

# Draft Genome Sequence of *Pediococcus parvulus* 2.6, a Probiotic $\beta$ -Glucan Producer Strain

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**We report here the draft genome sequence of the probiotic *Pediococcus parvulus* 2.6, a lactic acid bacterial strain isolated from ropy cider. The bacterium produces a prebiotic and immunomodulatory exopolysaccharide, and this is the first strain of the *P. parvulus* species whose genome has been characterized.**

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We report here the draft genome sequence of *Pediococcus parvulus* 2.6 (formerly *Pediococcus damnosus*), a lactic acid bacterium isolated from ropy cider (1). This is the first strain of *P. parvulus* whose genome has been characterized. The 2.6 strain produces the immunomodulatory exopolysaccharide 2-substituted (1,3)- $\beta$ -D-glucan (2), which is synthesized by a limited number of bacteria and confers probiotic properties to the producing strains. This polysaccharide differs from the  $\beta$ -glucans produced by plants and other microorganisms. The synthesis of 2-substituted (1,3)- $\beta$ -D-glucan by *P. parvulus* 2.6 is controlled by a single heterotransmembrane glucosyltransferase (GTF), which polymerizes glucosyl residues from UDP glucose (3–5). Some of the conditions that influence the homopolysaccharide (HoPS) synthesis by *P. parvulus* 2.6, as well as the enzymatic activities involved in sugar metabolism in this strain, have been examined (6, 7). The physicochemical properties of the HoPS have also been determined, and nuclear magnetic resonance (NMR) analysis showed that the same HoPS was synthesized, irrespective of the sugar source used for growth (8). The molecular masses of these  $\beta$ -glucans are high ( $>10^6$  Da), and their rheological properties showed that they have potential utility as biothickeners (8). An oat-based product fermented by *P. parvulus* 2.6 showed improved rheology (9), thereby decreasing the need for added stabilizers and texturizers.

The potential of *P. parvulus* 2.6 as a probiotic strain has also been examined; it resists gastrointestinal stress, adheres to Caco-2 cells, and its HoPS reduces the production of inflammatory cytokines by polarized macrophages (10). We have also shown that *P. parvulus* HoPS improves the growth and viability of probiotic microorganisms, as well as their adhesion to human enterocytes (11). The 2-substituted (1,3)- $\beta$ -D-glucan increases *in vitro* the ratio of interleukin 10 (IL10) (anti-inflammatory) to tumor necrosis factor alpha (TNF $\alpha$ ) (inflammatory) in human macrophages and decreases the levels of the proinflammatory IL8 in human intes-

tine organ cultures (reference 12 and Notararigo S., Antolin M., Guarner F., López P., unpublished data).

An oat-based product fermented by *P. parvulus* 2.6 had a bifidogenic effect and decreased serum cholesterol levels in humans (13). Possibly, the 2-substituted (1,3)- $\beta$ -D-glucan has a synergistic effect with the hypocholesterolemic action of oat  $\beta$ -glucans. Finally, *P. parvulus* 2.6 displays antibacterial activity against several bacterial species (14), including natural contaminants in oats, a property that reduces the need for chemical preservatives and improves the functionality of the final product.

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 used the Illumina GAIIx at the Genomics Research Centre (Fiorenzuola d'Arda, Italy). A total of 26,018,224 paired-end reads ( $2 \times 110$ -bp length) were assembled into 115 contigs. The genome was calculated to be 2,236,754 long. The size of the shortest contig was 206 bp, while the length of the longest contig was 171,226 bp. The genome sequence was annotated by the NCBI Prokaryotic Genomes Annotation Pipeline. A total of 2,241 genes were predicted to encode 2,069 proteins, three rRNAs, 60 tRNAs, and four noncoding RNAs (ncRNAs), and 105 are pseudogenes.

**Accession number(s).** The complete genome of *P. parvulus* 2.6 has been deposited at DDBJ/EMBL/GenBank under accession number [LXND000000000](https://www.ncbi.nlm.nih.gov/nuccore/LXND000000000).

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