Complete genome sequence of *Lactobacillus fermentum* SRCM103285 isolated from Korean rice wine, makgeolli

Woorim Kang†, Seong-Yeop Jeong††, In-seong Cha†, Min Seok Cho†, Do-Youn Jeong‡, Byung-Yong Kim†, and Je Hee Lee*†

†ChunLab, Inc., Seoul 06725, Republic of Korea
‡Microbial Institute for Fermentation Industry (MIFI), Sunchang 56048, Republic of Korea


Lactobacillus fermentum SRCM103285 was isolated from Korean rice wine, makgeolli. Here, we report the complete genome sequence of *L. fermentum* SRCM103285. Strain SRCM 103285 showed 99.87% of 16S rRNA gene similarity and 99.17% of OrthoANIu value with *L. fermentum* B1 28T. The complete genome sequence was obtained by using PacBio RS II platform. Strain SRCM103285 has single circular chromosome of 1,905,587 bp and the G + C contents is 52.3%. The genome contains 1,864 coding sequences, 15 rRNA genes, and 58 tRNA genes. There are at least five genes involved in acetate fermentation and five alcohol tolerance genes.

**Keywords:** Lactobacillus fermentum, SRCM103285, complete genome sequence, fermentation

Makgeolli is a traditional Korean rice wine that brewed with steamed rice and nuruk, fermenting agent used to make alcohol in a Korean traditional way. Nuruk is made by breeding koji mold by floating grains such as wheat or steamed beans (Aidoo et al., 2006). Even after brew, makgeolli still contains microorganisms, especially lactate-producing bacteria, derived from nuruk due to its unique brewing method (Song and Park, 2003). We isolated a *L. fermentum* strain designated SRCM103285 from makgeolli by using MRS agar medium at 20°C. The strain was deposited in the Korean Culture Center of Microorganisms (KCCM) with the accession number of KCCM 12742P.

Strain SRCM103285 was closely related to *Lactobacillus fermentum* through 16S rRNA gene similarity value, 99.87%. *Lactobacillus fermentum* is an economically important species of lactic acid bacterium used in fermented food (Yeung et al., 2002) and probiotics (Maldonado et al., 2012). The members of *L. fermentum* are known to produce short-chain fatty acids (SCFA) vigorously (Kahouli et al., 2015). In this report, we investigate the genome of strain SRCM103285, focusing on SCFA production and alcohol resistance.

Genomic DNA was extracted using the Fast DNA Spin Kit for Soil (MP Bio) and checked by 1% agarose gel electrophoresis and quantified by a QuantiFluor (Promega). The complete genome of strain SRCM103285 was sequenced using the PacBio RS II platform (Pacific Biosciences) with a 20 kb SMRTbell template at Macrogen Inc. and the reads were
assembled using HGAP version 2.3. The genome was annotated using the NCBI Prokaryotic Genome Annotation Pipeline (https://www.ncbi.nlm.nih.gov/genome/annotation_prok/) with the best-placed reference protein set and GeneMarkS methods.

We obtained the complete genome sequence of strain SRCM103285 that has a single circular chromosome of 1,905,587 bp with 52.3% G + C contents. The genome of strain SRCM103285 contains 1,864 coding sequences (CDSs), 15 rRNA genes, and 58 tRNA genes.

Genome-derived 16S rRNA gene sequence of strain SRCM103285 was compared to other type strains, including the members of Lactobacillus using EzBioCloud server (Yoon et al., 2017a). Genomic relatedness between strain SRCM103285 and L. fermentum B1 28T was evaluated with average nucleotide identify (ANI) calculator (Yoon et al., 2017b). OrthoANIu value between strain SRCM103285 and L. fermentum B1 28T was 99.17%.

Acetate is one of the most representative bacterial SCFAs (LeBlanc et al., 2017). Pyruvate, made from glucose through glycolysis, is decarboxylated by pyruvate dehydrogenase (PDH) to acetyl-CoA and acetyl-CoA is used for acetate production by acetate kinase (Zaunmüller et al., 2006). Four pyruvate dehydrogenase related genes (pdhA, pdhB, pdhC, and ldhA) and an acetate kinase gene (ackA) were found from the genome of strain SRCM103285. Furthermore, strain SRCM103285 potentially utilize ethanol as an energy source and produce acetate as a by-product. Ethanol is catabolized to acetaldehyde by alcohol dehydrogenase and acetaldehyde dehydrogenase (Arndt et al., 2008). We found two alcohol dehydrogenase genes (adh) and an acetaldehyde dehydrogenase gene (adhE) in the genome of strain SRCM103285.

As a member of makgeolli ecosystem, strain SRCM103285 should have alcohol resistance to survive. One of the most representative strategies for alcoholic stress is suppressing the metabolism through the stalling of the ribosome, and RelA/SpoT family, NusA, and GppA are related genes (Haft et al., 2014). We found these genes in the genome of strain SRCM103285. Also, members of the genus Lactobacillus, especially, are known to replace fatty acids in the cell membrane with long-chain to gain alcohol tolerance (Gold et al., 1992). We found two genes that encode Beta-ketoacyl synthase, which is involved in the synthesis of long-chain fatty acid. Taken together, strain SRCM103285 is expected to ribosome stalling and convert cell membrane composition to long-chain fatty acid to resist ethanol in the makgeolli ecosystem.

Nucleotide sequence accession number

The complete genome sequence of Lactobacillus fermentum SRCM103285 was deposited at NCBI under the GenBank accession no. CP035054.

Acknowledgments

This research was supported by the Ministry of Trade, Industry & Energy (MOTIE), Korea Institute for Advancement of Technology (KIAT) and Establishment of Infrastructure for Industrialization of Korean Useful Microbes (R0004073).

References


