



Genome Announcements

Draft genome sequence of alcohol-tolerant bacteria *Pediococcus acidilactici* strain K3

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ABSTRACT

Pediococcus acidilactici strain K3 is an alcohol-tolerant lactic acid bacterium isolated from nuruk, which is a traditional Korean fermentation starter for makgeolli brewing. Draft genome of this strain was approximately 1,991,399 bp (G+C content, 42.1%) with 1525 protein-coding sequences (CDS), of which 44% were assigned to recognized functional genes. This draft genome sequence data of the strain K3 will provide insights into the genetic basis of its alcohol-tolerance.

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Introduction

Lactic acid bacteria (LAB) of the genus *Pediococcus* that have been isolated and characterized to date, have mostly been found as probiotics and used in many fermented foods and beverages.¹ Previous studies have been reported that the makgeolli, a traditional Korean rice wine contains many different types of LAB.² An alcohol-tolerant bacterium, *Pediococcus acidilactici* strain K3 was isolated from nuruk, the traditional

fermentation starter for makgeolli brewing, which can survive in 13% of ethyl alcohol.³ The isolated alcohol-tolerant LAB could be used for makgeolli brewing as a starter or supplementation on either way.⁴ Here we report the draft genome sequence of *P. acidilactici* strain K3.

The genome of strain K3 was sequenced using the Ion Torrent Personal Genome Machine (PGM) sequencer system.⁵ A total of 4,064,182 reads were generated at an average read length of 249 bp. *De novo* assembly of the reads was performed using Mimicking Intelligent Read Assembly (MIRA) 4.0

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and CLC Genomics Workbench version 7.5. The best assembly results comprised 67 contigs, with the N_{50} contig length of 78,870 bp, and the largest contig was 245,802 bp with $385\times$ coverage. The draft genome consists of 1,991,399 bp, which covers almost all of the predicted average genome, with a G+C content of 42.1%. Genome annotation was done using the NCBI Prokaryotic Genomes Annotation Pipeline (PGAP).⁶ The RAST annotation server (<http://rast.nmpdr.org/>) was also used for subsystem classification and functional annotation.⁷ This analysis predicted 1525 protein-coding sequences (CDS), of which 44% were assigned to recognized functional genes. Furthermore, 50 tRNA and 8 rRNA genes were predicted.

The genome also harbored a complete cluster genes coding for alcohol-tolerance. These genes include those encoding for alcohol-tolerant enzymes, such as aldehyde dehydrogenase (477 aa; locus tag AN404.00595; accession number LJBS01000002), malate dehydrogenase (379 aa; locus tag AN404.03730; accession number LJBS01000008, 542 aa; locus tag AN404.05615; accession number LJBS01000016), alcohol dehydrogenase (337 aa; locus tag AN404.03925; accession number LJBS01000009, 167 aa; locus tag AN404.03980; accession number LJBS01000010) and aryl-alcohol dehydrogenase (373 aa; locus tag AN404.05340; accession number LJBS01000014).^{8–10} This draft genome sequence of *P. acidilactici* strain K3 will further help us in understanding the genetic level potential of *Pediococcus* spp. for alcohol-tolerance.

Nucleotide sequence accession numbers

The draft sequence of *P. acidilactici* strain K3 obtained in this Whole Genome Shotgun project has been deposited at GenBank under the accession no. LJBS00000000. The version described in this paper is the first version, with accession, no. LJBS01000000.

Conflicts of interest

The authors declare no conflicts of interest

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