Lactobacillus saniviri sp. nov. and *Lactobacillus senioris* sp. nov., isolated from human faeces

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Two Gram-stain-positive strains, YIT 12363^T and YIT 12364^T, were isolated from human faeces. They were rod-shaped, non-motile, asporogenous, facultatively anaerobic and did not exhibit catalase activity. Comparative analyses of 16S rRNA, *pheS* and *rpoA* gene sequences demonstrated that the novel strains were members of the genus *Lactobacillus*. On the basis of 16S rRNA gene sequence similarity, the type strains of *Lactobacillus casei* (95.3% similarity), *Lactobacillus paracasei* subsp. *paracasei* (95.6%), *Lactobacillus paracasei* subsp. *tolerans* (95.3%) and *Lactobacillus rhamnosus* (95.4%) were the closest neighbours to strain YIT 12363^T. For strain YIT 12364^T, the highest similarity values were observed with the type strains of *Lactobacillus diolivorans*, *Lactobacillus parafarraginis* and *Lactobacillus rapi* (95.8, 96.0 and 96.0%, respectively). Phenotypic and genotypic features demonstrated that these strains each represent a separate novel species of the genus *Lactobacillus*, and the names *Lactobacillus saniviri* sp. nov. (type strain YIT 12363^T=JCM 17471^T=DSM 24301^T) and *Lactobacillus senioris* sp. nov. (type strain YIT 12364^T=JCM 17472^T=DSM 24302^T), respectively, are proposed.

Lactobacillus strains are among the most familiar microorganisms to humans, not only because of their association with a wide range of naturally fermented dairy products, grain crops and vegetables but also because they inhabit the gastrointestinal tracts of humans and animals, and are the most widely used probiotics aimed at promoting a healthy lifestyle. Currently, the genus *Lactobacillus* comprises about 140 species, although only a few species – *Lactobacillus brevis*, the *Lactobacillus casei* group, *Lactobacillus delbrueckii*, *Lactobacillus gasseri*, *Lactobacillus parabuchneri*, the *Lactobacillus plantarum* group, *Lactobacillus reuteri* and *Lactobacillus sakei* – have been found in human faeces (Dal Bello *et al.*, 2003; Walter, *et al.*, 2001). Although the names of around 80 species have been validly published in the last decade, no novel species isolated from human faeces

have been described during this time (J. P. Euzéby: List of Prokaryotic names with Standing in Nomenclature; <http://www.bacterio.cict.fr/index.html>).

While exploring novel *Lactobacillus* strains from the culture collection of the Yakult Central Institute, 328 strains isolated from the faeces of 61 healthy Japanese subjects in different age-groups – neonates, infants, adults, elderly people and centenarians – were reanalysed by determining 16S rRNA gene sequence similarity values and using DNA–DNA hybridization tests. As a result, two strains that could not be clearly placed within any recognized species of the genus *Lactobacillus* were discovered. In the present study, further phenotypic and genotypic research revealed that strains YIT 12363^T and YIT 12364^T represent two novel species of the genus *Lactobacillus*. The following *Lactobacillus* strains were obtained from the culture collection of Yakult Central Institute (YIT, Tokyo, Japan) and were used as references: *L. casei* YIT 0078^T, *Lactobacillus paracasei* subsp. *paracasei* YIT 0209^T and *Lactobacillus rhamnosus* YIT 0105^T (for isolate YIT 12363^T); and *Lactobacillus parafarraginis* YIT 12274^T and *Lactobacillus rapi* YIT 11204^T (for isolate YIT 12364^T). The strains used in this study were cultivated and maintained in MRS broth (BD, Difco; pH 6.8) (De Man *et al.*, 1960) at 37 °C (or 30 °C for *L. parafarraginis* YIT 12274^T) for 16 h, unless indicated otherwise. Modified MRS broth [MRS broth supplemented with 1% (w/v) L-arabinose and 1% (w/v) maltose instead of glucose] was used for *L. rapi* YIT 11204^T.

Chromosomal DNA used as a template for 16S rRNA, *rpoA* and *pheS* gene sequence amplification was prepared

The GenBank/EMBL/DDBJ accession numbers for the 16S rRNA gene sequences of strains *Lactobacillus saniviri* sp. nov. YIT 12363^T and *Lactobacillus senioris* sp. nov. YIT 12364^T are AB602569 and AB602570, respectively; those for the *pheS* gene sequences are AB602775 and AB602776, respectively; and those for the *rpoA* gene sequences are AB602777 and AB602778, respectively. Accession numbers for the *pheS* gene sequences of *L. camelliae* YIT 12276^T, *L. farraginis* YIT 12273^T, *L. kisonensis* YIT 11168^T, *L. otakiensis* YIT 11163^T, *L. parafarraginis* YIT 12274^T, *L. rapi* YIT 11204^T and *L. sunkii* YIT 11161^T are AB602819–AB602825, respectively; and those for the *rpoA* gene sequences are AB602828–AB602834, respectively. Accession numbers for the *rpoA* gene sequences of *L. buchneri* YIT 0077^T and *L. diolivorans* YIT 10368^T are AB602826 and AB602827, respectively.

Three supplementary figures are available with the online version of this paper.

according to the method of Watanabe *et al.* (2008). The conditions for PCR amplification of the partial 16S rRNA gene and subsequent DNA sequencing have been described previously (Chao *et al.*, 2008). The *pheS* and *rpoA* gene sequences for YIT 12363^T, YIT 12364^T, *Lactobacillus buchneri* YIT 0077^T (*rpoA* gene only), *Lactobacillus camelliae* YIT 12276^T, *Lactobacillus diolivorans* YIT 10368^T (*rpoA* gene only), *Lactobacillus farraginis* YIT 12273^T, *Lactobacillus kisonensis* YIT 11168^T, *Lactobacillus otakiensis* YIT 11163^T, *L. parafarraginis* YIT 12274^T, *L. rapi* YIT 11204^T and *Lactobacillus sunkii* YIT 11161^T were amplified by PCR with primers *rpoA*-21F (5'-ATGATYGARTTTGAAAAACC-3') and *rpoA*-23R (5'-ACHGTRTTRATDCCDGCRCG-3') (Naser *et al.*, 2005), and *pheS*-21F (5'-CAYCCNGCHCGY-AYATGC-3') and *pheS*-952R (5'-TATTTCAAATGCR-AAACGRTC-3') (for YIT 12363^T, YIT 12364^T) or *pheS*-23R (5'-GGRTGTACCATVCCNGCHCC-3') (Naser *et al.*, 2005), respectively. The PCR mixture (25 µl) contained 1 × Ex *Taq* Buffer, 200 µM of each dNTP, 0.4 µM of each primer, 1 U Ex *Taq* HS polymerase (Takara Bio) and 10 ng template DNA. The amplification program consisted of: one cycle of 95 °C for 2 min; 35 cycles of 95 °C for 20 s, 55 °C (for *pheS* gene) or 46 °C (for *rpoA* gene) for 30 s, 72 °C for 1 min 15 s; and finally one cycle of 72 °C for 3 min. For amplification of the *pheS* gene of strains YIT 12363^T and YIT 12364^T, 1 × *Taq* buffer and *Taq* polymerase (Takara Bio) were used and the annealing temperature was changed to 42 °C. For amplification of the *pheS* gene of *L. rapi* YIT 11204^T, the annealing temperature was changed to 42 °C. For amplification of the *rpoA* gene of *L. farraginis* YIT 12274^T, the annealing and elongation steps were modified to 48 °C for 20 s and 72 °C for 5 s, respectively.

The amplified 16S rRNA, *pheS* and *rpoA* genes were purified by using an AMPure kit (Beckman Coulter) and were subsequently sequenced using the ABI PRISM BigDye Terminator v3.1 cycle sequencing kit (Applied Biosystems). The closest known species to the novel isolates were determined by FASTA and sequences of members of the most closely related species were extracted from GenBank/EMBL/DBJ. Multiple alignment and the construction of phylogenetic trees were performed with the program CLUSTAL_X v. 2.0.12. (Thompson *et al.*, 1997). For strain YIT 12363^T, strain YIT 12364^T and related strains, approximately 1390 bp of the 16S rRNA gene, approximately 280 bp of the *pheS* gene and approximately 350 bp of the *rpoA* gene sequences were used for constructing phylogenetic trees by the neighbour-joining method (Saitou & Nei, 1987). The statistical reliability of trees was evaluated by bootstrap analysis of 1000 replicates (Felsenstein, 1985) and tree topologies were also confirmed with the minimum-evolution (Rzhetsky & Nei, 1992) and maximum-parsimony (Fitch, 1971) methods, by using MEGA v4.1 software (Tamura *et al.*, 2007), according to the Kimura two-parameter model (Kimura, 1980).

Phylogenetic analysis based on 16S rRNA gene sequences showed that isolate YIT 12363^T was a close neighbour to the *L. casei* group of lactobacilli (Fig. 1). 16S rRNA gene sequence similarities between strain YIT 12363^T and its

closest neighbours, *L. casei* YIT 0078^T, *L. paracasei* subsp. *paracasei* YIT 0209^T, *L. paracasei* subsp. *tolerans* NBRC 15906^T and *L. rhamnosus* YIT 0105^T were high, with values of 95.3, 95.6, 95.3 and 95.4 %, respectively. Similar topologies were obtained by the minimum-evolution (Supplementary Fig. S1, available in IJSEM Online) and maximum-parsimony (data not shown) methods. Similarities between the *pheS* and *rpoA* gene sequences of strain YIT 12363^T and the most closely related strains ranged from 73.5 to 75.2 %, and from 79.5 to 80.4 %, respectively (Supplementary Figs S2 and S3, available in IJSEM Online). Phylogenetic analysis based on 16S rRNA gene sequences placed isolate YIT 12364^T in the *L. buchneri* group of lactobacilli (Fig. 1). 16S rRNA gene sequence similarities between strain YIT 12364^T and its closest neighbours, *L. diolivorans* YIT 10368^T, *L. parafarraginis* NRIC 0677^T and *L. rapi* YIT 11204^T, were 95.8, 96.0 and 96.0 %, respectively; 16S rRNA gene sequence similarities with the type strains of all other species in this group were below 97 %. Similar topologies were obtained by the minimum-evolution (Supplementary Fig. S1) and maximum-parsimony (data not shown) methods. Similarities between the *pheS* and *rpoA* gene sequences of isolate YIT 12364^T and the most closely related strains ranged from 77.3 to 79.9 %, and from 79.9 to 80.0 %, respectively (Supplementary Figs S2 and S3). Interspecies gaps within the genus *Lactobacillus* based on *pheS* and *rpoA* gene sequences normally exceed 10 % and 5 %, respectively (Naser *et al.*, 2007), which suggested that the novel strains should be classified as members of two novel species.

For determination of DNA–DNA relatedness and the DNA G + C content, chromosomal DNA was extracted according to the method of Marmur (1961). DNA–DNA hybridization analyses were performed between strain YIT 12363^T, *L. casei* YIT 0078^T, *L. paracasei* subsp. *paracasei* YIT 0209^T and *L. rhamnosus* YIT 0105^T, and between strain YIT 12364^T, *L. parafarraginis* YIT 12274^T and *L. rapi* YIT 11204^T, respectively. The microdilution well technique was used as described by Ezaki *et al.* (1989) using a Spectra Max M2 (Molecular Devices) for fluorescence measurements. Reciprocal hybridization experiments were performed for every pair of strains at 44 °C (for YIT 12363^T and its reference strains) or 40 °C (for YIT 12364^T and its reference strains) for 2 h in the presence of 50 % formamide, using biotinylated DNA and unlabelled ssDNA, which was bound non-covalently to microplate wells. The highest and lowest values of eight replicate wells were excluded and the mean of the remaining values was calculated for each experiment. The levels of DNA–DNA relatedness of strain YIT 12363^T to *L. casei* YIT 0078^T, *L. paracasei* subsp. *paracasei* YIT 0209^T and *L. rhamnosus* YIT 0105^T were 22.3–30.0, 19.7–25.7 and 12.5–27.8 %, respectively; those of strain YIT 12364^T to *L. parafarraginis* YIT 12274^T and *L. rapi* YIT 11204^T were 11.6–26.3 and 15.9–23.1 %, respectively. All values among the reference strains were well below the 70 % cut-off value that indicates separate species status (Stackebrandt & Goebel, 1994). To assess the DNA G + C

Fig. 1. Phylogenetic tree based on 16S rRNA gene sequences showing the relationship of *Lactobacillus saniviri* sp. nov. YIT 12363^T and *Lactobacillus senioris* sp. nov. YIT 12364^T with strains of closely related species. The tree was constructed by the neighbour-joining method on the basis of a comparison of approximately 1390 bp, and *Lactobacillus vitulinus* JCM 8228^T was used as the outgroup. Bootstrap values (%) based on 1000 replications are given at nodes. Bar, 5% sequence divergence.

content, DNA was enzymically degraded into nucleosides as described previously (Mesbah *et al.*, 1989) and then separated by HPLC. The DNA G+C contents of strains YIT 12363^T and YIT 12364^T were 48.7 and 41.6 mol%, respectively, which are within the range for the genus *Lactobacillus* (32.0–53.0 mol%) (Kandler & Weiss, 1986).

Morphological, cultural and biochemical tests were performed according to standard techniques at 37 °C unless otherwise stated. Cell shape, cell size and Gram staining were determined by using cultures grown in MRS broth at 37 °C for 16 h. Motility was tested in MRS soft agar (0.15%). Catalase activity was determined by using cells

grown on MRS agar. Gas production from glucose was measured with a Durham tube in MRS broth. Production of dextran was assessed on MRS agar in which glucose was replaced with 2 % (w/v) sucrose. The methods of Barrow & Feltham (1993) were used to determine growth at various temperatures and pH, and in the presence of NaCl, reduction of nitrate and production of ammonia from arginine. Carbohydrate fermentation tests were conducted by using the API 50 CHL system (bioMérieux) according to the manufacturer's instructions. The presence of diaminopimelic acid in the cell-wall peptidoglycan was determined

according to Kandler & Weiss (1986). Cell-wall peptidoglycan for analysis of amino acid composition was prepared and hydrolysed according to the method of Schleifer & Kandler (1972). Cell-wall amino acids were analysed by HPLC (Alliance 2695 HPLC system; Waters) equipped with a fluorescence detector (model 474 Fluorescence Detector; Waters) and an AccQ-Tag column (3.9 × 150 mm; Waters), and using an AccQ-Fluor reagent KIT (6-aminoquinolyl-N-hydroxysuccinimidylcarbamate; Waters) for derivatization. Cellular fatty acid methyl esters were obtained from cells grown in MRS broth at 37 °C (or 30 °C for *L. rapi* YIT

Table 1. Differential characteristics of *Lactobacillus saniviri* sp. nov. YIT 12363^T and closely related lactobacilli

Strains: 1, *Lactobacillus saniviri* sp. nov. YIT 12363^T; 2, *L. casei* YIT 0078^T; 3, *L. paracasei* subsp. *paracasei* YIT 0209^T; 4, *L. rhamnosus* YIT 0105^T. All strains were able to ferment D-galactose, D-glucose, D-fructose, D-mannose, D-mannitol, N-acetylglucosamine, amygdalin, cellobiose, maltose, trehalose, D-tagatose and gluconate (weakly). All strains were able to grow at pH 4.0 and 15 °C, and hydrolyse aesculin. No strains were able to ferment erythritol, D- or L-arabinose, D- or L-xylose, D-adonitol, methyl β-D-xylopyranoside, dulcitol, inositol, methyl α-D-mannopyranoside, inulin, glycogen, xylitol, D- or L-fucose, D- or L-arabitol, or 5-ketogluconate. None of the strains grew in 8 % NaCl. Strains were not motile and did not produce gas from glucose, dextran from sucrose, ammonia from arginine, or reduce nitrate. +, Positive; −, negative; w, weakly positive reaction; ND, no data.

Characteristic	1	2	3	4
Growth at:				
10 °C	+	w	w	w
45 °C	−	−	−	+
pH 8.5	+	+	−	+
Tolerance to 5 % salt	+	+	−	+
Acid production from:				
Glycerol	+	−	−	−
D-Ribose	+	−	+	+
L-Sorbose	−	−	−	+
L-Rhamnose	−	−	−	w
D-Sorbitol	−	−	−	+
Methyl α-D-glucopyranoside	−	−	w	+
Arbutin	+	+	+	w
Salicin	+	+	+	w
Lactose	−	+	+	+
Melibiose	+	−	−	−
Sucrose	+	w	+	+
Melezitose	+	+	+	w
Raffinose	+	−	−	−
Starch	w	−	−	−
Gentiobiose	+	+	+	w
Turanose	−	−	+	+
D-Lyxose	−	−	−	+
2-Ketogluconate	w	−	−	−
Optical form of lactic acid	DL	L	L	L
Peptidoglycan				
Type	L-Lys-D-Asp	ND	L-Lys-D-Asp	ND
meso-DAP*	−	+	−	−
DNA G + C content (mol%)	48.1	48.7	47.5	46.8

*DAP, Diaminopimelic acid.

11204^T) for 18 h by saponification, methylation and extraction using the method of Miller (1982) with minor modifications (Kuykendall *et al.*, 1988). FAMES were determined by using the MIDI system with MOORE5 of the MIS Standard Libraries. The isomers of lactic acid formed from glucose were determined with a TC D-/L-lactic acid test kit (Boehringer Mannheim).

Various phenotypic characteristics of isolate YIT 12363^T differed from those of *L. casei* YIT 0078^T, *L. paracasei* subsp. *paracasei* YIT 0209^T and *L. rhamnosus* YIT 0105^T. Likewise, isolate YIT 12364^T had different phenotypic characteristics from *L. parafarraginis* YIT 12274^T and *L. rapi* YIT 11204^T (Tables 1, 2 and 3). According to the genotypic and phenotypic data obtained, it is proposed that the novel strains should be classified as representatives of two novel *Lactobacillus* species: *Lactobacillus saniviri* sp. nov. (YIT 12363^T) and *Lactobacillus senioris* sp. nov. (YIT 12364^T).

Description of *Lactobacillus saniviri* sp. nov.

Lactobacillus saniviri (sa.ni.vi'ri. L. adj. *sanus* healthy; L. gen. n. *viri* of an adult male; N.L. gen. n. *saniviri* of a healthy adult male, indicating the source of the type strain).

Cells are rod-shaped (1.0 × 1.5–3.0 µm) and occur singly, in pairs or in short chains comprising three to six cells. Cells are Gram-stain-positive, non-motile, asporogenous and facultatively anaerobic. Catalase and pseudocatalase are not produced. After anaerobic growth at 37 °C for 72 h, colonies on MRS agar are circular to slightly irregular, 1.5–2.0 mm in diameter and beige with a smooth surface. After aerobic growth at 37 °C for 72 h on blood agar, α-haemolysis is observed. In MRS broth, growth occurs at 10 °C but not at 45 °C. Growth occurs at pH 4.0 and pH 8.5. Growth occurs in the presence of 5 % NaCl but not in the presence of 8 % NaCl. Gas is not produced from glucose. Both L- (49 %) and D-lactate (51 %) are produced as end products from glucose.

Table 2. Differential characteristics of *Lactobacillus senioris* sp. nov. YIT 12364^T and closely related lactobacilli

Strains: 1, *Lactobacillus senioris* sp. nov. YIT 12364^T; 2, *L. rapi* YIT 11204^T; 3, *L. parafarraginis* YIT 12274^T. All strains were able to ferment L-arabinose, D-ribose, D-xylose and D-glucose. No strains were able to ferment glycerol, erythritol, D-arabinose, L-xylose, D-adonitol, D-mannose, L-sorbose, L-rhamnose, dulcitol, inositol, D-mannitol, D-sorbitol, methyl α-D-mannopyranoside, amygdalin, arbutin, salicin, cellobiose, trehalose, inulin, starch, glycogen, xylitol, gentiobiose, D-lyxose, D-tagatose, D- or L-fucose, D- or L-arabitol or 2-ketogluconate. None of the strains grew in 8 % NaCl or at 10 °C, 45 °C and pH 8.5. Strains were not motile, did not contain meso-diaminopimelic acid in their peptidoglycan, and were not able to produce dextran from sucrose, reduce nitrate or hydrolyse aesculin. +, Positive; –, negative; w, weakly positive reaction; ND, no data.

Characteristic	1	2	3
Growth at:			
15 °C	+	–	+
pH 4.0	–	+	+
Tolerance to 5 % salt	w	–	–
Ammonia production from arginine	+	+	–
Acid production from:			
Methyl β-D-xylopyranoside	–	+	–
D-Galactose	–	–	w
D-Fructose	+	w	+
Methyl α-D-glucopyranoside	–	+	–
N-Acetylglucosamine	w	–	–
Maltose	–	+	+
Lactose	–	–	w
Melibiose	–	+	+
Sucrose	–	w	+
Melezitose	–	+	+
Raffinose	–	+	+
Turanose	–	+	–
Gluconate	+	w	w
5-Ketogluconate	–	w	w
Optical form of lactic acid	DL	L	DL
Peptidoglycan type	L-Lys-D-Asp	L-Lys-D-Asp	ND
DNA G+C content (mol%)	39.8	41.6	42.0

Table 3. Cellular fatty acid compositions of the novel strains and genetically closely related lactobacilli

Strains: 1, *L. saniviri* sp. nov. YIT 12363^T; 2, *L. paracasei* subsp. *paracasei* YIT 0209^T; 3, *L. senioris* sp. nov. YIT 12364^T; 4, *L. rapi* YIT 11204^T. Values are percentages of total fatty acids. Data are from the present study. —, Not detected. DMA, dimethylacetal. ECL, equivalent chain-length.

Fatty acid	1	2	3	4
Saturated				
C _{14:0}	1.16	11.98	—	1.22
C _{16:0}	4.1	17.88	2.23	18.2
C _{16:0} 3OH	—	0.36	—	—
C _{18:0}	0.82	0.56	1.53	0.59
C _{18:0} 12OH	4.42	4.74	—	—
Unsaturated				
C _{16:1} ω5c	—	0.56	—	—
C _{16:1} ω7c	—	4.63	—	2.28
C _{18:1} ω9c	56.61	30.32	57.22	28.18
C _{18:1} ω7c DMA	0.71	0.76	0.57	—
C _{18:2} ω6,9c	—	—	1.09	—
Cyclopropane				
C ₁₉ cyc 9,10	29.29	18.66	34.39	14.9
C ₁₉ cyc 11,12	—	—	—	5.41
Summed features*				
10	2.3	7.94	2.05	29.22
12	—	0.54	0.93	—
Unknown fatty acid (ECL 18.199)	0.59	1.05	—	—

*Summed feature 10: C_{18:1}ω7c and/or unknown fatty acid (ECL 17.834). Summed feature 12: unknown fatty acid (ECL 18.622) and/or iso-C_{19:0}.

Ammonia is not produced from arginine. Nitrate is not reduced. Acid is produced from glycerol, D-ribose, D-galactose, D-glucose, D-fructose, D-mannose, D-mannitol, N-acetylglucosamine, amygdalin, arbutin, salicin, cellobiose, maltose, melibiose, sucrose, trehalose, melezitose (weakly), raffinose, starch (weakly), gentiobiose, D-tagatose, gluconate (weakly) and 2-ketogluconate. Aesculin is hydrolysed. Dextran is not produced from sucrose. Cells do not contain *meso*-diaminopimelic acid in their cell-wall peptidoglycan. Peptidoglycan structure is of the L-Lys-D-Asp type in the presence of Lys, Glu, Ala and Asp. The major cellular fatty acids (>10 %) are unsaturated fatty acid C_{18:1}ω9c and cyclopropane C₁₉ cyc 9,10. Phylogenetic analysis of the 16S rRNA gene sequence indicates that members of the *L. casei* group of lactobacilli are the closest neighbours.

The type strain, YIT 12363^T (=JCM 17471^T=DSM 24301^T), was isolated from faeces of a healthy Japanese adult male in Tokyo, Japan. The DNA G+C content of the type strain is 48.7 mol%.

Description of *Lactobacillus senioris* sp. nov.

Lactobacillus senioris (se.ni'ō.ris. L. gen. n. *senioris* of/from an elderly person, indicating the source of the type strain).

Cells are rod-shaped (0.7 × 1.0–10.0 μm) and occur singly, in pairs or in chains comprising three to four cells. Cells are

Gram-stain-positive, non-motile, asporogenous and facultatively anaerobic. Catalase and pseudocatalase are not produced. After anaerobic growth at 37 °C for 72 h, colonies on MRS agar are circular, 1–2 mm in diameter and beige with a smooth or rough surface. In MRS broth, growth occurs at 15 °C but not at 10 °C or 45 °C. Growth does not occur at pH 4.0 or pH 8.5. Growth occurs weakly in the presence of 5 % NaCl but not in the presence of 8 % NaCl. Gas is produced from glucose. Both L- (72 %) and D-lactate (28 %) are produced as the end products from glucose. Ammonia is produced from arginine. Nitrate is not reduced. Acid is produced from L-arabinose, D-ribose, D-xylose, D-glucose, D-fructose, N-acetylglucosamine (weakly) and gluconate. Aesculin is not hydrolysed. Dextran is not produced from sucrose. Cells do not contain *meso*-diaminopimelic acid in their cell-wall peptidoglycan. Peptidoglycan structure is of the L-Lys-D-Asp type in the presence of Lys, Glu, Ala and Asp. The major cellular fatty acids are unsaturated fatty acid C_{18:1}ω9c and cyclopropane C₁₉ cyc 9,10. Phylogenetic analysis of the 16S rRNA gene sequence places the species in the *L. buchneri* group of lactobacilli.

The type strain, YIT 12364^T (=JCM 17472^T=DSM 24302^T), was isolated from faeces of a 100-year-old elderly female person in Okinawa, Japan. The DNA G+C content of the type strain is 41.6 mol%.

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