Maribacter gen. nov., a new member of the family *Flavobacteriaceae*, isolated from marine habitats, containing the species *Maribacter sedimenticola* sp. nov., *Maribacter aquivivus* sp. nov., *Maribacter orientalis* sp. nov. and *Maribacter ulvicola* sp. nov.

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Six novel gliding, heterotrophic, Gram-negative, yellow-pigmented, aerobic, oxidase- and catalase-positive bacteria were isolated from the green alga *Ulva fenestrata*, sea water and a bottom sediment sample collected in the Gulf of Peter the Great, Sea of Japan. 16S rRNA gene sequence analysis revealed that the strains studied were members of the family *Flavobacteriaceae*. On the basis of their phenotypic, chemotaxonomic, genotypic and phylogenetic characteristics, the novel bacteria have been assigned to the new genus *Maribacter* gen. nov., as *Maribacter sedimenticola* sp. nov., *Maribacter orientalis* sp. nov., *Maribacter aquivivus* sp. nov. and *Maribacter ulvicola* sp. nov., with the type strains KMM 3903^T (=KCTC 12966^T=CCUG 47098^T), KMM 3947^T (=KCTC 12967^T=CCUG 48008^T), KMM 3949^T (=KCTC 12968^T=CCUG 48009^T) and KMM 3951^T (=KCTC 12969^T=DSM 15366^T), respectively.

INTRODUCTION

The gliding agarolytic bacteria belonging to the family *Flavobacteriaceae* are often isolated from different marine environments. Many novel bacteria that decompose agar, a polysaccharide of the red alga, have been collected from

coastal bottom sediments. For example, a single strain of *Zobellia uliginosa* ATCC 14397^T, formerly *Flavobacterium uliginosum* (ZoBell & Upham, 1944), was found in a beach mud sample collected near California (Barbeyron *et al.*, 2001). A common coastal dweller, *Cellulophaga lytica*, formerly [*Cytophaga*] *lytica* (Reichenbach, 1989), was originally isolated from beach sand in Costa Rica (Lewin, 1969; Johansen *et al.*, 1999). Some of the agar-degrading bacteria are associated with algae. For example, two species of the genus *Cellulophaga*, *Cellulophaga baltica* and *Cellulophaga fucicola*, were isolated from brown alga *Fucus serratus* collected in the North Sea (Johansen *et al.*, 1999). The diatom *Melosira* sp. and an unidentified macrophyte have been colonized by representatives of another species of the genus *Cellulophaga*, *Cellulophaga algicola* (Bowman, 2000).

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The GenBank/EMBL/DDBJ accession numbers for *Maribacter sedimenticola* KMM 3903^T, *Maribacter orientalis* KMM 3947^T, *Maribacter aquivivus* KMM 3949^T and *Maribacter ulvicola* KMM 3951^T are AY271623, AY271624, AY271625 and AY271626, respectively.

Micrographs of some of the strains described in this study are available from IJSEM Online.

The type strain of the type species of the genus *Zobellia*, *Zobellia galactanivorans* Dsij^T, was isolated from surfaces of the red alga *Delesseria sanguinea* (Barbeyron *et al.*, 2001).

In this study, we describe the phenotypic and genotypic characteristics of six gliding, Gram-negative bacteria isolated from the green alga *Ulva fenestrata*, sea water and a bottom sediment collected in the Gulf of Peter the Great, Sea of Japan. A 16S rRNA gene-based phylogenetic analysis revealed that the strains studied should be assigned to a new genus, *Maribacter* gen. nov., as four species within the *Muricauda*–*Zobellia*–*Arenibacter* cluster of the family *Flavobacteriaceae*. The names *Maribacter aquivivus* sp. nov., *Maribacter orientalis* sp. nov., *Maribacter sedimenticola* sp. nov. and *Maribacter ulvicola* sp. nov. are proposed for the novel marine bacteria.

METHODS

Organisms. Strains KMM 3947^T, KMM 3948 and KMM 3949^T were isolated from sea water; KMM 3903^T was isolated from a bottom sediment sample; KMM 3951^T and KMM 3952 were isolated from the green alga *Ulva fenestrata* collected in the Gulf of Peter the Great, Sea of Japan, during June 2000. Strains were cultivated at 28 °C on marine agar (Difco) and stored at –80 °C in marine broth (Difco) supplemented with 20 % (v/v) glycerol.

Phenotypic characterization. Oxidative or fermentative utilization of glucose was determined using the Hugh–Leifson medium modified for marine bacteria (Lemos *et al.*, 1985). Degradation of agar, starch, casein, gelatin, cellulose (filter paper and CMC), chitin, DNA, urea and alginic acids, flexirubin pigment production, growth at different NaCl concentrations or pH, production of acid from carbohydrates and susceptibility to antibiotics were tested as described previously (Nedashkovskaya *et al.*, 2003a, b). Gram-staining reaction; hydrolysis of Tween 20, Tween 40 and Tween 80; nitrate reduction; production of hydrogen sulphide and indole; and β -galactosidase, oxidase, catalase and alkaline phosphatase activities were tested according to the methods of Gerhardt *et al.* (1994). To examine carbon source utilization, a medium containing 0.2 g NaNO₃, 0.2 g NH₄Cl, 0.05 g yeast extract (Difco) and 0.4 % (w/v) carbon source in 1 litre of artificial sea water and the commercial API 20NE identification strips, following the instructions of the manufacturers, were used. To study the growth temperature ranges of the strains, bacteria were cultivated on medium A consisting of (l⁻¹) 5 g Bacto peptone (Difco), 2 g Bacto yeast extract (Difco), 1 g glucose, 0.02 g KH₂PO₄ and 0.05 g MgSO₄·7H₂O in 50 % (v/v) natural sea water and 50 % (v/v) distilled water. Spread growth was observed by cultivation on medium B which contained (l⁻¹) 1 g Bacto peptone (Difco), 1 g yeast extract (Difco), 15 g agar and half-strength natural sea water under high-moisture conditions. Gliding motility was determined as described by Bowman (2000). The cell movement at the edges of colonies was verified by using phase-contrast microscopy.

Scanning electron microscopy. The bacteria were fixed with a solution containing 2 % glutaraldehyde and 3 % formaldehyde in cacodylate buffer (0.1 M cacodylate, 0.09 M sucrose, 0.01 M CaCl₂, 0.01 M MgCl₂, pH 6.9) for 1 h on ice and washed with cacodylate buffer. After being washed several times in TE buffer (20 mM Tris, 1 mM EDTA, pH 7.0), samples were dehydrated with a graded series of acetone (10, 30, 50, 70, 90, 100 %) on ice, each step 15 min, followed by critical-point drying with liquid CO₂. Samples were sputter-coated with an ~10 nm thick gold film before being examined in a Zeiss field emission scanning electron microscope

DSM982 Gemini at an acceleration voltage of 5 kV using the Everhart Thornley SE detector and the inlens-SE detector in a 50:50 ratio.

Cellular fatty acid composition and respiratory quinone analyses. The analysis of fatty acid methyl esters was carried out according to the standard protocol of the Microbial Identification System (Microbial ID). Isoprenoid quinones were extracted from lyophilized cells and analysed as described by Akagawa-Matsushita *et al.* (1992). Isoprenoid quinone composition was characterized by HPLC (Shimadzu instruments) using a reversed-phase type Zorbax ODS column (250 × 4.6 mm) and acetonitrile/2-propanol (65:35, v/v) as a mobile phase at a flow rate of 0.5 ml min⁻¹. The column was kept at 40 °C. Menaquinones were detected by monitoring at 270 nm and were identified by comparison with known quinones from a reference strain, *Salegentibacter salegens* DSM 5424^T.

DNA base content and DNA–DNA reassociation. DNA was isolated following the method of Marmur (1961) and the G + C content (mol%) of the DNA was determined by the thermal denaturation method (Marmur & Doty, 1962). DNA–DNA hybridization was performed spectrophotometrically and initial renaturation rates were recorded as described by De Ley *et al.* (1970).

16S rRNA gene sequencing and phylogenetic analysis. DNA extraction, PCR and sequencing of 16S rRNA gene followed previously described procedures (Kim *et al.*, 1998). The obtained sequence data were aligned together with those of representative members of selected genera belonging to the family *Flavobacteriaceae* using PHYDIT version 3.2 (<http://plaza.snu.ac.kr/~jchun/phydit/>). Phylogenetic trees were inferred using suitable programs of the PHYLIP package (Felsenstein, 1993). Phylogenetic distances were calculated from the models of Jukes & Cantor (1969), and the trees were constructed on the basis of the neighbour-joining (Saitou & Nei, 1987), least squares (Fitch & Margoliash, 1967) and maximum-likelihood (Felsenstein, 1993) algorithms. Bootstrap analysis was performed with 1000 resampled data sets, using SEQBOOT and CONSENSE programs of the PHYLIP package.

RESULTS AND DISCUSSION

Bacteria isolated in this study were gliding, Gram-negative, chemo-organotrophic organisms with a respiratory type of metabolism. They were non-motile, single, flexible rods, of 0.5–0.7 µm in diameter and 2–10 µm in length (micrographs, supplementary data in IJSEM Online). On marine agar, colonies of strains studied were round, yellow-pigmented, shiny, with entire edges, and were 2–4 mm in diameter. Colonies of strains KMM 3903^T, KMM 3948, KMM 3949^T and KMM 3951^T were weakly sunken into the agar. The bacteria studied were oxidase-, catalase- and alkaline phosphatase-positive, and required Na⁺ ions for growth. Growth of strains KMM 3947^T, KMM 3951^T and KMM 3952 occurred in the presence of 1–5 % NaCl, strain KMM 3903^T grew in media containing 1–6 % NaCl and strain KMM 3949^T grew in the presence of 1–7 % NaCl; optimal growth for all strains was observed at 1.5–2.0 % NaCl. All strains grew at 4 °C. The maximum temperatures for growth of strains KMM 3903^T, KMM 3947^T, KMM 3949^T and KMM 3951^T were 33, 32, 30 and 32 °C, respectively. The pH range for growth was 5.5–10.0, with optimum growth occurring between pH 7.5 and 8.5. Other physiological and biochemical characteristics of the KMM strains described in this study are listed in Table 1.

Table 1. Phenotypic characteristics of *Maribacter* species

Species: 1, *M. sedimenticola* KMM 3903^T; 2, *M. orientalis* KMM 3947^T; 3, *M. aquivivus* KMM 3949^T; 4, *M. ulvicola* KMM 3951^T. All strains were positive for: respiratory metabolism; gliding motility; oxidase, catalase and alkaline phosphatase activity; NaCl requirement for growth; growth at 4–30 °C and in the presence of 1–5 % NaCl; hydrolysis of Tween 40; susceptibility to carbenicillin, lincomycin and oleandomycin. All strains were negative for: hydrolysis of casein, cellulose (CMC, filter paper), chitin and urea; production of flexirubin pigments; acid formation from raffinose, sorbose, *N*-acetylglucosamine, citrate, adonitol, glycerol, inositol, mannitol and sorbitol; utilization of mannitol, inositol, sorbitol, malonate and citrate; indole, H₂S, acetoin (Voges–Proskauer reaction); susceptibility to benzylpenicillin, gentamicin, kanamycin, neomycin, polymyxin B and streptomycin. +, Positive test result; –, negative test result.

Characteristic	1	2	3	4
Nitrate reduction	+	–	+	–
β-Galactosidase	–	+	+	+
Growth at:				
6 % NaCl	+	–	+	–
32 °C	+	+	–	+
Hydrolysis of:				
Agar	+	–	+	+
Gelatin	–	+	+	–
Starch	+	–	–	–
Alginate	+	+	+	–
DNA	–	–	+	–
Tween 20	+	+	–	+
Tween 80	+	–	+	+
Acid from:				
Arabinose	+	+	–	–
Cellobiose	–	+	–	+
L-Fucose	–	–	–	+
Galactose	–	+	–	–
Glucose	–	+	–	+
Lactose	–	+	–	+
Maltose	–	+	–	+
Melibiose	–	+	–	–
Rhamnose	–	–	–	+
Sucrose	–	+	–	+
Xylose	–	+	–	–
Utilization of:				
Arabinose	–	+	–	–
Glucose, lactose, mannose, sucrose	–	+	+	+
Susceptibility to:				
Ampicillin	–	–	–	+
Tetracycline	+	–	–	–
G + C content (mol%)	37.5	39	35	35–37, (36.7)*

*Determined for the type strain.

Predominant cellular fatty acids of strains studied were of the branched-chain unsaturated and straight-chain saturated types, namely *i*-C_{15:0}, *i*-C_{15:1}, C_{15:0} and *i*-C_{17:0}3-OH

Table 2. Whole-cell fatty acid profiles (percentage composition) of *Maribacter* species

Species: 1, *M. sedimenticola* KMM 3903^T; 2, *M. aquivivus* KMM 3949^T; 3, *M. ulvicola* KMM 3951^T; 4, *M. orientalis* KMM 3947^T.

Fatty acid	1	2	3	4
C _{13:1}	0.7	1.1	1.1	0.3
C _{14:0}	0.5	1.0	0.9	0.5
C _{14:1ω5}		1.0	0.9	
<i>i</i> -C _{15:0}	20.5	12.3	13.6	10.6
<i>a</i> -C _{15:0}	1.2	1.3	1.9	2.3
<i>i</i> -C _{15:1}	16.9	13.6	18.9	10.1
C _{15:0}	6.3	14.5	8.1	12.3
C _{15:1ω6c}	1.7	4.8	1.6	2.5
<i>i</i> -C _{16:0}	1.1	0.7	0.3	0.3
C _{16:0}	1.0	0.5	1.0	1.2
C _{16:1ω7/i} -C _{15:0} 2-OH	5.8	12.9	12.2	11.4
<i>i</i> -C _{17:1ω5c}		1.4	1.2	
<i>i</i> -C _{17:1ω9c}	2.3	2.2	2.2	4.0
C _{17:1ω6c}	0.5	1.7	0.5	1.3
<i>i</i> -C _{15:0} 3-OH	5.4	3.2	4.1	2.9
C _{15:0} 3-OH	2.4	2.3	1.5	1.5
<i>i</i> -C _{16:0} 3-OH	1.7	2.5	1.7	2.1
C _{16:0} 3-OH	2.2	2.9	3.7	3.0
<i>i</i> -C _{17:0} 3-OH	20.4	11.6	14.5	18.8
<i>i</i> -C _{18:1}				2.4
Unknown	7.9	10.2	10.3	5.9

fatty acids (Table 2). The main respiratory quinone was MK-6. The DNA base contents of strains KMM 3903^T, KMM 3947^T, KMM 3949^T, KMM 3951^T and KMM 3952 were 37.5, 39.0, 35.0, 36.7 and 35.9 mol%, respectively, as determined by the thermal denaturation method. The level of DNA–DNA reassociation between strains KMM 3948 and KMM 3949^T, KMM 3951^T and KMM 3952, and KMM 3949^T and KMM 3951^T was 85, 93 and 51 %, respectively.

A phylogenetic analysis of almost-complete 16S rRNA gene sequences revealed that the strains studied formed a distinct lineage within the phylum *Cytophaga–Flavobacterium–Bacteroides* and created a cluster with *Arenibacter latericius*, *Muricauda ruestringensis* and *Zobellia* species (Fig. 1). The sequence identities of KMM strains with *Arenibacter latericius* and *Muricauda ruestringensis* were 90.9–91.5 % and 89.9–90.4 %, respectively. The 16S rRNA gene sequence similarity values for KMM strains and their nearest neighbour, *Z. uliginosa*, were 92.9, 93.1, 94.3 and 93.8 %, respectively, but their relationships were without significant bootstrap support. Differential features of strains KMM 3903^T, KMM 3947^T, KMM 3949^T and KMM 3951^T and related members of the phylum *Cytophaga–Flavobacterium–Bacteroides* are presented in Table 3. The production of flexirubin-type pigments, casein hydrolysis and maximum growth temperature (42–43 °C) differentiate members of the genus *Zobellia* from the strains studied. The low level of sequence similarity of the strains tested with other

Fig. 1. Phylogenetic tree based on the 16S rRNA gene sequences of the KMM strains described in this study and representative members of related genera in the family *Flavobacteriaceae*. The asterisks indicate branches that were also recovered using least-squares and maximum-likelihood algorithms. The numbers at nodes indicate bootstrap values (%). Bar, 0.01 substitutions per nucleotide position.

Cytophaga-like bacteria described to date (84.5–91.6%) clearly demonstrates that the bacteria isolated in this study represent a new genus. The 16S rRNA gene sequences of the novel strains showed between 95.1 and 97.4% similarity; only the 16S rRNA gene sequence similarity value between strains KMM 3949^T and KMM 3951^T was higher than 97%. It is known that strains which demonstrate less than 3% difference in their 16S rRNA gene sequences may belong to the same species (Stackebrandt & Goebel, 1994). The DNA–DNA hybridization experiment carried out between strains KMM 3949^T and KMM 3951^T showed a DNA–DNA reassociation value of 51%. Consequently, strains KMM 3949^T and KMM 3951^T were shown to be separate species.

Thus, sequence distinctiveness and DNA–DNA reassociation data define strains KMM 3903^T, KMM 3947^T, KMM 3949^T and KMM 3951^T as separate genospecies. Phenotypic findings support the data from the genomic analyses of the strains studied (Table 1). Physiologically, strain KMM 3903^T may be differentiated from other strains studied by the absence of β -galactosidase activity, non-utilization of the majority of carbohydrates tested, growth at 37 °C, starch hydrolysis and susceptibility to tetracycline; strain KMM 3947^T does not hydrolyse Tween 80, but forms acid from galactose, xylose and melibiose; strain KMM 3949^T produces DNase, does not hydrolyse Tween 20 and grows at 30 °C. Also, strain KMM 3951^T may be easily separated from the above strains by the absence of alginate hydrolysis,

Table 3. Characteristics that differentiate the genus *Maribacter* from other, related, genera of the family *Flavobacteriaceae*

Genus: 1, *Maribacter*; 2, *Zobellia*; 3, *Arenibacter*; 4, *Muricauda*; 5, *Vitellibacter*; 6, *Aequorivita*; 7, *Cellulophaga*; 8, [*Cytophaga*] *marinoflava*. Data are from Reichenbach (1989), Johansen *et al.* (1999), Bowman (2000), Ivanova *et al.* (2001), Barbeyron *et al.* (2001), Bruns *et al.* (2001), Bowman & Nichols (2002), Nedashkovskaya *et al.* (2003a, b) and this study. A, Aerobic; F, facultative; +, positive test result; –, negative test result; V, variable; ND, not determined.

Test	1	2	3	4	5	6	7	8
Reaction to oxygen	A	A	A	F	A	A	A	A
Oxidase/catalase	+ / +	+ / +	+ / +	+ / –	+ / +	– / +	+ / +	+ / +
Gliding motility	+	+	–	–	–	–	+	+
Flexirubin	–	+	–	–	+	–	–	–
Requirement for Na ⁺ or sea water for growth	+	+	+	+	+	V	+	–
Growth at 42 °C	–	+	+	–	+	–	–	–
Acid formation from carbohydrates	V	+	+	ND	–	–	+	+
Hydrolysis of:								
Agar	V	+	–	–	–	–	+	–
Casein	–	+	–	ND	+	V	V	–
Gelatin	V	+	V	–	+	+	+	ND
Starch	V	+	–	–	–	–	+	+
Alginate	V	+	–	ND	–	ND	+	ND
DNA	V	+	+	ND	+	–	+	ND
Urea	–	–	V	ND	–	V	V	ND
Nitrate reduction	V	+	+	–	–	–	V	+
DNA G + C content (mol%)	35–39	42–43	37–40	41	41	33–39	33–38	37

fucose and rhamnose oxidation and susceptibility to ampicillin.

Thus, our conclusion, supported by the polyphasic analysis data presented in this report, is that the bacteria studied here could not be assigned to any of the taxa currently included in the phylum *Cytophaga–Flavobacterium–Bacteroides*. Consequently, we propose that strains KMM 3903^T, KMM 3947^T, KMM 3949^T and KMM 3948, and KMM 3951^T and KMM 3952 be placed in a new genus, *Maribacter*, as *Maribacter sedimenticola*, *Maribacter orientalis*, *Maribacter aquivivus* and *Maribacter ulvicola*, respectively.

Description of *Maribacter* gen. nov.

Maribacter (Ma.ri.bac'ter. L. neut. n. *mare* the sea; N.L. masc. n. *bacter* from Gr. n. *bakteron* rod; N.L. masc. n. *Maribacter* rod inhabiting marine environments).

Rod-shaped cells. Non-motile. Gram-negative. Do not form endospores. Require Na⁺ ions for growth. Strictly aerobic. Produce non-diffusible yellow pigments. No flexirubins are formed. Chemo-organotroph. Cytochrome oxidase-, catalase- and alkaline phosphatase-positive. Predominant cellular fatty acids are straight-chain saturated, branched-chain saturated and unsaturated fatty acids i-C_{15:0}, i-C_{15:1}, C_{15:0} and i-C_{17:0}3-OH. The main lipoquinone is MK-6. As determined by 16S rRNA gene sequence analysis, the genus *Maribacter* is a member of the family *Flavobacteriaceae*, phylum *Cytophaga–Flavobacterium–Bacteroides*.

Type species is *Maribacter sedimenticola*.

Description of *Maribacter sedimenticola* sp. nov.

Maribacter sedimenticola (se.di.men.ti.co'la. L. masc. n. *sedimentum* sediment; L. suffix *-cola* dweller; N.L. masc. n. *sedimenticola* sediment dweller).

Main characteristics are the same as those given for the genus. In addition, cells range in size from 0.5 to 0.7 µm in width and 2 to 10 µm in length. On marine agar, colonies are 2–4 mm in diameter, circular, shiny with entire edges, yellow pigmented and weakly sunken into agar. Grows at 4–33 °C; optimal temperature for growth is between 22 and 24 °C. Grows in the presence of 1–6 % NaCl. Decomposes agar, gelatin, alginate, DNA, Tween 40 and Tween 80. Does not hydrolyse casein, starch, Tween 20, cellulose (carboxymethylcellulose and filter paper) or chitin. Forms no acid from cellobiose, fucose, galactose, glucose, lactose, maltose, melibiose, raffinose, rhamnose, sucrose, xylose, citrate, adonitol, dulcitol, glycerol, inositol or mannitol. Does not utilize glucose, lactose, mannose, sucrose, mannitol, inositol, sorbitol, malonate or citrate. Nitrate is not reduced. H₂S, indole and acetoin (Voges–Proskauer reaction) production are negative. Susceptible to carbenicillin, lincomycin, oleandomycin and tetracycline; resistant to ampicillin, benzylpenicillin, gentamicin, kanamycin, neomycin, polymyxin B and streptomycin.

Type strain is KMM 3903^T (=KCTC 12966^T=CCUG 47098^T). G + C content of its DNA is 37.0 mol%. Isolated from a bottom sediment sample collected in the Gulf of Peter the Great, Sea of Japan.

Description of *Maribacter orientalis* sp. nov.

Maribacter orientalis (o.ri.en.ta'lis. L. adj. *orientalis* eastern, bacterium inhabiting the East).

Main characteristics are the same as those given for the genus. In addition, cells range in size from 0.5 to 0.7 µm in width and 2 to 10 µm in length. On marine agar, colonies are 2–4 mm in diameter, circular, shiny with entire edges and yellow–orange pigmented. Grows at 4–32 °C; optimal temperature for growth is between 21 and 23 °C. Grows in the presence of 1–5 % NaCl. Decomposes gelatin, alginate, Tween 20 and Tween 40. Does not hydrolyse agar, casein, DNA, starch, urea, Tween 80, cellulose (carboxymethylcellulose and filter paper) or chitin. Forms acid from arabinose, cellobiose, galactose, glucose, lactose, maltose, melibiose, sucrose and xylose, but not from fucose, raffinose, rhamnose, citrate, adonitol, dulcitol, glycerol, inositol or mannitol. Utilizes arabinose, glucose, lactose, mannose and sucrose, but not mannitol, inositol, sorbitol, malonate or citrate. Nitrate is not reduced. H₂S, indole and acetoin (Voges–Proskauer reaction) production are negative. Susceptible to carbenicillin, lincomycin and oleandomycin; resistant to ampicillin, bensylpenicillin, gentamicin, kanamycin, neomycin, polymyxin B, streptomycin and tetracycline.

Type strain is KMM 3947^T (=KCTC 12967^T=CCUG 48008^T). G+C content of its DNA is 39.0 mol%. Isolated from a sea water sample collected in the Gulf of Peter the Great, Sea of Japan.

Description of *Maribacter aquivivus* sp. nov.

Maribacter aquivivus (a.qui.vi'vus. L. fem. n. *aqua* water; N.L. adj. *vivus* alive; N.L. *aquivivus* living in water).

Main characteristics are the same as those given for the genus. In addition, cells range in size from 0.4 to 0.5 µm in width and 1.2 to 1.4 µm in length. On marine agar, colonies are 2–4 mm in diameter, circular, shiny with entire edges, yellow pigmented and sunken into agar. Grows at 4–30 °C; optimal temperature for growth is between 21 and 23 °C. Grows in the presence of 1–7 % NaCl. Decomposes agar, starch, alginate, Tween 20, Tween 40 and Tween 80. Does not hydrolyse gelatin, casein, DNA, cellulose (carboxymethylcellulose and filter paper) or chitin. Does not form acid from arabinose, cellobiose, fucose, galactose, glucose, lactose, maltose, melibiose, raffinose, rhamnose, sucrose, xylose, citrate, adonitol, dulcitol, glycerol, inositol or mannitol. Utilizes glucose, lactose, mannose and sucrose, but not arabinose, mannitol, inositol, sorbitol, malonate or citrate. Nitrate is reduced. H₂S, indole and acetoin (Voges–Proskauer reaction) production are negative. Susceptible to carbenicillin, lincomycin and oleandomycin; resistant to ampicillin, bensylpenicillin, gentamicin, kanamycin, neomycin, polymyxin B, streptomycin and tetracycline.

Type strain is KMM 3949^T (=KCTC 12968^T=CCUG 48009^T). G+C content of its DNA is 35.0 mol%. Isolated

from a sea water sample collected in the Gulf of Peter the Great, Sea of Japan.

Description of *Maribacter ulvicola* sp. nov.

Maribacter ulvicola (ul.vi.co'la. N.L. fem. n. *Ulva* generic name of green alga *Ulva fenestrata*; L. suffix *-cola* dweller; N.L. n. *ulvicola* a green alga *Ulva fenestrata* dweller).

Main characteristics are the same as those given for the genus. In addition, cells are flexible rods ranging in size from 0.25 to 0.3 µm in width and 4 to 6 µm in length. On marine agar, colonies are 2–4 mm in diameter, circular, shiny with entire edges, yellow pigmented and weakly sunken into agar. Grows at 4–32 °C; optimal temperature for growth is between 21 and 23 °C. Grows in the presence of 1–4 % NaCl. Does not decompose casein, gelatin, DNA, starch, alginate, urea, Tween 20, Tween 40, Tween 80, cellulose (carboxymethylcellulose and filter paper) or chitin. Agar is hydrolysed weakly. Forms acid from cellobiose, fucose, glucose, lactose, maltose, rhamnose and sucrose, but not from arabinose, galactose, melibiose, raffinose, xylose, citrate, adonitol, dulcitol, glycerol, inositol or mannitol. Utilizes glucose, lactose, mannose and sucrose, but not arabinose, mannitol, inositol, sorbitol, malonate or citrate. Nitrate is not reduced. H₂S, indole and acetoin (Voges–Proskauer reaction) production are negative. Susceptible to ampicillin, carbenicillin, lincomycin and oleandomycin; resistant to bensylpenicillin, gentamicin, kanamycin, neomycin, polymyxin B, streptomycin and tetracycline.

Type strain is KMM 3951^T (=KCTC 12969^T=DSM 15366^T). G+C content of its DNA is 35–37 mol%. Isolated from the green alga *Ulva fenestrata*.

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