Lactobacillus thermotolerans sp. nov., a novel thermotolerant species isolated from chicken faeces

Piyanuch Niamsup,1 I Nengah Sujaya,2 Michiko Tanaka,2 Teruo Sone,2 Satoshi Hanada,3 Yoichi Kamagata,3 Saisamorn Lumyong,4 Apinya Assavanig,5 Kozo Asano,2 Fusao Tomita2 and Atsushi Yokota1

Correspondence
Atsushi Yokota
yokota@chem.agr.hokudai.ac.jp

1,2Laboratory of Microbial Resources and Ecology 1, Laboratory of Applied Microbiology 2, Graduate School of Agriculture, Hokkaido University, Kita-9 Nishi-9, Kita-ku, Sapporo 060-8589, Japan
3Research Institute of Biological Resources, National Institute of Advanced Industrial Science and Technology (AIST), Tsukuba Central 6, Higashi 1-1-1, Tsukuba, Ibaraki 305-8566, Japan
4Department of Biology, Faculty of Science, Chiang Mai University, Huay Kaew Road, Muang District, Chiang Mai 50200, Thailand
5Department of Biotechnology, Faculty of Science, Mahidol University, Rama 6 Road, Bangkok 10400, Thailand

Five strains of thermotolerant lactic acid bacteria (G 12, G 22, G 35T, G 43 and G 44) isolated from chicken faeces were characterized taxonomically. The strains were facultatively anaerobic, Gram-positive, catalase-negative, non-motile, non-spore-forming rods. They were heterofermentative lactobacilli that produced DL-lactic acid. Growth of the strains occurred at 45 °C but not at 15 °C. The optimum temperature for growth was 42 °C, as determined from the specific growth rate. The highest permissive temperatures for growth were 50 °C for strain G 35T and 48 °C for the other four strains. DNA G+C content of the strains was between 49 and 51 mol%. Complex fatty acid patterns of the strains showed the presence of C14:0, C16:0, sometimes C18:0, C18:1 and C19:0 cyclo in the cell walls. Phylogenetic analysis of the 16S rRNA gene sequences of the five strains placed them in the Lactobacillus casei/Pediococcus group, with Lactobacillus fermentum as their closest relative (about 95% sequence similarity). DNA–DNA hybridization data indicated that the thermotolerant strains were not L. fermentum. Taken together, the findings of this study show that the five strains isolated from chicken faeces represent a novel species within the genus Lactobacillus, for which the name Lactobacillus thermotolerans is proposed (G 35T = DSM 14792T = JCM 11425T).

Lactic acid bacteria (LAB) comprise a diverse group of Gram-positive, non-spore-forming bacteria (Kandler & Weiss, 1986), and are widely involved in the production of fermented foods. Recently, a great deal of interest has been focused on some members of the LAB with regard to their use as probiotics (Tannock, 1999). LAB belonging to the genus Lactobacillus have been isolated from a variety of habitats, including plant and dairy products, meat products, sewage and manure, and humans and animals (Kandler & Weiss, 1986). Some species of Lactobacillus isolated from chicken faeces and intestine have been reported previously. Fujisawa et al. (1984) isolated a novel Lactobacillus species, Lactobacillus aviarius, from the intestine of chickens, which consists of two subspecies, L. aviarius subsp. aviarius and L. aviarius subsp. araffinosus. Fujisawa et al. (1992) also isolated other novel Lactobacillus spp. from chicken faeces, namely Lactobacillus gallinarum and Lactobacillus johnsonii. When investigating acid and bile tolerance among intestinal strains of Lactobacillus, Jin et al. (1998) isolated 12 Lactobacillus strains (six strains of Lactobacillus brevis, three of Lactobacillus
fermentum, two of Lactobacillus acidophilus and one of Lactobacillus crispatus) from chicken intestine. Gusils et al. (1999) isolated L. fermentum, L. fermentum subsp. cellobiosus and Lactobacillus animalis, when studying lectin-like protein fractions in Lactobacillus strains isolated from the gastrointestinal tracts of chickens. Although several Lactobacillus spp. have been isolated from chicken faeces, most of the strains isolated so far have been mesophiles. The isolation of Lactobacillus spp. from chicken faeces under high temperatures has not been reported. Some LAB used in the dairy industry, for example, Lactobacillus delbrueckii, Lactobacillus helveticus and Streptococcus thermophilus, are already known as thermotolerant starter species from their temperature range for growth (Delcour et al., 2000). However, we still have little knowledge about the biodiversity of thermotolerant lactic acid bacteria (TLAB) in nature, because very few studies have been done that focus on LAB from the standpoint of their thermostolerance.

In the course of studies to isolate thermotolerant microorganisms for use in the fermentation industry, we have isolated a large number of LAB from various types of natural samples at relatively high temperatures, i.e. 40–50°C. 16S rDNA sequence analysis of these LAB raised the possibility that some of the TLAB included from chicken faeces comprised a novel species within the genus Lactobacillus. In the present study, five Lactobacillus strains isolated from chicken faeces that were known to be TLAB were characterized. On the basis of physiological, biochemical and genetic data, it is shown that the five strains represent a novel species within the genus Lactobacillus, for which the name Lactobacillus thermostolera is proposed.

Strains G 12, G 22, G 35, G 43 and G 44, isolated as TLAB, were used in this work. For the isolation of TLAB, fresh faecal samples from chickens were collected from the chicken coop of Kasetsart University, Bangkok, Thailand. These faecal samples were inoculated into glucose/peptone/yeast extract (GPY) broth and incubated anaerobically at 40, 45 and 50°C for 24 h using mixed gases (N2/H2/CO2, 8:1:1). GPY broth contained (g l–1): glucose, 10; peptone, 5; yeast extract, 10; sodium acetate trihydrate, 2; NaCl, 0.01; Tween 80, 0.5; MgSO4?7H2O, 0.2; MnSO4?4H2O, 0.01; FeSO4?7H2O, 0.035. NaOH was used to adjust the broth to pH 6.8. After appropriate dilutions had been prepared, culture broths were spread onto GPY/BCP agar plates which were prepared by the addition of 5 g CaCO3 l–1, 0.06 g bromocresol purple l–1, 0.05 g cycloheximide l–1 and 20 g agar l–1 to GPY broth. The plates were incubated anaerobically at 40, 45 and 50°C in anaerobic jars having the H2 + CO2 environment generated with a BBL GasPack (Becton Dickinson Microbiology Systems). Colonies that were yellow in colour and formed clear zones were selected as TLAB. In the experiments detailed in this study, cultures were routinely grown anaerobically in MRS broth (Difco) using mixed gases at 42°C (for strains G 12, G 22, G 35, G 43 and G 44) and 37°C (for reference strains). For the preparation of DNA for DNA–DNA hybridization studies and PCR, cells grown in MRS broth were harvested in the late-exponential phase and DNA was extracted essentially as described by Marmur (1961). The 16S rRNA genes of the five novel strains (corresponding to positions 27–1522 of the Escherichia coli 16S rRNA gene) were amplified by PCR. The six oligonucleotide primers used in the PCR amplification have been described previously (Mori et al., 1997). The purified PCR products were sequenced directly using a dRhodamine dye terminator cycle sequencing kit (Applied Biosystems) and an automated DNA sequencer (model 377; Applied Biosystems). The resulting sequences were subjected to similarity searches against sequences within the public databases, to determine a possible phylogenetic classification for the novel strains. To determine the closest known relatives of the novel strains, based on 16S rDNA sequences, primary searches were performed in GenBank using the FASTA program (Devereux et al., 1984). The database sequences representing the best matches to the 16S rDNA sequences of the novel strains were retrieved, and all of the sequences were aligned using the CLUSTAL W software (Thompson et al., 1994). Sequences in the alignment were corrected manually; approximately 1500 nt, covering the whole range of 16S rDNA sequences, were used in the phylogenetic analysis. A distance matrix was calculated using DNADIST, contained within the PHYLIP package (Felsenstein, 1993), and the Kimura two-correction parameter, and a phylogenetic tree was constructed using the PHYLIP package. The reliability of the individual branches of the tree was assessed by the bootstrap method (1000 replications) using SEQBOOT, DNADIST, NEIGHBOR and CONSENSE (all within the PHYLIP package).

The novel strains were further distinguished from their nearest relatives on the basis of physiological and biochemical comparisons. Cells were grown anaerobically on MRS agar or in MRS broth at 42°C (strains G 12, G 22, G 35, G 43 and G 44) or 37°C (reference strains) for 24 h. Catalase and oxidase activity, gas production from glucose, ammonia production from arginine and isomeric type of lactic acid were determined for each strain after they had been cultured in MRS broth. Configuration of the lactic acid was determined by HPLC using an Aminex HPX-87H 300×7.8 mm column (Bio-Rad) by the method described by Otsuka et al. (1994). The production of organic acids by each strain was determined by ion-exclusion HPLC using the culture supernatants as samples by the method described by Hoshi et al. (1994). Carbohydrate utilization and acid production by the strains were determined using the API 50 CHL system (bioMérieux) with CHL medium, as recommended by the manufacturer. API strips were incubated at 42°C (novel strains) and 37°C (reference strains) for up to 48 h. Tests for growth of the strains at 15 and 45°C were performed in MRS broth; results were recorded after 48 h. To evaluate the thermostolerance of the strains isolated from chicken faeces, optimum temperatures for growth of the novel strains were determined in comparison with reference strains. Each strain was cultured in half-strength MRS broth at temperatures ranging between 15 and 50°C in waterbaths with standard
thermometers. Growth of the strains was determined by measuring the OD_{660} values of the culture broths with a 20D spectrophotometer (Milton Roy). To determine the optimum temperature for growth of each of the strains, the specific growth rate was calculated from each growth curve for each strain. Detection of dianaminopimelic acid in the cell walls of the strains was done with 50–100 mg washed cells that had been suspended in 100 μl of potassium phosphate buffer (pH 6.8) containing 0.38 g KH₂PO₄ 1⁻¹, 0.39 g K₂HPO₄ 1⁻¹ and 7.46 g KCl 1⁻¹. The cell suspension was treated with 1 ml of 6 M HCl at 100 °C for 18 h. The hydrolysate was applied to a cellulose TLC plate (no. 1.05552; Merck), and developed using methanol/water/6 M HCl/pyridine (80:26:3:10, by vol.) (Komagata & Suzuki, 1987). The resulting spots were visualized with ninhydrin. For the analysis of the cellular fatty acid composition of the strains, whole-cell fatty acids were converted to methyl esters by treatment with anhydrous methanolic HCl. Methyl esters were extracted with n-hexane (Komagata & Suzuki, 1987) and analysed by using a GC-MS (Hitachi M7200A GC/3DQMS) equipped with a DB-5ms capillary column coated with 5% phenylmethylpolysiloxane to a thickness of 250 nm (Hanada et al., 2002). DNA base content of the strains was determined by the method of Tamaoka & Komagata (1984) using HPLC following enzymatic digestion of genomic DNA to deoxyribonucleotides. DNA–DNA hybridization was performed essentially according to the membrane method described by Johnson (1973). Tritium-labelled DNA for DNA–DNA hybridization studies was prepared by using the nick-translation system (Amersham Pharmacia Biotech).

Strains G 12, G 22, G 35ᵀ, G 43 and G 44, which were isolated from chicken faeces, were Gram-positive, non-motile, non-spore-forming rods. When grown in MRS broth at 42 °C, cells appeared as short rods of 1 × 2–3 μm in size, which occurred singly, in pairs or occasionally in short chains. Good growth of the strains was observed when they were grown under anaerobic conditions in liquid and on solid media. After incubation on MRS agar for 2 days, colonies were white, circular, convex, smooth, opaque and approximately 1–1.5 mm in diameter. The 16S rDNA sequences of the novel strains were subjected to similarity searches against sequences within GenBank, to infer a possible phylogenetic classification for the strains. The results of these searches revealed that the five novel strains were members of the genus Lactobacillus. This classification was confirmed by a 16S-rDNA-based phylogenetic analysis (Fig. 1) and by nucleotide sequence similarity values. The phylogenetic tree revealed that the novel strains were included in the Lactobacillus casei/Pediococcus group of the genus Lactobacillus (Collins et al., 1991). The closest relatives of strain G 35ᵀ were found to be Lactobacillus mucosae DSM 13345ᵀ (Roos et al., 2000) and L. fermentum ATCC 14931ᵀ, with moderate similarity values of 95.1 and 95.0%, respectively (Fig. 1). The branching pattern of the strain cluster with L. fermentum ATCC 14931ᵀ was supported by a high bootstrap value (95%) (Fig. 1). A fuller phylogenetic tree showing the placement of the five novel strains within the genus Lactobacillus is available as supplementary data in IJSEM Online (Fig. I; http://ijs.sgmjournals.org).

The novel strains were further distinguished from their closest relatives, L. mucosae DSM 13345ᵀ [obtained from the Deutsche Sammlung von Mikroorganismen und Zellkulturen (DSMZ)] and L. fermentum JCM 1173ᵀ [obtained from the Japan Collection of Microorganisms (JCM)], on the basis of physiological and biochemical comparisons. None of the five novel strains exhibited oxidase or catalase activities. No dianaminopimelic acid was detected in their cell walls. The five strains produced D₃-lactic acid and gas from glucose. The amounts of lactate and other organic acids produced from glucose are shown in Table 1. Analyses revealed that the novel strains apparently produced about 100 mM of lactate and 67–95 mM of acetate as the main products when 111 mM glucose (20 g l⁻¹) in MRS broth was completely consumed, indicating that these organisms were obligately heterofermentative, as were the reference strains L. fermentum JCM 1173ᵀ and L. mucosae DSM 13345ᵀ. Results of carbohydrate fermentation tests determined using the API 50 CHL system are shown in Table 1. Only those carbohydrates that gave different fermentation patterns for the novel strains and the reference strains are listed. Clear differences were found between the novel strains and the reference strains in the fermentation of L-arabinose and galactose. All the novel strains fermented L-arabinose, whereas it was not fermented by the reference strains. However, the reference strains fermented galactose,
which was not utilized by any of the novel strains. D-Xylose, which was fermented by all the novel strains, was not
fermented by L. fermentum JCM 1173T, the species most
closely related to the novel strains. Also, fermentation of
lactose occurred only in L. fermentum JCM 1173T. Among
the novel strains, strain G 44 showed a rather distinct
fermentation pattern as demonstrated by its lack of raffinose
and gluconate fermentation. The optimum temperature for
growth of all the novel strains, determined from the specific
growth rate, was 42 °C, whereas it was 40 °C for
L. helveticus JCM 1173T. Among the reference strains were 20–50 °C for
L. fermentum and L. mucosae DSM 13345T, the species most closely related to the novel strains, suggesting that the novel strains isolated
from chicken faeces represented a separate genomic species.

Table 1. Physiological and biochemical characteristics of the novel strains, G 12, G 22, G 35<sup>T</sup>, G 43 and G 44, and
selected reference organisms

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
<th>5</th>
<th>6</th>
<th>7</th>
</tr>
</thead>
<tbody>
<tr>
<td>Organic acid productivity (mM):</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Lactate</td>
<td>98:0</td>
<td>102:9</td>
<td>103:5</td>
<td>104:3</td>
<td>103:3</td>
<td>111:5</td>
<td>109:3</td>
</tr>
<tr>
<td>Succinate</td>
<td>0:6</td>
<td>0:4</td>
<td>0:4</td>
<td>0:4</td>
<td>0:4</td>
<td>0:7</td>
<td>10:7</td>
</tr>
<tr>
<td>Propionate</td>
<td>1:5</td>
<td>1:3</td>
<td>1:4</td>
<td>1:3</td>
<td>1:6</td>
<td>1:9</td>
<td>2:1</td>
</tr>
<tr>
<td>Acid production from:</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>L-Ascorbic acid</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>D-Xylose</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Galactose</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
</tr>
<tr>
<td>D-Fructose</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Lactose</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
</tr>
<tr>
<td>Melibiose</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>−</td>
<td>−</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Raffinose</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>−</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Gluconate</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>−</td>
<td>+</td>
<td>+</td>
</tr>
</tbody>
</table>

As shown in Table 2, strains G 12, G 22, G 35<sup>T</sup> and G 43
contained an unsaturated straight chain acid, C<sub>18:1</sub>, as their
major component, and strain G 44 contained both C<sub>18:1</sub>
and C<sub>16:0</sub> as major components. Straight chain acids of C<sub>14:0</sub>
and C<sub>18:0</sub> (occasionally), and a cyclopropane acid, C<sub>19:0</sub>
cyclo
were also detected. Therefore, the profiles of the novel strains
were clearly different from those of L. fermentum JCM 1173<sup>T</sup>
and L. mucosae DSM 13345<sup>T</sup>, in which C<sub>16:0</sub> was found to
be the major component. The DNA G+C contents of strains G 12, G 22, G 35<sup>T</sup>, G 43 and G 44 were 50:6, 50:8,
50:5, 49:4 and 50:4 mol%, respectively. These G+C values are
within the range reported for members of the genus
Lactobacillus, i.e. 32–53 % (Kandler & Weiss, 1986). The
DNA G+C contents of L. fermentum JCM 1173<sup>T</sup> and L. mucosae DSM 13345<sup>T</sup>, the species most closely related to the
novel strains, were 53:5 and 48:4 mol%, respectively. DNA–
DNA reassociation tests were performed between the five
novel strains, L. fermentum JCM 1173<sup>T</sup> and L. mucosae DSM 13345<sup>T</sup>
Strain G 35<sup>T</sup> and L. fermentum JCM 1173<sup>T</sup> exhibited reciprocal values of DNA–DNA relatedness of 18:4 and
17:6 %. Reciprocal values between strain G 35<sup>T</sup> and L. mucosae DSM 13345<sup>T</sup> were 21:4 and 14:3 %. The other
novel strains also showed low reciprocal values with the reference strains, suggesting that the novel strains isolated
from chicken faeces represented a separate genomic species.
The reciprocal values between the five novel strains were
about 70 %, except for strain G 44. This strain showed levels of
DNA homology of between 53 and 68 %. These values are
not above the 70 % level seen as being indicative of single
species status (Wayne et al., 1987), but they may be seen as
being indicative of closely related species or subspecies.

According to the phylogenetic analysis of the 16S rRNA gene
sequences of the novel strains and related Lactobacillus spp.
(Fig. 1), strain G 44 formed a different branch to the other
novel strains. Moreover, strain G 44 showed a rather distinct
fermentation pattern as demonstrated by its lack of raffinose
and gluconate fermentation (Table 1), and contained C<sub>18:1</sub>
and C<sub>16:0</sub> fatty acids as major components, whereas the
other novel strains contained only an unsaturated straight chain fatty acid, C\textsubscript{18:1}, as their major component (Table 2).

From the results presented here, it can be seen that the novel strains isolated from chicken faeces can be distinguished from all validly described Lactobacillus spp. on the basis of their biochemical, physiological and chemotaxonomic characteristics, their 16S rDNA sequences and the results of DNA–DNA hybridization studies. Consequently, we conclude that the TLAB strains isolated from chicken faeces represent a novel species within the genus Lactobacillus, for which we propose the name Lactobacillus thermotolerans.

**Description of Lactobacillus thermotolerans**


Cells are Gram-positive, non-motile, non-spore-forming, catalase-negative rods of 1×2–3 μm in size, which occur singly, in pairs or as short chains. After anaerobic growth at 42 °C for 2 days, colonies on MRS agar are 1–1.5 mm in diameter, white, circular, convex, smooth and opaque. Obligately heterofermentative and produces D- and L-lactic acid. Grows up to 50 °C, but not at 15 °C; optimum temperature for growth is 42 °C. Aesculin is hydrolysed. Arginine is cleaved. Hydrogen sulfide is not produced. Gelatin is not liquefied. No dextran is produced from sucrose. Acid is produced from glucose, ribose, L-arabinose, D-xylene and D-fructose. The majority of strains also ferment melibiose and D-raffinose. Glycerol, erythritol, D-arabinose, L-xylene, adonitol, methyl \(\beta\)-xyloside, dulcitol, inositol, methyl \(\alpha\)-D-mannoside, arbutin, lactose, inulin, melezitose, starch, glycosgen, xylitol, D-turanose, D-lyxose, D-tagatose, D-fucose, D-arabitol, L-arabitol, gluconate, 2-ketogluconate and 5-ketogluconate are not fermented. *meso*-Diaminopimelic acid is not present in the cell wall. DNA G+C content of the type strain is 50·5 mol%. Major cellular fatty acid is a straight chain unsaturated acid, C\textsubscript{18:1}. Isolated from the faeces of chickens in Thailand. The type strain is G 35\textsuperscript{T} (=DSM 14792\textsuperscript{T} = JCM 11425\textsuperscript{T}).

### Acknowledgements

Part of this work was done by collaboration in a Core University Programme between Yamaguchi University and Kasetsart University, supported by the Scientific Cooperation Programme agreed by Japan Society for the Promotion of Science (JSPS) and National Research Council of Thailand (NRCT). Piyanuch Niamsup received a scholarship from the Ministry of Education, Science, Sports and Culture of Japan to support her studies in Japan.

### References


