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GENOME ANNOUNCEMENT

Genome Sequence of *Lactobacillus salivarius* SMXD51, a Potential Probiotic Strain Isolated from Chicken Cecum, Showing Anti-*Campylobacter* Activity

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We report the draft genome sequence of *Lactobacillus salivarius* SMXD51, isolated from the cecum of healthy chickens showing an activity against *Campylobacter*—the food-borne pathogen that is the most common cause of gastroenteritis in the European Union (EU)—and potentially interesting features for a probiotic strain, explaining our interest in it.

Lactobacillus salivarius is a lactic acid bacterium usually found in human and animal gastrointestinal tracts whose probiotic properties and genomic diversity have recently been described (18, 19).

In a previous study (16), we isolated *Lactobacillus salivarius* SMXD51 from the cecum of a healthy Tunisian chicken and reported an antimicrobial activity against *Campylobacter*, a food-borne pathogen, the most common cause of gastroenteritis in the European Union (EU) (9). Only a few bacterial strains show a peptide anti-*Campylobacter* activity (15, 20–23), and to our knowledge, none of them has yet been sequenced.

Additional studies (data not yet published) indicate that this strain is a good probiotic candidate due to its high survival rates when exposed to gastrointestinal tract conditions, its strong adherence to intestinal cells, its absence of cytotoxicity, and its benefit in barrier integrity and modulation of immunity.

The sequence data were obtained using a 454 GS FLX Titanium pyrosequencing system (Roche Diagnostic, Branford, CT) with 3 different libraries: a fragment library (169,277 reads produced, 56.1 Mb), a 3-kb mate-pair library (196,906 reads produced, 62.5 Mb), and an 8-kb mate-pair library (369,135 reads produced, 152.1 Mb). All reads were assembled into 18 contigs using MIRA3 Assembler (4). The functional annotation of predicted genes was achieved using a RAST server (2) to predict open reading frames (ORFs) using the Glimmer 3 modeling software package (7). The predicted ORFs were annotated by searching against the COG (Clusters of Orthologous Groups) (17) and SEED (8) databases.

The draft genome includes 1,967,690 bp divided into one chromosome (6 contigs) of 1.7 Mb with a 33.1% G+C ratio and four single-contig plasmids: a megaplasmid (pLS51A) which reaches approximately 143 kb with a 32.2% G+C ratio, a large plasmid (pLS51B) of 85 kb with a 32.3% G+C ratio, and two plasmids of 31 kb (pLS51C) and 9 kb (pLS51D) with G+C ratios of 32.6% and 29%, respectively. This strain contains 1,795 coding sequences and 103 RNAs, including 78 genes for tRNA.

Comparative genome analysis with other published *L. salivarius* sequences (5, 6, 13, 14) revealed some unique predicted proteins: a DNA adenine methylase, a restriction endonuclease (AlwI), several translocases, and hypothetical proteins.

Several genes known to be important for gastrointestinal survival and adherence were found. First, 2 genes shown to be involved in acid tolerance (1) and coding for an ornithine decarboxylation-antiporter system were found. Then, 2 genes involved in bile salt resistance were found: one encoding the well-known bile salt hydrolase (BSH) family protein choloylglycine hydrolase (10) and one encoding aggregation-promoting factor (12). Concerning adhesion capacity, 2 genes encoding cell wall-anchored adhesin were found: one encoding a fibronectin binding protein (FbpA) (3) and one encoding a potential mucus adhesion-promoting protein (MapA) (25). Furthermore, the *lspA* gene from *Lactobacillus salivarius* UCC118, reported to mediate adhesion, was found with 92.6% identity (24).

In addition, a megaplasmid-located bacteriocin gene cluster homologous to salivaricin ABP-118 (11) was found. The synteny and the homology are conserved except for the bacteriocin-producing gene. Its role in the antimicrobial activity remains to be confirmed.

Nucleotide sequence accession numbers. This Whole Genome Shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. AICL00000000. The version described in this paper is the first version, AICL01000000.

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