

Supplementary file to:

Identification of Lactic Acid Bacteria Strains Isolated from Sourdoughs Prepared with Different Flour Types

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Table S1. Cell morphology of the obtained isolates grown on MRS-agar. Observations were performed after methylene blue staining, magnification 1000 x.

Ech1 – short/medium rods	X1 - cocci
Ech2 – short/medium rods	X2 – medium/single long rods
Ech3 – short/medium rods	X4 – short/medium/single long rods
Ech4 – short/medium rods	L1- short/medium rods
Ech6 - short rods/volutine	L2- short/medium/single long rods
Ech7 - short rods	El1 - short rods/volutine
Ph1 – short/medium/long rods	El2 - cocci
Ph2 - short rods	Ch42 - cocci
Ph3 – medium/long rods	Ch53 - slightly elongated cocci
Ph5 – short/single long rods	Ch54 - slightly elongated cocci
Ph4 - medium rods	Car - short rods/volutin
Cn1 – short/medium rods	
Cn2 - short rods	
Cn3 - short rods	
Cn4 - short rods	
Cn5 - short rods/volutine	
Cn6 - short rods X1 – cocci	

Table S2. Most discriminative carbohydrate utilization patterns of the tested isolates*

Isolate	Ech1	Ech3	L1	L2	X2	X4	El1	Cn1	Ph1	Ph2	Ph3	Ph5	Car
L-arabinose	+	-	+	+	+	+	+	+	+	-	-	-	+
D-xylose	-	+	-	+	+	+	+	-	+	-	-	-	+
Galactose	+	-	+	-	-	-	-	+	-	+	+	+	-
b-mannose	+	-	+	-	-	-	-	+	-	+	+	+	-
Rhamnose	-	-	+	-	-	-	-	-	-	+	+	-	-
Mannitol	+	-	+	-	-	-	-	+	-	+	+	+	-
Sorbitol	+	-	+	-	-	-	-	+	-	+	+	+	-
Amygdaline	+	-	+	-	-	-	-	+	-	+	+	+	-
Arbutine	+	-	+	-	-	-	-	+	-	+	+	+	-
Esculine	+	-	+	-	-	-	-	+	-	-	+	+	-
Salicine	+	-	+	-	-	-	-	+	-	+	+	+	-
Cellobiose	+	-	+	+	-	-	-	+	-	+	+	+	-
Lactose	+	-	+	-	-	-	-	+	-	+	+	+	-
Melibiose	+	w	+	+	-	w	-	+	-	+	+	+	w
Saccharose	+	-	+	-	-	-	-	+	-	+	+	+	-
Trehalose	+	-	+	-	-	-	-	+	-	+	+	+	-
Melezitose	+	-	+	-	-	-	-	+	-	-	-	-	-
D-raffinose	+	-	+	-	-	-	-	+	-	-	+	-	-
B-gentiobiose	+	-	+	-	-	-	-	+	-	+	+	+	-
D-turanose	+	-	+	-	-	-	-	+	-	+	-	-	-

*All tested strains were positive for ribose, D-glucose, D-fructose, N-acetyl-glucosamine and maltose; w- weak

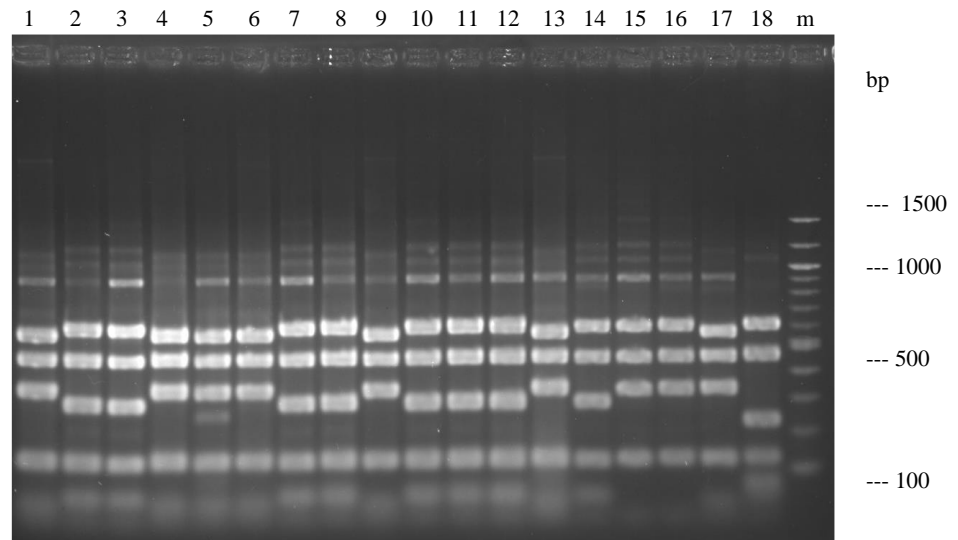


Figure S1. Restriction profiles of 16S-ribosomal DNA of the studied isolates treated with the restriction enzyme *Hae*III. Lanes-isolate: 1-Ech1; 2- Ech3; 3 – Ph1; 4 - Ph2; 5 – Ph3; 6 – Ph5; 7 – X2; 8 – X4; 9 – L1; 10 – L2; 11 – El1; 12 – Car; 13 – Cn1; 14 - *Levilactobacillus brevis* LMG 6906; 15 – *Lacticaseibacillus rhamnosus* LMG 6400; 16 – *Lacticaseibacillus paracasei* LMG 13087; 17 - *Lactiplantibacillus plantarum* DSM 20174; 18 – *Limosilactobacillus fermentum* DSM 20052; m – 100-bp DNA ladder.

Table S3. Hits from the NCBI database with $\geq 99\%$ similarity to the partial 16S-rDNA sequences of the studied isolates. The number of base pairs (bp) of the partial 16S rDNA sequence read for each isolate is shown in parentheses.

Isolate	Species/subspecies	Number of hits
Ech1 (1426 bp)	<i>Lactiplantibacillus</i>	101
	. <i>Lactiplantibacillus plantarum</i>	56
	. <i>Lactiplantibacillus argentoratensis</i>	44
	. <i>Lactiplantibacillus</i> sp.	1
Ech3 (1410 bp)	<i>Levilactobacillus</i>	101
	. <i>Levilactobacillus brevis</i>	100
	. <i>Levilactobacillus</i> sp.	1
L1 (1399 bp)	<i>Lactiplantibacillus</i>	100
	. <i>Lactiplantibacillus plantarum</i>	69
	. <i>Lactiplantibacillus argentoratensis</i>	30
	. <i>Lactiplantibacillus</i> sp.	1
L2 (1403 bp)	<i>Levilactobacillus</i>	100
	. <i>Levilactobacillus brevis</i>	99
	. <i>Levilactobacillus</i> sp.	1
El1 (1397 bp)	<i>Levilactobacillus</i>	100
	. <i>Levilactobacillus brevis</i>	99
	. <i>Levilactobacillus</i> sp.	1
X2 (1415 bp)	<i>Levilactobacillus</i>	105
	. <i>Levilactobacillus brevis</i>	104
	. <i>Levilactobacillus brevis</i> BSO 464	1
	. <i>Lactobacillus</i> sp.	1
X4 (1405 bp)	<i>Levilactobacillus</i>	100
	. <i>Levilactobacillus brevis</i>	99
	. <i>Levilactobacillus</i> sp.	1
Cn1 (1395 bp)	<i>Lactiplantibacillus</i>	101
	. <i>Lactiplantibacillus plantarum</i>	50
	. <i>Lactiplantibacillus argentoratensis</i>	51
Ph1 (1417 bp)	<i>Levilactobacillus</i>	101
	. <i>Levilactobacillus brevis</i>	100
	. <i>Levilactobacillus</i> sp.	1
Ph2 (1431 bp)	<i>Lactiplantibacillus</i>	100
	. <i>Lactiplantibacillus pentosus</i>	44
	. <i>Lactiplantibacillus plantarum</i>	54
	. <i>Lactiplantibacillus argentoratensis</i>	2
Ph3 (1399 bp)	<i>Lactiplantibacillus</i>	102
	. <i>Lactiplantibacillus plantarum</i>	61
	. <i>Lactiplantibacillus pentosus</i>	35
	. <i>Lactiplantibacillus plantarum</i> subsp. <i>plantarum</i>	1
Ph5 (1412 bp)	<i>Lactiplantibacillus</i>	102
	. <i>Lactiplantibacillus plantarum</i>	65
	. <i>Lactiplantibacillus pentosus</i>	29
	. <i>Lactiplantibacillus argentoratensis</i>	1
Car (1418 bp)	<i>Levilactobacillus</i>	101
	. <i>Levilactobacillus brevis</i>	100
	. <i>Levilactobacillus</i> sp.	1

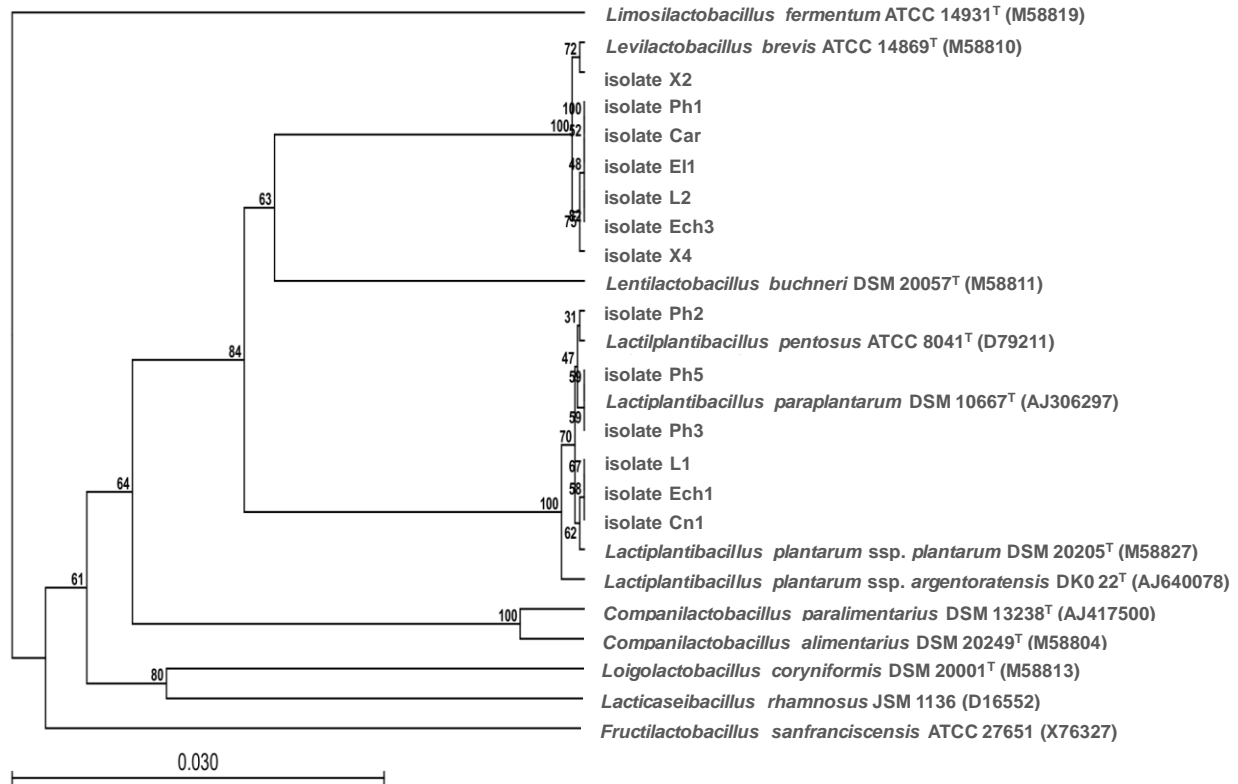


Figure S2. Phylogenetic tree of the most common *Lactobacillus* species found in sourdough and the isolates obtained in this study based on ca. 1356 bp partial sequence of the 16S rRNA gene. The tree was generated by the CLC Sequence Viewer software ver. 6.6.1 (www.clcbio.com, CLC bio A/S) by the UPGMA algorithm. Bootstrap values displayed at nodes were obtained based on 100 replicates. Sequences were derived from GenBank (NCBI). Type strains are labeled with superscript “T”.