JOURNAL OF BACTERIOLOGY, Aug. 2009, p. 5020–5021 Vol. 191, No. 15
0021-9193/09/$08.00+0 doi:10.1128/JB.00587-09

GENOME ANNOUNCEMENT

Complete Genome Sequence of *Lactobacillus plantarum* JDM1[▽]

Zhuo-Yang Zhang,[1] Chang Liu,[1] Yong-Zhang Zhu,[1] Yi Zhong,[1] Yong-Qiang Zhu,[2] Hua-Jun Zheng,[2] Guo-Ping Zhao,[2] Sheng-Yue Wang,[2] and Xiao-Kui Guo[1]*

Department of Medical Microbiology and Parasitology, Institutes of Medical Sciences, Shanghai Jiao Tong University School of Medicine, Shanghai 200025, China,[1] and Shanghai-MOST Key Laboratory of Health and Disease Genomics, Chinese National Human Genome Center at Shanghai, Shanghai, China[2]

Received 6 May 2009/Accepted 12 May 2009

Lactobacillus plantarum **is a lactic acid bacterium (LAB) species commonly used as a probiotic. We have sequenced the genome of *Lactobacillus plantarum* JDM1, which is a Chinese commercial LAB with several probiotic functions, using a GS 20 system. We recommend that each commercial probiotic strain should undergo complete genome sequencing to ensure safety and stability.**

Lactic acid bacteria (LAB) play a prominent role in the world food supply, performing the main bioconversions in fermented food, and are also used as probiotic supplements in dairy products and other foods. *Lactobacillus plantarum* is a LAB species commonly used as a probiotic. We have sequenced the genome of *Lactobacillus plantarum* JDM1, which is a widely used Chinese commercial LAB with several probiotic functions, using a GS 20 system (454 Life Science Corporation) (11). Two hundred thirty-six thousand, five hundred sixty-three high-quality reads were assembled with the 454 assembly tool, which had an average depth of 18.6-fold coverage of the genome and yielded 367 contigs. Among these, 225 large contigs represented 99.17% of the draft sequence. In the finishing process, the order of the selected large contigs was determined by BLAST analysis with the originally published genome sequence of strain WCFS1 (GenBank accession number AL935263) (8). Physical gaps were filled through sequencing of PCR products that spanned these regions using ABI 3730 xl DNA sequencers. Sequence assembly was accomplished by using the Phred/Phrap/Consed software package (4, 7). To ensure final accuracy, the errors in homopolymer sites that arose from the pyrosequencing method were solved via comparison with the corresponding sites on WCFS1 and then resequencing of the ambiguous bases using the ABI 3730 xl DNA sequencer.

The complete genome of *Lactobacillus plantarum* JDM1 contains a single, circular chromosome of 3,197,759 bp and two plasmids (pLP2000 [2,062 bp] and pLP9000 [9,254 bp]). The two plasmids have been sequenced and published, with GenBank accession numbers AY096004 and AY096005 (3). The overall GC content of the chromosome is 44.66%, whereas the plasmids have a GC content slightly lower than that of the chromosome. The entire genome of JDM1 contains 2,948 protein-coding genes, 62 tRNA-encoding genes, and 16 rRNA-encoding genes. Several repeated sequences, designated IS*P2*, were found in the chromosome which were almost the same as those in WCSF1, identified as a class of transposase-encoding regions representing mobile genetic elements. The other repeated sequence, IS*P1* of WCSF1, was absent in JDM1.

The entire genomic sequence of *L. plantarum* JDM1 was a little shorter than that of *L. plantarum* WCSF1 (3.3 Mb). The two genomes were highly similar (>90% by BLASTN analysis) with respect to genome structure and gene order. Intraspecies diversity may be required for successful adaptation in a complex ecological habitat (2). *L. plantarum* JDM1 has been grown as a probiotic in rich nutritional medium for so long that the genome may have gradually contracted. As supporting evidence, many sugar transport and metabolism genes in WCFS1 were absent in JDM1.

The prophage sequences and locations of JDM1 and WCFS1 are highly variable. *L. plantarum* JDM1 contains three prophage elements in its genome. R-Pg1, representing a short prophage remnant, is about 14 kb in size, which is similar to R-Lp3 in WCFS1. Pg2 and Pg3 are two ~39-kb-long prophages that are closely related to *Listeria* phage B025 (accession no. DQ003639) and the phage *Pediococcus pentosaceus* ATCC 25745 (accession no. CP000422), respectively.

The genomes of LAB evolve actively to adapt to nutritionally rich environments. Even for two strains of the same species, differences obviously exist. The degradation of the genome appears to be an ongoing process not only in all species of *Lactobacillus* (10) but also in different strains of the same species(2).

With the development of better living conditions, the biosafety of food and medicine has received more attention. *Lactobacillus* bacteria have been supposed to have a "generally accepted as safe" status, but they still have been associated with negative reports (1, 6, 9). More about the functional mechanisms of JDM1 and potential side effects would be explored by complete genome sequencing and data mining. Furthermore, comparative genomics analysis could be carried out with Chinese and European strains. We believe the complete

* Corresponding author. Mailing address: Department of Medical Microbiology and Parasitology, Shanghai Jiao Tong University School of Medicine, Shanghai 200025, China. Phone and fax: 86-21-64453285. E-mail: microbiology@sjtu.edu.cn.

▽ Published ahead of print on 22 May 2009.

genome of each probiotic strain should be sequenced to ensure safety and stability. At the end of the day, we will get what we pay for in terms of microbial genome sequencing projects (5).

Nucleotide sequence accession number. Genome information for the chromosome of *L. plantarum* JDM1 was deposited in GenBank under the accession number CP001617.

This research was supported in part by the National Natural Science Foundation of China (no. 30830002, 30670102, and 30770820), the National Key Program for Infectious Diseases of China (no. 2008ZX10004002, 200810002X4009, and 2009ZX10004712), and the National High Technology Research and Development Program of China.

REFERENCES

1. **Aguirre, M., and M. D. Collins.** 1993. Lactic acid bacteria and human clinical infection. J. Appl. Bacteriol. **75:**95–107.
2. **Chaillou, S., M. Daty, F. Baraige, A. M. Dudez, P. Anglade, R. Jones, C. A. Alpert, M. C. Champomier-Verges, and M. Zagorec.** 2009. Intraspecies genomic diversity and natural population structure of the meat-borne lactic acid bacterium *Lactobacillus sakei*. Appl. Environ. Microbiol. **75:**970–980.
3. **Daming, R., W. Yinyu, W. Zilai, C. Jun, L. Hekui, and Z. Jingye.** 2003. Complete DNA sequence and analysis of two cryptic plasmids isolated from Lactobacillus plantarum. Plasmid **50:**70–73.
4. **Ewing, B., L. Hillier, M. C. Wendl, and P. Green.** 1998. Base-calling of automated sequencer traces using phred. I. Accuracy assessment. Genome Res. **8:**175–185.
5. **Fraser, C. M., J. A. Eisen, K. E. Nelson, I. T. Paulsen, and S. L. Salzberg.** 2002. The value of complete microbial genome sequencing (you get what you pay for). J. Bacteriol. **184:**6403–6405.
6. **Gasser, F.** 1994. Safety of lactic acid bacteria and their occurrence in human clinical infections. Bull. Inst. Pasteur **92:**45–67.
7. **Gordon, D., C. Abajian, and P. Green.** 1998. Consed: a graphical tool for sequence finishing. Genome Res. **8:**195–202.
8. **Kleerebezem, M., J. Boekhorst, R. van Kranenburg, D. Molenaar, O. P. Kuipers, R. Leer, R. Tarchini, S. A. Peters, H. M. Sandbrink, M. W. Fiers, W. Stiekema, R. M. Lankhorst, P. A. Bron, S. M. Hoffer, M. N. Groot, R. Kerkhoven, M. de Vries, B. Ursing, W. M. de Vos, and R. J. Siezen.** 2003. Complete genome sequence of Lactobacillus plantarum WCFS1. Proc. Natl. Acad. Sci. USA **100:**1990–1995.
9. **Ku, W. H., D. C. Y. Lau, and K. F. Huen.** 2006. Probiotics provoked D-lactic acidosis in short bowel syndrome: case report and literature review. Hong Kong J. Paediatr. **11:**246–254.
10. **Makarova, K., A. Slesarev, Y. Wolf, A. Sorokin, B. Mirkin, E. Koonin, A. Pavlov, N. Pavlova, V. Karamychev, N. Polouchine, V. Shakhova, I. Grigoriev, Y. Lou, D. Rohksar, S. Lucas, K. Huang, D. M. Goodstein, T. Hawkins, V. Plengvidhya, D. Welker, J. Hughes, Y. Goh, A. Benson, K. Baldwin, J. H. Lee, I. Diaz-Muniz, B. Dosti, V. Smeianov, W. Wechter, R. Barabote, G. Lorca, E. Altermann, R. Barrangou, B. Ganesan, Y. Xie, H. Rawsthorne, D. Tamir, C. Parker, F. Breidt, J. Broadbent, R. Hutkins, D. O'Sullivan, J. Steele, G. Unlu, M. Saier, T. Klaenhammer, P. Richardson, S. Kozyavkin, B. Weimer, and D. Mills.** 2006. Comparative genomics of the lactic acid bacteria. Proc. Natl. Acad. Sci. USA **103:**15611–15616.
11. **Margulies, M., M. Egholm, W. E. Altman, S. Attiya, J. S. Bader, L. A. Bemben, J. Berka, M. S. Braverman, Y. J. Chen, Z. Chen, S. B. Dewell, L. Du, J. M. Fierro, X. V. Gomes, B. C. Godwin, W. He, S. Helgesen, C. H. Ho, G. P. Irzyk, S. C. Jando, M. L. Alenquer, T. P. Jarvie, K. B. Jirage, J. B. Kim, J. R. Knight, J. R. Lanza, J. H. Leamon, S. M. Lefkowitz, M. Lei, J. Li, K. L. Lohman, H. Lu, V. B. Makhijani, K. E. McDade, M. P. McKenna, E. W. Myers, E. Nickerson, J. R. Nobile, R. Plant, B. P. Puc, M. T. Ronan, G. T. Roth, G. J. Sarkis, J. F. Simons, J. W. Simpson, M. Srinivasan, K. R. Tartaro, A. Tomasz, K. A. Vogt, G. A. Volkmer, S. H. Wang, Y. Wang, M. P. Weiner, P. Yu, R. F. Begley, and J. M. Rothberg.** 2005. Genome sequencing in microfabricated high-density picolitre reactors. Nature **437:**376–380.