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## Taxono-genomics description of ‘*Lactobacillus raoultii* sp. nov.’, strain Marseille-P4006T, a new *Lactobacillus* species isolated from the female genital tract of a patient with bacterial vaginosis

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1 **Taxonogenomics description of “*Lactobacillus raoultii* sp. nov”, strain Marseille-P4006<sup>T</sup>,**  
2 **a new *Lactobacillus* species isolated from the female genital tract of a patient with**  
3 **bacterial vaginosis**

4  
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20  
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25 **References:** 43

**Table 3** Univariate and multivariate logistic regression analyses for mortality

Parameter	Univariate analysis		Multivariate analysis <sup>a</sup>	
	Odds ratio (95% CI)	<i>P</i>	Odds ratio (95% CI)	<i>P</i>
Age	1.009 (0.982, 1.038)	0.509		
Male	0.952 (0.503, 1.802)	0.881		
BMI	1.090 (0.960, 1.237)	0.184		
Hypertension	1.164 (1.094, 1.238)	<0.001	1.112 (1.040, 1.188)	0.011
Diabetes	1.786 (0.906, 3.522)	0.094		
Smoking history	2.360 (1.555, 3.583)	<0.001	1.709 (1.058, 2.761)	0.009
Drinking history	0.935 (0.470, 1.863)	0.849		
Family history of ischemic stroke	1.544 (0.763, 3.125)	0.227		
TC	1.004 (0.997, 1.011)	0.238		
TG	1.002 (0.996, 1.007)	0.591		
HDL-C	1.317 (1.028, 1.626)	<0.001	1.474 (1.154, 1.882)	0.002
LDL-C	1.633 (1.308, 2.038)	<0.001	1.381 (1.100, 1.732)	0.005
Lp(a)	1.093 (1.034, 1.156)	0.002	1.091 (1.021, 1.165)	0.010
Apo A/Apo B	1.804 (1.392, 2.337)	<0.001	1.907 (1.425, 2.552)	<0.001
NLR	1.317 (1.028, 1.626)	<0.001	1.474 (1.154, 1.882)	0.002
PLR	0.998 (0.972, 1.026)	0.908		
hs-CRP	1.633 (1.308, 2.038)	<0.001	1.381 (1.100, 1.732)	0.005
TNF- $\alpha$	1.009 (1.001, 1.019)	0.021	1.015 (1.006, 1.315)	0.037

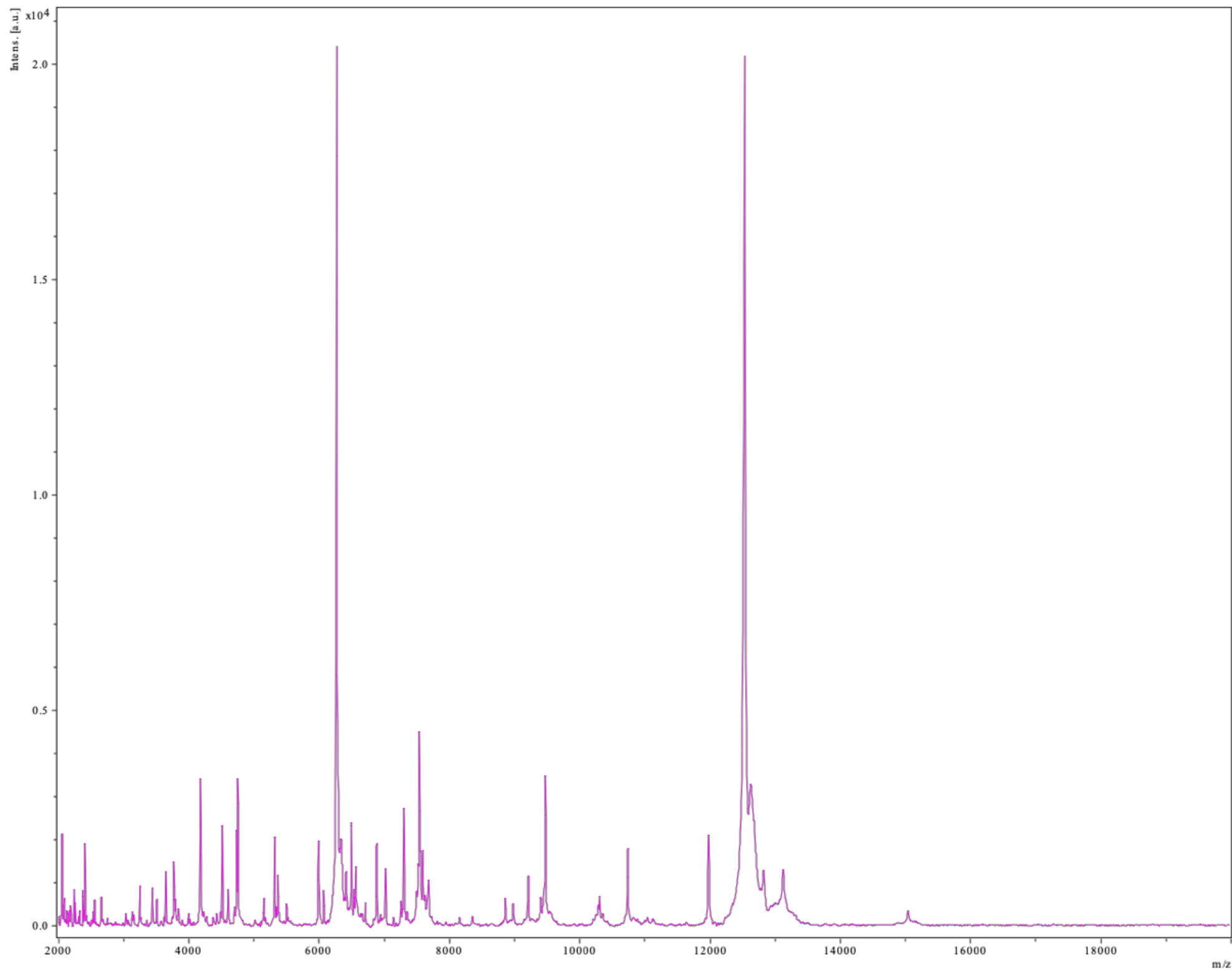
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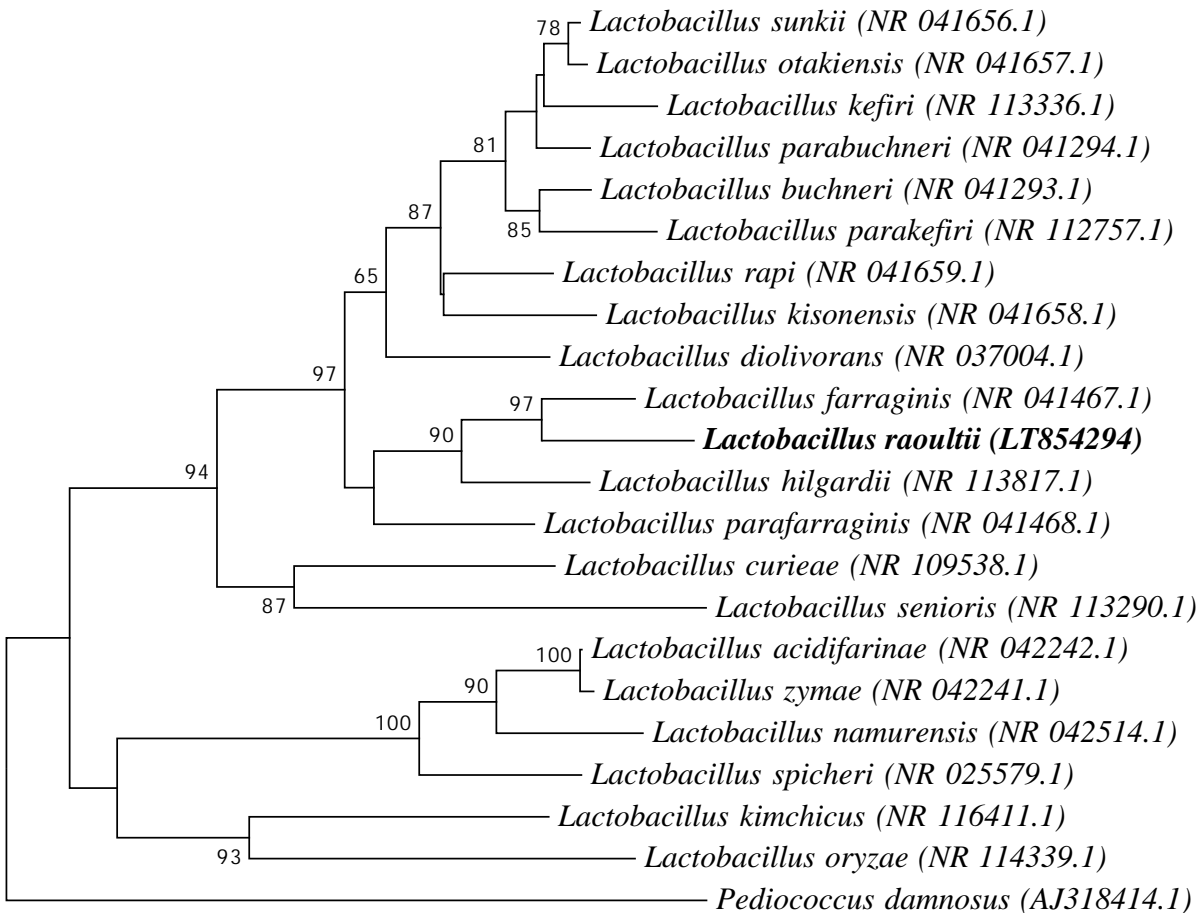
IL-6	1.265 (1.060, 1.508)	0.009	1.171 (1.059, 1.430)	0.022
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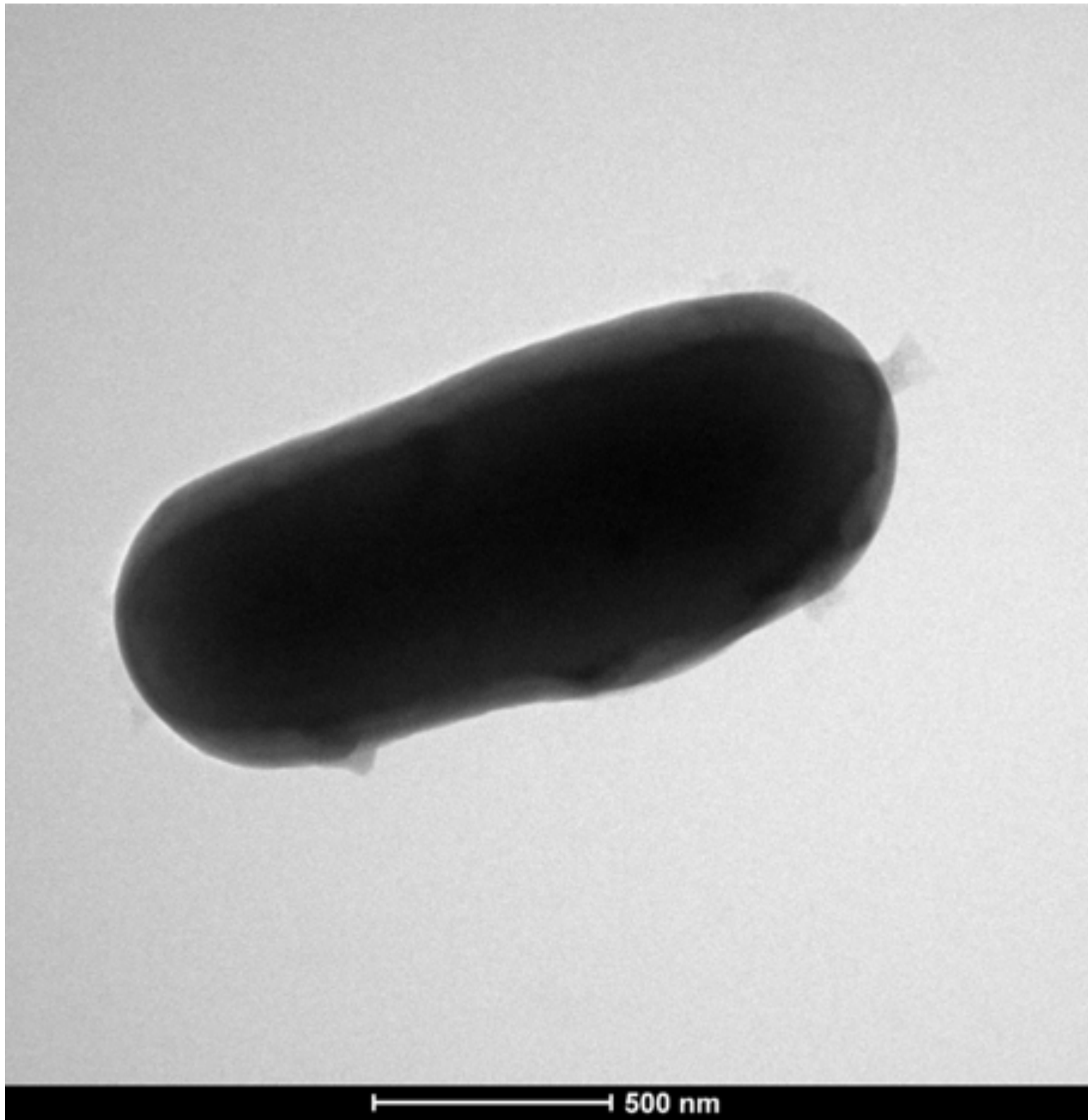
Abbreviation: NLR: neutrophil to lymphocyte ratio; hs-CRP: hypersensitive C-reactive protein; TNF- $\alpha$ : tumor necrosis factor- $\alpha$ ; IL-6: interleukin 6; HDL-C: high-density lipoprotein cholesterol; LDL-C: low-density lipoprotein cholesterol; Lp(a): lipoprotein (a); Apo A/Apo B: apolipoprotein A/ apolipoprotein B

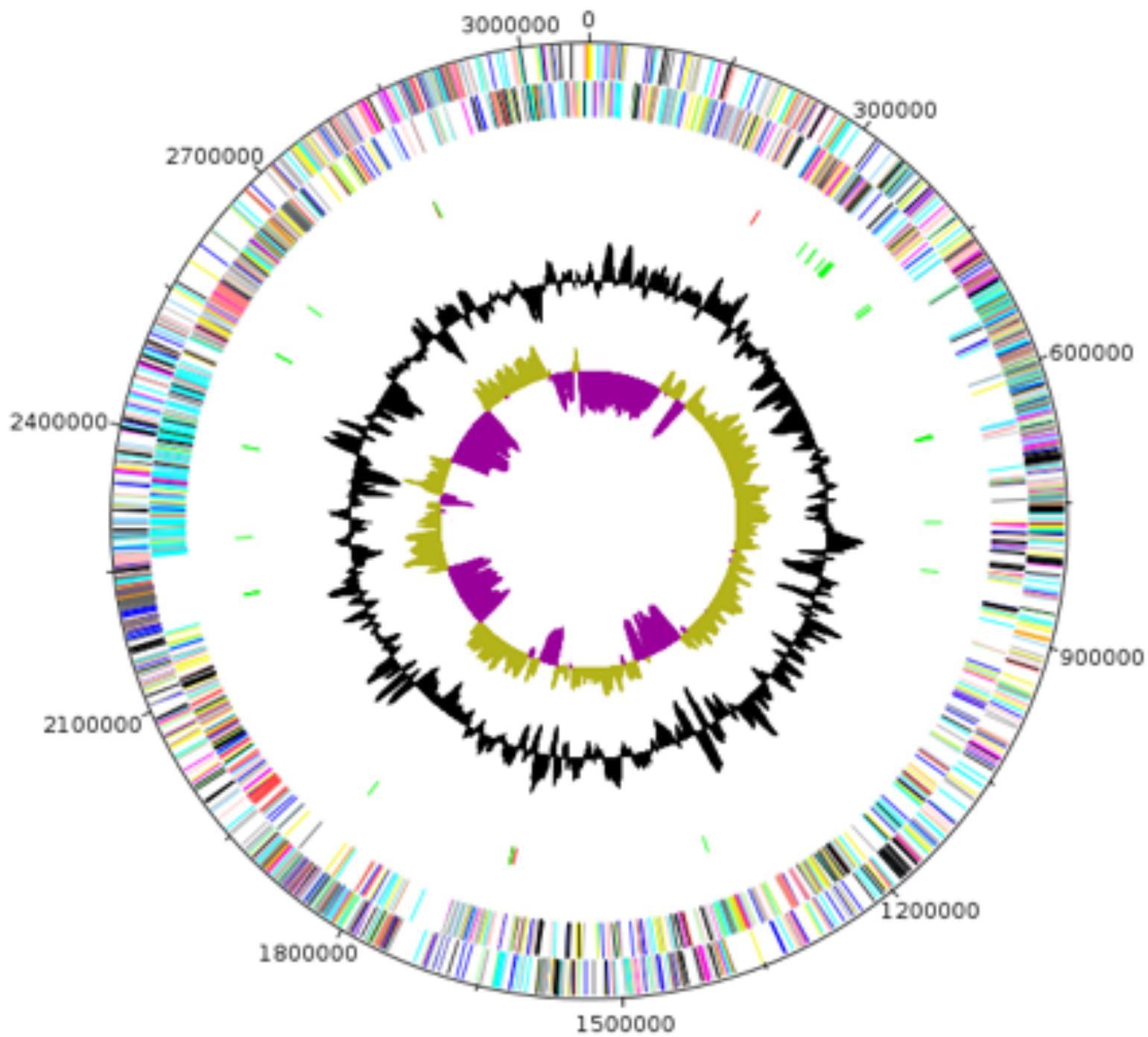
<sup>a</sup> The odds ratio was adjusted for all significant variables of the univariate logistic regression analysis



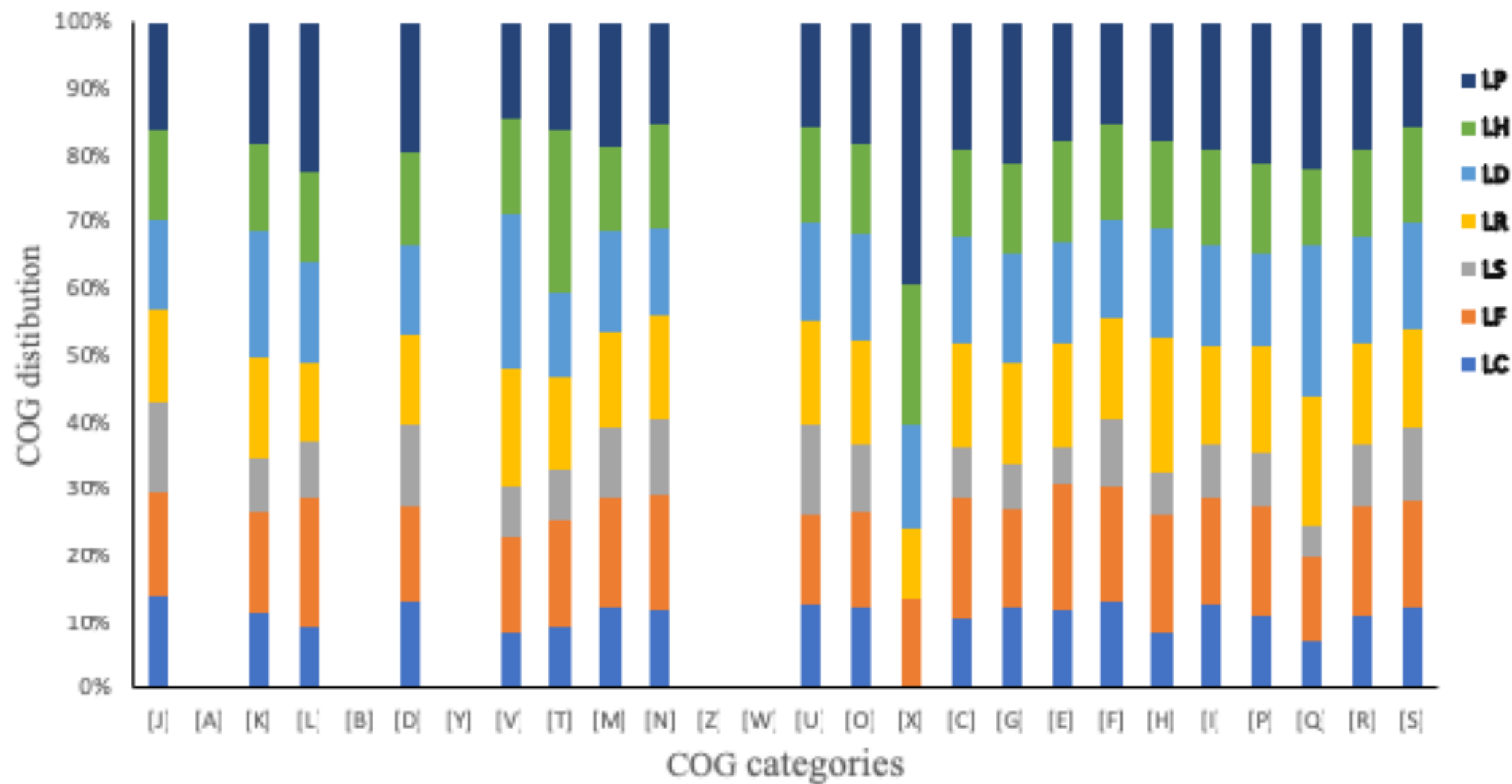


0.005









1 **Table 1.** Classification and general features of *Lactobacillus raoultii* strain Marseille-P4006<sup>T</sup>.

<b>Properties</b>	<b>Terms</b>
Taxonomy	<p><b>Kingdom:</b> <i>Bacteria</i></p> <p><b>Phylum:</b> <i>Firmicutes</i></p> <p><b>Class:</b> <i>Bacilli</i></p> <p><b>Order:</b> <i>Lactobacillales</i></p> <p><b>Family:</b> <i>Lactobacillaceae</i></p> <p><b>Genus:</b> <i>Lactobacillus</i></p> <p><b>Species:</b> <i>Lactobacillus raoultii</i></p>
Type strain	Marseille-P4006
Isolation site	Human vagina
Isolation country	France
Gram stain	Positive
Cell shape	Rod
Motility	Non
Oxygen requirements	Facultative anaerobic
Optimal temperature	37°C
Temperature range	Mesophilic
Habitat	Host associated
Biotic relationship	Free living
Host name	<i>Homo sapiens</i>
Sporulation	Non-sporulating

2

3 **Table 2.** Cellular fatty acid composition (%).

<b>Fatty acids</b>	<b>Name</b>	<b>Mean relative %<sup>(a)</sup></b>
16:0	Hexadecanoic acid	47.7 ± 1.2
19:1n9	10-Nonadecenoic acid	13.5 ± 0.5
18:00	Octadecanoic acid	11.2 ± 3.3
19:1n7	12-Nonadecenoic acid	9.1 ± 0.8
18:1n9	9-Octadecenoic acid	8.3 ± 0.5
18:1n7	11-Octadecenoic acid	3.5 ± 0.4
18:2n6	9,12-Octadecadienoic acid	2.2 ± 0.2
15:0	Pentadecanoic acid	1.6 ± 0.1
14:0	Tetradecanoic acid	1.0 ± 0.2
17:0	Heptadecanoic acid	TR
16:1n9	7-Hexadecenoic acid	TR
16:1n7	9-Hexadecenoic acid	TR
17:0 anteiso	14-methyl-Hexadecanoic acid	TR

4 <sup>a</sup>Mean peak area percentage; ± standard deviation; TR = trace amounts < 1%

5

6 **Table 3.** Differential characteristics of *Lactobacillus raoultii* strain Marseille-P4006<sup>T</sup>,  
7 *Lactobacillus senioris* strain DSM 24302, *Lactobacillus farraginis* strain DSM 18382,  
8 *Lactobacillus parafarraginis* strain DSM 18390, *Lactobacillus diolivorans* strain DSM 14421,  
9 *Lactobacillus hilgardii* Bergey's manual, *Lactobacillus curieae* strain JCM 18524 (39–  
10 41,43,42).

Properties	<i>L. raoultii</i>	<i>L. senioris</i>	<i>L. farraginis</i>	<i>L. parafarraginis</i>	<i>L. diolivorans</i>	<i>L. hilgardii</i>	<i>L. curieae</i>
<b>Cell diameter (µm)</b>	0.7 x 1.6	0.7 x 1.0-10.0	0.8 x 3-6	0.8 x 2-4	1 x 2	0.5-0.8 x 2-4	0.6x 1.2-3
<b>Major fatty acid</b>	C <sub>16:0</sub> (48%)	C <sub>18:1ω9</sub> (57%)	na	na	na	na	C <sub>18:1ω7c</sub> / C <sub>18:1ω9c</sub> (46.36%)
<b>DNA G+C content (%mol/L)</b>	41.4	39.1	42.1	45.2	40	39.6	39.8
<b>Production of</b>							
Catalase	-	-	-	-	-	na	-
Oxidase	-	na	na	na	na	na	na
<b>Acid production from</b>							
D-Galactose	+	-	+	+	+	v	+
D-Fructose	+	+	+	+	+	na	+
Melibiose	+	-	+	+	+	-	+
5-Ketogluconate	+	-	na	na	w	na	-
D-Xylose	+	+	-	+	+	+	-
L-Arabinose	+	+	+	+	+	-	-
D-Ribose	+	+	+	+	+	+	na
D-Glucose	+	+	+	+	+	na	na
Esculin	+	-	na	na	-	-	w
Maltose	+	-	+	+	+	+	+
Gluconate	+	+	w	w	+	na	na
D-Mannose	-	na	-	-	-	-	w
Methyl αD- glucopyranoside	-	-	na	na	w	na	+
Lactose	-	-	-	-	-	na	w
Sucrose	-	-	+	+	-	v	+
Melezitose	-	-	+	+	-	v	+
Raffinose	-	-	+	+	-	-	+
Turanose	-	-	na	na	-	na	+
Methyl βD- xylopyranoside	-	-	na	na	+	na	-
N-acetylglucosamine	-	W	na	na	-	na	-
<b>Habitat</b>	Human vagina	Human Faeces	Shochu residue	Shochu residue	Maize silage	Wine	Stinky tofu brine

11 +, positive reaction; -, negative reaction; v, variable; w, weakly positive; na, no available data.  
12 Data are from literature except DNA G+C content which was calculated by RAST online  
13 software.

14 **Table 4.** Nucleotide content and gene count levels of the genome.

15

<b>Attribute</b>	<b>Value</b>	<b>% of total</b>	16
			17
Size (bp)	3,070,142	100%	18
G+C content (bp)	1,271,038	41.4%	19
			20
Coding region (bp)	2,627,322	85.57%	21
			22
Total genes	2,924	100%	23
			24
RNA genes	68	2.35%	25
			26
Protein-coding genes	2,855	97.64%	27
Genes with function prediction	2,047	70.00%	
Genes assigned to COGs	2,195	75.06%	
Genes with peptide signals	210	7.18%	
Genes with transmembrane helices	828	28.31%	
Protein associated with ORFans	606	20.72%	

28 **Table 5.** Number of genes associated with 25 general COG functional categories.

<b>Code</b>	<b>Value</b>	<b>% value<sup>a</sup></b>	<b>Description</b>
<b>J</b>	141	4.82	Translation
<b>A</b>	0	0	RNA processing and modification
<b>K</b>	178	6.09	Transcription
<b>L</b>	119	4.07	Replication, recombination and repair
<b>B</b>	0	0	Chromatin structure and dynamics
<b>D</b>	22	0.75	Cell cycle control, mitosis and meiosis
<b>Y</b>	0	0	Nuclear structure
<b>V</b>	60	2.05	Defense mechanisms
<b>T</b>	61	2.09	Signal transduction mechanisms
<b>M</b>	112	3.83	Cell wall/membrane biogenesis
<b>N</b>	8	0.27	Cell motility
<b>Z</b>	0	0	Cytoskeleton
<b>W</b>	0	0	Extracellular structures
<b>U</b>	15	0.51	Intracellular trafficking and secretion
<b>O</b>	74	2.53	Posttranslational modification, protein turnover, chaperones
<b>X</b>	4	0.14	Mobilome: prophages, transposons
<b>C</b>	109	3.73	Energy production and conversion
<b>G</b>	200	6.84	Carbohydrate transport and metabolism
<b>E</b>	250	8.55	Amino acid transport and metabolism
<b>F</b>	87	2.98	Nucleotide transport and metabolism
<b>H</b>	107	3.66	Coenzyme transport and metabolism
<b>I</b>	65	2.22	Lipid transport and metabolism
<b>P</b>	117	4.00	Inorganic ion transport and metabolism
<b>Q</b>	25	0.85	Secondary metabolites biosynthesis, transport, and catabolism
<b>R</b>	239	8.17	General function prediction only
<b>S</b>	202	6.91	Function unknown
<b>_</b>	729	24.93	Not in COGs

29 <sup>a</sup>The total is based on the total number of protein-coding genes in the annotated genome.

31 **Table 6.** Genomic comparison of *L. raoultii* with closely related *Lactobacillus* species

<b>Species</b>	<b>Strain</b>	<b>Genome accession number</b>	<b>Genome size (Mb)</b>	<b>GC content (%)</b>	<b>Gene content</b>
<i>Lactobacillus raoultii</i>	<b>Marseille-P4006</b>	<b>OVSN00000000</b>	<b>3.07</b>	<b>41.4</b>	<b>2,855</b>
<i>Lactobacillus parafarraginis</i>	DSM 18390	NZ_BBAR00000000	3.10	45.2	3,053
<i>Lactobacillus farraginis</i>	DSM 18382	NZ_BAKI00000000	2.84	42.1	3,079
<i>Lactobacillus diolivorans</i>	DSM 14421	NZ_AZEY00000000	3.26	40	2,962
<i>Lactobacillus hilgardii</i>	DSM 20176	NZ_ACGP00000000	2.61	39.6	2,599
<i>Lactobacillus curieae</i>	JCM 18524	NZ_CP018906	2.09	39.8	1,960
<i>Lactobacillus senioris</i>	DSM 24302	NZ_AYZR00000000	1.56	39.1	1,539

32

**Table 7.** Genomic comparisons of *L. raoultii* with closely related *Lactobacillus* species †

Strains	<i>L. raoultii</i>	<i>L. senioris</i>	<i>L. farraginis</i>	<i>L. curieae</i>	<i>L. diolivorans</i>	<i>L. hilgardii</i>	<i>L. parafarraginis</i>
<i>Lactobacillus raoultii</i>	<b>2,855</b>	1,118	1,658	1,476	1,794	1,743	1,55
<i>Lactobacillus senioris</i>	68.79%	<b>1,569</b>	974	1,080	1,112	1,094	930
<i>Lactobacillus farraginis</i>	76.87%	68.00%	<b>3,170</b>	1,298	1,572	1,593	1,385
<i>Lactobacillus curieae</i>	69.56%	69.20%	68.80%	<b>1,992</b>	1,470	1,426	1,199
<i>Lactobacillus diolivorans</i>	73.46%	69.16%	73.00%	70.03%	<b>3,053</b>	1,706	1,482
<i>Lactobacillus hilgardii</i>	77.75%	68.82%	78.17%	69.85%	74.26%	<b>2,592</b>	1,461
<i>Lactobacillus parafarraginis</i>	73.50%	67.07%	74.05%	68.38%	71.84%	74.40%	<b>3,629</b>

† numbers of orthologous proteins shared between genomes (above diagonal), AGIOS values (below diagonal) and numbers of proteins per genome (bold numbers).



**Table 8.** dDDH values obtained by comparing all genomes studied using GGDC, Formula 2.

Strain	<i>L. raoultii</i>	<i>L. senioris</i>	<i>L. farraginis</i>	<i>L. curieae</i>	<i>L. diolivorans</i>	<i>L. hilgardii</i>	<i>L. parafarraginis</i>
<i>Lactobacillus raoultii</i>	100%±00	21.3%±2.30	20.4%±2.30	19.8%±2.30	19.8%±2.30	20.8%±2.30	19.7%±2.30
<i>Lactobacillus senioris</i>		100%±00	20.0%±2.30	18.7%±2.30	18.8%±2.25	19.6%±2.30	20.0%±2.30
<i>Lactobacillus farraginis</i>			100%±00	19.4%±2.30	20.5%±2.35	19.0%±2.30	21.2%±2.35
<i>Lactobacillus curieae</i>				100%±00	19.9%±2.30	21.5%±2.35	21.1%±2.35
<i>Lactobacillus diolivorans</i>					100%±00	20.8%±2.35	20.5%±2.35
<i>Lactobacillus hilgardii</i>						100%±00	20.4%±2.35
<i>Lactobacillus parafarraginis</i>							100%±00