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GENOME SEQUENCES

Draft Genome Sequence of *Lactobacillus reuteri* Strain LR CGMCC 11154, Isolated from the Feces of Healthy Weaned Piglets

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ABSTRACT *Lactobacillus reuteri* strain LR CGMCC 11154, which was isolated from the feces of healthy weaned piglets, was experimentally proven to be a probiotic bacterium. The whole genome was sequenced on the Illumina Miseq platform to obtain the draft genome, which consists of 120 contigs totaling 1.9 Mbp encoding 1,854 genes.

Lactobacillus reuteri is a strain of lactic acid bacterium which belongs to the *Lactobacillus* genus. It is a well-known probiotic bacterium (1, 2). We isolated a strain of the probiotic bacterium from the feces of five healthy 35-day-old weaned piglets (duroc × Landrace × large white) at the Guangdong Academy of Agricultural Sciences. Briefly, about 1 g of feces per piglet was collected by using sterile swabs and stored in sterilized sampling bags with cryopreservation. The swabs were repeatedly and rapidly rinsed with quantitative sterilized phosphate-buffered saline (PBS) and were gradually diluted to 10^6 cells/ml. Then, a 200-μl liquid sample was coated on a 5-ml Rogosa SL agar plate and cultured anaerobically at 37°C for 48 h. Finally, the strain was identified as *Lactobacillus reuteri* using 16S rRNA gene sequencing (3) (GenBank accession number KT205306) and named strain LR1 by Z.W. This strain provided excellent health benefits to the weaned piglets (4). At present, this strain is stored in the China General Microbiological Culture Collection Center (CGMCC) under access number 11154. To avoid confusion in the database, we used the unique accession number LR CGMCC 11154 instead of the nonunique name LR1. To further investigate LR CGMCC 11154, we performed its genome sequencing using next-generation sequencing technology. The genomic DNA was extracted using the E.Z.N.A. bacterial DNA kit (product number D3350-01, Omega, USA) following the manufacturer's instructions, and the library was constructed using the NEBNext Ultra II DNA library prep kit for Illumina (product number E7645L). The whole genome was sequenced on the Illumina MiSeq platform using the 2 × 150-bp MiSeq reagent kit v2 (Illumina, USA). Then, 1,161,442 raw paired-end sequences were generated, and the Q30 quality reached 97%. The raw sequences without trimming because of good quality were used for the *de novo* genome assembly using the IDBA assembler (5) with the default parameters, including precorrection before assembly. The draft genome was assembled into 120 contigs with an N_{50} contig size of 30,797 bp and a median coverage depth of 100×. The draft genome of LR CGMCC 11154 is composed of 1,910,900 bp with an average G+C content of 38.6%. Genome annotation was done using the Rapid Annotations using Subsystems Technology (RAST) server (6). A total of 1,854 coding genes and 60 RNAs (including 7 rRNAs and 53 tRNAs) were predicted. Among the coding genes, 1,447 genes (78%) had functional assignments or exhibited homology to proteins with

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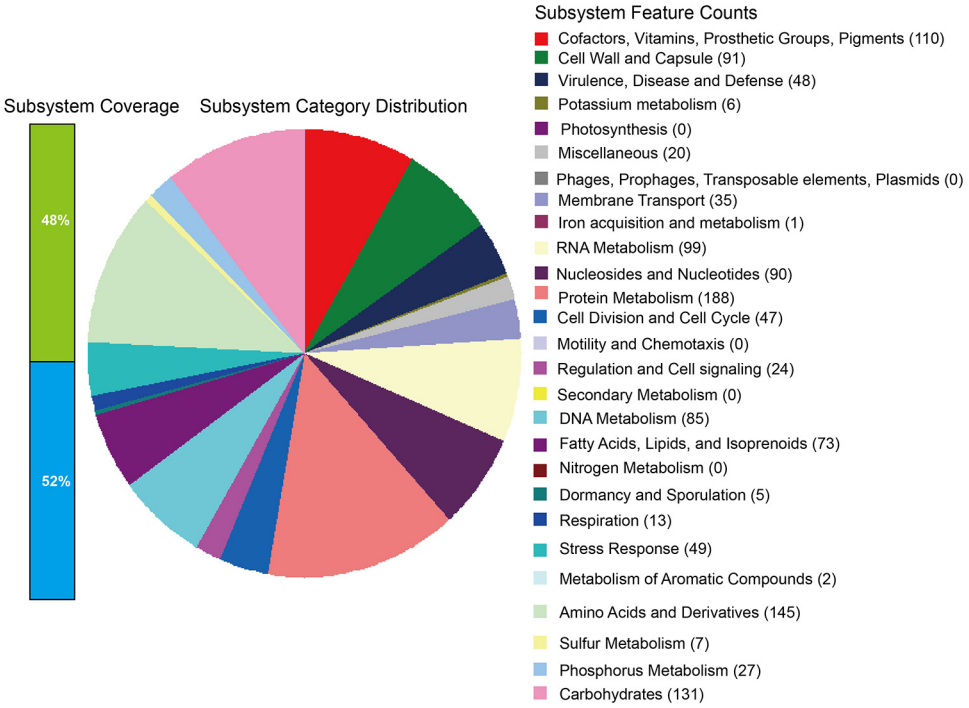

FIG 1 Genes connected to subsystems and their distribution in different categories.

previously known functions, while 407 genes (22%) remained hypothetical proteins. Eighteen subsystem categories in the RAST system were assigned, and the maximum gene count was functionally associated with the amino acids and derivatives (145 coding genes), followed by carbohydrates (131 coding genes) and the category of cofactors, vitamins, prosthetic groups, and pigments (110 coding genes) (Fig. 1). The genome sequence will be useful for genetic modifications of the strain.

Data availability. This whole-genome shotgun project of *Lactobacillus reuteri* strain LR CGMCC 11154 has been deposited at GenBank under the accession number QRDF00000000. The draft genome sequence described in this paper is the first version (QRDF01000000). Raw sequencing reads have been submitted to the Sequence Read Archive (SRA accession number SRR8182721) and are available in the NCBI under BioProject number PRJNA505088 and BioSample number SAMN10410839.

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The authors' contributions are as follows: Z.C. and Z.J. designed the research. Z.W. provided the strain. T.Y. analyzed the data and wrote the manuscript. X.Y. submitted the data to NCBI and revised the manuscript. W.L. and Q.Z. conducted the sequencing. C.Z., J.B., and L.W. took part in the research. All of the authors read and approved the final version of the manuscript.

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