Sphingomicrobium marinum sp. nov. and Sphingomicrobium flavum sp. nov., isolated from surface seawater, and emended description of the genus Sphingomicrobium

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Two Gram-staining-negative, yellow-pigmented, rod-shaped, strictly aerobic, non-flagellated and non-spore-forming amylolytic marine bacterial strains, designated CC-AMZ-30MT and CC-AMZ-30NT, were isolated from coastal surface seawater in Taiwan. Strain CC-AMZ-30MT shared pairwise 16S rRNA gene sequence similarities of 95.8, 95.0 and 94.0 % to Sphingomicrobium lutaoense CC-TBT-3T, Sphingomicrobium astaxanthinifaciens CC-AMO-30BT and other sphingomonads, respectively. Strain CC-AMZ-30NT shared 97.0, 96.7, 95.0 and 95.1 % similarities to strain CC-AMZ-30MT, Sphingomicrobium lutaoense CC-TBT-3T, Sphingomicrobium astaxanthinifaciens CC-AMO-30BT and other sphingomonads, respectively.

The common polar lipids of the two strains include a signature glycolipid (GL2), diphosphatidylglycerol, phosphatidylglycerol, phosphatidylethanolamine and sphingoglycolipid in major amounts besides moderate-to-trace amounts of an unidentified aminolipid and several unidentified glycolipids. Both strains contained C18 : 1\(^\text{v}\)/C18 : 1\(^{\text{v}}\)/C18 : 1\(^{6}\), C16 : 1\(^{7}\)/C18 : 1\(^{6}\), C16 : 0 and C18 : 2-OH as major (>5 % of the total) fatty acids. Strains CC-AMZ-30MT and CC-AMZ-30NT had DNA G+C contents of 64.2 and 65.2 mol%, respectively. The major polyamine was spermidine in strain CC-AMZ-30MT and triamine sym-homospermidine in strain CC-AMZ-30NT. Both strains contained ubiquinone Q-10 as the predominant respiratory quinone.

Differential phylogenetic and chemotaxonomic evidence including the presence of characteristic GL2, C18 : 1 2-OH and several other phenotypic features supported the classification of strains CC-AMZ-30MT and CC-AMZ-30NT as two novel species of the genus Sphingomicrobium, for which we propose the names Sphingomicrobium marinum sp. nov. and Sphingomicrobium flavum sp. nov., respectively; corresponding type strains are Sphingomicrobium marinum CC-AMZ-30MT (=JCM 18554\(^T\)=BCRC 80466\(^T\)) and Sphingomicrobium flavum CC-AMZ-30NT (=JCM 18555\(^T\)=BCRC 80467\(^T\)). An emended description of the genus Sphingomicrobium is also proposed.

Abbreviations: DPG, diphosphatidylglycerol; PC, phosphatidylcholine; PE, phosphatidylethanolamine, PG, phosphatidylglycerol; RP-HPLC, reversed-phase HPLC; SGL, sphingoglycolipid.

The GenBank/EMBL/DDBJ accession numbers for the 16S rRNA gene sequences of strains CC-AMZ-30MT and CC-AMZ-30NT are JX235672 and JX393854, respectively.

Three supplementary figures are available with the online version of this paper.

The family Sphingomonadaceae was proposed by Kosako et al. (2000) that presently accommodates 13 validly established genera including Zymomonas (De Ley & Swings, 1976), Sphingomonas (Yabuuchi et al., 1990, 1999), Blastomonas (Sly & Cahill, 1997), Sandaracinobacter (Yurkov et al., 1997), Sphingobium, Novosphingobium, Sphingopyxis (Takeuchi et al., 2001), Sphingosinicella (Maruyama et al., 2006), Sandarakinorhabdus (Gich &
Overmann, 2006), Stakelama (Chen et al., 2010), Sphingomicrobium (Kämpfer et al., 2012), Paraphosphopyx (Uchida et al., 2012) and Sphingorhabdus (Jogler et al., 2012). At the time of writing, the genus Sphingomicrobium accommodated two established species Sphingomicrobium luteaense (Kämpfer et al., 2012) and Sphingomicrobium astaxanthinifaciens (Shahina et al., 2013). Here, based on a polyphasic approach (Vandamme et al., 1996), we investigated the taxonomic position of strains CC-AMZ-30MT and CC-AMZ-30NT that appeared to be closely related to the species of the genus Sphingomicrobium.

Strains were isolated from seawater sample collected at 10 cm depth near Taichung harbour, Taiwan (24.307512° N, 120.518572° E) on 26 May 2012. The seawater sample was subjected to standard dilution-to-extinction plating method using marine agar (MA; Difco) and incubated at 30°C for 48–96 h. Colonies of strains were isolated, primarily based on their differential yellow-pigmentation, purified and preserved as 20% (v/v) glycerol stocks. Taxonomic analyses were carried out according to the published guidelines (Tindall et al., 2010). Direct comparative analyses were made with reference to Sphingomicrobium luteaense CC-TBT-3T (type species) and Sphingomicrobium astaxanthinifaciens CC-AMO-30B. All these strains were cultured on MA or in marine broth (MB) for 48 h at 30°C, unless specified otherwise.

Colonies were examined for morphological features such as appearance, size, shape, texture and pigmentation. 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 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% uranyl acetate for 5–10 s, brief air-drying and transmission electron microscopy (JEM-1400; JEOL). Gram-staining was performed according to the protocol of Murray et al. (1994). After 48 h of incubation on MA, colonies were ≤0.5 mm in diameter, circular, convex and yellow-pigmented; pigmentation was relatively intense in CC-AMZ-30NT as compared with CC-AMZ-30MT. Cells of the strains were Gram-staining-negative, non-flagellated and non-sore-forming, strictly aerobic rods. During exponential growth phase, strain CC-AMZ-30MT formed rod-shaped non-flagellated cells, which were 1.2–2.0 μm in length and 0.5–0.6 μm in diameter. In contrast, cells of strain CC-AMZ-30NT were relatively slender and longer non-flagellated rods, which were 1.2–3.1 μm in length and 0.3–0.5 μm in diameter.

Growth was tested using the media such as nutrient agar (NA; Himedia), tryptic soy agar (TSA; Bacto) and R2A (Oxoid) agar. Growth under anaerobic condition was tested by streaking bacterial strains on MA and MA supplemented with 0.1% KNO₃ followed by incubation in an anaerobic chamber (Coy) for a week. The pH range for growth was determined in MB, which was adjusted before sterilization to pH 3.5–12.5 (at 1.0 pH unit intervals) using appropriate buffers. Growth at 10, 20, 25, 30, 37, 40, 45, 50 and 55°C was tested in MB after 72 h of incubation. Survival at 55°C for 20 min was determined by growing the cells in MB. Cells grew well on MA and showed weak growth on NA; however, no growth was observed on TSA and R2A agar. Growth does not occur under anaerobic conditions. Strain CC-AMZ-30NT was able to grow at 10–45°C, pH 6.5–10.5 and NaCl concentration of 1–3%, whereas strain CC-AMZ-30NT exhibited growth at 10–40°C, pH 6.5–9.5 and NaCl concentrations of 1–2%. Strains survived after incubation at 55°C for 20 min.

Activities of catalase and oxidase and hydrolysis of starch (0.2%), egg yolk (1.0%), Tween 20 (1.0%) and Tween 80 (1.0%) were tested on MA according to the protocol of Smibert & Krieg (1994). Degradation of casein (1.0% skimmed milk), colloidal chitin (1.0%), CM-cellulose (1.0%) and xylan (1.0%) were tested on MA. Degradation was revealed by the clear zone formed around colonies, either directly or after flooding with appropriate stains (Teather & Wood, 1982). Hydrolysis of L-tyrosine (0.5%) was tested on MA (Barrow & Feltham, 1993). All results were recorded after incubating the agar plates at 30°C for 10 days. DNase activity was assessed using DNase test agar (Himedia) supplemented with 3.2% sea salts (Sigma Aldrich). Carbon source utilization was determined using GN2 MicroPlate (Biolog). Reduction of nitrate, production of indole, D-glucose fermentation, activities of arginine dihydrolase, urease, p-nitrophenyl β-D-galactopyranosidase, hydrolysis of aesculin and gelatin and growth on D-glucose, L-arabinose, D-mannose, D-mannitol, N-acetylglucosamine, maltose, potassium glutonate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid were tested by using API 20 NE strips (bioMérieux). Activities of lysine decarboxylase, ornithine decarboxylase, tryptophan deaminase and production of H₂S and acetoin were assessed by using API 20 E strips (bioMérieux). Other enzyme assays and acid production tests were performed by using API ZYM and API 50CH strips (bioMérieux), respectively. All kit-based assays were performed according to the manufacturers’ instructions, except that the inoculation fluids were supplemented with sterile 3.2% sea salt solution (final concentration); results were recorded after 48 h of incubation at 30°C.

The strains showed positive reactions for catalase, oxidase, alkaline phosphatase, esterase C4, esterase lipase C8, leucine arylamidase, valine arylamidase, cystine arylamidase, trypsin and naphthol-AS-BI-phosphohydrolase activities; negative reactions for lipase, x-chymotrypsin, x-galactosidase, β-galactosidase, β-glucuronidase, α-glucosidase, β-glucosidase, N-acetyl β-glucosaminidase, α-mannosidase, α-fucosidase and p-nitrophenyl β-D-galactopyranosidase activities; and variable reactions for acid phosphatase
activity. The strains hydrolysed L-tyrosine and starch but
did not hydrolyse casein, xylan, CM-cellulose, chitin,
Tween-80 and DNA. Weak hydrolysis of Tween-20 and
egg yolk were recorded only for CC-AMZ-30M T. Additionally,
the strains produced several enzymes, assimilated and
produced acid from a variety of compounds as
listed in the species description. Differential biochemical
and phenotypic characteristics that distinguished the
strains from other established members of the genus
*Sphingomicrobium* are given in Table 1.

The genomic DNA of the strains was isolated and partial
16S rRNA genes were amplified via PCR according to the
method of Shahina et al. (2013). The PCR products were
sequenced by using the Bigdye terminator kit (Heiner et al.,
1998) and an automatic DNA sequencer (ABI PRISM 310,
Table 1. Differential phenotypic characteristics of strains CC-AMZ-30M T, CC-AMZ-30N T and the other two species of the genus
*Sphingomicrobium*

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
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<tbody>
<tr>
<td>Colony pigmentation</td>
<td>Light-yellow</td>
<td>Bright-yellow</td>
<td>Reddish-orange</td>
<td>Light-yellow</td>
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<td>Cell size (μm)</td>
<td>1.2–2.0×0.5–0.6</td>
<td>1.2–3.1×0.3–0.5</td>
<td>1.1–2.8×0.5–0.7</td>
<td>1.5±0.5×1.0±0.1*</td>
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<td>Growth in NaCl (%) (optimum)</td>
<td>1–3 (1)</td>
<td>1–2 (1)</td>
<td>1–4 (3)</td>
<td>1–4 (1)</td>
</tr>
<tr>
<td>Reduction of nitrate to N₂</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>W</td>
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<tr>
<td>Acetoin production</td>
<td>w</td>
<td>w</td>
<td>w</td>
<td>W</td>
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<td>Hydrolysis of:</td>
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<tr>
<td>Starch</td>
<td>+</td>
<td>+</td>
<td>–</td>
<td>+</td>
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<tr>
<td>L-Tyrosine</td>
<td>+</td>
<td>+</td>
<td>–</td>
<td>+</td>
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<td>Tween-20</td>
<td>w</td>
<td>+</td>
<td>–</td>
<td>W</td>
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<tr>
<td>Egg yolk</td>
<td>w</td>
<td>+</td>
<td>W</td>
<td>W</td>
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<tr>
<td>Aesculin</td>
<td>+</td>
<td>–</td>
<td>+</td>
<td>–</td>
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<td>Assimilation of:</td>
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<tr>
<td>L-Arabinose</td>
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<td>+</td>
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<td>Malate</td>
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<td>Lipase</td>
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<td>α-Glucosidase</td>
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<td>–</td>
<td>–</td>
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<tr>
<td>β-Glucosidase</td>
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<td>–</td>
<td>–</td>
<td>W</td>
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<tr>
<td>N-acetyl-β-glucosaminidase</td>
<td>–</td>
<td>–</td>
<td>+</td>
<td>–</td>
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<td>DNA G+C content (mol%)</td>
<td>64.2</td>
<td>65.2</td>
<td>70.6</td>
<td>67.7 (63.4)*</td>
</tr>
</tbody>
</table>

*Data taken from Kämpfer et al. (2012).
Sphingomicrobium lutaoense

Similarities to

Maximum-likelihood (Felsenstein, 1981) parameter model; Kimura, 1980) including clustering by method (distance options according to the Kimura two-parameter model; Kimura, 1980) including clustering by neighbour-joining (Saitou & Nei, 1987), discrete-character-based maximum-parsimony (Fitch, 1971) and maximum-likelihood (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 16S rRNA gene sequence analysis revealed that CC-AMZ-30MT shared 95.8, 95.0 and <94% pairwise similarities to Sphingomicrobium lutaoense CC-TBT-3T, Sphingomicrobium astaxanthinifaciens CC-AMO-30BT and other sphingomonads, respectively. In contrast, CC-AMZ-30NT shared 97.0, 96.7, 95.0 and <95.1% similarities to CC-AMZ-30MT, Sphingomicrobium lutaoense CC-TBT-3T, Sphingomicrobium astaxanthinifaciens CC-AMO-30BT and other sphingomonads, respectively. In the neighbour-joining phylogenetic tree, the novel strains occupied discrete phyletic lineages tightly associated with each other (99% confidence for the node) as well as within the clade that accommodated species of the genus Sphingomicrobium (Fig. 1). Similarly, in the maximum-likelihood (Fig. S1) and maximum-parsimony phylogenetic trees (not shown), the novel strains were found to be clustered together within the genus Sphingomicrobium.

For cellular fatty acid analysis, the fatty acid methyl esters of the strains were extracted from cells cultivated on MA at 30 °C. Cell samples were harvested during mid-exponential growth phase, subjected to saponification, methylation and extraction as described previously (Kämpfer & Kroppenstedt, 1996) and analysed by gas chromatography (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 RTSBA6. Both strains possessed C_{18:1} \text{OH} and C_{16:0} \text{OH} as major (>5%) of the total fatty acids. Strain CC-AMZ-30MT additionally contained C_{17:0} \text{OH} and C_{18:1} \text{11-methyl} in major amounts (Table 2). Both strains displayed the predominance of C_{18:1} \text{OH} and/or C_{18:1} \text{11-methyl} in their fatty acid profiles, similar to the two reference strains of species of the genus Sphingomicrobium. The presence of major amounts of C_{18:1} \text{2-OH} is a characteristic feature attributed to the genus Sphingomicrobium (Kämpfer et al., 2012).

The respiratory quinones were extracted according to the method of Collins (1985) with slight modifications (Shahina et al., 2013). Strains produced ubiquinone Q-10 as the predominant respiratory quinone besides trace amounts of Q-9, which were in line with that of species of the genus Sphingomicrobium (Kämpfer et al., 2012; Shahina et al., 2013).

For the determination of the DNA G+C content, the DNA of strains were prepared by thermal denaturation and enzymic digestion into nucleosides as described previously (Mesbah et al., 1989). The resultant nucleoside mixture was separated and quantified by RP-HPLC with the conditions specified by Shahina et al. (2013). Strains CC-AMZ-30MT and CC-AMZ-30NT respectively contained 64.2 and 65.2 mol% DNA G+C. These values were slightly lower when compared with that of Sphingomicrobium lutaoense CC-TBT-3T, as determined under identical conditions (Table 1).

The polyamines were extracted and analysed by RP-HPLC according to the method of Scherer & Kniefl (1983) with slight modifications (Shahina et al., 2013). The polyamine profile of strain CC-AMZ-30MT consisted of major amounts of spermidine followed by triamine sym-homospermidine and trace amounts of putrescine and cadaverine (Fig. S2). In contrast, strain CC-AMZ-30NT possessed triamine sym-homospermidine in major amounts besides having moderate amounts of spermidine; no other polyamines were detected. Species of the genus Sphingomicrobium have been found to produce triamine sym-homospermidine as a predominant polyamine (Kämpfer et al., 2012; Shahina et al., 2013). Kämpfer et al. (2012) reported that Sphingomicrobium lutaoense CC-TBT-3T can also produce minor amounts of spermidine, putrescine and cadaverine besides trace amounts of spermine. Thus, the differential polyamine profiles identified in this study probably reflect the species-specific polyamine biosynthetic disparity existing within the species of the genus Sphingomicrobium.

The polar lipids of the novel strains were extracted and analysed by TLC (Embley & Wait, 1994). The strains possessed diphasphatidylglycerol (DPG), phosphatidylglycerol (PG), phosphatidylethanolamine (PE), sphingoglycolipid (SGL) and a signature glycolipid (GL2) in major amounts besides several unidentified glycolipids and an unidentified aminolipid in moderate-to-trace amounts (Fig. 2). The major polar lipids were very similar to the polar lipids reported previously for the other two species of the genus Sphingomicrobium (Kämpfer et al., 2012; Shahina et al., 2013). In addition, strain CC-AMZ-30NT possessed phosphatidylcholine (PC), which was detected also in Sphingomicrobium lutaoense CC-TBT-3T but not in Sphingomicrobium astaxanthinifaciens CC-AMO-30BT (Shahina et al., 2013) and strain CC-AMZ-30MT (Fig. S3). Strain CC-AMZ-30MT completely lacked unidentified phospholipids (PL1–3) and an aminophospholipid (APL) that were found in strain CC-AMZ-30NT (Fig. 2) as well as in
Sphingomicrobium lutaoense CC-TBT-3^T (Shahina et al., 2013). Furthermore, a glycolipid spot designated GL6 was detected exclusively in strain CC-AMZ-30MT. Thus, it can be concluded that species of the genus Sphingomicrobium can produce PC, several unidentified glycolipids, unidentified phospholipids and an aminophospholipid heterogeneously. Nevertheless, GL2 appears to be an important chemotaxonomic marker that can differentiate species of the genus Sphingomicrobium from other members of the family Sphingomonadaceae.

Molecular and phylogenetic evidence presented here clearly distinguished the strains from each other as well as from other sphingomonads. Furthermore, the detection of signature glycolipid (GL2), significant amounts of C_{18:1} 2-OH and several phenotypic and biochemical features supported the classification of strains CC-AMZ-30M^T and CC-AMZ-30N^T as two novel species within the genus Sphingomicrobium, for which the names Sphingomicrobium marinum sp. nov. and Sphingomicrobium flavum sp. nov. are proposed, respectively. Based on the new data obtained in this study, an emended description of the genus Sphingomicrobium is also proposed.


The genus description is as given by Kämpfer et al. (2012) and Shahina et al. (2013) with the following amendments: triamine sym-homospermidine is a major polyamine in the polyamine pattern but spermidine may be predominant. The presence of PC is variable.

**Description of Sphingomicrobium marinum sp. nov.**

*Sphingomicrobium marinum* (ma.ri’num. L. neut. adj. marinum of or belonging to the sea, marine).

Cells are Gram-staining-negative, strictly aerobic, non-flagellated and non-spore-forming rods. The cell size...
The polar lipid profile features DPG, PG, PE, SGL, six unidentified glycolipids (GL1–6) and an unidentified aminolipid (AL). The major polyamines are spermidine and triamine sym-homospermidine. The predominant respiratory quinone is ubiquinone Q-10.

The type strain is CC-AMZ-30MT (\(=\)JCM 18554\(^T\)) \(=\)BCRC 80466\(^T\), which was isolated from surface seawater (10 cm depth) collected near Taichung harbour, Taiwan. The DNA G+C content of the type strain is 64.2 mol%.
Description of *Sphingomicrobium flavum* sp. nov.

*Sphingomicrobium flavum* (fla’vum. L. neut. adj. flavum yellow, the colour of colonies or pigments that the bacterium produces).

Cells are Gram-staining-negative, strictly aerobic, non-spor-forming and non-motile rods. The cell size ranges from 1.2 to 3.1 μm in length and from 0.3 to 0.5 μm in diameter. Colonies are ≤0.5 mm in diameter, circular and bright-yellow-pigmented after 48 h of incubation on MA. Cells grow well on MA, weakly on NA but not on R2A and TSA. Growth occurs at pH 6.5–9.5 (optimum 6.5–8.5), at 10–40 °C (optimum 30–37 °C) and in the presence of 1–2% NaCl (optimum 1.0%). Catalase- and oxidase-positive. Can hydrolyse starch, Tween 20, L-tyrosine and egg yolk but not CM-cellulose, casein, chitin, xylan, Tween 80 and DNA. According to the API 20 NE strip, positive for assimilation of D-glucose, L-arabinose, D-mannitol, D-mannose, N-acetylglucosamine, maltose and phenylacetic acid; negative for nitrate reduction, indole production, D-glucose fermentation, hydrolysis of ascelin and gelatin, arginine dihydrolase, urease and p-nitrophenyl β-D-galactopyranosidase activities and assimilation of capric acid, adipic acid, malic acid, trisodium citrate and potassium gluconate. According to the API 20 E strip, weakly positive for acetoin production; negative for citrate utilization, o-nitrophenyl β-D-galactopyranosidase, arginine dihydrolase, lysine decarboxylase, ornithine decarboxylase, urease, indole production, gelatinase and tryptophan deaminase activities, H2S production and fermentation/oxidation of D-glucose, D-mannitol, inositol, D-sorbitol, L-rhamnose, sucrose, melibiose, amygdalin and L-arabinose. In the API ZYM strip, positive for alkaline phosphatase, esterase (C4), esterase lipase (C8), leucine arylamidase, valine arylamidase, cystine arylamidase, trypsin and naphthol-AS-BI-phosphohydrolase activities; negative for acid phosphatase, N-acetyl-β-glucosaminidase, lipase, α-chymotrypsin, α-galactosidase, β-galactosidase, β-glucuronidase, α-glucosidase, β-glucosidase, α-mannosidase and α-fucosidase activities. According to the API 50 CH strip, acid is produced only from aesculin ferric citrate and potassium-S-ketogluconate. According to the GN2 MicroPlate, the following carbon sources are utilized: x-cyclodextrin, glycogen, N-acetyl-D-galactosamine, N-acetyl-D-glucosamine, adonitol, D-arabitol, L-fucose, D-galactose, gentiobiose, x-glucose, inositol, α-lactose, maltose, lactulose, D-mannitol, β-methyl D-glucoside, melibiose, D-psicose, raffinose, L-rhamnose, D-sorbitol, trehalose, turanose, xyitol, succinic acid monomethyl ester, citric acid, D-galacturonic acid, D-glucuronic acid, D-glucuronic acid, glucuronamide, D-glucosaminic acid, β-hydroxybutyric acid, α-ketobutyric acid, α-ketoacetic acid, Di-lactic acid, malonic acid, D-saccharic acid, succinic acid, succinamic acid, succrose, acetic acid, cis-aconitic acid, L-alanine, L-alaninamide, L-alanyl glycine, L-aspartic acid, L-asparagine, DL-carnitine, L-glutamic acid, glycyl-L-aspartic acid, L-histidine, hydroxy-L-proline, L-ornithine, L-phenylalanine, L-proline, L-pyroglutamic acid, quinic acid, urocanic acid, D-serine, L-serine, L-threonine, thymidine and D-glucose 6-phosphate; the remaining substrates are not utilized. The major (>5% of the total) fatty acids are summed feature 8 (C18:1ω7d C18:1ω6c), summed feature 3 (C16:1ω7d C16:1ω6c), C18:1 2-OH and C16:0. The polar lipid profile includes DPG, PG, PE, SGL, PC, five unidentified glycolipids (GL1–5), three unidentified phospholipids (PL1–3), one unidentified aminolipid (AL) and one unidentified aminophospholipid (APL). The predominant polyamine is triamine sym-homospermidine. The respiratory quinone is ubiquinone Q-10.

The type strain is CC-AMZ-30NT (=JCM 18555T = BCRC 80467T), which was isolated from surface seawater (~10 cm depth) near Taichung harbour, Taiwan. The DNA G+C content of the type strain is 65.2 mol%.

Acknowledgements

The authors would like to thank the editor and anonymous reviewers for providing constructive comments on this manuscript. The present work was supported in part by the Ministry of Education, Taiwan, ROC under the Aim at Top University (ATU) plan. Mariyah Shahina is grateful to the Ministry of Economic Affairs and National Chung Hsing University, Taiwan, for award of a doctoral scholarship.

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