Meridianimaribacter flavus gen. nov., sp. nov., a member of the family *Flavobacteriaceae* isolated from marine sediment of the South China Sea

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A Gram-staining-negative, rod-shaped marine bacterium, designated strain NH57N^T, isolated from sandy sediment in the Mischief Reef of the South China Sea, was characterized based on its physiological and biochemical features, fatty acid profile and phylogenetic position. 16S rRNA gene sequence analysis revealed a clear affiliation with the family *Flavobacteriaceae*. Strain NH57N^T showed the closest phylogenetic relationship with members of the genera *Gaetbulibacter*, *Gelidibacter*, *Subsaxibacter*, *Subsaximicrobium* and *Yeosuana*; levels of 16S rRNA gene sequence similarity between strain NH57N^T and the type strains of related species ranged from 94.9 to 91.2%. Cells of strain NH57N^T were motile by gliding and grew on solid media as yellow colonies at 9–37 °C, pH 6.5–8.5 and in the presence of 0.5–4.0% NaCl. The DNA G+C content was 32.7 mol% and the predominant fatty acids were iso-C_{15:1} (22.7% of the total), iso-C_{15:0} (20.7%), iso-C_{17:0} 3-OH (9.5%), iso-C_{16:0} 3-OH (8.3%), C_{15:0} (7.8%) and iso-C_{15:0} 3-OH (5.8%). Based on the physiological and phylogenetic data, and on the fatty acid composition, strain NH57N^T is considered to represent a novel species of a new genus in the family *Flavobacteriaceae*, for which the name *Meridianimaribacter flavus* gen. nov., sp. nov. is proposed. The type strain of *Meridianimaribacter flavus* is NH57N^T (=CCTCC AB 208318^T=LMG 24839^T=MCCC 1A03544^T).

The family *Flavobacteriaceae*, proposed by Jooste (1985), is one of the most widely expanding families in the phylum *Bacteroidetes*: more than 50 genera have been described, most of them in recent years. The genus *Gaetbulibacter* was erected by Jung *et al.* (2005) to accommodate the novel species *Gaetbulibacter saemankumensis*, isolated from a tidal flat sediment in the Yellow Sea in Korea. A second species of this genus, *Gaetbulibacter marinus*, was subsequently described from coastal surface seawater, also from the Yellow Sea (Yang & Cho, 2008). Species assigned to this genus are yellow-pigmented, aerobic, rod-shaped, catalase- and alkaline-phosphatase-positive, and have the ability to degrade aesculin. Oxidase activity and gliding motility are species-dependent.

Strain NH57N^T was isolated recently from the South China Sea. It is considered to represent a new lineage closely related to the genus *Gaetbulibacter*. Although strain NH57N^T shares many physiological and biochemical characteristics with species of the genus *Gaetbulibacter*, it differs from them in its narrower pH and salinity ranges for growth, lower DNA

G+C content and ability to degrade gelatin. In addition, moderate levels of 16S rRNA gene sequence similarity and differences in cellular fatty acid composition also support the suggestion that strain NH57N^T represents a novel species of a new genus in the family *Flavobacteriaceae*.

Strain NH57N^T was isolated from a sandy sediment sample with coral granules collected in May 2007 at a water depth of 12 m from the seafloor of a lagoon of the Mischief Reef of the South China Sea (115.4617° E 9.9217° N). This work was part of a taxonomic survey of the broad biodiversity of free-living microbial populations of the South China Sea. In the laboratory, sediment slurry was spread on M2 agar plates, which were then incubated at 25 °C for 1 week. The medium consisted of (per litre seawater): 5 g CH₃COONa, 0.5 g peptone, 0.5 g yeast extract, 0.5 g glucose, 0.5 g sucrose, 0.5 g starch, 0.05 g trisodium citrate, 0.05 g malic acid, 0.05 g potassium sodium tartrate, 1.0 g NH₄NO₃, 0.2 g NH₄Cl and 15 g agar, adjusted to pH 7.5–7.6. Strain NH57N^T was isolated and subsequently purified on fresh M2 agar four times and stored at –80 °C in M2 broth supplemented with 20% (v/v) glycerol.

The 16S rRNA gene of strain NH57N^T was amplified from a single colony by PCR with *Taq* DNA polymerase (MBI)

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The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain NH57N^T is FJ360684.

and two universal primers (Lane, 1991). Purification of the PCR product was carried out according to the protocol of the TIANquick midi purification kit (TIANGEN). Sequencing of the 16S rRNA gene was performed with an Applied Biosystems automatic sequencer (ABI3730XL). The 16S rRNA gene sequence (1470 bp) of strain NH57N^T was compared with others in the NCBI database via BLAST searches. Closely related sequences were retrieved and aligned. Evolutionary distances were then calculated according to the Kimura two-parameter model (Kimura, 1980) with DNAMAN software (version 6). Phylogenetic trees were constructed by using the neighbour-joining (Saitou &

Nei, 1987) method, and were evaluated by bootstrap analysis based on 1000 replicates.

Phylogenetic analysis of 16S rRNA gene sequences revealed that strain NH57N^T is a member of the family *Flavobacteriaceae* and forms a distinct lineage with species of the genera *Gaetbulibacter*, *Gelidibacter*, *Subsaxibacter*, *Subsaximicrobium* and *Yeosuana* (Fig. 1). Its nearest phylogenetic neighbours are *Gaetbulibacter marinus* IMCC1914^T and *Gaetbulibacter saemankumensis* SMK-12^T, with which it shared 16S rRNA gene sequence similarities of 94.9 and 94.2 %, respectively. Although the

Fig. 1. Neighbour-joining phylogenetic tree based on 16S rRNA gene sequences showing the position of strain NH57N^T among representative members of related genera in the family *Flavobacteriaceae*. Bootstrap values above 50 % (based on 1000 replicates) are given at nodes. *Capnocytophaga ochracea* ATCC 27872^T was used as an outgroup. GenBank accession numbers are shown in parentheses. Bar, 0.05 substitutions per nucleotide position.

branching of strain NH57N^T with *Gaetbulibacter* species in the phylogenetic tree was not supported strongly by bootstrap analysis (Fig. 1), the trees generated with the distance matrix by using the Jukes–Cantor and maximum-likelihood models showed the same topology (data not shown). Levels of 16S rRNA gene sequence similarity between strain NH57N^T and the type strains of other related species were 93.4–91.2 %. These relatively low levels of 16S rRNA gene sequence similarity to its most closely related genera suggest that strain NH57N^T may represent a novel species of a new genus.

Cell morphology and motility were observed by using phase-contrast light microscopy (model 50i; Nikon) and transmission electron microscopy (model JEM-1230; JEOL), with cells from the early exponential phase grown on M2 agar. Gliding motility was determined as described by Bowman (2000). Growth was tested at pH 3–10 by using 5 ml HLB medium supplemented with 200 µl M2 medium, adjusted with NaOH and HCl solutions. HLB was modified from Luria–Bertani medium (Sambrook *et al.*, 1989), with the NaCl concentration increased to 30 g l⁻¹. Growth was tested at 4–45 °C and in the presence of 0.5–25 % (w/v) NaCl on M2 agar. The requirement for NaCl was studied on M2 agar devoid of NaCl obtained by replacing seawater with distilled water. The oxidase reaction was tested by using oxidase reagent (bioMérieux). Catalase activity was tested by using a 3 % H₂O₂ solution. Hydrolysis of starch and Tweens 20, 40 and 80 were determined as described by Cowan & Steel (1965). Casein hydrolysis was tested according to the method of Smibert & Krieg (1994). Other physiological and biochemical tests were performed with the API 20E and API 20NE systems (bioMérieux) and the inoculum was prepared by suspending cells in a 3 % (w/v) NaCl solution. The API ZYM system (bioMérieux) was used to determine the activity of 19 enzymes. Oxidation of 95 carbon sources was determined by using GN2 microplates (Biolog) as described by Ivanova *et al.* (1998). Cupules were inoculated with 150 µl liquid culture, with the NaCl concentration increased to 2.4 %. All above-mentioned tests were conducted at 30 °C.

Susceptibility to antibiotics was tested on M2 agar at 30 °C for 2 days by using the following discs (Oxoid): ceftriaxone (30 µg), cephradine (30 µg), chloramphenicol (30 µg), gentamicin (10 µg), erythromycin (15 µg), cefoperazone (75 µg), ciprofloxacin (5 µg), clindamycin (2 µg), doxycycline hydrochloride (30 µg), neomycin (10 µg), tetracycline (30 µg), cephalixin (30 µg), ampicillin (10 µg), furazolidone (15 µg), metronidazole (5 µg), cephalolin (30 µg), lincomycin (2 µg), minocycline (30 µg), norfloxacin (10 µg), kanamycin (30 µg), vancomycin (30 µg), trimethoprim (25 µg), piperacillin (100 µg), ofloxacin (5 µg), rifampicin (5 µg), carbenicillin (100 µg), polymyxin B (300 U), streptomycin (10 µg), oxacillin (1 µg) and penicillin G (10 U). The physiological and biochemical characteristics of strain NH57N^T are given in the genus and species descriptions and in Table 1.

For cellular fatty acid analysis, strain NH57N^T was harvested from MA plates after cultivation for 3 days at 30 °C. *Gaetbulibacter* species had also been grown on MA for 3 days; growth temperature was 30 °C for *Gaetbulibacter saemankumensis* (Jung *et al.*, 2005) and 25 °C for *Gaetbulibacter marinus* (Yang & Cho, 2008). Fatty acids were extracted according to the standard protocol of the Microbial Identification System (MIDI; Sherlock). Analysis of fatty acid methyl esters was performed using a gas chromatograph (6850; Agilent), and peaks were identified with the MIDI software (version 6.0). The main cellular fatty acids were branched-chain unsaturated and saturated, and straight-chain saturated components, namely iso-C_{15:1} (22.7 % of the total), iso-C_{15:0} (20.7 %), iso-C_{17:0} 3-OH (9.5 %), iso-C_{16:0} 3-OH (8.3 %), C_{15:0} (7.8 %) and iso-C_{15:0} 3-OH (5.8 %). High levels of branched-chain and 3-hydroxy C₁₅–C₁₇ fatty acids are typical for members of the family *Flavobacteriaceae* (Bowman *et al.*, 1998). The presence of significant amounts of iso-C_{17:0} 3-OH and branched-chain fatty acids supports the placement of strain NH57N^T in the family *Flavobacteriaceae*.

The DNA G+C content of strain NH57N^T was 32.7 mol%, as determined by reversed-phase HPLC according to the method of Tamaoka & Komagata (1984).

Separation of the novel strain from members of related genera was supported by comparison of their phenotypic and genotypic characteristics (Tables 1 and 2). Strain NH57N^T exhibited narrower pH and salinity ranges for growth. In addition, it could be distinguished from its closest relatives, *Gaetbulibacter marinus* and *Gaetbulibacter saemankumensis*, based on hydrolysis of gelatin and susceptibility to ampicillin. The ability to produce oxidase, inability to generate acid from glucose and requirement of Na⁺ ions for growth distinguished strain NH57N^T from members of the genus *Gelidibacter*. Weak degradation of starch and failure to hydrolyse casein or Tween 80 differentiated the novel strain from *Subsaxibacter* and *Subsaximicrobium* species. The difference of more than 10 mol% in DNA G+C content readily distinguished strain NH57N^T from *Yeosuana aromativorans* GW1-1^T. Moreover, strain NH57N^T was clearly differentiated from members of all phylogenetically related genera based on differences in the presence and proportions of several fatty acids (Table 2).

Overall, the low levels of 16S rRNA gene sequence similarity, together with differences in chemotaxonomic, physiological and biochemical properties, indicate that strain NH57N^T represents a novel species of a new genus, for which the name *Meridianimaribacter flavus* gen. nov., sp. nov. is proposed.

Description of *Meridianimaribacter* gen. nov.

Meridianimaribacter (Me.ri.di.a.ni.ma.ri.bac'ter. L. adj. *meridianus* of or belonging to the south, southern, meridional; L. n. *mare* the sea; N.L. masc. n. *bacter* a rod;

Table 1. Differential phenotypic characteristics between strain NH57N^T and closely related members of the family *Flavobacteriaceae*

Taxa: 1, strain NH57N^T (*M. flavus* gen. nov., sp. nov.); 2, *Gaetbulibacter* (*n*=2; data from Jung *et al.*, 2005; Yang & Cho, 2008); 3, *Gelidibacter* (*n*=4; Kwon *et al.*, 2006; Bowman & Nichols, 2005); 4, *Subsaxibacter broadyi* P7^T (Bowman & Nichols, 2005; Kwon *et al.*, 2006); 5, *Subsaximicrobium* (*n*=2; Bowman & Nichols, 2005; Kwon *et al.*, 2006); 6, *Yeosuana aromatorans* GW1-1^T (Kwon *et al.*, 2006); 7, *Algibacter* (*n*=2; Nedashkovskaya *et al.*, 2004, 2007); 8, *Bizionia* (*n*=6; Kwon *et al.*, 2006; Bercovich *et al.*, 2008; Bowman & Nichols, 2005); 9, *Formosa* (*n*=2; Nedashkovskaya *et al.*, 2006). *n*, Number of type strains in each genus. +, Positive; –, negative; w, weakly positive; ND, no data available; v, variable. All taxa are positive for catalase and negative for indole and H₂S production.

Characteristic	1	2	3	4	5	6	7	8	9
Gliding motility	+	v	+	+	+	–	+	–	+
Production of acetoin	+	ND	ND	ND	ND	ND	–	–*	–
Urease activity	–	–	–	–	–	–	–	v	–
Oxidase activity	+	v	–	ND	ND	–	+	+	+
Nitrate reduction	–	v	–	–	–	–	v	–	v
Requirement for:									
Na ⁺	+	+	–	+	+	+	+	+	v
Oxygen	+	v	+	+	+	+	v	+	v
Temperature (°C)†	9–37 (30–37)	3–40 (25)	0–37 (15–18)	–2 to 20	–2 to 25	23–39 (33–36)	4–37 (23)	4–36 (23–25)	4–34
pH†	6.5–8.5 (7.8)	5.5–11	ND	ND	ND	5–8 (7)	ND	ND	5–10
NaCl (%)†	0.5–4.0 (0.5–2.0)	0.5–7	0–15	0.5–7.3 (1.8–2.3)	0.5–12	0.5–4.0 (2.0)	1–6	1–17.6	0–8
Degradation of:									
Agar	–	–	–	–	–	–	+	–	v
Casein	–	v	v	–	+	–	–	+	–
Gelatin	+	–	v	+	+	+	+	+	+
Starch	w	v	v	–	+	–	v	–	v
Tween 80	–	–	v	+	+	ND	–	+‡	–
Aesculin	+	+	+	w	+	ND	+	–	+
Acid production from glucose	–	v	+	–	–	–	v	–	+
Susceptibility to:									
Ampicillin	+	–	ND	ND	ND	ND	–	ND	v
Penicillin G	+	+	ND	ND	ND	ND	–	ND	–
DNA G + C content (mol%)	32.7	34.7–38.1	36–42	35	38–41	51.4	31–35.1	34–45	34–36

*Only the type strain of *Bizionia paragorgiae* was negative.

†Ranges with optima in parentheses.

‡Only the type strain of *Bizionia argentinensis* was negative.

N.L. masc. n. *Meridianimaribacter* a rod of the southern sea, isolated from the South China Sea).

Cells are strictly aerobic, Gram-staining-negative, non-spore-forming, rod-shaped and motile by gliding. Yellow colonies are formed on M2 plates. The major cellular fatty acids are straight-chain saturated, branched-chain saturated and unsaturated compounds. Oxidase- and catalase-positive. As determined by 16S rRNA gene sequence analysis, the genus is a member of the family *Flavobacteriaceae*, phylum *Bacteroidetes*. The type species is *Meridianimaribacter flavus*.

Description of *Meridianimaribacter flavus* sp. nov.

Meridianimaribacter flavus (fla'vus. L. masc. adj. *flavus* yellow, reflecting the colour of colonies).

Has the following characteristics in addition to those given for the genus. Cells are 1.15–2.3 µm in length and 0.3–0.55 µm in diameter, surrounded by an unidentified extracellular compound (Fig. 2). Growth occurs at 9–37 °C (optimum, 30–37 °C), at pH 6.5–8.5 (optimum, pH 7.8) and in the presence of 0.5–4.0 % NaCl (optimum, 0.5–2.0 %). NaCl is essential for growth. Colonies on M2 are circular, smooth, glistening, moist in appearance, convex with entire margins and 1–2 mm in diameter after 3 days incubation at 30 °C. Gelatin is hydrolysed. Starch and Tween 40 are weakly hydrolysed. Agar, casein and Tweens 20 and 80 are not hydrolysed. Nitrate is not reduced. Acetoin is produced, but H₂S and indole are not. With API 20E and 20NE strips, positive for β-glucosidase (=aesculinase) and β-galactosidase activity, but negative for urease, arginine dihydrolase, ornithine decarboxylase, tryptophan deaminase and lysine decarboxylase activities.

Table 2. Cellular fatty acid compositions (% of the total) of strain NH57N^T and closely related members of the family Flavobacteriaceae

Taxa: 1, strain NH57N^T (*M. flavus* gen. nov., sp. nov.); 2, *Gaetbulibacter* ($n=2$; data from Yang & Cho, 2008); 3, *Gelidibacter* ($n=4$; Bowman & Nichols, 2005); 4, *Subsaximicrobium* ($n=2$; Bowman & Nichols, 2005); 5, *Subsaxibacter broadyi* P7^T (two strains analysed; data from Bowman & Nichols, 2005); 6, *Yeosuana aromativorans* GW1-1^T (Kwon *et al.*, 2006); 7, *Algibacter* ($n=2$; Nedashkovskaya *et al.*, 2004, 2007); 8, *Bizionia* ($n=6$; Bowman & Nichols, 2005; Bercovich *et al.*, 2008); 9, *Formosa* ($n=2$; Nedashkovskaya *et al.*, 2006). *n*, Number of type strains in each genus. For taxa 2, 3, 4, 5, 7, 8 and 9, values shown are the range of percentages for all species in the genus or for all strains of the species. br, Branched (in which branching positions have not been determined) fatty acids; tr, trace (<0.3%); ND, not detected. Fatty acids amounting to <0.3% of the total fatty acids in all strains listed were omitted.

Fatty acid	1	2	3	4	5	6	7	8	9
iso-C _{13:0}	0.5	0.6–2.0			ND to tr			tr to 3.0	
anteiso-C _{13:0}					ND to tr			0.3–0.4	
C _{14:0}	0.3		0.3–0.6	tr to 0.5	0.6–0.7			0.4–0.8	
iso-C _{14:0}	1.2	ND to 1.0	0.4–2.8	tr to 0.7	0.4–0.6			1.2–2.5	
iso-C _{14:0} 3-OH	0.4								
br-C _{14:1}			0.3–1.7	0.3–0.5	0.4–0.5			0.7–1.1	
C _{15:0}	7.8	1.3–3.9	2.4–5.3	0.6–1.1	0.7–1	5.3	7–13.4	2.3–6.0	8.7–15.5
anteiso-C _{15:0}	1.3	4–10.8	10.5–17.7	9.9–17.1	14.3–14.5	14.9	4.6–7.2	10.1–20.8	1.6–4.7
iso-C _{15:0}	20.7	20.6–24.3	3.4–8.8	7.4–10.4	6.3–6.4	21.7	11.3–12.5	3.1–17.3	12.7–17.2
iso-C _{15:0} 3-OH	5.8	4.8–8.6	2.2–6.2	2.4–5.4	1.9–2.3		5.8–9.4	1.2–9.3	6.7–10.5
anteiso-C _{15:0} 3-OH			0.3–10.6	3.6–8.7	5.2			3.4–22.9	
C _{15:0} 2-OH	0.9	0.6–1.6					ND to 2.4	ND to 2.1	1.5–1.8
C _{15:0} 3-OH	1.3		tr to 1.5	ND to 0.8	ND to 0.5		ND to 1.3	tr to 2.0	2.3–4.0
C _{15:1} ω6c			2.7–4.2	tr to 1.0	1.3–2.0		1.7–10.9	1.2–3.0	6.0–8.5
anteiso-C _{15:1}	0.4	1.4–3.4	11.8–16.6	5.9–14.7	9.9–15.5		ND to 2.1	3.6–14.0	ND to 1.0
iso-C _{15:1}	22.7	12.5–32.1	5.3–11.4	6.7–13.4	6.2–6.7	14.8	13–13.4	2.1–18.1	6.5–11.4
Summed feature 3*	9.2	4.5–10.4	4.3–9.5	9.5–13.4	8.3–13.1	10.9	22.2	2.6–6.3	5.9–15.8
C _{16:0}	1.4	0.9–1.3	1.2–2.2	1.9–2.7	1.6–2		ND to 2.3	1.2–3.4	ND to 1.6
C _{16:0} 10-methyl						4.7	ND to 2.1		
C _{16:0} 3-OH	1.1	ND to 1.2					ND to 1.4		tr to 2.1
iso-C _{16:0}	0.9	ND–1.2	1.4–4.4		1.5–1.7			1.1–5.8	ND to 2.1
iso-C _{16:0} 3-OH	8.3	2.0–5.5	4.1–12.2	8.8–13.7	5.0–6.0			1.3–8.5	3.1–8.9
C _{16:1} ω5c			ND to 1.1	ND to 0.5	1.1–1.2			0.4–0.8	
br-C _{16:1}			1.4–10.3	1.9–4.7	3.5–7.7			1.1–5.4	
iso-C _{16:1}	0.4						ND to 2.0		ND to 2.5
anteiso-C _{17:0}	0.3					4.2			
C _{17:0} 2-OH	0.3	1.0–2.4					ND to 2.4	ND to 1.8	ND to 1.5
C _{17:0} 3-OH	0.5								
iso-C _{17:0} 3-OH	9.5	7.8–16.0	ND to 3.1	1.0–3.4			9.1–13.0	0.4–9.2	8.5–10.7
anteiso-C _{17:0} 3-OH			1.0–11.3	2.7–5.3	2.3–3.2			0.5–2.9	
anteiso-C _{17:1} ω9c			1.9–3.4	2.1–3.8	4.0–7.4			1.5–4.6	
iso-C _{17:1} ω9c		0.3–2.4	1.1–2.3	3.5–5.1	2.3–2.6			1.7–15.1	tr to 1.4
C _{17:1} ω6c	0.3	tr to 1.1							1.4–3.5
C _{18:0}			0.5–1.2	1.2–2.1	ND to 0.5			0.5–1.1	
C _{18:1} ω9c					8.2–18.7				

*Summed features are groups of two or three fatty acids that could not be separated by GC with the MIDI system. Summed feature 3 contains C_{16:1}ω7c and/or iso-C_{15:0} 2-OH.

With API ZYM strips, positive for alkaline phosphatase, esterase lipase (C8), leucine arylamidase, valine arylamidase, α -chymotrypsin, acid phosphatase and naphthol-AS-BI-phosphohydrolase activities, weakly positive for esterase

(C4), cystine arylamidase, trypsin and α -glucosidase activities, but negative for lipase (C14), α -galactosidase, β -glucuronidase, *N*-acetyl- β -glucosaminidase, α -mannosidase and α -fucosidase activities. The following carbon

Fig. 2. Cell morphology of strain NH57N^T grown on M2 agar for 24 h at 30 °C as revealed by phase-contrast (a) and transmission electron microscopy of negatively stained cells (b, c). Bars, 10 μm (a), 0.5 μm (b) and 1 μm (c).

substrates are oxidized in GN2 microplates: α -cyclodextrin, dextrin, *N*-acetyl-D-galactosamine, cellobiose, gentiobiose, α -D-glucose, *myo*-inositol, D-mannose, trehalose, acetic acid, γ -hydroxybutyric acid, α -ketovaleric acid, propionic acid and L-proline. The following carbon substrates are weakly oxidized: lactulose, raffinose, sucrose, α -ketobutyric acid and DL-lactic acid. All other substrates in the GN2 microplates are not oxidized. Susceptible to trimethoprim, ofloxacin, carbenicillin, cephradine, doxycycline hydrochloride, chloramphenicol, ciprofloxacin, cefoperazone, erythromycin, clindamycin, ceftriaxone, cephalixin, furazolidone, ampicillin, lincomycin, minocycline, norfloxacin, tetracycline, piperacillin, penicillin G, rifampicin and vancomycin, but resistant to kanamycin, polymyxin B, cephalosporin, metronidazole, streptomycin, oxacillin, gentamicin and neomycin. The predominant fatty acids (>5% of the total) are iso-C_{15:1}, iso-C_{15:0}, iso-C_{17:0} 3-OH, iso-C_{16:0} 3-OH, C_{15:0}, iso-C_{15:0} 3-OH and summed feature 3 (comprising C_{16:1} ω 7c and/or iso-C_{15:0} 2-OH). The DNA G+C content of the type strain is 32.7 mol%. Other phenotypic characteristics are given in Table 1.

The type strain, NH57N^T (=CCTCC AB 208318^T=LMG 24839^T=MCCC 1A03544^T), was isolated from a sandy sediment sample of the South China Sea taken at a water depth of 12 m.

Acknowledgements

This work was financially supported by the National Key Technology R&D Program of China (no. 2006BAB19B02) and National

Infrastructure of Natural Resources for Science and Technology Program of China (no. 2005DKA21209).

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