



Draft Genome Sequence of *Faecalimonas umbilicata* JCM 30896^T, an Acetate-Producing Bacterium Isolated from Human Feces

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ABSTRACT Here, we report the draft genome sequence of *Faecalimonas umbilicata* JCM 30896^T, an acetate-producing bacterium isolated from human feces. The genomic analysis reveals genes for acetate and vitamin B₁₂ synthesis and will facilitate the study of the role of this strain in the human gut.

Acetate is one of the metabolic end products of anaerobic fermentation. Butyrate-producing bacteria, such as *Faecalibacterium prausnitzii* and *Roseburia* spp., can be net utilizers of acetate (1). The butyrate formed by the above-mentioned acetate-consumers has important roles in colonic health (1). Recently, we isolated a new acetate-producing bacterium, *Faecalimonas umbilicata* JCM 30896^T, from a fecal sample from a healthy Japanese man (2). This species is a member of the family *Lachnospiraceae*. Anaerobic bacteria affiliated with the family *Lachnospiraceae* make up the majority of highly prevalent bacteria in the human intestinal tract (3). We analyzed the draft genome sequence of *F. umbilicata* JCM 30896^T to improve our understanding of the physiology and potential health contribution of this strain in the human gut.

F. umbilicata JCM 30896^T was grown on Eggerth-Gagnon agar (Merck) supplemented with 5% (vol/vol) horse blood for 4 days at 37°C under a H₂-CO₂-N₂ (1:1:8, by volume) gas mixture. Total genomic DNA was extracted from *F. umbilicata* JCM 30896^T using a Genomic-tip 100/G kit (Qiagen). Labiase (5.0 mg/ml; Cosmo Bio) was used to lyse bacterial cells. A whole-genome shotgun library was constructed using a SMRTbell template prep kit 1.0 (Pacific Biosciences), followed by single-molecule real-time (SMRT) sequencing conducted on the PacBio RS II sequencing system (Pacific Biosciences) by Takara. A total of 97,745 reads (311-fold coverage) with an average length of 13,372 bp were assembled *de novo* using Hierarchical Genome Assembly Process version 3.0 (HGAP3.0) in SMRT Analysis version 2.3.0 (4), resulting in 8 contigs with an *N*₅₀ value of 1,731,485 bp. The default settings for genome assembly were used. This assembly resulted in a draft genome sequence of 3,262,821 bp with a G+C content of 41.6%. Analysis of the genome sequences was performed using the DDBJ Fast Annotation and Submission Tool (DFAST; <https://dfast.nig.ac.jp/>) (5). A total of 3,210 protein-coding sequences, 60 tRNAs, and 18 rRNAs were detected.

The genome of *F. umbilicata* JCM 30896^T contained genes involved in acetate synthesis, such as formate acetyltransferase (EC 2.3.1.54), phosphotransacetylase (EC 2.3.1.8), and acetate kinase (EC 2.7.2.1). In addition, *F. umbilicata* JCM 30896^T was predicted to possess a vitamin B₁₂ biosynthesis pathway. Vitamin B₁₂ is an important cofactor for a variety of enzymes. In the systematic genome assessment of B vitamin biosynthesis, vitamin B₁₂ biosynthesis was present in 42% of the genomes of 256 common human gut bacteria (6). Furthermore, nearly half of the *Firmicutes* genomes (43%; 56/130) were predicted to synthesize vitamin B₁₂ (6). Recently, true bidirectional metabolic cross-feeding dependent on vitamin B₁₂ was observed between the mucin-

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degrading bacterium *Akkermansia muciniphila* and the butyrate-producing bacterium *Eubacterium hallii* (7). The production of vitamin B₁₂ and acetate by *F. umbilicata* might be beneficial for growth with other bacteria lacking the vitamin B₁₂ biosynthesis pathway, such as *A. muciniphila* (8), and production of butyrate by butyrate-producing bacteria, such as *F. prausnitzii*.

The genome sequence will facilitate further studies of the beneficial role of this strain in the human gut.

Data availability. This whole-genome shotgun project has been deposited in DDBJ/ENA/GenBank under the accession no. [BHEO0000000](https://doi.org/10.1093/bioinformatics/btq000). The version described in this paper is the first version, BHEO01000000.

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