Lactobacillus satsumensis sp. nov., isolated from mashes of shochu, a traditional Japanese distilled spirit made from fermented rice and other starchy materials

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During a study of lactic acid bacteria originating from plant material, 62 strains were isolated from mashes of shochu, a traditional Japanese distilled spirit made from fermented rice, sweet potato, barley and other starchy materials, together with Saccharomyces cerevisiae and Aspergillus niger. Fermented mashes contain 15–18 % alcohol and they are kept at acidic pH (3–0–4–0) as a result of the production of citric acid by the mould during fermentation. The mash is therefore a harsh environment for lactic acid bacteria. After 16S rRNA gene sequence analysis of all the isolates, four strains (NRIC 0603, NRIC 0604T, NRIC 0605 and NRIC 0606) underwent subsequent study because they clustered separately from recognized species of lactic acid bacteria. Levels of DNA–DNA relatedness also separated the strains from related species. This paper details the taxonomic study of the four strains and their proposed classification in a novel species, Lactobacillus satsumensis sp. nov.

The enrichment culture approach was employed for isolation of lactic acid bacteria from fermented mashes of shochu made from sweet potato that were collected at a shochu distillery in the South Kyushu district of Japan. The enrichment medium comprised 1·0 % D-glucose, 1·0 % yeast extract, 0·5 % polypeptone, 0·2 % sodium citrate, 10 p.p.m. sodium azide and 10 p.p.m. cycloheximide, and was then incubated. Colonies were picked on MRS agar and maintained on MRS agar containing 0·5 % CaCO₃.

Chromosomal DNA was prepared from bacterial strains by the method of Zhu et al. (1993) and was then used as a template for 16S rRNA gene sequence amplification. Large fragments of the 16S rRNA gene sequence were amplified by PCR using two primers: 8F (5’-AGAGTTTGATCMT-TGGCTCAG-3’), 1400F (5’-TCGTTG-3’), 933–954), 1400F (5’-AGGGTTGCGC-3’), positions 8–27) and 15R (5’-AAGGAGGTGATCCARCCGCA-3’, positions 1541–1522); position numbers were based on the Escherichia coli numbering system (GenBank accession no. V00348; Brosius et al., 1981). The PCR products were purified using a QIAquick PCR purification kit (Qiagen) according to the manufacturer’s instructions. They were sequenced using a BigDye Terminator cycle sequencing kit (Applied Biosystems) and an automatic DNA sequencer (model 310; Applied Biosystems). The following seven primers were used: 8F, 930F (5’-GCACAAGCGGTGAGCATGTGG-3’, positions 933–954), 1400F (5’-TGTACACACCGCCCGT-3’, positions 1391–1406), 520R (5’-ACCGCGGCTGCTGGC-3’, positions 531–517), 800R (5’-CAGGACTACAGGGTATCT-TATT-3’, positions 804–787), 1100R (5’-AGGGTTGCGCTCGTGG-3’, positions 1115–1100) and 15R. The closest recognized relatives of the isolates were retrieved from GenBank. Multiple alignments of the sequences were carried out with the program CLUSTAL X (version 1.18) (Thompson et al., 1997). Distance matrices for the aligned sequences were calculated using the two-parameter method of Kimura (1980).
The neighbour-joining method was used to construct a phylogenetic tree (Saitou & Nei, 1987). The robustness of individual branches was estimated by bootstrapping with 1000 replicates (Felsenstein, 1985). The 16S rRNA gene sequence (positions 8–1541) was determined for NRIC 0604T, and this was used to search for sequence similarity using Database. The highest sequence similarity to NRIC 0604T was found with Lactobacillus nagelii, Lactobacillus mali, Lactobacillus murinus and Pediococcus damnosus, the values being 95–99 %, respectively; these species belong to the Lactobacillus casei–Pediococcus group (Fig. 1). Partial sequences (positions 8–351) of the 16S rRNA gene were determined for strains NRIC 0603, NRIC 0605 and NRIC 0606; these partial sequences were identical to one another and to that of NRIC 0604T (positions 8–351). Therefore, we concluded that the four isolates belong to the same taxon and that this is located in the Lactobacillus casei–Pediococcus group.

Extraction and isolation of bacterial DNA were performed by the method of Marmur (1961) as modified by Ezaki et al. (1983). DNA–DNA hybridization was carried out by the microdilution well technique using photobiotin for labelling of DNA (Ezaki et al., 1989). DNA base compositions (G+C content) of strains tested were determined by HPLC as described by Tamaoka & Komagata (1984). Strains NRIC 0603, NRIC 0604T, NRIC 0605 and NRIC 0606 showed high levels of DNA–DNA relatedness (96–99 %) to one another. By contrast, NRIC 0604T showed low levels of DNA–DNA relatedness to the type strains of L. nagelii (6 %) and L. mali (7 %). The DNA G+C content of the four isolates ranged from 39 to 41 mol%.

Cell shape, cell size and Gram staining (Hucker & Conn, 1923) were determined on cultures grown in MRS broth at 30 °C for 24 h. Motility was tested in MRS soft agar and flagella were stained by the method of Toda (1928). Catalase activity was determined on cells grown on MRS agar. Gas production from glucose was determined using a Durham tube in MRS broth. Nitrate reduction, acid formation from carbohydrates and production of dextran from sucrose were determined by the methods described by Tanasupawat et al. (1998). The effects of temperature and various initial pH levels were tested in MRS broth. Resistance to NaCl and ethanol was examined in MRS broth containing 5 % (w/v) NaCl or 10 % (v/v) ethanol after incubation for 5 days at 30 °C. Type of fermentation was determined enzymically using the F-kit ethanol (Roche Diagnostics) as described by Okada et al. (1991). The isomer type of lactic acid was analysed by HPLC as described by Manome et al. (1998). Preparation of cell walls and determination of peptidoglycans were carried out by the methods described by Komagata & Suzuki (1987), except that TLC was performed on cellulose sheets. Various phenotypic characteristics of the isolates were similar to those of L. nagelii (Edwards et al., 2000) and L. mali (Carr & Davies, 1970; Nonomura, 1983; Kaneuchi et al., 1988), which are the phylogenetically closest related species (Table 1). In addition to the strains tested, L. nagelii and L. mali are motile, have meso-diaminopimelic acid in the cell wall and produce dextran from sucrose. These characteristics are unique in the genus Lactobacillus. The strains investigated cannot be distinguished from L. nagelii and L. mali based on their phenotypic characteristics, and levels of DNA–DNA relatedness were therefore used to provide accurate classification.

Based on the data provided, the four isolates are genetically distinguishable from recognized species of lactic acid bacteria, and thus represent a novel species, for which the name Lactobacillus satsumensis sp. nov. is proposed.

Table 1. Characteristics of Lactobacillus satsumensis sp. nov. and genetically closely related lactobacilli

Data for reference species are from Kaneuchi et al. (1988) (L. mali) and Edwards et al. (2000) (L. nagelii); motility and the presence of meso-diaminopimelic acid in the cell wall of L. nagelii NRIC 0559T were determined in the present study. +, Positive; −, negative; v, variable. All three species are motile, produce acid from D-fructose, D-trehalose and D-salicin and have meso-diaminopimelic acid in the cell wall. All three species are negative for acid production from D-ribose, D-xylene and lactose.

<table>
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<tr>
<th>Characteristic</th>
<th>L. satsumensis</th>
<th>L. mali</th>
<th>L. nagelii</th>
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<tr>
<td>Catalase production</td>
<td>−</td>
<td>v</td>
<td>−</td>
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<td>Acid from D-cellobiose</td>
<td>−</td>
<td>v</td>
<td>+</td>
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<td>Growth in MRS broth containing 5 % NaCl</td>
<td>+</td>
<td>v</td>
<td>+</td>
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A simple method for estimating evolutionary rates of base substitutions through comparative studies of nucleotide sequences. 

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References


