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PROKARYOTES

Draft Genome Sequence of *Lawsonibacter asaccharolyticus* JCM 32166^T, a Butyrate-Producing Bacterium, Isolated from Human Feces

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ABSTRACT Here, we report the draft genome sequence of *Lawsonibacter asaccharolyticus* JCM 32166^T, a butyrate-producing bacterium, isolated from human feces. The genomic analysis reveals genes for butyrate synthesis and will facilitate the study on the role of this strain in the human gut.

Human gut microbiome research has become increasingly important. During our attempts to recover microbes with beneficial properties, such as butyrate-producing bacteria or flavonoid-degrading bacteria, we have successfully isolated a butyrate-producing bacterium, designated strain 3BBH22^T (= JCM 32166^T), from a feces sample from a healthy Japanese woman. Recently, strain 3BBH22^T was proposed to belong to a novel species in a novel genus of the family *Ruminococcaceae*, for which the name *Lawsonibacter asaccharolyticus* was given (1). Members of *Lachnospiraceae* and *Ruminococcaceae* have received the most attention (2) because they are very abundant in the human colon, comprising 10 to 20% of the total bacteria. There are four main pathways known for butyrate production, the acetyl-coenzyme A (acetyl-CoA), glutarate, 4-aminobutyrate, and lysine pathways (3). We analyzed the draft genome sequence of *L. asaccharolyticus* JCM 32166^T to elucidate the mechanisms of the butyrate synthesis pathway.

Chromosomal DNA was extracted from *L. asaccharolyticus* JCM 32166^T using a Genomic-tip 100/G kit (Qiagen). Labiase (5.0 mg/ml; Cosmo Bio) was used to lyse bacterial cells. The whole genome of *L. asaccharolyticus* JCM 32166^T was sequenced using the PacBio RS II sequencing system (Pacific Biosciences) by TaKaRa. The reads were assembled *de novo* using Hierarchical Genome Assembly Process version 3.0 (HGAP3.0) in SMRT Analysis version 2.3.0 (4), resulting in 7 contigs with an N_{50} length of 3,503,692 bp. This assembly resulted in a draft genome sequence of 4,282,156 bp, with a G+C content of 58.4%. Analysis of the genome sequences was performed using the Microbial Genome Annotation Pipeline (MiGAP; https://www.migap.org/index.php/en) (5). A total of 4,461 protein-coding sequences (CDSs), 85 tRNAs, and 6 rRNAs were detected.

As expected, the genome of *L. asaccharolyticus* JCM 32166^T contained an acetyl-CoA acetyltransferase (AtoB or Thl; EC 2.3.1.9) gene, 3-hydroxybutyryl-CoA dehydrogenase (Hbd; EC 1.1.1.157) gene, 3-hydroxybutyryl-CoA dehydratase (Crt; EC 4.2.1.55) gene, butyryl-CoA dehydrogenase (Bcd; EC 1.3.8.1, including electron transfer flavoprotein α,β-subunits; FixB and FixA) gene, phosphate butyryltransferase (Ptb; EC 2.3.1.19) gene, and butyrate kinase (Buk; EC 2.7.2.7) gene, verifying that it possesses the acetyl-CoA pathway (3). Although *Intestinimonas butyriciproducens* (6), which is phylogenetically related to *L. asaccharolyticus* JCM 32166^T (1), possesses the lysine pathway (7, 8), *L. asaccharolyticus* JCM 32166^T did not. It has been reported that the acetyl-CoA pathway is the most prevalent, followed by the lysine pathway (3). In this strain, butyrate is

Received 17 May 2018 **Accepted** 22 May 2018 **Published** 21 June 2018

Citation Sakamoto M, Ikeyama N, Yuki M, Ohkuma M. 2018. Draft genome sequence of *Lawsonibacter asaccharolyticus* JCM 32166^T, a butyrate-producing bacterium, isolated from human feces. Genome Announc 6:e00563-18. https://doi.org/10.1128/genomeA.00563-18.

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produced via Buk, leading to the formation of ATP. The genome sequence will facilitate further studies on the beneficial role of this strain in the human gut.

Accession number(s). The draft genome sequence of *L. asaccharolyticus* JCM 32166^T has been deposited in DDBJ/EMBL/GenBank under the accession numbers BFBT01000001 to BFBT01000007.

ACKNOWLEDGMENTS

We thank Wakako Bunryo and Naomi Sakurai for their technical assistance.

This work was supported by PRIME, the Japan Agency for Medical Research and Development (AMED), under grant JP17gm6010007 to M.S., and by a RIKEN Competitive Program for Creative Science and Technology (to M.O.).

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