

Genome Sequence of *Lactobacillus pentosus* IG1, a Strain Isolated from Spanish-Style Green Olive Fermentations

Antonio Maldonado-Barragán,* Belén Caballero-Guerrero,
Helena Lucena-Padrós, and José Luis Ruiz-Barba

Departamento de Biotecnología de Alimentos, Instituto de la Grasa, Consejo Superior de Investigaciones Científicas (CSIC),
Avda. Padre García Tejero, 4, Aptdo. 1078, 41012 Seville, Spain

Received 6 July 2011/Accepted 18 July 2011

***Lactobacillus pentosus* is the most prevalent lactic acid bacterium in Spanish-style green olive fermentations. Here we present the draft genome sequence of *L. pentosus* IG1, a bacteriocin-producing strain with biotechnological and probiotic properties isolated from this food fermentations.**

Lactobacilli have been largely associated with food fermentations, and more recently, they have been used as probiotics, since they may promote health in humans and animals (6). *Lactobacillus pentosus* is the lactic acid bacterium most frequently isolated from Spanish-style green olive fermentations, and it has been successfully used as a starter culture for these fermentations (8). In addition, certain strains of *L. pentosus* have been shown to exert probiotic effects, improving the mucosal immunity and the resistance to bacterial infections (2, 5). The genome sequence of *Lactobacillus pentosus* IG1, a bile-resistant strain displaying bacteriocin activity against a wide range of spoilage and pathogen bacteria, will allow us to explore its biotechnological and probiotic properties.

The whole genome of IG1 was sequenced using a paired-end strategy by pyrosequencing technology with the platform 454 Life Sciences, GS FLX Titanium system. The sequence data consisted of 8-kb paired-end libraries (481,661 reads totaling ~175.5 Mb, ~45-fold coverage of the genome). The paired-end reads were assembled into 13 scaffolds (3,982,537 nt), of which scaffold 1 (3,687,424 nt) corresponds to the entire chromosome, while scaffolds 2 (125,904 nt), 3 (77,782 nt), 4 (36,648 nt), 5 (21,059 nt), 6 (10,521 nt), 11 (2,654 nt), and 12 (2,509 nt) seem to belong to seven distinct plasmids, according to the plasmid profile obtained for *L. pentosus* IG1.

The draft genome of *L. pentosus* IG1 includes 3,982,537 nucleotide bases, making it the biggest lactobacillus genome described to date. The G+C content of the chromosome (scaffold 1) was determined to be 44.9 mol%. There is a single predicted copy of the 16S and 23S rRNAs, 3 copies of the 5S rRNA, and 44 predicted tRNAs. The genome contains 3,133 predicted coding sequences, of which 2,972 belong to scaffold 1.

Comparative genomic analysis indicated that the closest genome is that of *Lactobacillus plantarum* (4, 9, 10). Putative functions could be assigned to 82% of the encoded proteins, and the remaining 18% could not be placed (putative uncharacterized proteins). Remarkably, this strain harbors 16 putative two-component regulatory systems, which may reflect an extensive ability

to adapt to changing environmental conditions. *L. pentosus* IG1 contains several genes that could encode putative probiotic functions involved in adhesion (collagen-binding proteins, exopolysaccharides, lipoteichoic acids), resistance to stress (mannose phosphotransferase systems, bile salt hydrolases), and microbial competition (LuxS-mediated production of AI-2- and AI-3-like molecules and bacteriocin production). The genes responsible for the bacteriocin activity of *L. pentosus* IG1 are identical to those of the two-component class IIb bacteriocin plantaricin S of *L. plantarum* LPCO10 (3). Finally, we found a locus that resembles the gene cluster of plantaricins, which is typical of *L. plantarum* (1, 7).

Nucleotide sequence accession numbers. The 13 scaffold sequences of *Lactobacillus pentosus* IG1 were deposited in the EMBL database with accession numbers FR874848 to FR874860.

This research was funded by the Spanish Ministry of Science and Innovation (MICINN) through Project AGL2009-07861 and by the Junta de Andalucía Excellence Project AGR-04621. A.M.-B. and H.L.-P. were the recipients of grants awarded by the Spanish National Research Council (CSIC) through the JAE Doc and JAE predoctoral Programmes, respectively.

REFERENCES

1. Diep, D. B., D. Straume, M. Kjos, C. Torres, and I. F. Nes. 2009. An overview of the mosaic bacteriocin *pln* loci from *Lactobacillus plantarum*. A review. *Peptides* **30**:1562–1574.
2. Izumo, T., et al. 2011. Influence of *Lactobacillus pentosus* S-PT84 ingestion on the mucosal immunity of healthy and *Salmonella* Typhimurium-infected mice. *Biosci. Microflora* **30**:27–35.
3. Jiménez-Díaz, R., et al. 1995. Purification and partial amino acid sequence of plantaricin S, a bacteriocin produced by *Lactobacillus plantarum* LPCO10, the activity of which depends on the complementary action of two peptides. *Appl. Environ. Microbiol.* **61**:4459–4463.
4. Kleerebezem, M., et al. 2003. Complete genome sequence of *Lactobacillus plantarum* WCF51. *Proc. Natl. Acad. Sci. U. S. A.* **100**:1990–1995.
5. Kotani, Y., et al. 2010. Oral intake of *Lactobacillus pentosus* strain b240 accelerates salivary immunoglobulin A secretion in the elderly: a randomized, placebo-controlled, double-blind trial. *Immun. Ageing* **7**:11.
6. Lebeer, S., J. Vanderleyden, and S. C. J. De Keersmaecker. 2008. Genes and molecules of lactobacilli supporting probiotic action. *Microbiol. Mol. Biol. Rev.* **72**:728–764.
7. Maldonado, A., R. Jiménez-Díaz, and J. L. Ruiz-Barba. 2004. Induction of plantaricin production in *Lactobacillus plantarum* NCS after coculture with specific Gram-positive bacteria is mediated by an autoinduction mechanism. *J. Bacteriol.* **186**:1556–1564.
8. Ruiz-Barba, J. L., D. P. Cahtcart, P. J. Warner, and R. Jiménez-Díaz. 1994. Use of *Lactobacillus plantarum* LPCO10, a bacteriocin producer, as a starter culture in Spanish-style green olive fermentations. *Appl. Environ. Microbiol.* **60**:2059–2064.
9. Wang, Y., et al. 2011. Complete genome sequence of the probiotic *Lactobacillus plantarum* ST-III. *J. Bacteriol.* **193**:313–314.
10. Zhang, Z. Y., et al. 2009. Complete genome sequence of *Lactobacillus plantarum* JDM1. *J. Bacteriol.* **191**:5020–5021.

* Corresponding author. Mailing address: Departamento de Biotecnología de Alimentos, Instituto de la Grasa, Consejo Superior de Investigaciones Científicas (CSIC), Avda. Padre García Tejero, 4, Aptdo. 1078, 41012 Seville, Spain. Phone: 34 54691054. Fax: 34 54691262. E-mail: maldoantonio@gmail.com.