

1 **Table S1.** Changes of pH and TTA of UHT milks added with the rennet pastes.

Trials	pH			TTA <sup>a</sup>		
	T <sub>0</sub>	3 d	6d	T <sub>0</sub>	3 d	6d
Control	6.70±0.01	6.56±0.07	6.29±0.05	1.6±0.5	1.7±0.5	2.4±0.6
T1	6.73±0.04	4.56±0.01	4.56±0.04	1.6±0.5	7.1±0.4	6.9±0.7
T2	6.67±0.08	4.58±0.08	4.51±0.03	1.8±0.6	7.9±0.6	8.3±0.4
T3	6.73±0.04	4.65±0.09	3.70±0.01	1.6±0.3	9.9±0.2	19.3±0.2
T4	6.71±0.05	4.59±0.09	4.49±0.02	1.5±0.3	8.2±0.3	9.3±0.7
T5	6.67±0.07	4.62±0.03	4.48±0.02	1.7±0.4	7.7±0.7	9.1±0.1
T6	6.71±0.02	4.51±0.06	4.38±0.07	1.7±0.3	8.5±0.3	9.2±0.6
T7	6.66±0.09	4.61±0.03	4.60±0.04	1.8±0.2	7.5±0.2	7.9±0.8
T8	6.68±0.03	4.80±0.10	4.80±0.06	1.6±0.3	9.4±0.8	10.3±0.3
T9	6.71±0.02	4.57±0.01	4.45±0.05	1.6±0.3	7.5±0.7	8.4±0.1
T10	6.71±0.03	5.07±0.02	4.92±0.06	1.5±0.4	6.6±0.5	6.9±0.2
T11	6.71±0.01	3.60±0.01	3.48±0.03	1.5±0.2	15.6±0.6	21±0.6

2 <sup>a</sup> Determined by titration with 0.1 N NaOH and expressed in terms of ml of NaOH.  
 3 Lowercase (a,b) and uppercase (A, B) letters indicate different statistical significances for pairwise comparison with control at P values of <0.05 and <0.01, respectively.  
 4

5 **Table S2.** Microbial evolution ( $\text{Log}_{10}$  CFU/ml) of UHT milks added with the rennet pastes.

Time of analysis	Microbial groups	Trials											
		Control	T1	T2	T3	T4	T5	T6	T7	T8	T9	T10	T11
T <sub>0</sub>	TPC	<1	<1	<1	<1	<1	<1	<1	<1	<1	<1	<1	<1
	TMC	<1	<1	<1	<1	<1	<1	<1	<1	<1	<1	<1	1.3±0.1
	Mesophilic rod LAB	0	0	0	0	0	0	0	0	0	0	0	0.8±0.5
	Thermophilic rod LAB	0	0	0	0	0	0	0	0	0	0	0	0
	Mesophilic coccus LAB	0	0.3±0.6	0.3±0.4	0.5±0.1	0.7±0.4	0.9±0.7	1.0±0.4	0.5±0.3	0.3 ±0.2	0.7±0.5	0.8±0.7	1.7±0.4
	Thermophilic coccus LAB	0	0	0	0	0	1.0±0.7	0	0	0	0	0	0.5±0.3
6 d	TPC	2.9±0.3	3.4±0.6	2.3±0.4	4.0±0.7	6.5±0.1	5.8±0.4	5.0±0.3	2.3±0.5	2.4±0.3	2.4±0.4	7.4±0.1	3.9±0.5
	TMC	3.5±0.4	7.4±0.5	7.6±0.4	7.5±0.7	7.4±0.1	7.9±0.5	8.0±0.6	7.9±0.7	8.1±0.4	7.9±0.7	7.9±0.6	7.6±0.7
	Mesophilic rod LAB	2.2±0.5	5.0±0.3	5.1±0.6	5.0±0.3	4.9±0.5	5.2±0.3	6.2±0.1	4.8±0.3	5.0±0.3	5.2±0.5	4.9±0.5	5.0±0.4
	Thermophilic rod LAB	2.4±0.6	7.6±0.7	5.1±0.3	5.4±0.2	7.9±0.1	5.0±0.4	7.1±0.6	5.0±0.3	5.2±0.3	7.8±0.3	5.1±0.5	6.2±0.4
	Mesophilic coccus LAB	4.2±0.4	8.0±0.9	7.9±0.4	8.2±0.4	8.5±0.3	8.5±0.3	8.2±0.6	6.7±0.8	7.1±0.5	8.3±0.7	5.0±0.4	7.1±0.5
	Thermophilic coccus LAB	3.4±0.2	7.8±0.2	7.9±0.5	8.0±0.5	8.7±0.7	8.5±0.6	8.4±0.4	5.1±0.5	3.9±0.3	8.4±0.6	5.1±0.3	8.3±0.5

6 Abbreviations: TPC, total psychrotrophic counts; TMC, total mesophilic counts; LAB, lactic acid bacteria.  
7 The results represent mean values of three replicates.  
8

9 **Table S3.** Phenotypic grouping of LAB isolated from high dilutions of milks acidified with animal rennet pastes.

Characters	Clusters							10
	I (n = 3)	II (n = 3)	III (n = 1)	IV (n = 14)	V (n = 4)	VI (n = 3)	VII (n = 4)	11
Morphology <sup>a</sup>	R	C	C	C	C	C	C	12
Cell disposition <sup>b</sup>	sc	lc	sc	sc	sc	sc	sc	13
Growth:								14
15°C	-	-	+	+	-	+	+	15
45°C	+	+	+	+	+	+	+	16
pH 9.2	nd	-	+	+	+	+	+	17
6.5% NaCl	nd	-	+	+	+	+	+	18
Hydrolysis of:								19
arginine	-	-	+	+	+	+	+	20
esculin	-	-	+	+	+	-	+	21
Acid production from:								22
arabinose	-	+	+	+	+	+	-	23
ribose	-	+	+	-	-	-	-	24
xylose	-	+	+	-	-	-	-	25
fructose	+	+	+	+	+	+	+	26
galactose	+	+	+	+	+	+	+	27
lactose	+	+	+	+	+	+	+	28
sucrose	+	+	+	+	+	+	+	29
glycerol	+	+	+	+	+	+	+	30
CO <sub>2</sub> from glucose	-	-	-	-	-	-	-	31
								32
								33
								34

35 <sup>a</sup> R, rod; C, coccus.

36 <sup>b</sup> sc, short chain; lc, long chain.

37 nd, not determined.

### **Legend to supplementary figures.**

**Fig. S1.** Dendrogram obtained from combined RAPD-PCR patterns of the fastest acidifier rennet LAB. Scale bar indicates the percentage of similarity.

**Fig. S2.** Phylogenetic tree of unspiciated enterococci isolated from animal rennet pastes based on 16S rRNA gene sequences. Sequence alignment was performed with CLUSTAL-X (43). Sequence and alignment manipulations and calculation of similarity values and nucleotide compositions of sequences were performed with GeneDoc program version 2.5.000 (Nicholas and Nicholas, unpublished data). Positions available for analysis were ca. 1080 bp. Phylogenetic and molecular evolutionary analyses were conducted using MEGA version 3.1 (44). The bar indicates the number of nucleotide substitutions per site.

### **REFERENCES**

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44. **Kumar S, Tamura K, Nei M.** 2004. MEGA3: Integrated software for molecular evolutionary genetics analysis and sequence alignment. *Brief Bioinform* **5**:150–163.

Fig. S1

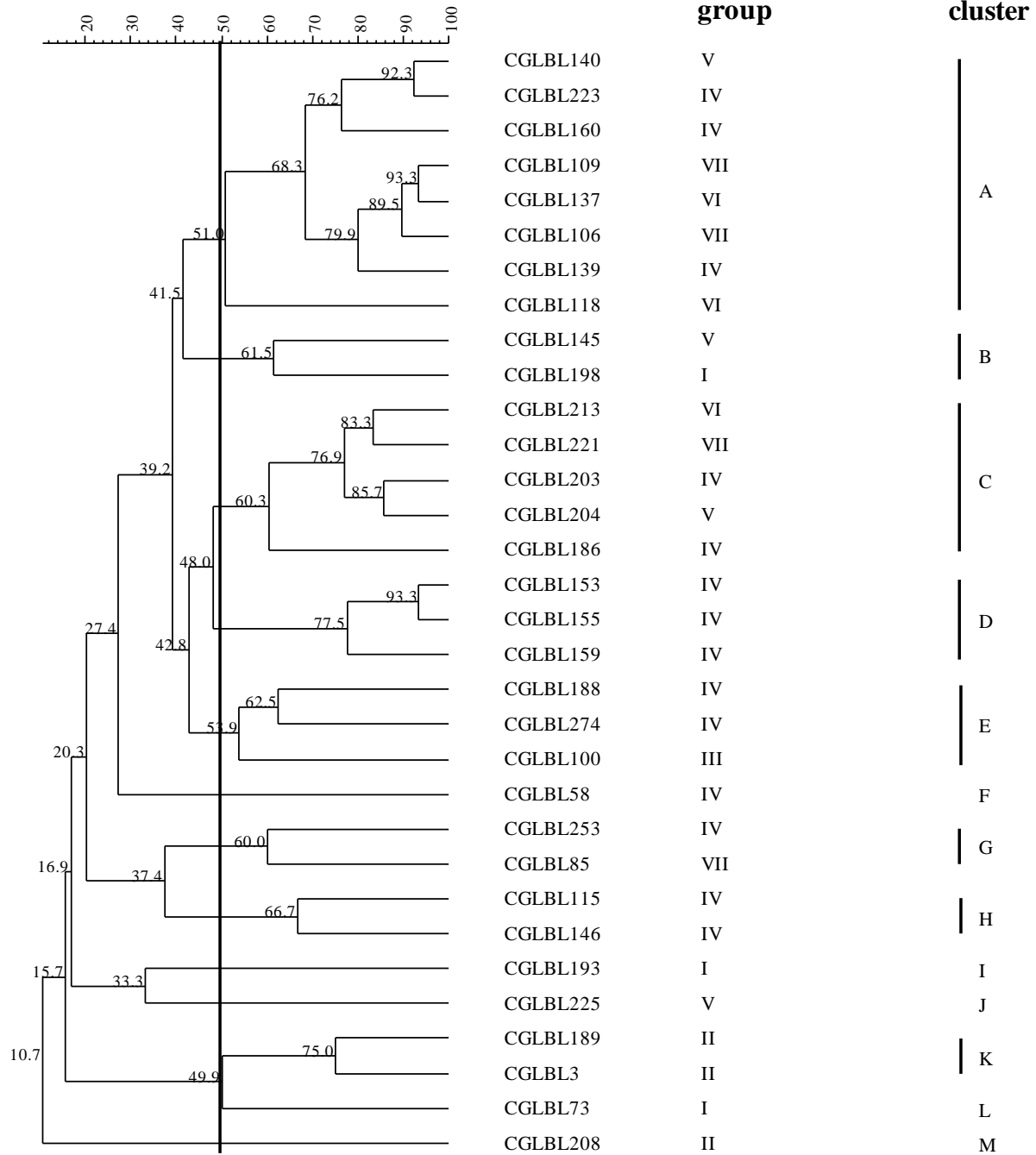


Fig. S2

