Gluconobacter thailandicus sp. nov., an acetic acid bacterium in the \( \alpha \)-Proteobacteria

Somboon Tanasupawat,1,* Chitti Thawai,1 Pattaraporn Yukphan,5 Duangtip Moonmangmee,2 Takashi Itoh,3 Osao Adachi,4 and Yuzo Yamada5,**

1 Department of Microbiology, Faculty of Pharmaceutical Sciences, Chulalongkorn University, Bangkok 10330, Thailand
2 Department of Microbiology, Faculty of Science, King Mongkut’s University of Technology, Thonburi, Bangkok 10140, Thailand
3 Japan Collection of Microorganisms, RIKEN BioResource Center, Wako, Saitama 351–0198, Japan
4 Department of Biological Chemistry, Faculty of Agriculture, Yamaguchi University, Yamaguchi 753–8515, Japan
5 BIOTEC Culture Collection, BIOTEC Central Research Unit, National Center for Genetic Engineering and Biotechnology, National Science and Technology Development Agency, Pathumthani 12120, Thailand

(Received March 1, 2004; Accepted June 27, 2004)

Four strains of acetic acid bacteria were isolated from flowers collected in Thailand. In phylogenetic trees based on 16S rRNA gene sequences and 16S–23S rDNA internal transcribed spacer (ITS) region sequences, the four isolates were located in the lineage of the genus *Gluconobacter* and constituted a separate cluster from the known *Gluconobacter* species, *Gluconobacter oxydans*, *Gluconobacter cerinus*, and *Gluconobacter frateurii*. In addition, the isolates were distinguished from the known species by restriction analysis of 16S–23S rDNA ITS region PCR products using three restriction endonucleases *Bsp*1286I, *Mbo*II, and *Ava*II. The DNA base composition of the isolates ranged from 55.3–56.3 mol% G+C. The four isolates constituted a taxon separate from *G. oxydans*, *G. cerinus*, and *G. frateurii* on the basis of DNA-DNA similarities. Morphologically, physiologically, and biochemically, the four isolates were very similar to the type strains of *G. oxydans*, *G. cerinus*, and *G. frateurii*; however, the isolates were discriminated in their growth at 37°C from the type strains of *G. cerinus* and *G. frateurii*, and in their growth on L-arabitol and meso-ribitol from the type strain of *G. oxydans*. The isolates showed no acid production from myo-inositol or melibiose, which differed from the type strains of the three known species. The major ubiquinone homologue was Q-10. On the basis of the results obtained, *Gluconobacter thailandicus* sp. nov. was proposed for the four isolates. The type strain is isolate F149-1\(^T\) (=BCC 14116\(^T\)=NBRC 100600\(^T\)=JCM 12310\(^T\)=TISTR 1533\(^T\)=PCU 225\(^T\)), which had

---

* Address reprint requests to: Dr. Somboon Tanasupawat, Department of Microbiology, Faculty of Pharmaceutical Sciences, Chulalongkorn University, 254 Phayathai Road, Wangmai, Pathumwan, Bangkok 10330, Thailand.
E-mail: Somboon.T@chula.ac.th

** JICA Senior Overseas Volunteer; Visiting Professor, Laboratory of General and Applied Microbiology, Department of Applied Biology and Chemistry, Faculty of Applied Bioscience, Tokyo University of Agriculture, Setagaya-ku, Tokyo 156–8502, Japan.

Abbreviations: BCC, BIOTEC Culture Collection, BIOTEC Central Research Unit, National Center for Genetic Engineering and Biotechnology, National Science and Technology Development Agency, Pathumthani, Thailand; NBRC, Biological Resource Center (NBRC), Department of Biotechnology, National Institute of Technology and Evaluation, Kisarazu, Chiba, Japan; JCM, Japan Collection of Microorganisms, RIKEN BioResource Center, Wako, Saitama, Japan; TISTR, Thailand Institute of Scientific and Technological Research, Bangkok, Thailand; PCU, Department of Microbiology, Faculty of Pharmaceutical Sciences, Chulalongkorn University, Bangkok, Thailand.
55.8 mol% G+C, isolated from a flower of the Indian cork tree (*Millingtonia hortensis*) collected in Bangkok, Thailand.

**Key Words**——acetic acid bacteria; Avall; Bsp1286I; Gluconobacter; Gluconobacter oxydans; *Gluconobacter thailandicus* sp. nov.; MboII; 16S–23S rDNA ITS region sequence analyses; 16S rRNA gene sequences

**Introduction**

In the genus *Gluconobacter* Asai 1935, 689, emend. mut. char. Asai et al. 1964, 100AL, three species are currently recognized: *Gluconobacter oxydans* (Henneberg 1897) De Ley 1961, 304AL, *Gluconobacter cerinus* Yamada and Akita 1984, 503VP, and *Gluconobacter frateurii* Mason and Claus 1989, 182VP (Katsura et al., 2002; Mason and Claus, 1989; Yamada and Akita, 1984; Yamada et al., 1999). *Gluconobacter asaii* Mason and Claus 1989, 183VP is a subjective junior synonym of *G. cerinus*, since the type strain and the representative strains of *G. asaii* showed very high DNA-DNA similarities to the type strain of *G. cerinus* (Katsura et al., 2002; Tanaka et al., 1999; Yamada and Akita, 1984; Yamada et al., 1999). *Gluconobacter asaii* Mason and Claus 1989, 183VP is a subjective junior synonym of *G. cerinus*, since the type strain and the representative strains of *G. asaii* showed very high DNA-DNA similarities to the type strain of *G. cerinus* (Katsura et al., 2002; Tanaka et al., 1999; Yamada and Akita, 1984; Yamada et al., 1999).

During the course of studies on diversity of acetic acid bacteria in Thailand, we found that four strains isolated from flowers and assigned to the genus *Gluconobacter* constitute a new species on the basis of DNA-DNA similarities, 16S rRNA gene sequences, and 16S–23S rDNA internal transcribed spacer (ITS) region sequences.

This paper describes *Gluconobacter thailandicus* sp. nov., the fourth species of the genus *Gluconobacter* in the family *Acetobacteraceae* Gillis and De Ley 1980, 23VP.

**Materials and Methods**

**Isolation of strains assigned to the genus *Gluconobacter***. Strains of acetic acid bacteria were isolated from natural sources by an enrichment culture approach, as described previously (Seeearunruangchai et al., 2004). The collected flowers were incubated at pH 4.5 and 30°C for 3–5 days in a liquid medium (15 ml/tube), which was composed of 2.0% D-glucose, 5.0% ethanol, and 1.0% yeast extract (GEY) (all by w/w). When microbial growth was found, the cultures were streaked onto GEY-CaCO₃ (0.3%, w/v) agar plates (Yamada et al., 1976, 1999). The acetic acid bacteria were selected as acid-producing bacterial strains, which formed clear zones around colonies on agar plates. The four isolated strains are listed in Table 1.

**Reference strains of acetic acid bacteria.** *Gluconobacter oxydans* NBRC 14819ᵀ, *G. cerinus* NBRC 3267ᵀ, *G. frateurii* NBRC 3264ᵀ, and *Gluconacetobacter liquefaciens* TISTR 1057ᵀ were used as reference strains.

**16S rRNA gene sequences.** The 16S rRNA genes of the isolates were sequenced, as described previously (Seeearunruangchai et al., 2004). The 16S rRNA genes were amplified by PCR with Taq DNA polymerase and primers 9F (5’S-GAGTGGTGGATCATCG-
GCTCAG-3', the *Escherichia coli* numbering system, Brosius et al., 1981) and 1541R (5'-AAGGAGGT-GATCCAGCC-3'). A PCR amplification was carried out on a GeneAmp PCR System 2400 (PEBiosystems, Foster, California, USA). Double-stranded DNA was cloned and sequenced with an ABI PRISM BigDye Terminator v3.1 Cycle Sequencing Kit (Applied Biosystems, Foster, California, USA) according to the manufacturer's instruction, by the use of the following eight primers; universal vector primers, T7 and SP6, 339F (5'-CTCCTACGGGAGGCACGG-3'), 357R (5'-CTGCTGCCTCCGTAG-3'), 785F (5'-GGATTAGATAC-CCTGGTAGTC-3'), 802R (5'-TACCAAGGTATCTAA-TCC-3'), 1099F (5'-GCAAAGCCGGCACCACCC-3'), and 1115R (5'-AGGGTTGCGCTCGTTG-3'). The PCR products were sequenced with an ABI PRISM 377 Genetic Analyzer (Applied Biosystems).

**Phylogenetic analyses based on 16S rRNA gene sequences.** The 16S rRNA gene sequences determined (ca. 1,440 bases) were aligned along with the selected sequences obtained from the GenBank/EMBL/DDBJ databases by using the program CLUSTAL X (version 1.81) (Thompson et al., 1997). Gaps and ambiguous bases were eliminated from the calculations. Distance matrices for aligned sequences were calculated by the two-parameter method of Kimura (1980). A phylogenetic tree was constructed by the neighbor-joining method (Saitou and Nei, 1987) with the program MEGA (version 2.1) (Kumar et al., 2001). Confidence values of individual branches in the phylogenetic tree were determined by using the bootstrap analysis of Felsenstein (1985) based on 1,000 samplings. Sequence similarities among the type strains of the new species and the known species of the genus *Gluconobacter* were calculated on ca. 715 bases.

**PCR amplification of 16S–23S rDNA ITS regions for digestion with restriction endonucleases.** Amplification of 16S–23S rDNA ITS regions with restriction endonucleases was performed, as described previously (Yukphan et al., 2004). The two primers used were: 5'-TGCGG(C/T)TGGAATAC-CTCCT-3' (positions 1522–1540 on 16S rDNA by the *Escherichia coli* numbering system; Brosius et al., 1981) and 5'-GTGCC(A/T)AGGCTACCCAGG-3' (positions 38–22 on 23S rDNA) (Trček and Teuber, 2002).

**Digestion of 16S–23S rDNA ITS region PCR products with restriction endonucleases.** The purified 16S–23S rDNA ITS region PCR products (ca. 715 bases) were digested separately with restriction endonucleases *Bsp*1286I and *Mbo*I, as described previously (Yukphan et al., 2004). In addition, the restriction analysis was made by digestion with restriction endonuclease *Avall* (Fermentas, Hanover, Maryland, USA). The digestion reactions of the three restriction endonucleases followed the manufacturer’s instructions. The resulting reaction products were analyzed by 2.5% (w/v) agarose gel electrophoresis developed at 100 V for 40 min in 1×Tris-acetate running buffer.

**DNA base composition and DNA-DNA hybridization.** The DNAs of the isolates were extracted and purified from their whole cells by the phenol method of Saito and Miura (1963). DNA base composition was determined by the method of Tamaoka and Komagata (1984). DNA-DNA hybridization was carried out by the
photbiotin-labeling method with microdilution wells in 2× SSC and 50% formamide at 47°C for 16 h (Ezaki et al., 1989). DNA-DNA similarity was determined colorimetrically, as described previously (Tanasupawat et al., 2000).

Ubiquinone analysis. The ubiquinone system of the isolates was determined, as described previously (Seearunruangchai et al., 2004). Ubiquinone was extracted from freeze-dried cells by shaking with a mixture of chloroform-methanol (2:1, v/v) and purified by thin-layer chromatography on a silica gel plate (20×20 cm, silica gel 60F254). Art 5715, E. Merck, Darmstadt, Germany) with a solvent system of pure benzene (Yamada et al., 1968). The purified ubiquinone preparations were analyzed for their homologues by reversed-phase paper chromatography (Yamada et al., 1968) and by HPLC on a Shimadzu model LC-3A high performance liquid chromatograph (Tamaoka et al., 1983).

Phenotypic characteristics. The isolates were examined for their phenotypic characteristics, as described previously (Seearunruangchai et al., 2004). Oxidation of acetate and lactate to carbon dioxide and water, oxidation of ethanol to acetic acid, growth on glutamate agar and mannitol agar, and acid production from different carbon sources were tested by the methods of Asai et al. (1964). Growth on d-arabitol, L-arabitol, meso-ribitol, dulcitol, and meso-erythritol was determined in a basal medium, as described by Katsura et al. (2002). Production of d-gluconate, 2-keto-d-gluconate, 5-keto-d-gluconate, and 2,5-diketo-d-gluconate from d-glucose and d-gluconate was mediated by the methods of Gosselé et al. (1980). The effect of temperature on growth at 30, 37, and 40°C was tested by using potato agar plates (Moonmanngme et al., 2000). The effect of different pH on growth at pH 3.0–8.0 was tested by using a GMYP broth, which was composed of 2.0% glycerol, 2.0% d-mannitol, 0.5% yeast extract, and 0.5% peptone (all by w/v).

Base sequence deposition numbers. All the base sequences determined were deposited in the DDBJ database. The 16S rRNA gene sequences were under the accession numbers AB128050 and AB128051 respectively for isolates F149-1T and F142-1. The 16S–23S rDNA ITS region sequences were under the accession numbers AB127941 and AB127942 for isolates F149-1T and F142-1.

Results

Phylogenetic analyses based on 16S rRNA gene sequences

In a phylogenetic tree based on 16S rRNA gene sequences, G. thailandicus F149-1T and F142-1, all of which were isolated from flowers, were located in the lineage of the genus Gluconobacter and constituted a cluster separate from the type strains of the three known species, G. oxydans, G. cerinus, and G. frateurii (Fig. 1). A sequence similarity was 99.8% between the two isolates, F149-1T and F142-1. Gluconobacter thailandicus F149-1T represented 98, 98.9, 99.6, 94.9, 94.9, 95.9, and 95% similarities respectively to the type strains of G. oxydans, G. cerinus, G. frateurii, Acetobacter aceti, Acidomonas methanolica, Asaia bogorensis, and Kozakia baliensis.

Phylogenetic analyses based on 16S–23S rDNA ITS region sequences

As shown in Fig. 2, the phylogenetic tree based on the 16S–23S rDNA ITS region sequences showed that G. thailandicus F149-1T and F142-1 were located in the lineage of the genus Gluconobacter and constituted a cluster separate from the type strains of the known species, G. oxydans, G. cerinus, and G. frateurii. A sequence similarity was 99.9% between the two isolates, F149-1T and F142-1. Gluconobacter thailandicus F149-1T represented 87.2, 96.8, 99.1, and 69.7% sequence similarities respectively to the type strains of G. oxydans, G. cerinus, G. frateurii, and A. aceti.

Digestion of 16S–23S rDNA ITS region PCR products with restriction endonucleases Bsp1286I, MboII, and Avall

The 16S–23S rDNA ITS region PCR products (ca. 715) of the four isolates of G. thailandicus were digested separately with restriction endonucleases Bsp1286I and MboII. The isolates showed different restriction patterns from the type strains of G. oxydans and G. cerinus, viz., respectively G. oxydans and G. cerinus types of patterns, but gave restriction patterns identical with one another, which were the same as those of the type strain of G. frateurii, viz., G. frateurii types of patterns (data not shown) (Yukphan et al., 2004). However, the four isolates were completely differentiated from the type strain of G. frateurii by digestion with restriction endonuclease Avall (5′-
GG(A/T)CC-3', which showed a unique restriction pattern, viz., *G. thailandicus* type of patterns (Fig. 3). The four isolates did not produce any restriction fragments, although the type strain of *G. frateurii* produced two fragments showing 610 and 105 bp.

**DNA base composition and DNA-DNA similarity**

The DNA base composition of the isolates ranged 55.3–56.3 mol% G+C with a range of 1.0 mol% (Table 2). These values were almost identical with those of the type strains of *G. cerinus* and *G. frateurii*, but lower than that of the type strain of *G. oxydans*.
As shown in Table 2, the four isolates had low DNA-DNA similarities (4–43%), when the type strains of *G. oxydans*, *G. cerinus*, and *G. frateurii* were labeled. On the other hand, high and low DNA-DNA similarities (79–102% and 4–38%) were found respectively among the isolates and to the type strains of *G. oxydans*, *G. cerinus*, and *G. frateurii*, when *G. thailandicus* F149-1T and F142-1 were labeled.

**Ubiquinone system**

The major ubiquinone homologue of the isolates was Q-10, as found in the type strains of *G. oxydans*, *G. cerinus*, and *G. frateurii*. The four isolates had 92.6–97.3% Q-10, 2.7–6.9% Q-9, and 0.5–0.6% Q-8 (Table 1).

**Phenotypic characteristics**

The four isolates were Gram-negative and rod shaped, measuring 0.6–1.0×1.0–2.5 µm on GEY-CaCO₃ agar. All the isolates were non-motile. Colonies were white, shiny, smooth, and raised with an entire margin on GEY-CaCO₃ agar. They were strictly aerobic. All isolates grew at pH 3.0, 7.5, and 37°C. However, their growth at 37°C was not so intense but weak. No growth was found at pH 8.0 or 40°C.

The four isolates did not oxidize acetate and lactate. They grew on mannitol agar but not on glutamate agar. They produced D-gluconate, 2-keto-D-gluconate, and 5-keto-D-glucuronate from D-glucose, but not 2,5-diketo-D-glucuronate or a water-soluble brown pigment. All produced 2-keto-D-glucuronate, and 5-keto-D-glucuronate from D-glucuronate, but not 2,5-diketo-D-glucuronate. The isolates produced dihydroxyacetone from glycerol. They grew on D-arabitol, L-arabitol, meso-ribitol, and meso-erythritol, but not on dulcitol; however, their growth was not so intense but weak in L-arabitol, and meso-ribitol.

Acid was produced from L-arabinose, D-fructose, D-galactose, D-glucose, glycerol, D-mannitol (variable and weak), D-ribose, L-sorbose (sometimes weak), D-xylose, and ethanol. In contrast, no acid production was found from amygdalin, cellobiose, myo-inositol, maltose, D-mannose, melibiose, melezitose, raffinose, L-rhamnose, salicin, D-sorbitol, sucrose, or trehalose.

**Discussion**

The acetic acid bacteria are currently classified in the six genera in the family *Acetobacteraceae*: *Acetobacter* Beijerinck 1898, *215AL* (the type genus), *Glu-

\[ \text{Gluconobacter thailandicus} \]

was proposed as the fourth species of the genus \textit{Gluconobacter}. In phylogenetic trees based on 16S rRNA gene sequences and 16S–23S rDNA ITS region sequences, the isolates (F149-1\textsuperscript{T} and F142-1) of \textit{G. thailandicus} were located in the lineage of the genus \textit{Gluconobacter}, especially in the sublineage that was comprised of the type strains of \textit{G. cerinus} and \textit{G. frateurii}, but constituted a cluster separate from the type strains of \textit{G. oxydans}, \textit{G. cerinus}, and \textit{G. frateurii}.

On digestion of 16S–23S rDNA ITS region PCR products with restriction endonucleases \textit{Bsp}1286I and \textit{Mbo}II, the four isolates of \textit{G. thailandicus} gave the same restriction pattern as the type strain of \textit{G. frateurii}. However, the two species were completely differentiated from each other by digestion with restriction endonuclease \textit{Ava}II (Table 3).

The DNA base composition of the four isolates (55.3–56.3 mol% G+C) was similar to that of the type strains of \textit{G. cerinus} (55.9 mol% G+C) and \textit{G. frateurii} (55.1 mol% G+C) and lower than that of the type strain of \textit{G. oxydans} (60.3 mol% G+C). The low DNA-DNA similarities (4–43%) of the isolates showed a taxon separate from \textit{G. oxydans}, \textit{G. cerinus}, or \textit{G. frateurii}. Yamada and Akita (1984) recognized that strains assigned to the genus \textit{Gluconobacter} are divided into two groups, viz., the higher DNA G+C content-having group including \textit{G. oxydans} and the lower DNA G+C content group including \textit{G. cerinus} (and \textit{G. frateurii}, Mason and Claus, 1989) on the basis of DNA base composition. The four isolates were actually an additional member of the lower DNA G+C content group.

### Table 3. Differential characteristics of \textit{Gluconobacter thailandicus}.

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>\textit{G. thailandicus}</th>
<th>\textit{G. frateurii}</th>
<th>\textit{G. cerinus}</th>
<th>\textit{G. oxydans}</th>
</tr>
</thead>
<tbody>
<tr>
<td>Growth at 37°C C</td>
<td>w</td>
<td>w</td>
<td>w</td>
<td>–</td>
</tr>
<tr>
<td>Growth at pH 3.0</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>–</td>
</tr>
<tr>
<td>Growth on</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>L-Arabinose</td>
<td>w</td>
<td>w</td>
<td>w</td>
<td>–</td>
</tr>
<tr>
<td>meso-Ribitol</td>
<td>w</td>
<td>w</td>
<td>w</td>
<td>–</td>
</tr>
<tr>
<td>Acid production from</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>D-Manose</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>D-Sorbitol</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>myo-Inositol</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Maltose</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Melibiose</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Sucrose</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Restriction-pattern type</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>\textit{Bsp}1286I</td>
<td>G. frateurii</td>
<td>G. frateurii</td>
<td>G. frateurii</td>
<td>G. frateurii</td>
</tr>
<tr>
<td>\textit{Mbo}II</td>
<td>G. thailandicus</td>
<td>G. thailandicus</td>
<td>G. thailandicus</td>
<td>G. thailandicus</td>
</tr>
<tr>
<td>\textit{Ava}II</td>
<td>G. thailandicus</td>
<td>G. thailandicus</td>
<td>G. thailandicus</td>
<td>G. frateurii</td>
</tr>
<tr>
<td>DNA G+C content (mol%)</td>
<td>55.3</td>
<td>55.4</td>
<td>56.3</td>
<td>55.8</td>
</tr>
</tbody>
</table>

ND, not determined.

All the isolates and the type strains of the three known \textit{Gluconobacter} species produced dihydroxyacetone from glycerol and 2-keto-D-gluconate and 5-keto-D-gluconate from D-glucose, and acid from D-glucose, D-galactose, D-xylose, L-arabinose, D-ribose, D-fructose, L-sorbose, D-mannitol, glycerol, and ethanol, and grew on mannitol agar, meso-erythritol, and at pH 3.5 and 7.5, but did not produce 2,5-diketo-D-gluconate or a water-soluble brown pigment from D-glucose or acid from amygdalin, cellobiose, melizitose, raffinose, L-rhamnose, salicin, and trehalose, and did not grow on glutamate agar or dulcitol, at pH 8.0, or at 40°C.
Phenotypically, the four isolates were distinguished in growth at 37°C from the type strains of *G. cerinus* and *G. frateurii* and in growth on l-arabitol and meso-arabitol from the type strains of *G. cerinus* and *G. oxydans*, but their growth was not so intense. In acid production from myo-inositol, d-mannose, and melibiose, the four isolates were distinguished in no acid production from the type strains of *G. cerinus* and *G. frateurii*. On the basis of the results obtained above, the four isolates can be discriminated genetically, molecular-biologically, and phenotypically from the known species of the genus *Gluconobacter*, and should be classified as a new species (Table 3). The name of *Gluconobacter thailandicus* is proposed for the four isolates.

**Description of *Gluconobacter thailandicus* sp. nov.**

*Gluconobacter thailandicus* (thai. lan’di. cus. N. L. masc. adj. thailandicus of Thailand, where the type strain was isolated).

Cells are Gram-negative and rod-shaped, measuring 0.6–1.0×1.0–2.5 μm and are nonmotile. Colonies are white, shiny, smooth, and raised. Strictly aerobic. Grows at pH 3.0 and 7.5. Growth at 37°C is positive but weak. Does not oxidize acetate or lactate. Grows on mannitol agar but not on glutamate agar. Produces 2-keto-D-gluconate and 5-keto-D-gluconate from D-gluconate but not 2,5-diketo-D-gluconate or meso-2-keto-D-gluconate and 5-keto-D-gluconate from D-gluconate and l-mannose, but not 2,5-diketo-D-gluconate or a water-soluble brown pigment. Production of dihydroxyacetone from glycerol is positive. Acid is produced from amygdalin, cellobiose, melibiose, raffinose, L-rhamnose, salicin, D-sorbitol, sucrose, or trehalose. The major ubiquinone is Q-10. DNA base composition is 55.3–56.3 mol% G+C with a range of 1.0 mol%. The type strain is F149-1T (=BCC 14116T=NBRC 100600T=JCM 12310T=TISTR 1533T=PCU 225T), which had 55.8 mol% G+C, isolated from a flower of the Indian cork tree (*Millingtonia hortensis*) collected in Bangkok, Thailand.

**Acknowledgments**

We thank Mr. Apisit Seearunruangchai for his technical assistance. This study was supported in part by Rachadapiseksompoj Research Grant, Chulalongkorn University (1998–1999).

**References**


