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

Baojiang Wang*, Fengqin Sun*, Yaping Du, Xiupian Liu, Guangyu Li, Qiliang Lai, Jie Luo and Zongze Shao¶

Key Laboratory of Marine Biogenetic Resources, the Third Institute of Oceanography, State Oceanic Administration, People's Republic of China

***Co-first author**: Baojiang Wang and Fengqin Sun contributed equally to the paper.

¶Author for correspondence: Zongze Shao. Tel/Fax: +86-592-2195321. E-mail: shaozz@163.com.

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The GenBank accession number for the 16S rRNA gene sequence of *Meridianimaribacter flavus* NH57N^T is FJ360684.

Summary: 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*; 16S rRNA gene sequence similarities between strain NH57N^T and the type strains of the 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 ℃, at 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%), 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 genus and species in the family *Flavobacteriaceae,* for which the name *Meridianimaribacter flavus* gen. nov., sp. nov. is proposed. The type strain is NH57N^T (=CCTCC AB 208318^T=LMG 24839^T =MCCC 1A03544^T).

The family *Flavobacteriaceae*, proposed by Jooste (1985), is one of the fastest growing families in the phylum *Bacteroidetes*: more than 50 genera have been described, most of them in recent years. The genus *Gaetbulibacter* was created by Jung *et al.* (2005) to accommodate the new species *Gaetbulibacter saemankumensis,* isolated from a tidal flat sediment in the Yellow Sea in Korea (Jung *et al.*, 2005). A second species, *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 represents a new lineage closely related to the genus *Gaetbulibacter*. Although NH57N^T shares many physiological and biochemical characteristics with species of the genus *Gaetbulibacter*, it differs from them by

narrower pH and salinity ranges for growth, lower G+C content and ability to degrade gelatin. In addition, moderate 16S rRNA gene sequence similarity and differences in cellular fatty acid composition also support the description of strain NH57N^T as a novel genus and species, for which the name *Meridianimaribacter flavus* gen. nov., sp. nov. is proposed.

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 (E115.4617°, N9.9217°). 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 was then incubated at 25 °C for 1 week. The medium consisted of (l^{-1} sea water): 5 g CH_3COONa, 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 NH_4NO_3, 0.2 g NH_4Cl 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 ℃ in M2 broth supplemented with 20% (v/v) glycerol.

The 16S rRNA gene was amplified from a single colony by PCR with Taq DNA polymerase (MBI) and two universal primers (Lane, 1991). The 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 (1470bp) of strain NH57N^T was blasted in NCBI. The closely related sequences were retrieved and aligned. Then, evolutionary distances were calculated according to the Kimura two-parameter model (Kimura, 1980) with the DNAMAN software (Version 6). Phylogenetic trees were constructed by using the Neighbor-Joining (Saitou & Nei, 1987) method, and 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). The nearest neighbours of this strain are *Gaetbulibacter marinus* IMCC1914^T and *G. saemankumensis* SMK-12^T, with 16S rRNA gene sequence similarities of 94.9% and 94.2%, respectively. Although

the branching of the tested strain with *Gaetbulibacter* species in the phylogenetic tree was not supported strongly by bootstrap analysis (Fig.1), the trees generated with the distance matrix using the Jukes-Cantor and Maximum-Likelihood models showed the same topology (data not shown). Sequence similarities between strain NH57N^T and other related type strains were 93.4-91.2%. The relatively low similarity values to members of the most closely related genera warrant classification of strain NH57N^T as the representative of a novel genus.

Cell morphology and motility were observed by phase-contrast light microscopy (model 50i; Nikon) and transmission electron microscopy (model JEM-1230; JEOL), using 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 using 5 ml HLB medium supplemented with 200 µl M2 medium, adjusted with NaOH and HCl solutions. HLB was modified from Luria-Bertani (LB) medium (Sambrook *et al*., 1989), with the concentration of NaCl 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 sea water by distilled water. Oxidase reaction was tested by using oxidase reagent (bioMérieux). Catalase activity was tested using a 3% H_2O_2 solution. Hydrolysis of starch and Tweens 20, 40 and 80 were determined as described by Cowan & Steel (1965). Casein hydrolysis was tested by 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. The oxidation of 95 carbon sources was determined by using the GN2 MicroPlate (BIOLOG) as described previously (Ivanova *et al*., 1998). Cupules were inoculated with 150 µl liquid culture, which NaCl concentration was increased to 2.4%. All above –mentioned tests were conducted at 30℃.

Susceptibility to antibiotics was tested on M2 agar at 30 ℃ 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), cephalexin (30 µg),

ampicillin (10 µg), furazolidone (15 µg), metronidazole (5 µg), cephazolin (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. As we know that *Gaetbulibacter* species had also been grown on MA for 3 days; growth temperature was 30℃ for *G. saemankumensis* (Jung *et al.*, 2005) and 25℃ for *G. marinus* (Yang & Cho, 2008). The fatty acids were extracted according to the standard protocol of the Microbial Identification System (MIDI, Sherlock). Analysis of the fatty acid methyl esters was performed on a GC (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, fatty acids, namely iso-$C_{15:1}$ (22.7%), 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 C_{15}-C_{17} fatty acids are typical for members of the family *Flavobacteriacea* (Bowman et. al., 1998). So, 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 was 32.7 mol% as determined by reverse HPLC according to the method of Tamaoka & Komagata (1984).

Separation of the tested strain from members of related genera was supported by the comparison of their phenotypic and genotypic characteristics (Tables). Strain NH57N^T exhibited narrower pH and salinity ranges for growth. In addition, it could be distinguished from its closest relatives *Gaetbulibacter marinus* and *G. saemankumensis* by the hydrolysis of gelatin and susceptibility to ampicillin. Ability to produce oxidase, inability to generate acid from glucose and requirement of Na^+ ions for growth distinguished the strain studied from members of the genus *Gelidibacter*. Weak degradation of starch and failure to hydrolyse casein and Tween 80 separated

the 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 by differences in the presence and proportions of several fatty acids (Table 2).

Overall, the low similarity of 16S rRNA gene sequence, together with differences in chemotaxonomic, physiological and biochemical properties, indicate that isolate NH57N^T should be classified as a novel genus and species, 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; N.L. masc. n. *Meridianimaribacter*, a rod of the southern sea, isolated from the 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 fatty acids. Oxidase- and catalase- positive. The DNA G+C content of the type strain of the type species is 32.7 mol%. As determined by 16S rRNA gene sequence analysis, the genus *Meridianimaribacter* 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, the colour of colonies).

In addition to the characteristics of 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 with 0.5-4.0% NaCl (optimum, 0.5-2.0%). NaCl is essential for growth. Colonies on M2 are circular, smooth, glistening, moist-appearing, convex with entire margins and 1-2 mm in diameter after 3 days of incubation at 30 °C. Gelatin is hydrolyzed. Starch and Tween 40 are weakly hydrolyzed. Agar, casein and Tweens 20 and 80 are not hydrolyzed. Nitrate is not reduced. Acetoin is produced, but H_2S and indole are not produced. In API 20E and 20NE strips, β-glucosidase, esculinase and

β-galactosidase activities are present, but urease, arginine dihydrolase, ornithine decarboxylase, tryptophan deaminase and lysine decarboxylase activities are absent. In the API ZYM strip, alkaline phosphatase, esterase lipase (C8), leucine arylamidase, valine arylamidase, α-chymotrypsin, acid phosphatase and naphtol-AS-BI-phosphohydrolase activities are present; weak esterase (C4), cystine arylamidase, trypsin and α-glucosidase activities are present; and lipase (C14), α-galactosidase, β-glucuronidase, *N*-acetyl-β-glucosaminidase, α-mannosidase and α-fucosidase activities are absent. The following carbon substrates are oxidized in GN2 MicroPlate: α-cyclodextrin, dextrin, *N*-acetyl-D-galactosamine, D-cellobiose, gentiobiose, α-D-glucose, m-inositol, D-mannose, D-trehalose, acetic acid, γ-hydroxy butyric acid, α-keto valeric acid, propionic acid and L-proline. The following carbon substrates are weakly oxidized: lactulose, D-raffinose, sucrose, α-keto butyric acid and D, L-lactic acid. All other substrates in the GN2 MicroPlate are not oxidized. Susceptible to trimethoprim, ofloxacin, carbenicillin, cephradine, doxycycline hydrochloride, chloramphenicol, ciprofloxacin, cefoperazone, erythromycin, clindamycin, ceftriaxone, cephalexin, furazolidone, ampicillin, lincomycin, minocycline, norfloxacin, tetracycline, piperacillin, penicillin G, rifampicin and vancomycin, but resistant to kanamycin, polymyxin B, cephazolin, metronidazole, streptomycin, oxacillin, gentamicin and neomycin. The predominant fatty acids (>5% of the total fatty acids) 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 $C_{16:1}\omega7c$ and/or iso-$C_{15:0}$ 2-OH). The DNA G+C content 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 at a water depth of 12 m.

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247 **Table 1.** Phenotypic characteristics that differentiate strain NH57N^T from closely related members of the family *Flavobacteriaceae*

248 Taxa: 1, strain NH57N^T (data from this study); 2, *Gaetbulibacter* (n=2; Jung *et al.*, 2005; Yang & Cho, 2008),; 3, *Gelidibacter* (n=4; Kwon *et al.*, 2006; Bowman &
249 Nichols, 2005); 4, *Subsaxibacter broadyi* P7^T (Bowman & Nichols, 2005; Kwon *et al.*, 2006;) ; 5, *Subsaximicrobium* (n=2; Bowman & Nichols, 2005; Kwon *et al.*,
250 2006); 6, *Yeosuana aromativorans* GW1-1^T (Kwon *et al.*, 2006); 7, *Algibacter* (n=2; Nedashkovskaya *et al.*, 2004, 2007); 8, *Bizionia* (n=6; Kwon *et al.*, 2006;
251 Bercovich *et al.*, 2008; Bowman & Nichols, 2005); 9, *Formosa* (n=2; Nedashkovskaya *et al.*, 2006b). n= the number of type strains in each genus is given in
252 parentheses. +, Positive; -, negative; W, weakly positive; ND, no data availabe; V, variable. All taxa are positive for catalase and negative for indole and H_2S
253 production.
254

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)	-2-20	-2-25	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 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

*Ranges with optima shown in parentheses.

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

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

Table 2. Cellular fatty acid composition (%) of strain NH57NT and closely related members of the family Flavobacteriaceae

Taxa: 1, strain NH57N^T (data from this study); 2, *Gaetbulibacter* (n=2; 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.*, 2006b). n= the number of type strains in each genus is given in parentheses. For taxa 2, 3, 4, 5, 7, 8 and 9, values shown are the range of percentage 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-tr			tr-3.0	
anteiso-$C_{13:0}$					ND-tr			0.3-0.4	
$C_{14:0}$	0.3		0.3-0.6	tr-0.5	0.6-0.7			0.4-0.8	
iso-$C_{14:0}$	1.2	ND-1.0	0.4-2.8	tr-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-2.4	ND-2.1	1.5-1.8
$C_{15:0}$ 3-OH	1.3		tr-1.5	ND-0.8	ND-0.5		ND-1.3	tr-2.0	2.3-4.0
$C_{15:1}\omega6c$			2.7-4.2	tr-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-2.1	3.6-14.0	ND-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-2.3	1.2-3.4	ND-1.6
$C_{16:0}$ 10-methyl						4.7	ND-2.1		
$C_{16:0}$ 3-OH	1.1	ND-1.2					ND-1.4		tr-2.1
iso-$C_{16:0}$	0.9	ND-1.2	1.4-4.4		1.5-1.7			1.1-5.8	ND-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
$C_{16:1}\omega5c$			ND-1.1	ND-0.5	1.1-1.2			0.4-0.8	

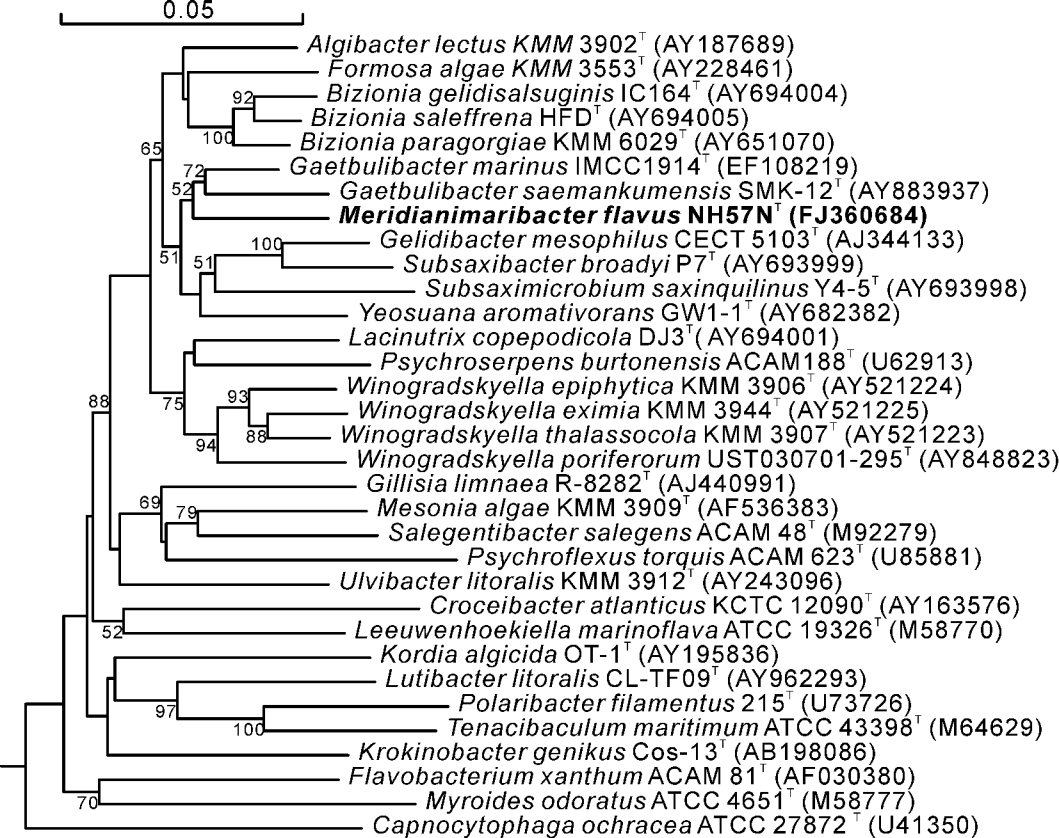
br-$C_{16:1}$			1.4-10.3	1.9-4.7	3.5-7.7			1.1-5.4	
iso-$C_{16:1}$	0.4						ND-2.0		ND-2.5
anteiso $C_{17:0}$	0.3					4.2			
$C_{17:0}$ 2-OH	0.3	1.0-2.4					ND-2.4	ND-1.8	ND-1.5
$C_{17:0}$ 3-OH	0.5								
iso-$C_{17:0}$ 3-OH	9.5	7.8-16.0	ND-3.1	1.0-3.4			9.1-13.0	0.4-9.2	8.5-10.7
anteiso-$C_{17:0}$ 3-OH			1.0-11.3	2.7-5.3	2.3-3.2			0.5-2.9	
anteiso-$C_{17:1}\omega 9c$			1.9-3.4	2.1-3.8	4.0-7.4			1.5-4.6	
iso-$C_{17:1}\omega 9c$		0.3-2.4	1.1-2.3	3.5-5.1	2.3-2.6			1.7-15.1	tr-1.4
$C_{17:1}\omega 6c$	0.3	tr-1.1							1.4-3.5
$C_{18:0}$			0.5-1.2	1.2-2.1	ND-0.5			0.5-1.1	
$C_{18:1}\omega 9c$					8.2-18.7				

*Summed features are groups of two or three fatty acids that could not be separated by GC using the MIDI system. Summed feature 3 comprised iso-$C_{15:0}$ 2-OH and/or $C_{16:1}\omega 7c$.

Legends to Figures:

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

Fig. 2. Cell morphology of strain NH57N^T grown on M2 agar for 24h at 30□: (a) phase contrast micrograph, Bar, 10 μm; (b-c), transmission electron micrographs of negatively stained cells (b: bar, 0.5μm and c: bar, 1 μm)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Formosa algae KMM 3553T (AY228461)
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Bizionia saleffrena HFDT (AY694005)
Bizionia paragorgiae KMM 6029T (AY651070)
Gaetbulibacter marinus IMCC1914T (EF108219)
Gaetbulibacter saemankumensis SMK-12T (AY883937)
Meridianimaribacter flavus NH57NT (FJ360684)
Gelidibacter mesophilus CECT 5103T (AJ344133)
Subsaxibacter broadyi P7T (AY693999)
Subsaximicrobium saxinquilinus Y4-5T (AY693998)
Yeosuana aromativorans GW1-1T (AY682382)
Lacinutrix copepodicola DJ3T (AY694001)
Psychroserpens burtonensis ACAM188T (U62913)
Winogradskyella epiphytica KMM 3906T (AY521224)
Winogradskyella eximia KMM 3944T (AY521225)
Winogradskyella thalassocola KMM 3907T (AY521223)
Winogradskyella poriferorum UST030701-295T (AY848823)
Gillisia limnaea R-8282T (AJ440991)
Mesonia algae KMM 3909T (AF536383)
Salegentibacter salegens ACAM 48T (M92279)
Psychroflexus torquis ACAM 623T (U85881)
Ulvibacter litoralis KMM 3912T (AY243096)
Croceibacter atlanticus KCTC 12090T (AY163576)
Leeuwenhoekiella marinoflava ATCC 19326T (M58770)
Kordia algicida OT-1T (AY195836)
Lutibacter litoralis CL-TF09T (AY962293)
Polaribacter filamentus 215T (U73726)
Tenacibaculum maritimum ATCC 43398T (M64629)
Krokinobacter genikus Cos-13T (AB198086)
Flavobacterium xanthum ACAM 81T (AF030380)
Myroides odoratus ATCC 4651T (M58777)
Capnocytophaga ochracea ATCC 27872T (U41350)
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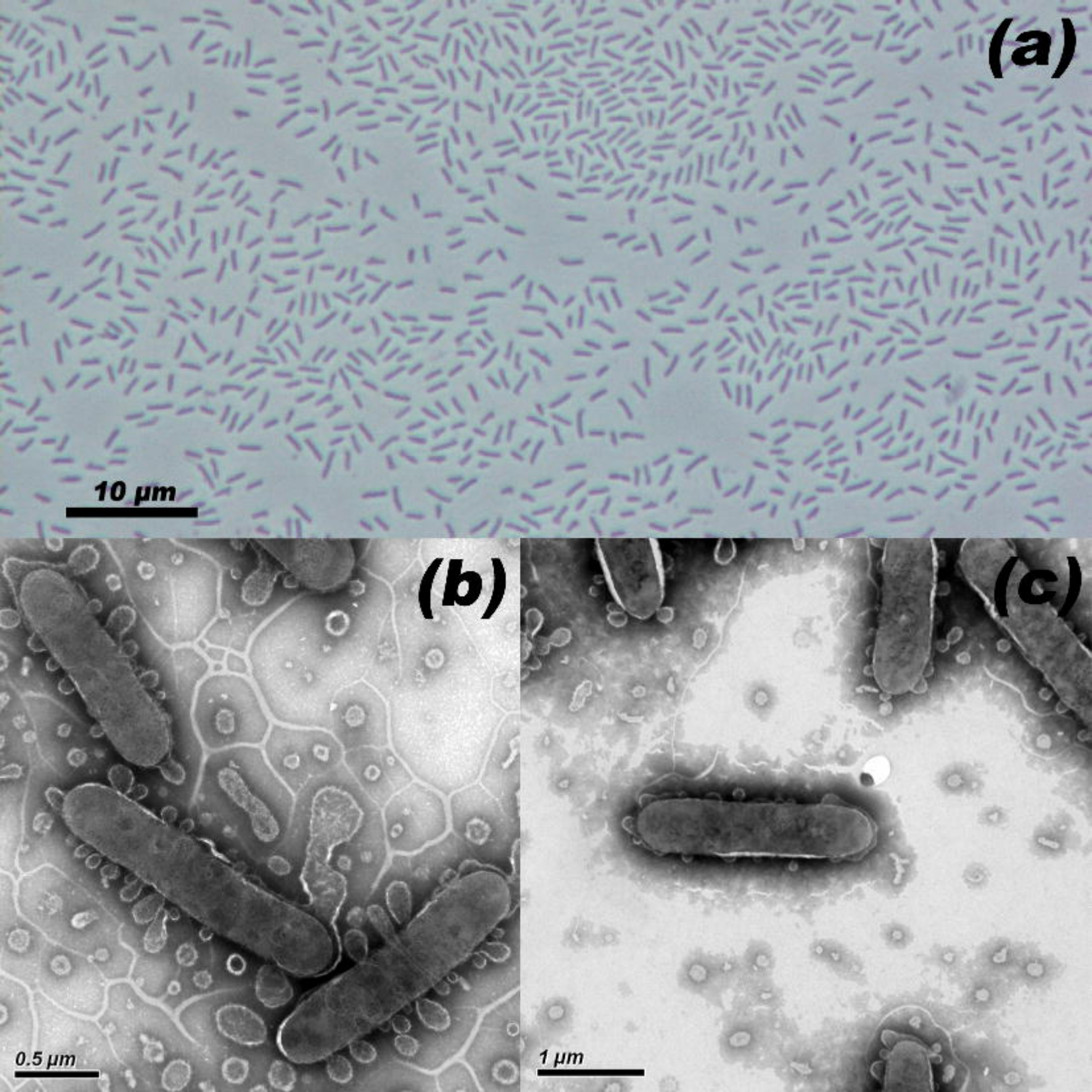
(a)
10 µm
(b)
0.5 µm
(c)
1 µm