Formosa agariphila sp. nov., a budding bacterium of the family *Flavobacteriaceae* isolated from marine environments, and emended description of the genus *Formosa*

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Two marine, heterotrophic, aerobic, yellow-pigmented, agarolytic bacterial strains that are motile by means of gliding were isolated from the green alga *Acrosiphonia sonderi* and from sea water. Comparative 16S rRNA gene sequence analysis revealed an affiliation between the strains studied and the genus *Formosa*, a member of the family *Flavobacteriaceae*. The level of sequence similarity between strain KMM 3901^T and *Formosa algae* KMM 3553^T was 99.1 %. The results of DNA–DNA hybridization experiments and phenotypic analysis indicated that the strains represent a novel species of the genus *Formosa*, for which the name *Formosa agariphila* sp. nov. is proposed, with KMM 3901^T (=KCTC 12365^T=LMG 23005^T=DSM 15362^T) as the type strain. The description of the genus *Formosa* is emended with newly obtained data.

The genus *Formosa* was proposed by Ivanova *et al.* (2004) for heterotrophic, Gram-negative, motile (by means of gliding), aerobic, halotolerant, saccharolytic, rod-shaped, yellow-pigmented strains isolated from an enrichment community degrading the brown alga *Fucus evanescens*. According to phylogenetic analysis, the genus was distantly related to the genera *Psychroserpens* and *Gelidibacter* within the family *Flavobacteriaceae*. Here, we report the establishment of the taxonomic position of two novel bacteria, and emend the

description of the genus *Formosa*, as a result of the new data obtained in this work.

Strain KMM 3901^T was isolated in Troitsa Bay, Gulf of Peter the Great, East Sea (also known as the Sea of Japan) from the green alga *Acrosiphonia sonderi*. Strain KMM 3962 (=LMG 23006) was isolated from sea water in Amursky Bay (Gulf of Peter the Great). All samples were collected in June 2000. For isolation, 0.1 ml algal homogenates or 0.1 ml sea water was transferred on marine agar 2216 (Difco) at 28 °C; the isolates were then purified and cultivated for further experiments under the same conditions and stored at –80 °C in marine broth (Difco) supplemented with 20 % (v/v) glycerol.

The GenBank/EMBL/DDBJ accession numbers for the 16S rRNA gene sequences of KMM 3901^T and KMM 3962 are AY187688 and AJ893518, respectively.

The phylogenetic position of strains KMM 3901^T and KMM 3962 was determined by means of complete 16S rRNA gene sequence analysis. For strain KMM 3901^T, genomic DNA extraction, PCR and 16S rRNA gene sequencing were performed according to the procedures of Kim *et al.* (1998). Genomic DNA of strain KMM 3962 was prepared according to the protocol of Niemann *et al.* (1997). The 16S rRNA gene was amplified using oligonucleotide primers complementary to highly conserved regions of the bacterial 16S rRNA genes. The forward primer was 5'-AGAGTTTGATCCTGG-CTCAG-3' (hybridizing at positions 8–27, according to the *Escherichia coli* numbering system) and the reverse primer was 5'-AAGGAGGTGATCCAGCCGCA-3' (hybridizing at positions 1541–1522). PCR products were purified using a QIAquick PCR purification kit (Qiagen) according to the manufacturer's instructions. Purified PCR products were sequenced by using the ABI Prism BigDye terminator cycle sequencing ready reaction kit and an Applied Biosystems 3100 DNA sequencer, using the protocols of the manufacturer (Applied Biosystems). The eight sequencing primers used are listed by Coenye *et al.* (1999). Sequence assembly was performed using the program AutoAssembler (Applied Biosystems). The 16S rRNA gene sequence data obtained were aligned together with those of representative members of selected genera belonging to the family *Flavobacteriaceae* by 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 model of Kimura (1980) and 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 datasets, using the SEQBOOT and CONSENSE programs of the PHYLIP package.

Phylogenetic analysis of the almost-complete 16S rRNA gene sequences of strains KMM 3901^T (1432 bp) and KMM 3962 (1472 bp) revealed that the marine isolates are members of the family *Flavobacteriaceae* and form a distinct lineage within the genus *Formosa* (Fig. 1). The topologies of phylogenetic trees constructed using neighbour-joining, maximum-likelihood and maximum-parsimony algorithms were similar, and the stability of the trees was supported by high bootstrap values. The level of sequence similarity between the strains studied and *Formosa algae* KMM 3553^T was 98.9–99.1%. Strains KMM 3901^T and KMM 3962 shared 99.6% sequence similarity.

For determination of the DNA G + C contents of strains KMM 3901^T and KMM 3962, DNA was extracted using the protocol described by Marmur (1961) and was analysed by the thermal denaturation method (Marmur & Doty, 1962). The DNA G + C contents of the strains studied and *Formosa algae* KMM 3553^T were also determined by HPLC (Mesbah *et al.*, 1989), with DNA preparation according to the protocol used for DNA–DNA hybridizations (see below). For the HPLC experiments, the nucleoside mixture was

Fig. 1. Phylogenetic tree, based on the neighbour-joining method, showing the relationship between KMM 3901^T and KMM 3962 and other representative members of the family *Flavobacteriaceae*. Asterisks indicate branches that were also recovered using the maximum-likelihood algorithm. Numbers at nodes indicate levels of bootstrap support (%) based on a dataset of 1000 resamplings. Bar, 0.01 substitutions per nucleotide position.

separated by using a Waters SymmetryShield C8 column maintained at a temperature of 37 °C. The solvent was 0.02 M NH₄H₂PO₄ (pH 4.0) with 1.5% acetonitrile. Non-methylated λ -phage DNA (Sigma) was used as the calibration reference. The DNA G + C contents of strains KMM 3901^T and KMM 3962 were 35.9 (*T_m*) and 33.6 mol% (HPLC) and 35.7 (*T_m*) and 34.1 mol% (HPLC), respectively. The value for *Formosa algae* KMM 3553^T was 34.3 mol% (HPLC), which is similar to the value [34.0 mol% (*T_m*)] from the literature (Ivanova *et al.*, 2004).

For DNA–DNA hybridization experiments among strains KMM 3901^T, KMM 3962 and *Formosa algae* KMM 3553^T, cells were cultivated on marine agar for 24 h at 30 °C. DNA was extracted from 0.75–1.25 g cells (wet weight) by using the DNA extraction protocol of Wilson (1987), as modified by Cleenwerck *et al.* (2002). Cells were lysed in a Tris/EDTA buffer (10 mM Tris/HCl with up to 200 mM EDTA, pH 8.0) containing RNase A (Sigma), SDS (Serva) and proteinase K (Merck) to final concentrations of 400 μ g ml⁻¹, 2% (w/v) and 200 μ g ml⁻¹, respectively. NaCl (5 M stock solution) and CTAB/NaCl solution (10% w/v CTAB in 0.7 M NaCl) were added to final concentrations of 1 M and 13.3% (v/v), respectively. For hybridization experiments, the microplate method was carried out as described by Ezaki *et al.* (1989) and Goris *et al.* (1998), using an HTS7000 BioAssay Reader (Perkin Elmer) for fluorescence measurements. Biotinylated

DNA was hybridized with unlabelled ssDNA, which was bound non-covalently to microplate wells. Hybridizations were performed at 37 °C in a hybridization mixture [$2 \times$ SSC, $5 \times$ Denhardt's solution, 2.5 % dextran sulfate, 50 % formamide, denatured salmon sperm DNA ($100 \mu\text{g ml}^{-1}$) and biotinylated probe DNA (1250 ng ml^{-1})]. Hybridization was carried out with three replications for each sample.

The value for DNA–DNA binding between strains KMM 3901^T and KMM 3962 was 97 %; this indicates that the strains represent a single species (Wayne *et al.*, 1987). DNA–DNA hybridizations performed between KMM 3901^T, KMM 3962 and *Formosa algae* KMM 3553^T revealed binding levels of 27 and 29 %, respectively. These data clearly demonstrate separate species status within the genus *Formosa* for the strains under study.

Isoprenoid quinones were extracted from lyophilized cells of strains KMM 3901^T, KMM 3962 and *Formosa algae* KMM 3553^T and analysed as described by Akagawa-Matsushita *et al.* (1992). The isoprenoid quinone composition was characterized by HPLC (Shimadzu instruments) using a reverse-phase type Zorbax ODS column ($250 \times 4.6 \text{ mm}$) 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 using monitoring at 270 nm and were identified by comparison with known quinones from reference strain *Salegendibacter salegens* DSM 5424^T. The major lipoquinone was MK-6. Polar lipids were determined as described previously (Nedashkovskaya *et al.*, 2004b). The only phospholipid of KMM 3901^T and KMM 3962 was phosphatidylethanolamine, in accordance with the results reported for *Formosa algae* by Ivanova *et al.* (2004).

For fatty acid methyl ester analysis, a loopful of well-grown cells of strains KMM 3901^T, KMM 3962 and *Formosa algae* KMM 3553^T were harvested. The fatty acid methyl esters were prepared as described previously (Vandamme *et al.*, 1992) and were separated and identified using the Sherlock Microbial Identification System (version 3.0; MIDI). The predominant cellular fatty acids for all strains analysed were C_{15:0}, iso-C_{15:1} G, C_{15:1}ω6c, iso-C_{15:0}, iso-C_{15:0} 3-OH, iso-C_{17:0} 3-OH and summed feature 3 (comprising any combination of C_{16:1}ω7c, C_{16:1}ω7t and iso-C_{15:0} 2-OH) (Table 1).

For pigment characterization, strains KMM 3901^T and *Formosa algae* KMM 3553^T were grown on marine agar for 48 h at 28 °C. The absorption spectrum of pigments extracted using acetone/methanol (7:2, v/v) was determined between 300 and 700 nm with a UV spectrophotometer (CE 7250, 7000 series; CECIL Instruments). Cells of strains KMM 3901^T and KMM 3553^T produced yellow carotenoid pigments with maximum absorption at 443.8 and 446.9 nm, respectively.

The cell morphology of strain KMM 3901^T was observed by using scanning and transmission electron microscopy as described by Bruns *et al.* (2001). These studies demonstrated

Table 1. Fatty acid content (percentage of total) of whole-cell hydrolysates of the *Formosa* strains

Values below 1 % for all strains are not shown. Summed feature 3 consisted of one or more of the following fatty acids, which could not be separated by the Microbial Identification System: iso-C_{15:0} 2-OH, C_{16:1}ω7c and C_{16:1}ω7t. tr, Trace amount (<1 % of total); –, not detected.

Fatty acid	<i>F. agariphila</i>		<i>F. algae</i> KMM 3553 ^T
	KMM 3901 ^T	KMM 3962	
C _{15:0}	8.7	11.4	15.5
C _{15:0} 2-OH	1.8	1.6	1.5
C _{15:0} 3-OH	2.4	4.0	2.3
C _{15:1} ω6c	6.0	11.8	8.5
iso-C _{15:0}	12.7	17.2	17.1
iso-C _{15:1} G	6.5	11.4	9.9
iso-C _{15:0} 3-OH	7.7	10.5	6.7
anteiso-C _{15:0}	3.4	1.6	4.7
anteiso-C _{15:1} A	tr	–	1.0
C _{16:0}	1.6	–	1.1
C _{16:0} 3-OH	2.1	tr	tr
iso-C _{16:0}	2.1	–	1.1
iso-C _{16:1} H	2.5	–	tr
iso-C _{16:0} 3-OH	8.9	3.1	4.0
C _{17:0} 2-OH	tr	–	1.5
C _{17:1} ω8c	tr	–	1.2
C _{17:1} ω6c	3.2	1.4	3.5
iso-C _{17:1} ω9c	1.4	tr	1.3
iso-C _{17:0} 3-OH	8.5	10.7	9.6
Summed feature 3	15.8	12.1	5.9

that cells of strain KMM 3901^T show budding fission (Fig. 2). To study the cell morphology of KMM 3962 and *Formosa algae* KMM 3553^T, samples were fixed in a 2.5 % paraformaldehyde/glutaraldehyde mixture buffered with 0.1 M phosphate (pH 7.2) for 2 h, fixed in 1 % osmium tetroxide in the same buffer for 1 h and then dehydrated in graded ethanol and substituted by isoamyl acetate. They were then dried at the critical point in CO₂. Finally, the samples were sputtered with gold in a sputter coater (SC502; Polaron) and observed using the scanning electron microscope (SEM 515; Philips).

The strains isolated in this study were Gram-negative, chemo-organotrophic, aerobic and motile by gliding. They comprised short rod-shaped cells, 0.5–0.6 μm in diameter and 0.8–1.0 μm long (Fig. 2a, b). Buds formed on mature cells of strain KMM 3901^T (Fig. 2). This is the first report of a budding process in marine flavobacteria. On marine agar, colonies formed by strain KMM 3901^T were round, flat, 3–4 mm in diameter, translucent, yellow in colour and sunken into the agar, while colonies of strain KMM 3962 were 2–3 mm in diameter, pale yellow in colour and only slightly sunken into the agar. In addition to producing buds, cells of KMM 3901^T formed threads that connected them to

Fig. 2. (a, b) Scanning electron micrographs of cells of strain KMM 3901^T, showing the rod-shaped morphology, budding (arrowheads) and thread-like structures formed by bacterial cells. (c–e) Transmission electron micrographs of ultrathin sections of cells of strain KMM 3901^T, showing thread-like structures (c, compare with b) and bud formation on mature cells (indicated by an arrowhead in d). Bars: 1 µm (a) and 0.5 µm (b–e).

each other. These structures were not observed for KMM 3962 or the type strain of *Formosa algae*. The formation of fibrillar networks connecting cells of flavobacteria was reported by Reichenbach (1989), and similar features were previously observed in strains of the genus *Winogradskyella*, another member of the family *Flavobacteriaceae* (Nedashkovskaya *et al.*, 2005). The ability of cells of strain KMM 3901^T to form fibrillar threads correlates well with results reported in the literature (Cooksey & Wigglesworth-Cooksey, 1995; Heissenberger *et al.*, 1996; Romanenko *et al.*, 2003). Cells of strain KMM 3901^T also produced a dense translucent slime on solid media. The extracellular fibrillar structures observed in this study could be involved in the attachment of the cells to suitable substrates and attachment to other cells, which are probably responsible for the formation of biofilms on the surface of algae and for the small aggregates observed in liquid cultures, respectively.

Biochemical tests and carbohydrate-oxidation tests were carried out as described previously (Nedashkovskaya *et al.*, 2003, 2004a), except that 50 % natural sea water (v/v) was

added to the base medium used for testing for acid production from carbohydrates. Additionally, the type strain of *Formosa algae* and the two isolates were tested using API 20E and API 20 NE galleries (bioMérieux). The ability to grow under anaerobic conditions was observed using the Oxoid Anaerobic System. Gliding motility was determined as described by Bowman (2000).

The phenotypic characteristics of the two strains studied are listed in Table 2 and summarized below in the species description. The strains shared a number of similar properties, but KMM 3901^T and KMM 3962 differed in maximum growth temperature (33 and 31 °C, respectively) and NaCl concentration (8 and 7 %, respectively). Also, strain KMM 3901^T did not oxidize *N*-acetylglucosamine or hydrolyse starch or Tween 40, in contrast to KMM 3962. While strain KMM 3901^T was susceptible to ampicillin, carbenicillin, lincomycin and oleandomycin, KMM 3962 was resistant to all antibiotics tested. Both strains studied can hydrolyse agar, form acid from D-galactose and utilize L-arabinose and D-lactose, in contrast with *Formosa algae*

Table 2. Phenotypic characteristics of the *Formosa* strains

All strains were positive for the following characteristics: gliding motility, oxidase, catalase and alkaline phosphatase activities, glucose fermentation, growth at 1–6% NaCl and at 4–30 °C, hydrolysis of gelatin and aesculin, acid formation from L-fucose, D-glucose, D-maltose, DL-xylose and mannitol and utilization of D-mannose. All strains were negative for the following characteristics: flexirubin pigments, urease activity, nitrate reduction, H₂S, indole and acetoin production, hydrolysis of casein, cellulose (CM-cellulose and filter paper), chitin, Tween 80 and DNA, acid formation from L-arabinose, D-cellobiose, D-lactose, D-melibiose, L-raffinose, L-rhamnose, L-sorbose, D-sucrose, acetate, citrate, fumarate, malate, adonitol, inositol and sorbitol, utilization of D-sucrose, inositol, sorbitol, citrate and malonate and susceptibility to benzylpenicillin, gentamicin, kanamycin, neomycin, polymyxin B and streptomycin. *n*, Number of strains.

Characteristic	<i>F. agariphila</i> (<i>n</i> = 2)	<i>F. algae</i> KMM 3553 ^T
β-Galactosidase activity	+	–
Hydrolysis of agar	+	–
Acid production from:		
D-Galactose	+	–
Glycerol	–	+
Utilization of L-arabinose and D-lactose	+	–
Susceptibility to tetracycline	–	+
DNA G + C content (mol%)	35–36	34.0

KMM 3553^T. Moreover, the latter strain differs from KMM 3901^T and KMM 3962 in its ability to produce acid from glycerol and its susceptibility to tetracycline. The genomic data obtained here, in combination with discriminative phenotypic findings (Table 2), support the conclusion that strains KMM 3901^T and KMM 3962 represent a separate species.

Although *Formosa algae* KMM 3553^T had originally been described as oxidase-negative and urease- and nitrate reductase-positive, in the course of the comparative phenotypic study of *Formosa algae* KMM 3553^T and the two novel isolates, we detected oxidase activities and the absence of urease and nitrate reductase activities for all strains, using the same methods (Ivanova *et al.*, 2004). As all strains studied fermented glucose, their ability to grow under anaerobic conditions was examined, but no growth was observed. The whole-cell fatty acid profiles of strains KMM 3901^T, KMM 3962 and *Formosa algae* KMM 3553^T were determined under the same conditions. The menaquinone composition, which was not reported by Ivanova *et al.* (2004) for *Formosa algae* strains, was also determined in this study. Differential phenotypic features for the genus *Formosa* and its close relatives are presented in Table 3. For most flavobacteria, generic affiliation on the basis of phenotypic traits is difficult. For instance, although the genera *Algibacter*, *Formosa* and *Gaetbulibacter* occupy distinct phylogenetic positions within the family *Flavobacteriaceae*, they share many similar phenotypic features (Table 3). Finding differential characteristics is especially difficult when most of them are variable between species; see, for instance, the genus *Gelidibacter* in Table 3.

Table 3. Differential characteristics of the genus *Formosa* and other allied genera of the family *Flavobacteriaceae*

Genera: 1, *Formosa*; 2, *Algibacter*; 3, *Gaetbulibacter*; 4, *Gelidibacter*; 5, *Lacinutrix*; 6, *Olleya*; 7, *Psychroserpens*; 8, *Subsaxibacter*; 9, *Subsaximicrobium*. Data are from Bowman *et al.* (1997), Macián *et al.* (2002), Ivanova *et al.* (2004), Nedashkovskaya *et al.* (2004b), Bowman & Nichols (2005), Nichols *et al.* (2005), Jung *et al.* (2005) and this study. Abbreviations: –, negative; +, positive; V, variable; ND, not determined.

Characteristic	1	2	3	4	5	6	7	8	9
Fermentation of glucose	+	+	+	–	–	–	–	–	–
Gliding motility	+	+	+	+	–	+	–	+	+
Presence of budding	+	–	–	–	–	–	–	–	–
Oxidase/catalase activity	+ / +	+ / +	+ / +	– / +	ND / +	+ / +	– / +	ND / +	ND / +
Acid formation from carbohydrates	+	+	+	+	–	+	–	–	–
Temperature range for growth (°C)	4–34	4–35	13–40	–2 to 37	–2 to 29	4–30	0–19	–2 to 20	–2 to 25
Salinity range for growth (%)	0–8	1–6	1–7	0–8	0.6–12	1.2–5	2.4–8	0.6–7	1.5–12
Hydrolysis of:									
Agar	V	+	–	–	–	–	–	–	–
Casein	–	–	–	V	–	–	+	–	V
Gelatin	+	+	–	V	+	+	V	+	+
Starch	V	+	+	V	–	–	–	–	V
Tween 80	–	–	–	V	+	+	+	+	+
Nitrate reduction	V	–	+	–	–	–	–	–	–
DNA G + C content (mol%)	34–36	31–33	34–35	36–42	37	49	27–29	35–36	38–41

Consequently, a polyphasic taxonomic approach is necessary to distinguish different members of the family *Flavobacteriaceae*.

Taking together the phenotypic and phylogenetic data described here, we conclude that the marine bacteria KMM 3901^T and KMM 3962 represent a novel species of the genus *Formosa*, for which the name *Formosa agariphila* sp. nov. is proposed. On the basis of the novel phenotypic and chemotaxonomic data obtained in this study, we also propose an emended description for the genus *Formosa*.

Emended description of the genus *Formosa* Ivanova *et al.* 2004

As the description given by Ivanova *et al.* (2004), with the following changes. Cells are motile by gliding. Buds may be produced. Do not form endospores or resting stages. Facultative anaerobes. Cytochrome oxidase-, catalase- and alkaline phosphatase-positive. May require Na⁺ ions for growth. Produces non-diffusible carotenoid pigments. The main cellular fatty acids are iso-C_{15:0}, C_{15:0}, iso-C_{15:1} G, C_{15:1}ω6c, iso-C_{15:0} 3-OH, iso-C_{17:0} 3-OH and summed feature 3 (comprising any combination of C_{16:1}ω7c, C_{16:1}ω7t and iso-C_{15:0} 2-OH). The major isoprenoid quinone is MK-6. Phosphatidylethanolamine is the only phospholipid identified. The G + C content of the DNA is 34–36 mol%. The type species is *Formosa algae*.

Emended description of *Formosa algae* Ivanova *et al.* 2004

The description is as given by Ivanova *et al.* (2004) with the following additions: the strains decompose aesculin and Tween 40 and can hydrolyse urea, grow in 0–8 % NaCl and at 4–34 °C. Strains form acid from L-fucose, D-glucose, D-maltose, DL-xylose and mannitol, but not from L-arabinose, D-cellobiose, D-lactose, D-melibiose, L-raffinose, L-rhamnose, L-sorbose, D-sucrose, acetate, citrate, fumarate, malate, adonitol, inositol or sorbitol. Utilizes D-mannose, but not D-sucrose, inositol, sorbitol, citrate or malonate. Hydrogen sulfide, indole and acetoin (Voges–Proskauer reaction) are not produced. Nitrate can be reduced to nitrite. The predominant fatty acids of the type strain are iso-C_{15:0} (17.1 %), C_{15:0} (15.5 %), iso-C_{15:1} G (9.9 %), C_{15:1}ω6c (8.5 %), iso-C_{15:0} 3-OH (6.7 %), anteiso-C_{15:0} (4.7 %), iso-C_{17:0} 3-OH (9.6 %) and summed feature 3 (5.9 %) (comprising any combination of C_{16:1}ω7c, C_{16:1}ω7t and iso-C_{15:0} 2-OH). The G + C content is 34–35 mol%.

The type strain is strain KMM 3553^T (=CIP 107684^T=KCTC 12364^T).

Description of *Formosa agariphila* sp. nov.

Formosa agariphila (a.ga.ri.phi'la. N.L. neut. n. *agarum* agar; Gr. adj. *philos* loving; N.L. fem. adj. *agariphila* agar-loving).

The main characteristics are the same as those given for the genus. In addition, cells are 0.4–0.6 µm in width and

0.8–1.2 µm in length and can be connected by thread-like structures. Budding morphology may be observed. On marine agar, colonies are 2–4 mm in diameter, circular, flat or convex, opaque or translucent, shiny with entire edges, sunken into the agar and yellow-pigmented. Growth occurs at 4–33 °C. The optimal temperature for growth is 21–23 °C. Growth occurs in 1–8 % NaCl. Decomposes agar, gelatin and aesculin. Does not hydrolyse casein, DNA, Tween 80, cellulose (CM-cellulose and filter paper) or chitin. Forms acid from L-fucose, D-galactose, D-glucose, D-maltose, DL-xylose and mannitol, but not from L-arabinose, D-cellobiose, D-lactose, D-melibiose, L-rhamnose, L-raffinose, L-sorbose, D-sucrose, adonitol, glycerol, dulcitol, inositol or sorbitol. Utilizes L-arabinose, D-lactose, D-mannose and D-sucrose, but not inositol, sorbitol, malonate or citrate. Produces β-galactosidase. Nitrate is not reduced to nitrite. H₂S, indole and acetoin (Voges–Proskauer reaction) production are negative. Some strains are susceptible to ampicillin, carbenicillin, lincomycin and oleandomycin. Resistant to benzylpenicillin, gentamicin, kanamycin, neomycin, polymyxin B, tetracycline and streptomycin. The predominant fatty acids are C_{15:0} (8.7–11.4 %), iso-C_{15:1} G (6.5–11.4 %), C_{15:1}ω6c (6–11.8 %), iso-C_{15:0} (12.7–17.2 %), iso-C_{15:0} 3-OH (7.7–10.5 %), iso-C_{17:0} 3-OH (8.5–10.7 %) and summed feature 3 (15.8–12.1 %, comprising any combination of C_{16:1}ω7c, C_{16:1}ω7t and iso-C_{15:0} 2-OH). The G + C content of the DNA is 35–36 mol% (T_m).

The type strain, KMM 3901^T (=KCTC 12365^T=LMG 23005^T=DSM 15362^T), was isolated from the green alga *Acrosiphonia sonderi*, collected in Troitsa Bay, Gulf of Peter the Great, East Sea (Sea of Japan). Strain KMM 3962 (=LMG 23006) was isolated from sea water collected in Amursky Bay, Gulf of Peter the Great.

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