

1 Genome Sequence of *Lactobacillus pentosus* IG1, a strain  
2 isolated from Spanish-style green olive fermentations

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20 **Running Title:** Genome Sequence of *Lactobacillus pentosus* IG1

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22 **Keywords:** Genome, *Lactobacillus pentosus*, bacteriocin

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26 **Abstract**

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

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32 *Lactobacilli* have been largely associated with food fermentations and, more recently,  
33 they have been used as probiotics since they may promote health in man and animals  
34 (6). *Lactobacillus pentosus* is the most frequent lactic acid bacteria isolated from  
35 Spanish-style green olive fermentations, and has been successfully used as starter  
36 cultures for these fermentations (8). In addition, certain strains of *L. pentosus* have  
37 shown to possess probiotic effects, improving the mucosal immunity and the resistance  
38 to bacterial infections (2, 5). This genome sequence will allow us to explore the  
39 biotechnological and probiotics properties of *Lactobacillus pentosus* IG1, a bile-  
40 resistant strain displaying bacteriocin activity against a wide range of spoilage and  
41 pathogen bacteria.

42 The whole genome of IG1 was sequenced using a paired-end strategy by  
43 pyrosequencing technology with the platform 454 Life Sciences, GS FLX Titanium  
44 system. The sequence data consisted of 8-kb paired-end libraries (481,661 reads  
45 totalling ~ 175, 5 Mb, ~ 45-fold coverage of the genome). The paired-end reads were  
46 assembled into 13 scaffolds (3,982,537 nt), of which the scaffold 1 (3,687,424 nt)  
47 corresponds to the entire chromosome, while scaffolds 2 (125,904 nt), 3 (77,782 nt), 4  
48 (36,648 nt), 5 (21,059 nt), 6 (10,521 nt), 11 (2,654 nt) and 12 (2,509 nt) seem to belong

49 to seven distinct plasmids, what is according to the plasmid profile obtained for *L.*  
50 *pentosus* IG1.

51 The draft genome of *L. pentosus* IG1 includes 3,982,537 nt bases, being the biggest  
52 genome of lactobacilli described to date. The G+C mol% content of the chromosome  
53 (scaffold 1) was determined to be 44, 9%. There is a single predicted copy of the 16S  
54 and 23S rRNA, 3 copies of the 5S rRNA and 44 predicted tRNAs. The genome contains  
55 3,133 predicted CDS, of which 2972 belong to scaffold 1.

56 Comparative genomic analysis indicated that the closest genome is that of  
57 *Lactobacillus plantarum* (4, 9, 10). Putative functions could be assigned to 82% of the  
58 encoded proteins, and the remaining 18% could not be placed (putative uncharacterized  
59 proteins). Remarkably, this strain harbours sixteen putative two-component regulatory  
60 systems, which may reflect a great ability of adaptation to the changing environmental  
61 conditions. *L. pentosus* IG1 presents several genes that could encode putative probiotic  
62 functions involved in adhesion (collagen-binding proteins, exopolysaccharides,  
63 lipoteichoic acids), resistance to stress (mannose phosphotransferase systems, bile salt  
64 hydrolases) and microbial competition (lux S-mediated production of AI-2 and AI-3-  
65 like molecules and bacteriocin production). The genes responsible for the bacteriocin  
66 activity of *L. pentosus* IG1 are identical to those of the two-component class IIb  
67 bacteriocin plantaricin S of *L. plantarum* LPCO10 (3). Finally, we found a locus that  
68 resembles the gene cluster of plantaricins, which is typical of the *L. plantarum* species  
69 (1, 7).

70 **Nucleotide sequence accession number.** The 13 scaffolds sequences of *Lactobacillus*  
71 *pentosus* IG1 were deposited in the EMBL database with accession numbers FR874848  
72 to FR874860.

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