Cane juice is the juice extracted from pressed sugarcane. It is consumed as a beverage worldwide and especially in regions where sugarcane is commercially grown, such as Southeast Asia, South Asia, and Latin America. The history of cane juice dates back thousands of years, running parallel to the history of sugar. Evaporated cane juice is chemically made up of a combination of sugars, such as fructose, glucose, and sucrose.

Our laboratory received the Leuconostoc pseudomesenteroides KCTC 3652 strain, which is known to be present in cane juice (2), from the Korean Collection for Type Cultures (KCTC), and it was grown under standard conditions (Lactobacilli MRS broth, 0881; Difco), at 30°C and 200 rpm. The genomic DNA was extracted from the cultured bacteria using the alkaline lysis method (3). We then sequenced the genome of Leuconostoc pseudomesenteroides KCTC 3652; genome sequencing of this organism had not been completed or initiated when our sequencing project was begun, according to the Genomes OnLine Database (GOLD) (7).

Here we report the genome sequence of Leuconostoc pseudomesenteroides KCTC 3652, obtained using a whole-genome shotgun strategy (5) using Roche 454 GS (FLX Titanium) pyrosequencing (190,210 reads, totaling 3,244,985 bp, with a G+C content of 38.3%), which consists of 1,160 large contigs (>100 bp in size). All of the contigs were assembled by the Newbler Assembler 2.3 software program (454 Life Sciences).

We announce the genome sequence of one of the most prevalent lactic acid bacteria present during the manufacturing process of cane juice, the type strain Leuconostoc pseudomesenteroides KCTC 3652 (3,244,985 bp, with a G+C content of 38.3%), which consists of 1,160 large contigs (>100 bp in size). All of the contigs were assembled by the Newbler Assembler 2.3 software program (454 Life Sciences).

ers. In addition, the contigs were searched against the KEGG, UniProt, and Clusters of Orthologous Groups (COG) databases to annotate the gene descriptions. The G+C mole percent measurements were calculated using the genome sequence. The DNA base composition was calculated using a Java programme developed.

The incomplete draft genome includes 3,244,985 bases and is comprised of 3,451 predicted coding sequences (CDSs), with a G+C content of 38.3%. There are single predicted copies of the 5S, 16S, and 23S rDNA genes and 56 predicted tRNAs. There are 264 subsystems that are represented in the genome, and we used this information to reconstruct the metabolic network (determined using the RAST server). There are many carbohydrate subsystem features, including genes involved in di- and oligosaccharides, central carbohydrate metabolism, monosaccharides, and sugar alcohols. The results from the study of Leuconostoc pseudomesenteroides derived from cane juice help to explain the rich characteristics of sugar cane.

Nucleotide sequence accession number. The draft genome sequence of Leuconostoc pseudomesenteroides KCTC 3652 is available in GenBank under the accession number AEOQ0000001 to AEOQ00001160.

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