



Genome Announcement

Whole genome sequence of lactic acid bacterium *Pediococcus acidilactici* strain S1



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ABSTRACT

Pediococcus acidilactici strain S1, a lactic acid-fermenting bacterium, was isolated from makgeolli—a Korean traditional fermented alcoholic beverage. Here we report the 1,980,172 bp (G + C content, 42%) genome sequence of *Pediococcus acidilactici* strain S1 with 1,525 protein-coding sequences (CDS), of which 47% could be assigned to recognized functional genes. The genome sequence of the strain S1 might provide insights into the genetic basis of the lactic acid bacterium with alcohol-tolerant.

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Introduction

Pediococcus acidilactici strain S1 is a gram-positive, coccus-shaped, lactic acid-fermenting bacterium that belongs to the *Lactobacillaceae* family. Several lactic acid bacteria (LAB) belonging to the genus *Pediococcus* have been isolated and characterized.¹ Most of them are found in fermented foods and beverages such as makgeolli, which is a traditional Korean rice wine.² *P. acidilactici* strain S1 was also isolated from makgeolli with alcohol-tolerant. The strain can be used for makgeolli brewing as a starter or supplementation.³ Here, we present

a description of the genome sequence and its annotation results.

The genome sequence of *P. acidilactici* strain S1 was revealed by using an Ion Torrent semiconductor sequencing machine.⁴ A total of 3,959,807 reads were generated at an average read length of 298 bp. The whole genome was assembled de novo from short shotgun sequence reads by using Mimicking Intelligent Read Assembly (MIRA) 4.0⁵ and CLC Genomics Workbench version 8.0. The best assembly results comprised 59 contigs with 531x coverage. The draft genome size was 1,980,172 bp with a G + C content of 42%. The assembled contigs were annotated by using NCBI Prokaryotic

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Genomes Annotation Pipeline (PGAP) version 3.0.⁶ RAST server (<http://rast.nmpdr.org/>) was used for subsystem classification and functional annotation.⁷ The annotation predicted 1,771 protein-coding sequences (CDS), of which 47% were assigned to recognized functional genes with 40 tRNA and 7 rRNA genes.

Among the protein coding genes alcohol-tolerance enzymes were identified such as aldehyde dehydrogenase (477 aa; locus tag ATO21.00425; accession number LNUM01000003, 456 aa; locus tag ATO21.02775; accession number LNUM01000010), malate transporter (296 aa; locus tag ATO21.00560; accession number LNUM01000003), alcohol dehydrogenase (385 aa; locus tag ATO21.04225; accession number LNUM01000015, 341 aa; locus tag ATO21.05320; accession number LNUM01000020) and aryl-alcohol dehydrogenase (373 aa; locus tag ATO21.06665; accession number LNUM01000025).^{8–10} The genome sequence of *P. acidilactici* strain S1 can provide the insights of genetic information for the alcohol-tolerance of *Pediococcus* spp. at genetic level.

Nucleotide sequence accession numbers

The draft sequence of *P. acidilactici* strain S1 obtained in this Whole Genome Shotgun project has been deposited to the GenBank under the accession no. LNUM00000000. The version described in this paper is the first version, with accession, no. LNUM01000000.

Conflicts of interest

The authors declare no conflicts of interest.

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