

Complete Genome Sequence of *Lactobacillus salivarius* CECT 5713, a Probiotic Strain Isolated from Human Milk and Infant Feces[∇]

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***Lactobacillus salivarius* is a homofermentative lactic acid bacterium and is frequently isolated from mucosal surfaces of healthy humans. *L. salivarius* CECT 5713, a strain isolated simultaneously from breast milk and infant feces of a healthy mother-infant pair, has immunomodulatory, anti-inflammatory, and anti-infectious properties, as revealed by several *in vitro* and *in vivo* assays. Here, we report its complete and annotated genome sequence.**

In the last years, culture-dependent and -independent analyses of the bacterial diversity of human milk and colostrum have revealed that these biological fluids are a source of live staphylococci, streptococci, lactic acid bacteria, and bifidobacteria in the infant gut (5, 6, 8, 9, 11, 13), where they play a key role in the initiation and development of the gut microbiota (12). In a previous study, we isolated *L. salivarius* CECT 5713 from human milk and infant feces of a mother-child pair (10). Subsequent studies revealed that this strain was a good probiotic candidate since it achieved high survival rates when exposed to the gastrointestinal tract conditions, showed a strong adherence to intestinal cells, stimulated the expression of mucin-encoding genes, produced antimicrobial compounds (lactate, acetate, and hydrogen peroxide), and displayed *in vivo* and *in vitro* immunomodulatory, anti-inflammatory, and antibacterial properties against pathogenic bacteria (2, 10, 15). Moreover, oral administration of *L. salivarius* CECT 5713 appears to be an efficient alternative for the treatment of infectious mastitis in lactating women (7). Similarly, studies with other *L. salivarius* strains in animal models and clinical trials have demonstrated their probiotic function and, particularly, their anti-inflammatory effects (3, 14, 16).

In order to interrogate the genome sequence of *L. salivarius* CECT 5713 with regard to its probiotic properties, the complete genome sequence was determined by a whole-genome shotgun strategy using pyrosequencing technology (454 Life Sciences, Banford, CT). The initial draft assembly provided by 454 Life Sciences was based on 444,604 high-quality pyrosequencing reads, which assembled into 59 contigs. The genome sequence of *L. salivarius* UCC118 (1), a well-characterized probiotic strain, was used to order these contigs into large scaffolds.

The genome of *L. salivarius* CECT 5713 consists of a circular chromosome of 1,828,169 bp, two plasmids (pHN1, 44,581 bp;

pHN2, 20,426 bp), and a megaplasmid (pHN3, 242,962 bp). The overall GC content of the chromosome is 32.93%, similar to that of the megaplasmid but lower than those of the plasmids (>38%). The entire genome of CECT 5713 contains 1,558 protein-, 87 tRNA-, and 51 rRNA-encoding genes. A comparison between the genomes of *L. salivarius* CECT 5713 and UCC118 revealed the presence of 52 protein-encoding genes that are exclusive for CECT 5713, including genes encoding a 6-phospho- β -glucosidase and three collagen-binding proteins, which may explain the high potential for competitive exclusion of pathogens displayed by this strain. The genes responsible for the bacteriocin activity of *L. salivarius* CECT 5713 are located in pHN3. This megaplasmid contains six open reading frames (ORFs) closely related, but not identical, to the genes responsible for the biosynthesis of salivaricin ABP-118, a two-component class II bacteriocin (4), in *L. salivarius* UCC118. Globally, several features of the *L. salivarius* CECT 5713 genome suggest a strong probiotic potential in humans.

Nucleotide sequence accession numbers. Genome information for the chromosome, the two plasmids, and the megaplasmid of *L. salivarius* CECT 5713 has been deposited in the EMBL and GenBank databases with accession numbers CP002034, CP002035 and CP002036, and CP002037, respectively.

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