SBM Sociedade Brasileira de Microbiologia

BRAZILIAN JOURNAL OF MICROBIOLOGY

http://www.bjmicrobiol.com.br/

Genome Announcements

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

Gun-Seok Park[a], Sung-Jun Hong[a], Seulki Park[b], Hyewon Jin[b], Sang-Jae Lee[b,c], Jae-Ho Shin[a,*], Han-Seung Lee[b,c,**]

[a] Kyungpook National University, School of Applied Biosciences, Daegu, Republic of Korea
[b] Silla University, College of Medical and Life Sciences, Major in Food Biotechnology, Busan, Republic of Korea
[c] Silla University, The Research Center for Extremophiles and Marine Microbiology, Busan, Republic of Korea

ARTICLE INFO

Article history:
Received 22 October 2015
Accepted 12 November 2015
Available online 26 July 2016

Associate Editor: John Anthony McCulloch

Keywords:
Pediococcus acidilactici
Makgeolli
Alcohol-tolerance
Ion torrent

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.

© 2016 Sociedade Brasileira de Microbiologia. Published by Elsevier Editora Ltda. This is an open access article under the CC BY-NC-ND license (http://creativecommons.org/licenses/by-nc-nd/4.0/).

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

---

* Corresponding author.
** Corresponding author.
E-mails: jhshin@knu.ac.kr (J.-H. Shin), hanslee@silla.ac.kr (H.-S. Lee).

http://dx.doi.org/10.1016/j.bjm.2016.07.021

1517-8382/© 2016 Sociedade Brasileira de Microbiologia. Published by Elsevier Editora Ltda. This is an open access article under the CC BY-NC-ND license (http://creativecommons.org/licenses/by-nc-nd/4.0/).

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× 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

Acknowledgments

This research was supported by the Basic Science Research Program through the National Research Foundation of Korea (NRF), which is funded by the Ministry of Education, Science and Technology (NRF-2014R1A1A1006415).

REFERENCES

1. Khani S, Hosseini MH, Taheri M, Nourani RM, Imani Fooladi AA. Probiotics as an alternative strategy for prevention and treatment of human diseases: a review. *Inflamm Allergy Drug Targets*. 2012;11(2):79–89.
2. Seo M-Y, Lee J-K, Ahn B-H, Cha S-K. The changes of microflora during the fermentation of Takju and Yakju. *Korean J Food Sci Technol*. 2005;37:61–66.
3. Jang D, Park S, Lee H, Pyo S, Lee H. Isolation of the alcohol-tolerant lactic acid bacteria *Pediococcus acidilactici* K3 and S1 and their physiological characterization. *Korean J Microbiolol Biotechnol*. 2013;41:442–448.
4. Jang D, Lee H, Pyo S, Roh SW, Rhee J-K, Lee H-S. Fermentation and quality evaluation of makgeolli, Korean rice wine supplemented with alcohol-tolerant *Pediococcus acidilactici* K3. *Korean J Microbiolol Biotechnol*. 2014;42:367–376.
5. Rothberg JM, Hinz W, Rearick TM, et al. An integrated semiconductor device enabling non-optical genome sequencing. *Nature*. 2011;475:348–352.
6. Angiuoli SV, Gussman A, Klimke W, et al. Toward an online repository of standard operating procedures (SOPs) for (meta) genomic annotation. *OMICS*. 2008;12:137–141.
7. Aziz RK, Bartels D, Best AA, et al. The RAST Server: rapid annotations using subsystems technology. *BMC Genomics*. 2008;9:75.
8. Ram S. Role of alcohol dehydrogenase, malate dehydrogenase and malic enzyme in flooding tolerance in *Brachiaria* species. *J Plant Biochem Biotechnol*. 2000;9:45–47.
9. Eanes WF, Merritt TJ, Flowers JM, Kumagai S, Zhu C-T. Direct evidence that genetic variation in glycerol-3-phosphate and malate dehydrogenase genes (Gpdh and Mdh1) affects adult ethanol tolerance in *Drosophila melanogaster*. *Genetics*. 2009;181:607–614.
10. Brown SD, Guss AM, Karpinets TV, et al. Mutant alcohol dehydrogenase leads to improved ethanol tolerance in *Clostridium thermocellum*. *Proc Natl Acad Sci USA*. 2011;108:13752–13757.