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Genome Sequences of Five *Lactobacillus* sp. Isolates from Traditional Turkish Sourdough

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ABSTRACT A high level of variation in microflora can be observed in profiles of lactic acid bacteria (LAB) from sourdoughs. Here, we present draft genome sequences of *Lactobacillus reuteri* E81, *L. reuteri* LR5A, *L. rhamnosus* LR2, *L. plantarum* PFC-311, and the novel *Lactobacillus* sp. strain PFC-70, isolated from traditional Turkish backslopped wheat sourdoughs.

Sourdough is a mixture of flour and water that is fermented mainly with naturally occurring lactic acid bacteria (LAB), although yeasts also contribute to this fermentation process (1, 2). The addition of sourdough to bread dough can improve its technological properties, enhance nutritional and sensory properties of the bread, and increase the shelf life of the bread (3, 4). These functional roles of sourdough mainly originate from the metabolism of LAB species occurring during fermentation that include their proteolytic activity (5), their formation of volatile antibacterial and antifungal compounds (6), and their exopolysaccharide (EPS) production characteristics (7). So far, several LAB species were reported to be present in sourdoughs from different origins, with a high level of diversity depending on cultural and geographical identities (8, 9). Among LAB strains, *Lactobacillus* species, especially heterofermentative ones, dominate the sourdough environment (10). *L. reuteri* and *L. plantarum* strains are among the well-known sourdough LAB species (11–13).

This study reports the draft genome sequences of *L. reuteri* E81, *L. reuteri* LR5A, *L. rhamnosus* LR2, *L. plantarum* PFC-311, and the novel *Lactobacillus* sp. strain PFC-70, isolated from traditional Turkish backslopped wheat sourdoughs. *L. reuteri* E81, *L. reuteri* LR5A, and *L. rhamnosus* LR2 were isolated from traditional sourdoughs. *L. plantarum* PFC-311 and *Lactobacillus* sp. strain PFC-70 were isolated from traditional sourdoughs prepared for tarhana production. All sourdoughs were collected at their final fermentation stage. The isolation and identification of five distinct strains were performed as described previously (9) and subjected to sequencing.

DNA libraries were prepared with an Illumina Nextera XT DNA preparation kit and sequenced on the Illumina MiSeq platform with the Illumina MiSeq reagent kit v3 (2 × 300 bp, 600 cycles). CLC Genomics Workbench (v 10.0.2) was used to trim sequence files using quality scores and then *de novo* assemble them. After removing contigs <1,000 bp, the draft assemblies were annotated using both the Rapid Annotations using Subsystems Technology (RAST) server and the NCBI Prokaryotic Genome Annotation Pipeline. The summary statistics for the assembled genomes are presented in Table 1.

The average read length was 223 bp (±20 bp) with total read counts of 3,306,384 bp for *L. reuteri* E81 and average read counts of 684,706 bp (±232,675 bp) for the remaining isolates, which were sequenced in a separate analysis. The calculated genome size, GC content, and number of coding regions (based on RAST) for each of the assemblies

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TABLE 1 Draft genome statistics of 5 bacterial strains isolated from traditional Turkish sourdough

Isolate	GenBank assembly no.	No. of contigs	Assembly size (bp)	N_{50} (bp)	G+C content (%)	Coverage (×)	No. of coding regions	GenBank accession no.
L. reuteri E81	GCA_003046135.1	55	1,987,461	39,453	38.6	463	1,977	PZQO00000000
L. reuteri LR5A	GCA_003046055.1	60	1,986,306	67,178	38.6	90	1,975	PZQN00000000
L. rhamnosus LR2	GCA_003046115.1	39	2,931,997	121,085	46.7	38	2,932	PZQM00000000
Lactobacillus sp. PFC-70	GCA_003046095.1	71	2,592,913	72,018	51.8	90	2,354	PZQL00000000
L. plantarum PFC-311	GCA_003046075.1	87	3,323,213	73,995	44.3	83	3,188	PZQK00000000

are consistent with the expected results for the taxonomic classifications of the closest neighbors in the RAST database. Preliminary analysis of the assemblies revealed several bacteriocins identified by BAGEL4 (14). *L. reuteri* E81 and LR5A were both found to contain a putative enterolysin-A, *L. rhamnosus* LR2 had a carnocin_CP52, and *L. plantarum* PFC-311 had plantaricin-A, -E, -F, –J, -K, and -N. The draft genomes for these LAB are key to providing a better understanding of the complex diversity of strains associated with fermented sourdough.

Accession number(s). The genome sequences of all 5 isolates have been deposited at DDBJ/ENA/GenBank under the accession numbers provided in Table 1.

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