AMERICAN SOCIETY FOR MICROBIOLOGY | genomeAnnouncements™

PROKARYOTES

Complete Genome Sequence of *Lactobacillus reuteri* WHH1689, Isolated from Traditional Chinese Highland Barley Wine

Su Chen,[a] Lin Chen,[a] Lie Chen,[a] Xueliang Ren,[a] Hongjuan Ge,[a] Guokai Kang,[a] Sheng Sun,[a] Zuoguo Chen,[a] Yong Sun,[a] Yanjun Li[a]

[a]Key Laboratory of Food and Biological Engineering of Zhejiang Province, Research and Development Department, Hangzhou Wahaha Technology Co. Ltd., Hangzhou Wahaha Group Co. Ltd., Hangzhou, China

ABSTRACT Here, we report the complete genome sequence of *Lactobacillus reuteri* WHH1689, which was isolated from traditional Chinese highland barley wine in the Tibetan Plateau of China. The genome consists of a circular chromosome (2.04 Mb).

Probiotics are live microorganisms that, when administered in adequate amounts, confer a health benefit on the host (1). Most probiotic bacteria are lactic acid bacteria (LAB). Because of their long history of safe use and potential therapeutic benefits for human health, LAB have received increasing attention (2). Among the LAB, *Lactobacillus* is the most common genus (3). *Lactobacillus reuteri* WHH1689 was isolated from highland barley wine in the Shigatse area of Tibet, China (4).

Genomic DNA was extracted and purified using a DNA extraction kit for bacteria (Promega, USA) according to the manufacturer's instructions. The genome was sequenced at the Majorbio Co., Ltd. (Shanghai, China). PacBio single-molecule real-time (SMRT) whole-genome sequencing was performed using a PacBio RS II sequencer with P6-C4 chemistry. Two SMRT cells were used for sequencing, thereby yielding 44,311 adapter-trimmed reads (subreads) with an average read length of approximately 7,467 bp, which corresponded to approximately 161-fold coverage. After filtering, the reads were assembled with the Hierarchical Genome Assembly Process (HGAP) 2.3.0 (5), resulting in one circular chromosome comprising 2,044,184 bp with a G+C content of 39.3%.

The tRNAs were predicted by tRNAscan-SE 1.3.1 (6), rRNAs were predicted by Barrnap 0.4.2 (https://github.com/tseemann/barrnap/). The coding DNA sequences (CDSs) were predicted by three software programs, Glimmer 3.02 (7), GeneMarkS 4.3 (8), and Prodigal 2.63 (9), and corrected manually. Finally, functional annotation was performed based on homology searches against the Cluster of Orthologous Groups (COG) protein database (10).

A total of 2,242 genes were identified in the genome sequence, including 69 tRNA genes and 18 complete rRNA operons. The COG annotation results revealed that approximately 69.8% of the protein-coding genes (proteins) were assigned to at least one functional category. A total of 327 CDSs were allocated to replication, recombination, and repair (category L), followed by translation, ribosomal structure, and biogenesis (J), with 136 proteins. Further comparison analysis of the genome with different strains in the same genus is now under way.

Accession number(s). This whole-genome sequence and the annotation data have been deposited at GenBank under the accession number CP027805.

ACKNOWLEDGMENT

The present work was supported by the Fund of the Major Science and Technology Projects of Zhejiang Province (2015C02039).

Received 27 April 2018 **Accepted** 29 April 2018 **Published** 7 June 2018

Citation Chen S, Chen L, Chen L, Ren X, Ge H, Kang G, Sun S, Chen Z, Sun Y, Li Y. 2018. Complete genome sequence of *Lactobacillus reuteri* WHH1689, isolated from traditional Chinese highland barley wine. Genome Announc 6:e00425-18. https://doi.org/10.1128/genomeA.00425-18.

Copyright © 2018 Chen et al. This is an open-access article distributed under the terms of the Creative Commons Attribution 4.0 International license.

Address correspondence to Su Chen, chensu@wahaha.com.cn.

REFERENCES

1. Hill C, Guarner F, Reid G, Gibson GR, Merenstein DJ, Pot B, Morelli L, Canani RB, Flint HJ, Salminen S, Calder PC, Sanders ME. 2014. Expert consensus document. The International Scientific Association for Probiotics and Prebiotics consensus statement on the scope and appropriate use of the term probiotic. Nat Rev Gastroenterol Hepatol 11:506–514. https://doi.org/10.1038/nrgastro.2014.66.
2. Saad N, Delattre C, Urdaci M, Schmitter JM, Bressollier P. 2013. An overview of the last advances in probiotic and prebiotic field. J Food Sci Technol 50:1–16. https://doi.org/10.1016/j.lwt.2012.05.014.
3. Argyri AA, Zoumpopoulou G, Karatzas K-AG, Tsakalidou E, Nychas G-JE, Panagou EZ, Tassou CC. 2013. Selection of potential probiotic lactic acid bacteria from fermented olives by *in vitro* tests. Food Microbiol 33:282–291. https://doi.org/10.1016/j.fm.2012.10.005.
4. Chen S, Chen L, Chen L, Ren XY, Ge HJ, Li BL, Ma GH, Ke XQ, Zhu J, Li L, Feng YH, Li YJ. 2018. Potential probiotic characterization of *Lactobacillus reuteri* from Chinese traditional highland barley wine and application for room-temperature-storage drinkable yogurt. J Diary Sci, in press. https://doi.org/10.3168/jds.2017-14139.
5. Chin CS, Alexander DH, Marks P, Klammer AA, Drake J, Heiner C, Clum A, Copeland A, Huddleston J, Eichler EE, Turner SW, Korlach J. 2013. Non-hybrid, finished microbial genome assemblies from long-read SMRT sequencing data. Nat Methods 10:563–569. https://doi.org/10.1038/nmeth.2474.
6. Lowe TM, Eddy SR. 1997. tRNAscan-SE: a program for improved detection of transfer RNA genes in genomic sequence. Nucleic Acids Res 25:955–964.
7. Delcher AL, Bratke KA, Powers EC, Salzberg SL. 2007. Identifying bacterial genes and endosymbiont DNA with Glimmer. Bioinformatics 23:673–679. https://doi.org/10.1093/bioinformatics/btm009.
8. Besemer J, Lomsadze A, Borodovsky M. 2001. GeneMarkS: a self-training method for prediction of gene starts in microbial genomes. Implications for finding sequence motifs in regulatory regions. Nucleic Acids Res 29:2607–2618. https://doi.org/10.1093/nar/29.12.2607.
9. Hyatt D, Chen G-L, LoCascio PF, Land ML, Larimer FW, Hauser LJ. 2010. Prodigal: prokaryotic gene recognition and translation initiation site identification. BMC Bioinformatics 11:119. https://doi.org/10.1186/1471-2105-11-119.
10. Tatusov RL, Fedorova ND, Jackson JD, Jacobs AR, Kiryutin B, Koonin EV, Krylov DM, Mazumder R, Mekhedov SL, Nikolskaya AN, Rao BS, Smirnov S, Sverdlov AV, Vasudevan S, Wolf YI, Yin JJ, Natale DA. 2003. The COG database: an updated version includes eukaryotes. BMC Bioinformatics 4:41. https://doi.org/10.1186/1471-2105-4-41.