicted the ability to utilise glucose, arbutin, salicin, starch, sulfide, and L-serine in all three strains. The genes for utilisation of trehalose were detected in both CLA-AA-H223 and CLA-AA-H254, whereas the genes for cellobiose utilisation were only found in CLA-AA-H223. The genes for production of acetate, propionate, L-glutamate, L-cysteine, cobalamin (vitamin B12), and riboflavin (vitamin B2) were present in all strains. As butyrate biosynthesis was not predicted, manual examination of the Prokka annotations identified genes assigned as 3-hydroxybutyryl-CoA dehydrogenase (EC 1.1.1.157) and butyryl-CoA:acetate CoA-transferase (EC 2.8.3.-). Antibiotic resistance genes were only detected in the genome of strain CLA-AA-H254: Erm 23S ribosomal RNA methyltransferase (ARO:3000560). The molecular G+C content of DNA is 56.4–56.9 mol%. The species was most prevalent in human gut microbiota (77.3–79.8% of 1,000 samples positive), followed by wastewater (60.9–68.1%), pig gut microbiota (57.4–67.4%), and activated sludge (60.9–65.0%). The type strain, CLA-AA-H223T (=DSM 113002T), was isolated from the faeces of a healthy 26-year-old woman. The other strain of this species, CLA-AA-H254 and CLA-AA-H283 (=DSM 113416) were isolated from the faeces of a healthy 36-year-old woman and 28-year-old man, respectively.

### Classification

*Bacteria* » *Bacillota* » *Clostridia* » *Eubacteriales* » *Oscillospiraceae* » *Faecalibacterium* » *Faecalibacterium hominis*

### Registry URL

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