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GENOME ANNOUNCEMENT

Draft Genome Sequence of *Lactobacillus rossiae* DSM 15814^T

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The draft genome sequence of *Lactobacillus rossiae* DSM 15814^T (CS1, ATCC BAA-88) was determined by a whole-genome shotgun approach. Reads were assembled to a 2.9-Mb draft version. RAST genome annotation evidenced 2,723 predicted coding sequences. Many carbohydrate, amino acid, and amino acid derivative subsystem features were found.

The genus *Lactobacillus* belongs to the phylum *Firmicutes*, class *Bacillus*, order *Lactobacillales*, and family *Lactobacillaceae*. Lactobacilli are Gram-positive, catalase-negative, non-spore-forming, rod-shaped bacteria that produce lactic acid as the major end product of fermentation. *Lactobacillus* is the largest genus within the group of lactic acid bacteria (5).

Lactobacillus rossiae was usually found within the autochthonous microbiota of sourdoughs (4, 11, 13, 14), spelt flour (3), pineapple (9), and the gastrointestinal tracts of humans (8) and animals (6). The genotypic and phenotypic diversity of *L. rossiae* strains isolated from sourdough was described previously (7, 13). Some strains were selected for antifungal activity (17) and used in sourdough biotechnology for glutamate production (15) and wheat germ fermentation (12). The genome sequence of *L. rossiae* DSM 15814^T (CS1, ATCC BAA-822) will be useful to explore its biotechnology properties.

A total of 30,544,098 whole-genome shotgun, 100-bp paired-end reads were generated using Illumina sequencing technology. Library preparation was carried out with minor modifications to the TruSeq DNA sample preparation protocol (Illumina, Inc., San Diego, CA). Briefly, 1 μg of bacterial DNA was sheared to an average length of 500 to 600 bp using the Diagenode Biorupter XL sonicator system (Sparta, NJ), and standard blunt ending with "A" base (paired-end DNA sample preparation kit; Illumina, Inc.) was performed. Illumina index adapters were ligated to the ends of the fragments. After ligation reaction and separation of nonligated adapters, samples were amplified by PCR to selectively enrich those fragments in the library having adapter molecules at both ends. The sample was quantified and the quality was tested using a NanoDrop ND-1000 UV-Vis spectrophotometer (Thermo Scientific, Wilmington, DE) and an Agilent 2100 bioanalyzer (Agilent Technologies, Santa Clara, CA). The library was pooled with the other eight bacterial genomes in equimolar ratios to yield a total concentration of 10 nM. Aliquots of pooled libraries (2 pmol) were processed with cBot (Illumina, Inc.) by following the manufacturer's recommendations. The HiSeq 2000 system was programmed for a paired-end sequencing run of 101 cycles. Raw images were processed using Illumina Pipeline software version RTA 2.8.0/OLB 1.8.0/CASAVA 1.7.0.

After filtering low-quality reads, 30,017,879 high-quality reads were assembled into contigs using CLC Genomics Workbench version 5.01 (CLC Bio, Denmark).

The annotation was done by merging the results obtained from the RAST server (1) and checked by BLAST analysis when needed. In addition, the scaffolds were searched against the KEGG (10), UniProt (2), and COG (16) databases to annotate the gene descriptions.

The draft genome includes 278 contigs covering 2,946,462 bp (N_{50} of 150,537 bp, average contig size of 11,466 bp, maximum contig size of 528,241 bp, with an average coverage of 1,000×). A total number of 2,723 predicted coding sequences were annotated.

There are 287 subsystems that are represented in the genome, and this information was used to reconstruct the metabolic network. The closest genome is that of *Lactobacillus brevis* (genome identification number 387344.13 [SEED Viewer version 2.0]). Many carbohydrate, amino acid, and amino acid derivative subsystem features were found, including genes involved in central carbohydrate, monosaccharide, and fermentation metabolisms. Many protein and DNA metabolism subsystem features were also identified.

Nucleotide sequence accession number. The whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession number AKZK00000000.

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