
Asif Hameed,1 Mariyam Shahina,1 Wei-An Lai,1 Shih-Yao Lin,1 You-Cheng Liu,1 Yi-Han Hsu1 and Chiu-Chung Young1,2

1Department of Soil & Environmental Sciences, College of Agriculture and Natural Resources, National Chung Hsing University, Taichung 402, Taiwan, ROC
2Agricultural Biotechnology Center, National Chung Hsing University, Taichung 402, Taiwan, ROC

A Gram-staining-negative, strictly aerobic, yellowish-orange, flexirubin-positive, rod-shaped, non-flagellated, non-spore-forming and non-gliding marine bacterium, designated strain CC-PY-50T, was isolated from estuarine water off Pingtung, Taiwan. The strain produced zeaxanthin as a major carotenoid pigment, and showed highest pairwise 16S rRNA gene sequence similarity to Bizonia hallyeanensis T-y7T (93.9 %) followed by Corallibacter vietnamensis KMM 6217T (93.8 %), Geojedonia litorea YCS-16T (93.7 %) and other members of the family Flavobacteriaceae (~<93.7 %). Strain CC-PY-50T established a distinct phyletic lineage associated with Mangrovimonas yunxiaonensis LYYY01T (93.1 % sequence similarity) with poor bootstrap support during neighbour-joining and maximum-likelihood phylogenetic analyses (37 % for each). The polar lipid profile of strain CC-PY-50T was determined to accommodate large numbers of unknown lipids including major amounts of three unidentified aminolipids and two unidentified lipids, and moderate amounts of an unidentified phospholipid, an unidentified glycolipid and an unidentified lipid. In addition, phosphatidylethanolamine was also detected in significant amounts. The major (>5 % of total) fatty acids were iso-C15 : 0, iso-C15 : 1G, iso-C17 : 03-OH, C16 : 0 and C16 : 17c and/or C16 : 17c. The DNA G+C content was 37.1 mol% and menaquinone-6 (MK-6) was the sole respiratory quinone. Based on the phylogenetic evidence and several distinguishing phenotypic and chemotaxonomic features, strain CC-PY-50T is proposed to represent a novel genus and species of the family Flavobacteriaceae, for which the name Hanstruepera neustonica gen. nov., sp. nov. is proposed. The type strain of the type species Hanstruepera neustonica gen. nov., sp. nov. is CC-PY-50T (=JCM 19743T=BCRC 80747T). Emended descriptions of the species Sediminibacter furfurcosus, Mangrovimonas yunxiaonensis, Antarcticimonas flava and Hoppeia youngheungensis are also proposed.

Abbreviations: ML, maximum-likelihood; MP, maximum-parsimony; NJ, neighbour-joining.

The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain CC-PY-50T is KF732814.

Three supplementary figures are available with the online Supplementary Material.

The family Flavobacteriaceae, affiliated to the phylum Bacteroidetes (formerly the Cytophaga–Flavobacterium–Bacteroides or Cytophaga–Flexibacter–Bacteroides group) (Garrity & Holt, 2001), was established, the name validly published and the description emended by Jooste (1985), Reichenbach (1992) and Bernardet et al. (1996, 2002), respectively. At the time of writing, the family accommodates
112 genera with validly published names (http://www.
bacterio.net) and the representatives are known to be
widespread in occurrence (O’Sullivan et al., 2002; Kirchman,
2002). They are among the major taxa of marine heterotrophic
bacterioplankton frequently found on macroscopic particles
of organic matter, as well as being free-living microbial
assemblages in nutrient-rich microenvironments (Bauer,
et al., 2006). Some strains have been identified to harbour
proteorhodopsin-based photophysiology (Gomez-Consarnau
et al., 2007; Gonzalez et al., 2008; Yoshizawa et al., 2012). The
number of representatives of the family Flavobacteriaceae
is constantly increasing through the continuous description of
ten taxa. We have characterized species such as Lutanaella
thermophila (Arun et al., 2014), Muricauda lutonensis
(Arun et al., 2009b), Siansiviga zeaxanthinificiens (Hameed
et al., 2012), Kordia aquimaris (Hameed et al., 2013), Gramella
planctonica (Shahina et al., 2014), Aquabacter zeaxanthini-
faciens (Hameed et al., 2014a), Robertkochia marina (Hameed
et al., 2014b) and Gramella oceanii (Hameed et al., 2014c)
from various marine locations in Taiwan. Here, we report on the
taxonomic characterization of a novel zeaxanthin-producing
flavobacterial strain, designated CC-PY-50T, which was
isolated from Formosan estuarine water.

While exploring the culturable bacterioplankton inhabiting
the marine environment, strain CC-PY-50T was isolated from a
surface water sample collected from an estuary near
Pingtung, Taiwan (22.466098’ N 120.444000’ E). The strain
was isolated after subjecting the water sample to standard
dilution-to-extinction plating on marine agar 2216 (MA; BD
Difco) and incubating at 30°C, for 48–96 h. The yellowish-
orange colony of strain CC-PY-50T was purified and pre-
served in marine broth (MB; BD Difco) supplemented with
20% (v/v) glycerol at −80°C. Taxonomic investigations
were carried out according to published guidelines and
minimal standards (Tindall et al., 2010; Bernardet et al., 2002).
Corallibacter vietnensis JCM 17525T, Geojedonia litorea
KCTC 32260T, Sediminibacter furfurosus NBRC 101622T,
Mangrovimonas yunxiaoensis JCM 27142T, Antarcticimonas
flava NBRC 103398T and Hoppeia youngheungensis JCM
19488T were used for direct comparative taxonomic analysis.
All strains (except for Antarcticimonas flava NBRC 103398T,
which was grown at 20°C) were cultured on MA or MB for
48 h at 30°C, unless specified otherwise.

The genomic DNA of strain CC-PY-50T was isolated using
an UltraClean Microbial Genomic DNA Isolation kit (MO
BIO) by following the manufacturer’s instructions. The
partial 16S rRNA gene was amplified via PCR according to
Shahina et al. (2013). Gene sequencing was performed by
using a BigDye terminator kit (Heiner et al., 1998) and an
automatic DNA sequencer (ABI PRISM 310, Applied Biosystems)
(Watts & MacBeath, 2001). Sequence fragment
ments were then assembled using the Fragment Assembly
System program from the Wisconsin Package (GCG,
1995). Sequence similarity values were computed using
BLAST searches (Altschul et al., 1990) and the EzTaxon-e
server (Kim et al., 2012a). Sequence data were analysed by
MEGA 5 (version 5.0; Tamura et al., 2011), after multiple
alignments by CLUSTAL X (Thompson et al., 1997). The
distance matrix method (distance options according to the
Kimura two-parameter model; Kimura, 1980) including clustering by neighbour-joining (NJ; Saitou & Nei, 1987), a
discrete character-based maximum-parsimony (MP; Fitch,
1971) and maximum-likelihood (ML; Felsenstein, 1981)
methods were used. The topologies of the trees were
evaluated by using the bootstrap resampling method based
on 1000 replications (Felsenstein, 1985).

The size of the amplified 16S rRNA gene of strain CC-PY-50T
was 1493 bp. Strain CC-PY-50T shared the highest pairwise
16S rRNA gene sequence similarities with Bizonia hallyeovenis
T-y7T (93.9%) followed by Corallibacter vietnensis KMM
6217T (93.8%), Geojedonia litorea YCS-16T (93.7%),
Meridiamiribacter flavus NH57NT (93.6%), Bizonia
echini KMM 6177T (93.6%), Winogradskyella wandosonensis
WD-2-2T (93.5%) and other members of the family
Flavobacteriaceae (≤93.5%). In the NJ phylogenetic tree,
strain CC-PY-50T established a distinct phyletic lineage in a
discrete clade associated with Mangrovimonas yunxiaoensis
LYY01T (37% bootstrap support), with which it shared a
sequence similarity of 93.1% (Fig. 1). The present clade
was also found to accommodate Sediminibacter furfurosus
MAOS-86T, Antarcticimonas flava IMCC3175T and Hoppeia
youngheungensis YIK12T, which shared a sequence similarity
of 93.5%, 93.0% and 91.4%, respectively, with the novel
strain. Although the phylogenetic association between strain
CC-PY-50T and Mangrovimonas yunxiaoensis LYY01T
was also conserved in the ML tree (Fig. S1 available in the
online Supplementary Material; 37% bootstrap support), the
association was found to be unstable through MP
analysis (Fig. S2). It is noteworthy that the novel strain was
found to be placed in a clade that accommodated
Corallibacter vietnensis KMM 6217T and Geojedonia
litorea YCS-16T in the MP tree. On the other hand, the
representatives of the genera Bizonia, Geojedonia and
Corallibacter occupied a distant phylogenetic neighbour-
hood in both NJ and ML trees. Taken together, phylogenetic
results did not support the classification of the novel strain
within any established genus. Thus, the type strains of type
species of the genera Geojedonia, Corallibacter, Mangrovimonas,
Sediminibacter, Hoppeia and Antarcticimonas were chosen to
resolve the taxonomic ambiguity of the novel strain and they
were all examined under identical experimental conditions.

The following tests were performed exclusively on strain
CC-PY-50T. Growth was tested on nutrient agar (NA;
Himedia), tryptic soy agar (TSA; BD Difco) and R2A
(Oxoid) agar. Colonies were examined for morphological
features such as colony appearance, size, shape, texture and
pigmentation. The presence of endospore was determined
by phase-contrast microscopy (model A3000, Zeiss) after
malachite-green staining (Smibert & Krieg, 1994) of the
cells grown on MA for 7 days. Cell morphology including
the presence of flagella was determined by placing the cells
(1–2 days old) on a carbon-coated copper grid followed by
staining with 0.2% (w/v) uranyl acetate for 5–10 s, brief
air-drying and observation under a transmission electron
microscope.
microscope (JEM-1400, JEOL). Gram staining was performed according to Murray et al. (1994). Gliding motility was investigated by using phase-contrast microscopy (model A3000, Zeiss) of a hanging-drop preparation from an MB culture (Bernardet et al., 2002). The presence of flexirubin-type pigments was investigated as described by Reichenbach (1992) and Bernardet et al. (2002). Carotenoids were extracted and analysed according to earlier descriptions (Hameed et al., 2012). The presence of the proteorhodopsin gene was tested using three pairs of degenerate primers (PR-Flavo-F and R, PR-Flavo-2F and 2R, and SA4-10 PRn30F and 3R) according to the descriptions of Yoshizawa et al. (2012). Growth under anaerobic conditions was tested using MA or MA supplemented with 0.1 % (w/v) KNO3 by incubating the culture plates in an anaerobic chamber (COY). The requirement for NaCl was tested on R2A agar (BD Difco) supplemented with 0–10 % (w/v) NaCl (at 1 % intervals). The pH range (pH 4.0–10.0, at 1.0 pH unit intervals) for growth was determined as described previously (Hameed et al., 2013). Growth at 10, 20, 25, 30, 37, 40, 45, 50 and 55 °C was tested in MB after 72 h of incubation. Cells were inoculated in API 50 CH strips (bioMérieux) and

**Fig. 1.** Neighbour-joining tree based on 16S rRNA gene sequences showing the phylogenetic relationship of strain CC-PY-50T and other representatives of the family *Flavobacteriaceae*. Bootstrap values (>70 %) based on 1000 replications are shown at the nodes. Bar, 0.02 substitutions per nucleotide position. *Microscilla marina* ATCC 23134T (AB078080) was used as an outgroup.
Antarcticimonas flava

Biolog GN2 MicroPlates according to the manufacturers’ instructions, except that the cell suspensions were prepared in sterile 3.2 % (w/v) sea salt (Sigma) solution.

The following tests were carried out on all seven strains. Catalase and oxidase activity, and hydrolysis of starch, egg yolk, Tweens 20 and 80, casein (skimmed milk), colloidal chitin, CM-cellulose, xylan, L-tyrosine and DNA were tested as described previously (Hameed et al., 2013). Triple-sugar iron agar (BD Difco) supplemented with 3.2 % (w/v) NaCl was used to determine H₂S production. Cells were subjected to API 20 NE and API ZYM (bioMérieux) tests as stated above.

Strain CC-PY-50ᵀ synthesized all-trans-zeaxanthin as a predominant (69.0 %) carotenoid pigment. In addition, significant amounts of cis-isomeric zeaxanthin (13 %) and some unidentified carotenoids (15 %) were also detected. The carotenoid profile was almost in line with our earlier data (Hameed et al., 2012, 2013, 2014a, c; Shahina et al., 2014). The gene encoding proteorhodopsin was not detected in strain CC-PY-50ᵀ after using the above-mentioned proteorhodopsin gene-targeted degenerate primer. The morphological features of strain CC-PY-50ᵀ are shown in Fig. S3. Other characteristics are listed in the genus and species descriptions. The features that distinguish the new isolate from its phylogenetic neighbours are given in Table 1.

For cellular fatty acid analysis, the fatty acid methyl esters of strain CC-PY-50ᵀ and reference strains (except for Antarciticimonas flava NBRC 103398ᵀ, which was grown at 20 °C) were extracted from cells cultivated on MA at 30 °C. Cell samples were harvested during the exponential growth phase, and subjected to saponification, methylation and extraction as described by Kämpfer & Kroppenstedt (1996) and then analysed by GC (model 7890A, Agilent). Peaks were automatically integrated, and fatty acid names and percentages were determined using the microbial identification standard software package MIDI (version 6) (Sasser, 1990) by adopting the database RTSSBA6.

The major (>5 % of total) fatty acids in strain CC-PY-50ᵀ were iso-C₁₅:₀ (22.3 %), iso-C₁₅:₁ G (20.3 %), iso-C₁₇:₀ 3-OH (15.6 %), C₁₆:₀ (6.2 %) and C₁₆:₁ω₆c and/or C₁₆:₁ω₇c (5.2 %) (Table 2). Strain CC-PY-50ᵀ could be distinguished from Mangrovinonas yunxiaonensis LMG 27142ᵀ, Antarcticimonas flava NBRC 103398ᵀ and Hoppeia younheungensis JCM 19488ᵀ have also been reported to possess MK-6 as the predominant respiratory quinone (Kim et al., 2012b; Park et al., 2013; Li et al., 2013; Yang et al., 2009; Kwon et al., 2014). Members of the family Flavobacteriaceae are known to possess MK-6 as their only or major respiratory quinone (Bernardet et al., 2002; Bernardet & Nakagawa, 2006). The DNA G+C content of strain CC-PY-50ᵀ was 37.1 mol%, a value well within the range of 34.7–40.4 mol% (Table 1) reported for other members of closely related genera. The low DNA G+C content is one of the characteristic features of representatives of the family Flavobacteriaceae (Bernardet et al., 2002).

The TLC patterns of the total polar lipids of strain CC-PY-50ᵀ and reference strains are given in Fig. 2 and summarized in Table 1. In line with the present phylogenetic neighbours and most of the previously described marine species of the family Flavobacteriaceae, strain CC-PY-50ᵀ also displayed complex unidentified polar lipids, with or without phospho-, amino- and glyco-moieties. Phosphatidylethanolamine was the only polar lipid to be identified in all the strains except for Corallibacter vietnamensis JCM 17525ᵀ, Geojedonia litorea KCTC 32260ᵀ, Mangrovinonas yunxiaonensis LMG 27142ᵀ, Antarcticimonas flava NBRC 103398ᵀ and Hoppeia younheungensis JCM 19488ᵀ. The polar lipids of strain CC-PY-50ᵀ contained major amounts of three unidentified aminolipids and two unidentified lipids, and moderate amounts of phosphatidylethanolamine and an unidentified phospholipid, an unidentified glycolipid and an unidentified lipid. In addition, trace amounts of an unidentified phospholipid, an unidentified glycolipid and an unidentified lipid were also detected. The unidentified lipid L2 was found in major amount in all seven strains, whereas unidentified phospholipid PL2 was found exclusively in strain CC-PY-50ᵀ. The unidentified aminolipids designated AL2 and AL3, detected in all seven strains, also showed significant quantitative variations at species-level. A moderate-to-minor amount of their only or major respiratory quinone (Bernardet et al., 2002; Bernardet & Nakagawa, 2006).
Table 1. Differential characteristics of strain CC-PY-50T and other members of the family Flavobacteriaceae

Strains: 1, CC-PY-50T; 2, Corallibacter vietnamensis JCM 17525T; 3, Geojedonia litorea KCTC 32260T; 4, Sediminibacter furfuratus NBRC 101622T; 5, Mangrovimonas yunxiaonensis LMG 27142T; 6, Antarctimonas flava NBRC 103398T; 7, Hoppeia youngheungensis JCM 19488T. All data from this study, except where indicated otherwise. All strains are positive for the following characteristics: activity of catalase; hydrolysis of egg yolk and gelatin; activity of alkaline phosphatase, esterase (C 4), esterase lipase (C 8), leucine arylamidase, valine arylamidase and acid phosphatase. All strains are negative for the following characteristics: H2S production; hydrolysis of DNA, colloidal chitin, xylan and CM-cellulose; nitrate reduction, indole production and fermentation of D-glucose; activity of arginine dihydrolase, urease, lipase (C 14), β-glucuronidase and α-fucosidase; assimilation of capric acid. YO, yellowish-orange; Y, yellow; DP, diffusible brown-pigments; PNPG, p-nitrophenyl β-D-galactopyranoside. +, Positive; −, negative; w, weakly positive; ND, not determined. Abbreviations for polar lipids are defined in Fig. 2.

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<th>Characteristics</th>
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<td>+ (DP +)</td>
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<td>+ (DP +)</td>
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unidentified glycolipid was also identified in Corallibacter vietnamensis JCM 17525T, Sediminibacter furfuratus NBRC 101622T and Mangrovimonas yunxiaonensis LMG 27142T. On
the contrary, the unidentified aminophospholipid APL2 was found to be present in major amounts in the strains *Sediminibacter furfurosus* NBRC 101622<sup>T</sup>, *Antarcticimonas flava* NBRC 103398<sup>T</sup> and *Hoppeia youngheungensis* JCM 19488<sup>T</sup>. The detection of significant amounts of the unidentified phospholipid PL2 and unidentified lipid L3 exclusively in strain CC-PY-50<sup>T</sup> and lack of the unidentified lipid L6 that was found only in *Mangrovimonas yunxiaonensis* LMG 27142<sup>T</sup> distinguished these two strains. The polar lipid patterns of *Corallibacter vietnamensis* JCM 17525<sup>T</sup> and *Geojedonia litorea* KCTC 32260<sup>T</sup> obtained in this study differed slightly compared to previously reported data (Kim et al., 2012b; Park et al., 2013), probably due to discrepancies in chromatographic run conditions. Nevertheless, the polar lipids served as an excellent chemotaxonomic marker that could clearly distinguish strain CC-PY-50<sup>T</sup> from its phylogenetic neighbours.

Taken together, the phylogenetic distinctiveness, chemotaxonomic features and phenotypic evidence presented here unambiguously supports the classification of strain CC-PY-50<sup>T</sup> as a novel taxon of the family *Flavobacteriaceae*. Strain CC-PY-50<sup>T</sup> could be further distinguished clearly from all reference strains as well as from *Mangrovimonas yunxiaonensis* LMG 27142<sup>T</sup> in many aspects including phylogenetic instability, polar lipid and fatty acid profiles and several additional features that are listed in Table 1. Thus, we propose the classification of strain CC-PY-50<sup>T</sup> as a representative of a novel genus and species of the family *Flavobacteriaceae*, for which the name *Hanstruepera neustonica* gen. nov., sp. nov. is proposed. In addition, on the basis of new data obtained in this study, emended descriptions of the species *Sediminibacter furfurosus, Mangrovimonas yunxiaonensis, Antarcticimonas flava* and *Hoppeia youngheungensis* are also proposed.

**Fig. 2.** Polar lipid profiles of strain CC-PY-50<sup>T</sup> (a), *Corallibacter vietnamensis* JCM 17525<sup>T</sup> (b), *Geojedonia litorea* KCTC 32260<sup>T</sup> (c), *Sediminibacter furfurosus* NBRC 101622<sup>T</sup> (d), *Mangrovimonas yunxiaonensis* LMG 27142<sup>T</sup> (e), *Antarcticimonas flava* NBRC 103398<sup>T</sup> (f) and *Hoppeia youngheungensis* JCM 19488<sup>T</sup> (g), as determined by two-dimensional TLC. The total polar lipids were visualized by spraying the plates with 10% (v/v) ethanolic molybdatophosphoric acid. PE, phosphatidylethanolamine; L1–9, unidentified lipids; AL1–5, unidentified aminolipids; PL1–3, unidentified phospholipids; GL1–2, unidentified glycolipids; APL1–2, unidentified aminophospholipids.

The description is according to Khan et al. (2007) and Kwon et al. (2014). In addition, cells are positive for egg yolk hydrolysis and negative for the hydrolysis of l-tyrosine, Tweens 20 and 80 and xylan. The major polar lipids are phosphatidylethanolamine, three unidentified aminolipids, an unidentified lipid and an unidentified aminophospholipid. In addition, moderate amounts of an unidentified phospholipid, an unidentified glycolipid and an unidentified lipid, and minor amounts of an unidentified aminolipid and an unidentified lipid are also present.

Emended description of Mangrovimonas yunxiaonensis Li et al. 2013

The description is according to Li et al. (2013). In addition, cells are positive for egg yolk hydrolysis. The major polar lipids are two unidentified aminolipids and two unidentified lipids. In addition, moderate amounts of an unidentified aminolipid and an unidentified lipid, and minor amounts of phosphatidylethanolamine, an unidentified phospholipid, two unidentified glycolipids and two unidentified aminolipids are also present.

Emended description of Antarcticimonas flava Yang et al. 2009

The description is according to Yang et al. (2009). In addition, cells are positive for egg yolk hydrolysis and negative for the hydrolysis of DNA, l-tyrosine, Tweens 20 and 80, CM-cellulose and xylan. The major polar lipids are phosphatidylethanolamine, an unidentified aminolipid, two unidentified lipids and an unidentified aminophospholipid. In addition, moderate amounts of an unidentified aminolipid, and minor amounts of an unidentified phospholipid, an unidentified aminolipid, two unidentified lipids and an unidentified aminophospholipid are also present.

Emended description of Hoppeia youngheungensis Kwon et al. 2014

The description is according to Kwon et al. (2014). In addition, cells are positive for Tween 20 and egg yolk hydrolysis and weakly positive for the hydrolysis of Tween 20. Negative for the hydrolysis of DNA, L-tyrosine, chitin and xylan. The major polar lipids are phosphatidylethanolamine, an unidentified aminolipid, two unidentified lipids and an unidentified aminophospholipid. In addition, moderate amounts of an unidentified aminolipid and an unidentified aminophospholipid. In addition, moderate amounts of an unidentified aminolipid, four unidentified lipids and an unidentified aminophospholipid are also present.

Description of Hanstruepera gen. nov.

Hanstruepera (Hans.true’pe.ra. N.L. fem. n. Hanstruepera after Hans Trüper, a German microbiologist).

Cells are Gram-staining-negative, strictly aerobic, non-spore-forming, chemoorganoheterotrophic, mesophilic, typically rod-shaped with rounded ends, non-flagellated and non-motile. Catalase- and oxidase-positive. Flexirubin-type pigments are present. Zeaxanthin is the major carotenoid pigment. The sole isoprenoid quinone is MK-6. The predominant fatty acids are iso-C15:1 G, iso-C15:0, iso-C17:0 3-OH. Three unidentified aminolipids and two unidentified lipids are present in major amounts, whereas phosphatidylethanolamine, an unidentified phospholipid, an unidentified glycolipid and an unidentified lipid are present in moderate amounts. As determined by 16S rRNA gene sequence analysis, the genus Hanstruepera is a member of the family Flavobacteriaceae. The type species is Hanstruepera neustonica.

Description of Hanstruepera neustonica sp. nov.

Hanstruepera neustonica (neus.to’ni.ca. N.L. fem. adj. neustonica pertaining to and living in the neuston).

Cells are rod-shaped, 0.4–0.5 μm in diameter and 1.0–2.0 μm in length. On MA, after 1–2 days of incubation at 30 °C colonies are circular, convex, yellowish-orange and 0.5–1.0 mm in diameter. Growth occurs at 20–40 °C (optimum, 30 °C), at pH 6.0–8.0 (optimum, 7.0) and in the presence of 2–4 % (w/v) NaCl (optimum, 3 %). Growth occurs on MA but not on NA, R2A or TSA agar. L-Tyrosine, starch and egg yolk are hydrolysed, whereas Tweens 20 and 80, chitin, casein, CM-cellulose, xylan and DNA are not. Diffusible brown-pigments are produced on L-tyrosine agar. In the API 20NE strip, positive for gelatin hydrolysis and assimilation of maltose; negative for nitrate reduction, indole production, D-glucose fermentation, arginine dihydrolase and urease activities, hydrolysis of aesculin and p-nitrophenol β-D-galactopyranoside, and assimilation of D-mannitol, potassium gluconate, capric acid and phenylacetic acid; and weakly positive for the assimilation of D-glucose, L-arabinose, D-mannose, N-acetylglucosamine, adipic acid, malic acid and trisodium citrate. In the Biolog GN2 MicroPlate, the following substrates are positive: α-D-glucose, myo-inositol, sucrose, trehalose, acetic acid, cis-aconitic acid, α-ketoglutaric acid, L-glutamic acid and L-proline; α-cyclodextrin, N-acetyl-D-galactosamine and turanose are weakly utilized; the remaining substrates are not utilized. In the API ZYM strip, positive for alkaline phosphatase, esterase (C 4), esterase lipase (C 8), leucine arylamidase, valine arylamidase, cystine arylamidase, trypsin, α-chymotrypsin, acid phosphatase and naphthol-AS-BI-phosphohydrolase activities; negative for lipase (C 14), α-galactosidase, β-galactosidase, β-glucuronidase, α-glucosidase, β-glucosidase, N-acetyl-β-glucosaminidase, α-mannosidase and α-fucosidase activities. In the API 50 CH strip, acid is produced from inositol and sucrose. In addition to the major fatty acids listed above, C16:0 and C16:1ω6c and/or C16:1ω7c are also present in significant amounts.

The type strain is CC-PY-50T (=JCM 19743T=BCRC 80747T), which was isolated from an estuarine water
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References


sample collected at Pingtung, Taiwan. The genomic DNA G+C content of the type strain is 37.1 mol%.


