Tuberibacillus calidus gen. nov., sp. nov., isolated from a compost pile and reclassification of Bacillus naganoensis Tomimura et al. 1990 as Pullulanibacillus naganoensis gen. nov., comb. nov. and Bacillus laevolacticus Andersch et al. 1994 as Sporolactobacillus laevolacticus comb. nov.

Kouta Hatayama,1 Hirofumi Shoun,2 Yasuichi Ueda3 and Akira Nakamura1

1Division of Integrative Environmental Sciences, Graduate School of Life and Environmental Sciences, University of Tsukuba, Tennodai 1–1–1, Tsukuba, Ibaraki 305–8572, Japan
2Department of Biotechnology, Graduate School of Agricultural and Life Sciences, The University of Tokyo, Yayoi 1–1–1, Bunkyo-ku, Tokyo 113–8657, Japan
3Institute of Hyperthermophiles, Motobu-Noge Hospital, Aza-Ohama 880–1, Motobu, Okinawa 905–0212, Japan

Two thermophilic strains, designated 607T and 606b, were isolated from a compost pile in Japan. The novel strains were Gram-positive, aerobic, spore-forming rods. Phylogenetic analyses based on 16S rRNA gene sequences revealed that strains 607T and 606b were closely related to Bacillus naganoensis (94.0–94.1% similarity) and separated from clusters of the related genera Bacillus (<91.9%) and Sporolactobacillus (91.0–92.5%). In addition, some chemotaxonomic and physiological characteristics of strains 607T and 606b differed from those of B. naganoensis and the two related genera. Several differences in physiological characteristics and 16S–23S rRNA gene internal transcribed spacer region nucleotide sequences were observed between strains 607T and 606b; however, DNA–DNA hybridization indicated that these two strains belonged to the same species. From these results, it is proposed that strains 607T and 606b represent the type species of a new genus, Tuberibacillus calidus gen. nov., sp. nov., with strain 607T (=JCM 13397T =DSM 17572T) as the type strain. In addition, the results of phylogenetic analyses, as well as chemotaxonomic and physiological characterization, indicated that B. naganoensis and B. laevolacticus did not belong to the genus Bacillus. Based on these results, it is proposed that B. naganoensis and B. laevolacticus should be transferred to Pullulanibacillus naganoensis gen. nov., comb. nov. and Sporolactobacillus laevolacticus comb. nov., respectively.

The genus Bacillus consists of many species which display a variety of physiological and chemotaxonomic characteristics (Claus & Berkeley, 1986). Recent studies have shown that this genus is in fact made up of heterogeneous genera and several new genera have been established from this genus (Niimura et al., 1990; Wisotzkey et al., 1992; Ash et al., 1993; Shida et al., 1996; Heyndrickx et al., 1998; Waino et al., 1999; Schlesner et al., 2001; Fortina et al., 2001; Nazina et al., 2001; Yoon et al., 2001). However, it has been noted that are still several species of the genus Bacillus which need to be reclassified into other genera (Xu & Côté, 2003).
In our study of the microbial flora associated with the hyperthermic composting process in Japan, several mesophilic and thermophilic strains have been previously isolated and characterized (Hatayama et al., 2005a, b). In this process, organic wastes were subjected to a rapid composting step at a high temperature using a hyperthermal composting machine followed by a further piling step in the atmosphere. In this latter step, the temperature of the compost piles was kept at approximately 60 °C for several weeks by the heat generated metabolically by the micro-organisms growing in the compost piles, as is the case for general composting (Fogarty & Tuovinen, 1991; Williams et al., 1992). After the easily metabolized organic compounds in the piles had been thoroughly utilized by the micro-organisms, the temperature of the piles decreased to the ambient temperature, indicating the maturation of the compost piles. We assumed that the microbial flora in the piles changed as the composting process progressed, as in other composting processes (Fogarty & Tuovinen, 1991; Ishii et al., 2000). We also assumed that when the easily metabolized organic compounds became scarce in the piles, such as during the later step in this process, the populations of some micro-organisms that utilize the corpses of previously dominant microbes might rise. To isolate these micro-organisms from the samples, we developed a medium containing microbial corpses as the sole nutrient source. Two thermophilic bacteria, 607 T and 606b, growing at around 60 °C, were isolated using this medium. From our phylogenetic analyses, based on 16S rRNA gene sequences and the sequences of the internal transcribed spacer (ITS) regions between the 16S and 23S rRNA genes, as well as chemotaxonomic and physiological characterizations of strains 607 T and 606b, we propose that the strains represent a new genus and novel species, Tuberibacillus calidus gen. nov., sp. nov. Furthermore, during the above-mentioned analyses, we found that Bacillus naganoensis and Bacillus laevolacticus should be reclassified into other genera than the genus Bacillus. B. naganoensis was isolated as a producer of pullulanase and proposed by Tomimura et al. (1990). However, this species was established mainly on the basis of the results of physiological characterization and not analysed according to its phylogenetic position based on 16S rRNA gene sequence. Although Goto et al. (2000) determined the 16S rRNA gene sequence for B. naganoensis, there has been no discussion on the taxonomic position of this species. B. laevolacticus, originally described by Nakayama & Yanoshi (1967), was proposed by Andersch et al. (1994). At the time of this proposal, the close relationship of this species to the genus Sporolactobacillus was discussed, but it was nonetheless classified in the genus Bacillus. On the basis of the data described here, we propose the reclassification of B. naganoensis as Pullulanibacillus naganoensis gen. nov., comb. nov. and B. laevolacticus as Sporolactobacillus laevolacticus comb. nov.

To isolate microbes that utilize the corpses of other microbes during the later piling step of the hyperthermal composting process, we used plates comprising microbial corpses, termed MC agar. To make these plates and to isolate such microbes, we used a sample from the compost pile obtained when the temperature of the pile was beginning to decrease, since this sample had the potential to contain various microbes related to the succession of the microbial flora. Microbes originating from this sample were cultured in Luria–Bertani (LB) medium at 37 °C overnight and the cells were collected by centrifugation. The cells were suspended in an equal volume of distilled water and sterilized by autoclaving at 121 °C for 20 min, after the addition of 1.5% agar. Using the MC agar made in this way, several micro-organisms growing at 60 °C were isolated from the same sample.

To determine the rough phylogenetic positions of the novel isolates, partial sequences of their 16S rRNA genes (approximately 500 bp) were analysed. DNA extraction from colonized cells was performed using the method of Zhu et al. (1993). PCR amplification and analysis of the partial 16S rRNA gene sequences were performed as previously described (Hatayama et al., 2005a) using Eubac27F (DeLong, 1992) and 518R (Ogino et al., 2001) primers. The results of a similarity search using BLASTN (Altschul et al., 1997) revealed that most of the isolates were closely related to Bacillus smithii (>99.6% similarity; data not shown). However, the sequences of two isolates, designated 607 T and 606b, showed high similarity (99.8 and 100%, respectively) to that of uncultured bacterial clone F2–7 isolated from a hydrogen sulfide and methanol biofilter (GenBank accession no. AY096130), but did not show any close relationships to recognized species.

To determine the phylogenetic position of strains 607 T and 606b in more detail, PCR amplification of their 16S rRNA genes (>95% of their full length) was performed with Eubac27F and 1492R (DeLong, 1992) primers. Sequencing and phylogenetic analyses were performed as previously described (Hatayama et al., 2005a). The 16S rRNA gene sequences were aligned at positions 28 to 1490 [Escherichia coli (DeLong, 1992)] using the CLUSTAL_X software package (Thompson et al., 1997). Distance values were calculated using the method described by Kimura (1980). These values were then used in CLUSTAL_X to construct a phylogenetic tree by the neighbour-joining method with bootstrap values based on 1000 replications. A maximum-likelihood analysis was performed in DNAML with bootstrap values based on 100 replications using the SEQBOOT and CONSENSE programs of the PHYLIP package, version 3.65 (Felsenstein, 2005). The results were visualized using TREEVIEW software (Page, 1996). The 16S rRNA gene sequences of strains 607 T and 606b were almost identical (99.9% similarity) and homology searches in BLASTN and FASTA (Pearson, 2000) revealed that the closest recognized species to these strains was Bacillus naganoensis (94.0–94.1% similarity). The novel strains showed relatively low 16S rRNA gene sequence similarities to members of the genera Bacillus (below
In order to clarify the phylogenetic position of the 16S–23S rRNA gene ITS (16S–23S ITS) region were conducted for strains 607 T and 606b, indicating that B. laevolacticus was not included in the cluster of the genus Bacillus, but was found in the cluster of the genus Sporolactobacillus (Fig. 1). However, Xu & Côté (2003) reported that B. laevolacticus was not included in the cluster of the genus Bacillus and members of the genus Sporolactobacillus according to the method of Xu & Côté (2003) and a phylogenetic analysis was performed with the sequence data for members of related genera. Our phylogenetic tree built via the neighbour-joining method, constructed via the neighbour-joining method, rather than the 3′-end of the 16S rRNA coding region (data not shown). These phylogenetic analyses strongly suggest that strains 607 T and 606b and B. naganoensis DSM 10191 T and B. laevolacticus DSM 442 T were subjected to physiological and chemotaxonomic characterization using Sporolactobacillus kofuensis JCM 3419 T, Sporolactobacillus inulinus DSM 20348 T, Sporolactobacillus nakayamae subsp. nakayamae DSM 11696 T and Sporolactobacillus terrae DSM 11697 T as reference strains.

The MC agar plates initially used for the isolation of the novel strains were not suitable for the maintenance and characterization of strains 607 T and 606b. A medium was selected in which strains 607 T and 606b would grow well. Although strains 607 T and 606b did not show any growth in LB medium, nutrient medium (nutrient broth; Difco) or GYP medium (Yanagida et al., 1997), they grew in CYC medium (33-4 g Czapek-Dox liquid medium, modified (Oxoid), 2-0 g Bacto yeast extract (Difco), 6-0 g Bacto vitamin assay Casamino acids (Difco), 1000 ml distilled water, pH 7-2] (Lacey & Cross, 1989) at 60 °C and this medium was used for further work. Colonies of strains 607 T and 606b were round, obscure-edged, translucent and cream in colour. The cells were Gram-positive rods (using Live BacLight Bacterial Gram Stain Kit; Invitrogen), 3–7 μm wide, non-motile and occurred singly or in chains. Strains 607 T and 606b both formed oval endospores which were 0–7–1-0 μm long and 0–5–0-7 μm wide and located terminally within swollen sporangia (see Supplementary Fig. S2 in IJSEM Online). The widths of

Fig. 1. Neighbour-joining phylogenetic tree based on the 16S rRNA gene sequences of strains 607 T and 606b, B. naganoensis, B. laevolacticus and recognized species of related genera. Bootstrap values are calculated from 1000 replications and values >50% are shown at branch points. GenBank accession numbers are shown in parentheses. Bar, 0.01 substitutions per nucleotide position.
the spores were greater than those of the cells. In CYC medium, growth of strains 607T and 606b was observed over a pH range of 5–7 and over a temperature range of 40 to 60°C, with optimal growth at between 50 and 55°C.

To examine strains 607T and 606b in more detail, their physiological characteristics were determined as described by Claus & Berkeley (1986). Lactic acid production was tested using an F-kit (D-lactic acid L-lactic acid; Roche Diagnostics). There were several differences in physiological characteristics between the novel strains and the other reference strains (Table 1). Notably, a marked difference was seen in the growth temperature: strains 607T and 606b grow at up to 60°C and can therefore be classified as thermophiles, whereas the reference strains, including the closest related species, *B. naganoensis*, are mesophiles.

Strains 607T and 606b and *B. naganoensis* showed some features that distinguished them from species of the genus *Sporolactobacillus* and *B. laevolacticus*, such as having catalase activities and not producing lactic acid. Strains 607T and 606b could also be distinguished from *B. naganoensis* by the presence of oxidase activity, the pH range for growth and the hydrolysis of starch and casein. Several differences were also detected between strains 607T and 606b, such as nitrate reduction ability, acid production from xylose and tolerance of NaCl. *B. laevolacticus* showed almost the same features as species of the genus *Sporolactobacillus* except for the hydrolysis of starch.

Chemotaxonomic characteristics and the DNA G+C content were determined as previously described (Hatayama *et al.*, 2005b) using cells of strains 607T and

<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>
<th>8</th>
</tr>
</thead>
<tbody>
<tr>
<td>Catalase activity</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>−∗</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
</tr>
<tr>
<td>Oxidase activity</td>
<td>+</td>
<td>+</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
</tr>
<tr>
<td>Motility</td>
<td>−</td>
<td>−</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Lactic acid production</td>
<td>−</td>
<td>−</td>
<td>ND</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Growth temperature range (°C)</td>
<td>40–60</td>
<td>40–60</td>
<td>28–33</td>
<td>15–40</td>
<td>25–40</td>
<td>25–40</td>
<td>15–40</td>
<td>15–40</td>
</tr>
<tr>
<td>NaCl tolerance (%)</td>
<td>0–4</td>
<td>0–2</td>
<td>0–5</td>
<td>0–5</td>
<td>0–7</td>
<td>0–7</td>
<td>0–7</td>
<td>0–5</td>
</tr>
<tr>
<td>pH range</td>
<td>5–0–7–0</td>
<td>5–0–7–0</td>
<td>4–0–6–0</td>
<td>4–5–7–7</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
</tr>
<tr>
<td>Hydrolysis of starch</td>
<td>−</td>
<td>−</td>
<td>+</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
</tr>
<tr>
<td>Hydrolysis of casein</td>
<td>+</td>
<td>+</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
</tr>
<tr>
<td>Nitrate reduction</td>
<td>+</td>
<td>+</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
</tr>
<tr>
<td>Acid production from:</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Arabinose</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
</tr>
<tr>
<td>Glucose</td>
<td>+</td>
<td>(weak)</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>(weak)</td>
<td>ND</td>
<td>−</td>
<td>−</td>
<td>−</td>
</tr>
<tr>
<td>Xylose</td>
<td>+</td>
<td>−</td>
<td>+</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
</tr>
<tr>
<td>Cell-wall sugars:</td>
<td></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>
<td>−</td>
</tr>
<tr>
<td>Glucose</td>
<td>−</td>
<td>−</td>
<td>+</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
</tr>
<tr>
<td>Mannose</td>
<td>−</td>
<td>−</td>
<td>+</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
</tr>
<tr>
<td>Rhamnose</td>
<td>−</td>
<td>−</td>
<td>+</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
</tr>
<tr>
<td>Predominant cellular fatty acids:†</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>C16:0</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
</tr>
<tr>
<td>iso-C16:0</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
</tr>
<tr>
<td>anteiso-C15:0</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
</tr>
<tr>
<td>anteiso-C17:0</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
</tr>
<tr>
<td>DNA G+C content (mol%)</td>
<td>46±0</td>
<td>47±3</td>
<td>45±2</td>
<td>43–45</td>
<td>47</td>
<td>43</td>
<td>43–47</td>
<td>43–46</td>
</tr>
</tbody>
</table>

*A positive reaction was reported by Andersch *et al.* (1994).
†Major components consisting of about 50% of total cellular fatty acids are regarded as predominant cellular fatty acids in taxa 1–3.
606b, B. naganoensis and the other reference strains cultured in CYC medium at 55 °C, CYC medium (pH was adjusted to 5.0) at 30 °C and GYP medium at 30 °C, respectively. The cell-wall peptidoglycan of strains 607T and 606b contained meso-diaminopimelic acid, alanine and glutamic acid as did that of the reference strains (data not shown). No sugars were detected in the cell walls of strains 607T and 606b, whereas those of the reference strains contained several sugars (Table 1). The predominant cellular fatty acid of strains 607T and 606b was anteiso-C17:0, which differed from those of the reference strains (Table 1 and Supplementary Table S1). Strains 607T and 606b and the reference strains contained menaquinone-7 as the predominant component of isoprenoid quinone and menaquinone-5 as the minor component (above 10% peak area ratio). The DNA G+C contents of strains 607T and 606b were 46.0 and 47.3 mol%, respectively, which were almost the same as those of the reference strains.

Our phylogenetic analyses based on 16S rRNA gene sequences and the nucleotide sequences of the 16S–23S ITS region (Fig. 1 and Supplementary Fig. S1) indicated that strains 607T and 606b could be classified as representing a novel species in a new genus. The differences found in growth temperatures, cell-wall sugar composition, cellular fatty acids and other physiological characteristics between strains 607T and 606b and related genera also support this proposal (Table 1). Although strains 607T and 606b showed differences in their nitrate reduction ability, acid production from xylose, tolerance of NaCl and in the nucleotide sequences of the 16S–23S ITS regions, DNA–DNA hybridization studies, using the method of Ezaki et al. (1989), indicated that the two strains belong to the same species (79–100% DNA–DNA relatedness). On the basis of these results, we propose that strains 607T and 606b be classified as Tuberibacillus calidus gen. nov., sp. nov., with strain 607T as the type strain.

On the basis of 16S rRNA gene sequence similarity (<92-9%, data not shown) and phylogenetic analyses (Fig. 1 and Supplementary Fig. S1), B. naganoensis showed a low relationship to the genera Bacillus and Sporolactobacillus. The cellular fatty acid profile of B. naganoensis also differed from those of related species (Table 1 and Supplementary Table S1). B. laevolacticus was included in the cluster of the genus Sporolactobacillus in both phylogenetic trees (Fig. 1 and Supplementary Fig. S1) and its physiological and chemotaxonomic characteristics mostly agreed with those of other species of this genus (Table 1). Therefore, we also propose that Bacillus naganoensis (Tomimura et al., 1990) is reclassified as Pullulanibacillus naganoensis gen. nov., comb. nov. and Bacillus laevolacticus is reclassified as Sporolactobacillus laevolacticus comb. nov.

**Description of Tuberibacillus gen. nov.**

Tuberibacillus (Tu.be ri.ba.ci'llus. L. neut. n. tuber swelling; L. masc. n. bacillus a small staff; N.L. masc. n. Tuberibacillus a small staff with a swelling).

Cells are aerobic, thermophilic, Gram-positive rods (3–7×0.3–0.5 μm), occur singly or in chains and are non-motile. Oval endospores (0.7–1.0×0.5–0.7 μm) are formed terminally within swollen sporangia. Catalase- and oxidase-positive. The cell-wall peptidoglycan contains meso-diaminopimelic acid, alanine and glutamic acid, but no sugars. The major menaquinone is MK-7. The predominant fatty acid is anteiso-C_{17:0}. The DNA G+C content is 46.0–47.3 mol%. The type species is Tuberibacillus calidus.

**Description of Tuberibacillus calidus sp. nov.**

Tuberibacillus calidus (ca.li’dus. L. adj. calidus hot, due to their growth temperature).

Displays the following properties in addition to those given in the genus description. Growth is observed on CYC medium [33·4 g Czapek-Dox liquid medium, modified (Oxoid), 2·0 g Bacto yeast extract (Difco), 6·0 g Bacto vitamin assay Casamino acids (Difco), 1000 ml distilled water, pH 7·2] under aerobic and thermophilic conditions. Colonies are round, obscure-edged, translucent and cream in colour. Growth occurs at a pH range of 5·0–7·0 and at 40–60 °C (with an optimum temperature of 50–55 °C) and 0–2 or 0–4% NaCl. Positive reactions are observed for catalase and oxidase activities and for the hydrolysis of casein. Negative reactions are observed for the deamination of phenylalanine, hydrolysis of starch and tyrosine, utilization of citrate and propionate and the production of lactic acid. Acid is produced from glucose and arabinose, but not from lactose. Nitrate reduction and acid production from xylose are dependent on the strain. DNA G+C content is 46·0–47·3 mol%. When grown in CYC medium at 55 °C, the predominant cellular fatty acid is anteiso-C_{17:0} with iso-C_{16:0} and iso-C_{15:0} as minor components.

The type strain, strain 607T (= JCM 13397T = DSM 17572T), was isolated from a compost pile undergoing a hyperthermal composting process in Okinawa Prefecture, Japan. Strain 606b is a reference strain.

**Description of Pullulanibacillus gen. nov.**

Pullulanibacillus (Pul.lu.la.ni.ba.ci’l’us. N.L. n. pullulanum pullulan; L. masc. n. bacillus a small staff; N.L. masc. n. Pullulanibacillus a small staff hydrolysing pullulan).

Cells are aerobic, non-motile, Gram-positive rods (0·5–1·0×2·1–10·0 μm) with rounded or square ends and occur singly or in chains. Endospores are oval and cause swelling of the sporangia. Mesophilic and moderately acidophilic. Catalase-positive. Tests for reduction of nitrate to nitrite and nitrite to NO_{2} are negative. When grown in nutrient broth containing 1% starch, the major fatty acid is iso-C_{16:0}. The DNA G+C content is 45±2 mol%. Additional characteristics found in this study are as follows: oxidase-negative, cell-wall peptidoglycan contains meso-diaminopimelic acid, alanine, glutamic acid, galactose, glucose and rhamnose and menaquinone-7 and menaquinone-5 are the major and minor isoprenoid quinones,
respectively. When grown in CYC (pH 5.0) medium, the predominant cellular fatty acids are C_{16:0} and iso-C_{16:0}, with iso-C_{15:0}, anteiso-C_{15:0} and anteiso-C_{17:0} as minor components. The type species is *Pullulanibacillus naganoensis*.

**Description of *Pullulanibacillus naganoensis* comb. nov.**


Basonym: *Bacillus naganoensis* Tomimura et al. 1990.

The description is the same as that given by Tomimura et al., 1990. Additional characteristics found in this study are given above in the genus description.

The type strain is DSM 10191^T (=ATCC 53909^T = LMG 12887^T).

**Description of *Sporolactobacillus laevolacticus* comb. nov.**

*Sporolactobacillus laevolacticus* [læ.vo.læ’v.ti.cus. N.L. adj. *laevolacticus* referring to D-(−)-lactic acid, the only lactic acid produced by the organisms].


The description is the same as that given by Andersch et al., 1994, except for the absence of catalase activity. Additional characteristics found in this study are as follows: cell-wall peptidoglycan contains meso-diaminopimelic acid, alanine, glutamic acid, galactose, mannose and rhamnose.

The type strain is DSM 442^T (=ATCC 23492^T).

**Acknowledgements**

We are grateful to Dr Hiroko Isoda (University of Tsukuba) for kindly permitting us to use a microplate fluorescent reader. This work was supported by a Grant-in-Aid of Open Competition for the Development of Innovative Technology from the Ministry of Education, Culture, Sports, Science and Technology.

**References**


