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# Draft Genome Sequence of *Lactobacillus fermentum* NB-22

**A. V. Chaplin, A. N. Shkoporov, B. A. Efimov, A. P. Pikina, O. Y. Borisova, I. A. Gladko, E. A. Postnikova, A. E. Lordkipanidze, L. I. Kafarskaia**

Pirogov Russian National Research Medical University, Moscow, Russian Federation

**We announce here a draft genome sequence of *Lactobacillus fermentum* NB-22, a strain isolated from human vaginal microbiota. The assembled sequence consists of 190 contigs, joined into 137 scaffolds, and the total size is 2.01 Mb.**

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Address correspondence to A. V. Chaplin, okolomedik@gmail.com.

*Lactobacillus fermentum* is a heterofermentative lactic acid bacterium (1) belonging to the phylum *Firmicutes*. It can be isolated from various sources, including mucosal microbiota of human and animals and fermented food. These bacteria are considered to possess probiotic properties, such as the absence of observed adverse effects related to their consumption (2), production of antimicrobial compounds (3), and immunomodulatory potential (4).

Multiple studies have explored the possibility of normalizing the vaginal microbiota using lactic acid bacteria. *L. fermentum* L23 was shown to produce both curative and protective effects in a murine model of vaginal tract infection caused by *Escherichia coli* (5). The combination of *L. fermentum* LF10 and *Lactobacillus acidophilus* LA02 was found to prevent recurrent vulvovaginal candidiasis in a small-scale clinical study without a control group (6). A large number of studies provided inconclusive but promising results of vaginal or oral administration of different combinations of *Lactobacillus* strains for the treatment of bacterial vaginosis and the prevention of its recurrence (7).

The molecular mechanisms of the putative probiotic activities of lactobacilli are largely unknown, and one of the ways to elucidate precise mechanisms and a diversity of host-microbe interactions is the collection and analysis of genomic data (8). This paper describes the draft genome sequence of *L. fermentum* NB-22, a strain that was isolated from human vaginal microbiota and was found to be perspective for usage as a probiotic due to its high adhesive and antagonistic properties.

Total culture DNA was sequenced using Illumina MiSeq. The reads were assembled *de novo* using CLC Genomics Workbench version 6.0.2. An assembly contained 190 contigs joined into 137 scaffolds using paired-end read data; the mean coverage was 114×. The total length of the sequence obtained was 2.01 Mb, showing a relatively small genome length in comparison with that of most other sequenced strains of *L. fermentum* (9–12); its genomic sequence was found to share 98.17% to 99.18% average nucleotide identity (ANI) with the other strains (13). The G+C content of the genome was 51.8%. An annotation made using PGAP (14) predicted 2,028 genes, including 1,938 protein-coding open reading frames. One of the small contigs (GenBank accession no. AYHA01000123) represented a unique 9-kb region without close homologs in complete and draft bacterial genomes; the genes within this locus encode the degradation of nitrogen-containing compounds, and one of the putative substrates might be allantoin.

**Nucleotide sequence accession numbers.** The *L. fermentum* NB-22 whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. AYHA00000000. The version described in this paper is version AYHA01000000.

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## REFERENCES

1. **Dellaglio F, Torriani S, Felis GE.** 2004. Reclassification of *Lactobacillus cellobiosus* Rogosa et al. 1953 as a later synonym of *Lactobacillus fermentum* Beijerinck 1901. Int J Syst Evol Microbiol **54:**809–812. http://dx.doi.org/10.1099/ijs.0.02947-0.
2. **López-Huertas E.** 2014. Safety and efficacy of human breast milk *Lactobacillus fermentum* CECT 5716. A mini-review of studies with infant formulae. Benef Microbes **6:**219–224. http://dx.doi.org/10.3920/BM2014.0091.
3. **Olivares M, Díaz-Ropero MP, Martín R, Rodríguez JM, Xaus J.** 2006. Antimicrobial potential of four *Lactobacillus* strains isolated from breast milk. J Appl Microbiol **101:**72–79. http://dx.doi.org/10.1111/j.1365-2672.2006.02981.x.
4. **Díaz-Ropero MP, Martín R, Sierra S, Lara-Villoslada F, Rodríguez JM, Xaus J, Olivares M.** 2007. Two *Lactobacillus* strains, isolated from breast milk, differently modulate the immune response. J Appl Microbiol **102:**337–343. http://dx.doi.org/10.1111/j.1365-2672.2006.03102.x.
5. **Pascual L, Ruiz F, Giordano W, Barberis IL.** 2010. Vaginal colonization and activity of the probiotic bacterium *Lactobacillus fermentum* L23 in a murine model of vaginal tract infection. J Med Microbiol **59:**360–364. http://dx.doi.org/10.1099/jmm.0.012583-0.
6. **Murina F, Graziottin A, Vicariotto F, De Seta F.** 2014. Can *Lactobacillus fermentum* LF10 and *Lactobacillus acidophilus* LA02 in a slow-release vaginal product be useful for prevention of recurrent vulvovaginal candidiasis? A clinical study. J Clin Gastroenterol **48**(Suppl 1):S102–S105. http://dx.doi.org/10.1097/MCG.0000000000000225.
7. **Homayouni A, Bastani P, Ziyadi S, Mohammad-Alizadeh-Charandabi S, Ghalibaf M, Mortazavian AM, Mehrabany EV.** 2014. Effects of probiotics on the recurrence of bacterial vaginosis: a review. J Low Genit Tract Dis **18:**79–86. http://dx.doi.org/10.1097/LGT.0b013e31829156ec.
8. **Ventura M, Turroni F, van Sinderen D.** 2012. Probiogenomics as a tool to obtain genetic insights into adaptation of probiotic bacteria to the human gut. Bioeng Bugs **3:**73–79. http://dx.doi.org/10.4161/bbug.18540.
9. **Karlyshev AV, Raju K, Abramov VM.** 2013. Draft genome sequence of

*Lactobacillus fermentum* strain 3872. Genome Announc **1**(6):-01006–13. http://dx.doi.org/10.1128/genomeA.01006-13.

10. **Jayashree S, Pooja S, Pushpanathan M, Vishnu U, Sankarasubramanian J, Rajendhran J, Gunasekaran P**. 2013. Genome sequence of *Lactobacillus fermentum* strain MTCC 8711, a probiotic bacterium isolated from yogurt. Genome Announc **1**(5):-13. http://dx.doi.org/10.1128/genomeA.00770-13.
11. **Sun Z, Zhang W, Bilige M, Zhang H**. 2015. Complete genome sequence of the probiotic *Lactobacillus fermentum* F-6 isolated from raw milk. J Biotechnol **194:**110–111. http://dx.doi.org/10.1016/j.jbiotec.2014.12.010.
12. **Jiménez E, Langa S, Martín V, Arroyo R, Martín R, Fernández L, Rodríguez JM**. 2010. Complete genome sequence of *Lactobacillus fermentum* CECT 5716, a probiotic strain isolated from human milk. J Bacteriol **192:**4800. http://dx.doi.org/10.1128/JB.00702-10.
13. **Richter M, Rosselló-Móra R**. 2009. Shifting the genomic gold standard for the prokaryotic species definition. Proc Natl Acad Sci U S A **106:** 19126–19131. http://dx.doi.org/10.1073/pnas.0906412106.
14. **Angiuoli SV, Gussman A, Klimke W, Cochrane G, Field D, Garrity G, Kodira CD, Kyrpides N, Madupu R, Markowitz V, Tatusova T, Thomson N, White O**. 2008. Toward an online repository of standard operating procedures (SOPs) for (meta)genomic annotation. Omics **12:**137–141. http://dx.doi.org/10.1089/omi.2008.0017.