

## PDF hosted at the Radboud Repository of the Radboud University Nijmegen

The following full text is a publisher's version.

For additional information about this publication click this link.

<http://hdl.handle.net/2066/155072>

Please be advised that this information was generated on 2020-09-08 and may be subject to change.

# Draft Genome Sequence of *Lactobacillus plantarum* Lp90 Isolated from Wine

Antonella Lamontanara,<sup>a</sup> Graziano Caggianiello,<sup>b</sup> Luigi Orrù,<sup>a</sup> Vittorio Capozzi,<sup>b</sup> Vania Michelotti,<sup>a</sup> Jumamurat R. Bayjanov,<sup>c</sup> Bernadet Renckens,<sup>c</sup> Sacha A. F. T. van Hijum,<sup>c,d</sup> Luigi Cattivelli,<sup>a</sup> Giuseppe Spano<sup>b</sup>

Consiglio Per la Ricerca e Sperimentazione in Agricoltura (CRA) Genomics Research Centre, Fiorenzuola d'Arda, Italy<sup>a</sup>; Department of Agriculture, Food and Environment Sciences, University of Foggia, Foggia, Italy<sup>b</sup>; Center for Molecular and Biomolecular Informatics, Radboud Institute for Molecular Life Sciences, Radboudumc, Nijmegen, The Netherlands<sup>c</sup>; NIZO food research, Ede, The Netherlands<sup>d</sup>

Here, we describe the draft genome sequence and annotation of *Lactobacillus plantarum* strain Lp90, the first sequenced genome of a *L. plantarum* strain isolated from wine. This strain has a noticeable ropy phenotype and showed potential probiotic properties. The genome consists of 3,324,076 bp (33 contigs) and contains 3,155 protein coding genes, 34 pseudogenes, and 84 RNA genes.

Received 27 January 2015 Accepted 2 February 2015 Published 12 March 2015

**Citation** Lamontanara A, Caggianiello G, Orrù L, Capozzi V, Michelotti V, Bayjanov JR, Renckens B, van Hijum SAFT, Cattivelli L, Spano G. 2015. Draft genome sequence of *Lactobacillus plantarum* Lp90 isolated from wine. *Genome Announc* 3(2):e00097-15. doi:10.1128/genomeA.00097-15.

**Copyright** © 2015 Lamontanara 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 Giuseppe Spano, giuseppe.spano@unifg.it.

*Lactobacillus plantarum* is a bacterial species found in many different ecological niches such as vegetables, meat, fish, and dairy products as well as in the gastrointestinal tract (1). *L. plantarum* is one of the dominant bacteria in fermented foods such as sauerkraut, pickles, olives, wine, sourdough, and kimchi (1). Some strains are claimed to provide a health benefit and are marketed as probiotics (2). Here, we report the genome sequence of *L. plantarum* strain Lp90, a strain isolated from “Nero di Troia,” a typical Apulian (South of Italy) wine and in particular, from the same *terroir* of six *Oenococcus oeni* strains whose genomes have been recently sequenced (3, 4). This strain is characterized by a distinctive ropy phenotype, which was ascribed to its capacity to overproduce exopolysaccharides (EPS) (5), and by potential probiotic properties (unpublished results). This strain was already characterized in a previous study on phenotypic and genomic diversity of *L. plantarum* strains isolated from various environmental niches (6) and in three studies dedicated to Lp90 genes coding for small heat shock proteins (7–9). It is the first *L. plantarum* genome sequenced coming from a strain of wine origin. Two micrograms of genomic DNA was subjected to library preparation using the TruSeq DNA sample prep kit FC-121-1001 according to the manufacturer's instructions. Whole-genome sequencing of Lp90 was performed using the Illumina GAIIX platform.

Prior to assembly, raw reads were filtered using the PRINSEQ v0.20.3 software (10). After filtering, a total of 16,574,199 paired-end reads ranging from 75 to 115 bp in length were obtained. The genome sequence was *de novo* assembled using the Ray v2.2.0 assembly program (11) with default parameters and using a Kmer size of 71. The assembly resulted in 33 contigs with an  $N_{50}$  length of 207,479 bp. The size of the shortest contig was 354 bp, while the length of the longest contig was 489,345 bp. The genome is 3,324,076 bp long with a GC content of 44.32%. Genome annotation was performed using the Rapid Annotation using Subsystem Technology (RAST) server (12). Functional annotations were re-

finied by aligning the protein sequences to the Cluster of Orthologous Groups (COG) database (13) using BLASTp and by using the functionality of InterProScan v5.0 in Blast2GO (14) searching for matches against the PRINTS (v42.0), Pfam (v27.0), and TIGRFAMs (v13.0) databases. The TMHMM (v2.0) and Phobius (v1.01) prediction search tools were used, respectively, to predict transmembrane domains and the presence of signal peptides. Of the 3,273 predicted genes, 3,155 were protein-coding genes, 34 were identified to be pseudogenes, while 84 were RNA-coding genes (70 tRNAs and 14 rRNAs).

**Nucleotide sequence accession number.** The whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number [JIBX000000000](https://www.ncbi.nlm.nih.gov/nuccore/JIBX000000000).

## ACKNOWLEDGMENTS

This research was partially supported by a grant from the project PON02\_00186\_3417512, “S.I. Mi.S.A.,” and by the Apulian Region in the framework of the “OenoMicroManagement” project (PIF—Progetti Integrati di Filiera no. 94750304571).

## 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. [http://dx.doi.org/10.1186/1475-2859-10-S1-S3](https://doi.org/10.1186/1475-2859-10-S1-S3).
2. De Vries MC, Vaughan EE, Kleerebezem M, de Vos WM. 2006. *Lactobacillus plantarum*—survival, functional and potential probiotic properties in the human intestinal tract. *Int Dairy J* 16:1018–1028. [http://dx.doi.org/10.1016/j.idairyj.2005.09.003](https://doi.org/10.1016/j.idairyj.2005.09.003).
3. Lamontanara A, Orrù L, Cattivelli L, Russo P, Spano G, Capozzi V. 2014. Genome sequence of *Oenococcus oeni* OM27, the first fully assembled genome of a strain isolated from an Italian wine. *Genome Announc* 2(4):e00658-14. [http://dx.doi.org/10.1128/genomeA.00658-14](https://doi.org/10.1128/genomeA.00658-14).
4. Capozzi V, Russo P, Lamontanara A, Orrù L, Cattivelli L, Spano G. 2014. Genome sequences of five *Oenococcus oeni* strains isolated from Nero Di Troia wine from the same *terroir* in Apulia, Southern Italy. *Genome Announc* 2(5):e01077-14. [http://dx.doi.org/10.1128/genomeA.01077-14](https://doi.org/10.1128/genomeA.01077-14).

5. Caggianiello G, Puertas A, Capozzi V, Russo P, Peña N, Spano G, Dueñas MT, Lopez P, Fiocco D. 2013. Ropy phenotype of *Lactobacillus plantarum* confers higher tolerances to acidic and bile stress. Proceedings of the Second International Conference on Microbial Diversity, Turin, Italy.
6. Siezen RJ, Tzeneva VA, Castioni A, Wels M, Phan HT, Rademaker JL, Starrenburg MJ, Kleerebezem M, Molenaar D, van Hylckama Vlieg JE. 2010. Phenotypic and genomic diversity of *Lactobacillus plantarum* strains isolated from various environmental niches. *Environ Microbiol* 12: 758–773. <http://dx.doi.org/10.1111/j.1462-2920.2009.02119.x>.
7. Spano G, Capozzi V, Vernile A, Massa S. 2004. Cloning, molecular characterization and expression analysis of two small heat shock genes isolated from wine *Lactobacillus plantarum*. *J Appl Microbiol* 97:774–782. <http://dx.doi.org/10.1111/j.1365-2672.2004.02359.x>.
8. Spano G, Beneduce L, Perrotta C, Massa S. 2005. Cloning and characterization of the *hsp 18.55* gene, a new member of the small heat shock gene family isolated from wine *Lactobacillus plantarum*. *Res Microbiol* 156:219–224. <http://dx.doi.org/10.1016/j.resmic.2004.09.014>.
9. Fiocco DF, Capozzi VC, Pepe DP, Crisetti EC, Spano GS. 2007. Sulphite stress induce small heat shock genes in wine *Lactobacillus plantarum*. *Res J Microbiol* 2:838–844. <http://dx.doi.org/10.3923/jm.2007.838.844>.
10. Schmieder R, Edwards R. 2011. Quality control and preprocessing of metagenomic datasets. *Bioinformatics* 27:863–864. <http://dx.doi.org/10.1093/bioinformatics/btr026>.
11. Boisvert S, Laviolette F, Corbeil J. 2010. Ray: simultaneous assembly of reads from a mix of high-throughput sequencing technologies. *J Comput Biol* 11:1519–1533. <http://dx.doi.org/10.1089/cmb.2009.0238>.
12. Aziz RK, Bartels D, Best AA, DeJongh M, Disz T, Edwards RA, Formsma K, Gerdes S, Glass EM, Kubal M, Meyer F, Olsen GJ, Olson R, Osterman AL, Overbeek RA, McNeil LK, Paarmann D, Paczian T, Parrello B, Pusch GD, Reich C, Stevens R, Vassieva O, Vonstein V, Wilke A, Zagnitko O. 2008. The RAST Server: Rapid Annotations using Subsystems Technology. *BMC Genomics* 9:75. <http://dx.doi.org/10.1186/1471-2164-9-75>.
13. 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. <http://dx.doi.org/10.1186/1471-2105-4-41>.
14. Conesa A, Gotz S, Garcia-Gomez LM, Terol J, Talon M, Robles M. 2005. Blast2GO: a universal tool for annotation, visualization and analysis in functional genomics research. *Bioinformatics* 21:3674–3676. <http://dx.doi.org/10.1093/bioinformatics/bti610>.