

Genome Sequence of *Lactobacillus plantarum* Strain UCMA 3037

Saima Naz,^a Raouf Tareb,^a Marion Bernardeau,^a Melissa Vaisse,^a Celine Lucchetti-Miganeh,^b Mathias Rechenmann,^b Jean-Paul Vernoux^a

Research Unit EA 4651, Aliments Bioprocédés Toxicologie Environnements (ABTE), Université de Caen Basse-Normandie, Esplanade de la paix, Caen, France^a; Genostar, Montbonnot, France^b

Nucleic acid of the strain *Lactobacillus plantarum* UCMA 3037, isolated from raw milk camembert cheese in our laboratory, was sequenced. We present its draft genome sequence with the aim of studying its functional properties and relationship to the cheese ecosystem.

Received 3 April 2013 Accepted 5 April 2013 Published 23 May 2013

Citation Naz S, Tareb R, Bernardeau M, Vaisse M, Lucchetti-Miganeh C, Rechenmann M, Vernoux J-P. 2013. Genome sequence of *Lactobacillus plantarum* strain UCMA 3037. Genome Announc. 1(3):e00251-13. doi:10.1128/genomeA.00251-13.

Copyright © 2013 Naz et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 3.0 Unported license](https://creativecommons.org/licenses/by/3.0/).

Address correspondence to Jean-Paul Vernoux, jean-paul.vernoux@unicaen.fr.

Lactobacillus plantarum is a lactic acid bacterium commonly found in numerous ecological niches such as vegetables, meat, fish, and dairy products (1). In dairy products, it is usually present in milk and cheeses as an adjunct starter or as a nonstarter lactic acid bacterium (NSLAB). *Lactobacillus plantarum* strain UCMA 3037, isolated in our laboratory from raw milk camembert cheese, is a probiotic candidate strain and is capable of surviving in various cheese matrices (2). For exploring its potentially functional and probiotic properties in detail, we sequenced its genome using high-throughput Illumina/paired-end technology.

The uncompleted draft genome sequence of *L. plantarum* UCMA 3037 was determined by paired-end sequencing using the Illumina GAIIX platform (6,570,144 reads) (Baseclear, Netherlands) with a coverage of >100×. The paired-end reads were assembled *de novo* using the CLC Genomics workbench 5.0 (CLC Bio). The resulting assembly consists of 92 contigs. The draft genome, of about 3.11 Mb, has a G+C content of 44.5%. These data are comparable to those of already reported sequenced genomes of *L. plantarum* strains (1).

At the time of genome submission to GenBank, genome annotation was requested to be performed by NCBI's Prokaryotic Genomes Annotation Pipeline (PGAAP), which predicted 2,932 protein coding sequences (CDSs).

An internal annotation of the assembled contig sequences was performed with the MetabolicPathwayBuilder system (Genostar). MetabolicPathwayBuilder, together with the reference MicroB database, is integrated bioinformatics interactive software dedicated to microbial genome analysis and comparison. MicroB integrates and updates data from several databases, i.e., NCBI Reference Sequence, UniProtKB, ENZYME, Gene Ontology, and KEGG. The GenoAnnot module was used to annotate our *L. plantarum* UCMA 3037 genome. A variant of the PRIAM algorithm (3) was used to predict the enzymatic activities of the proteins.

Within the reconstructed metabolic network, several pathways are representative of carbohydrate metabolism, protein and amino acid metabolism, nucleic acid metabolism, and fermentation metabolism, which correspond to 115 KEGG metabolic pathways. The products of some genes are found to confer an advan-

tage for adaptation to a cheese matrix; for example, malate lactate dehydrogenase (4) and histidine kinase for resistance to an acidic environment (5), two types of glycine/betaine transporter for osmoregulation (6), lipase/esterases for the production of cheese flavor compounds (7), and the serine protease HtrA domain (putative caseinase) (8).

L. plantarum UCMA 3037 has been predicted to carry two plasmids: plasmid NC11101, which shares a 64% sequence similarity to the *L. plantarum* plasmid pLTK13 (9), and plasmid NC06278, which shares a 96% sequence similarity to *L. plantarum* plasmid p256 (10). *L. plantarum* UCMA 3037 carries prophage elements similar in sequence to Lp1, Lp2, Lp3, and Lp4 prophages present in reference strains *L. plantarum* WCFS1 and JDM1 (11, 12).

A more detailed analysis is in progress in which we are evaluating the stability, safety, and functional and metabolic aspects of this strain and its relationship to the cheese ecosystem.

Nucleotide sequence accession numbers. This whole-genome-shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number [APH000000000](https://www.ncbi.nlm.nih.gov/nuccore/APH000000000). The version described in this paper is the first version, [APH000000000.1](https://www.ncbi.nlm.nih.gov/nuccore/APH000000000.1).

ACKNOWLEDGMENTS

We thank BaseClear BV, Leiden, Netherlands, for their work in sequencing. No external funding was received for this study.

REFERENCES

1. Siezen RJ, Van Hylckama Vlieg JE. 2011. Genomic diversity and versatility of *Lactobacillus plantarum*, a natural metabolic engineer. Microb. Cell Fact. 10(Suppl 1):S3.
2. Coeuret V, Gueguen M, Vernoux JP. 2004. In vitro screening of potential probiotic activities of selected lactobacilli isolated from unpasteurized milk products for incorporation into soft cheese. J. Dairy Res. 71:451–460.
3. Claudel-Renard C, Chevalet C, Faraut T, Kahn D. 2003. Enzyme-specific profiles for genome annotation: PRIAM. Nucleic Acids Res. 31:6633–6639.
4. Monnet V, Atlan D, Béal C, Champomier-Vergès MC, Chapot-Chartier MP, Chouayekh H, Coccagn-Bousquet M, Deghorain M, Gaudu P, Gilbert C, Guéden E, Guillaouard I, Goffin P, Guzzo J, Hols P, Juillard V, Ladero V, Lindley N, Lortal S, Loubière P, Maguin E, Monnet C, Rul F, Tourdot-Maréchal P, Yvon M. 2008. Métabolisme et ingénierie mé-

- tabolique, p 313–319. In *Bactéries lactiques: de la génétique aux ferments*. Editions TEC & DOC. Lavoisier, France.
5. Azcarate-Peril MA, McAuliffe O, Altermann E, Lick S, Russell WM, Klaenhammer TR. 2005. Microarray analysis of a two-component regulatory system involved in acid resistance and proteolytic activity in *Lactobacillus acidophilus*. *Appl. Environ. Microbiol.* 71:5794–5804.
 6. Romeo Y, Bouvier J, Gutierrez C. 2001. La réponse au stress osmotique des bactéries lactiques *Lactococcus lactis* et *Lactobacillus plantarum* (mini-revue). *Lait* 81:49–55.
 7. Holland R, Liu SQ, Crow VL, Delabre M-L, Lubbers M, Bennett M, Norris G. 2005. Esterases of lactic acid bacteria and cheese flavour: milk fat hydrolysis, alcoholysis and esterification. *Int. Dairy J.* 15:711–718.
 8. Kok J. 1990. Genetics of the proteolytic system of lactic acid bacteria. *FEMS Microbiol. Rev.* 7:15–41.
 9. Kim JH, Sunako M, Ono H, Murooka Y, Fukusaki E, Yamashita M. 2008. Characterization of gene encoding amylopullulanase from plant-originated lactic acid bacterium, *Lactobacillus plantarum* L137. *J. Biosci. Bioeng.* 106:449–459.
 10. Sørvig E, Skaugen M, Naterstad K, Eijsink VGH, Axelsson L. 2005. Plasmid p256 from *Lactobacillus plantarum* represents a new type of replicon in lactic acid bacteria, and contains a toxin-antitoxin-like plasmid maintenance system. *Microbiology* 151:421–431.
 11. Ventura M, Canchaya C, Kleerebezem M, de Vos WM, Siezen RJ, Brüssow H. 2003. The prophage sequences of *Lactobacillus plantarum* strain WCFS1. *Virology* 316:245–255.
 12. Zhang ZY, Liu C, Zhu YZ, Zhong Y, Zhu YQ, Zheng HJ, Zhao GP, Wang SY, Guo XK. 2009. Complete genome sequence of *Lactobacillus plantarum* JDM1. *J. Bacteriol.* 191:5020–5021.