Marinicella litoralis gen. nov., sp. nov., a gammaproteobacterium isolated from coastal seawater

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A Gram-negative, aerobic, greyish–yellowish-pigmented, stenohaline, rod-shaped, non-motile bacterium, strain KMM 3900^T, was isolated from a coastal seawater sample collected from the Sea of Japan. Based on phylogenetic analysis, strain KMM 3900^T was positioned within the *Gammaproteobacteria* on a separate branch adjacent to members of the genera *Reinekea* and *Kangiella*, sharing less than 88% 16S rRNA gene sequence similarity with all recognized species of the *Gammaproteobacteria*. The major isoprenoid quinone was Q-8. Polar lipids consisted of phosphatidylcholine, phosphatidylethanolamine, phosphatidylglycerol, diphosphatidylglycerol and two unknown phospholipids. Fatty acid analysis revealed iso-C_{15:0}, C_{16:1ω7c} and C_{16:0} as the dominant components. The DNA G + C content was 43.8 mol%. Based on its unique phenotypic characteristics and phylogenetic remoteness, marine isolate KMM 3900^T is considered to represent a novel genus and species, for which the name *Marinicella litoralis* gen. nov., sp. nov. is proposed. The type strain of *Marinicella litoralis* is KMM 3900^T (=NRIC 0758^T =JCM 16154^T).

There has been increasing interest in the investigation of microbial communities that are associated with marine coastal ecosystems; such ecosystems are known to be of ecological significance, providing favourable conditions for marine biota nursery, biocontrol and bioremediation activities. Sea coastal environments differ in physical parameters (such as sharp changes in temperature and salinity, agitation, terrestrial influx and radiation) from open or deep seawater, implying the existence of indigenous bacteria capable of adaptation to peculiar coastal conditions. Studies on micro-organisms recovered from tidal sediments and shallow waters of Pacific coastal habitats have led to the descriptions of novel genera of heterotrophic, non-fermentative bacteria in the *Gammaproteobacteria*, including *Hahella* (Lee *et al.*, 2001), *Zooshikella* (Yi *et al.*, 2003), *Aestuariibacter* (Yi *et al.*, 2004), *Kangiella* (Yoon *et al.*, 2004b) and *Simiduia* (Shieh *et al.*, 2008), demonstrating that coastal environments can serve as a source of novel gammaproteobacteria. In previous reports, we have

described *Oceanisphaera litoralis*, *Reinekea marinisedimentum* and *Marinobacter sediminum* (Romanenko *et al.*, 2003, 2004, 2005a) to accommodate heterotrophic gammaproteobacteria isolated from coastal sediments from the Sea of Japan. In the present study, we report the phenotypic and phylogenetic characterization of a Gram-negative, aerobic, greyish–yellowish-pigmented, non-motile bacterium, strain KMM 3900^T, recovered from a seawater sample during a survey of the biodiversity of micro-organisms associated with a coastal marine environment. On the basis of the phenotypic and molecular data obtained, a novel genus and species are described.

Strain KMM 3900^T was isolated from a seawater sample collected in June 2008 off the Russian coast of the Sea of Japan (42° 44.348' N 133° 14.490' E) at a depth of 2 m, as described previously (Romanenko *et al.*, 2004). Strain KMM 3900^T grew aerobically on marine 2216 agar (MA) or in marine broth (MB) at 25–28 °C and was stored at –80 °C in MB supplemented with 30% (v/v) glycerol. Motility and cellular morphology were observed by oil-immersion phase-contrast microscopy (AX70; Olympus) using cultures grown on MA for 36 h and 2 and 6 days at 25 °C. Gram staining, oxidase and catalase activities and hydrolytic reactions for gelatin, casein, chitin, starch, CM-cellulose, DNA and Tweens 20, 40 and 80 were tested according to the standard methods described by Smibert &

The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain KMM 3900^T is AB500095.

Results of 2D TLC of polar lipids of strain KMM 3900^T, 16S rRNA gene sequence-based maximum-likelihood and maximum-parsimony trees and a phase-contrast micrograph are available as supplementary material with the online version of this paper.

Krieg (1994). Growth under anaerobic conditions with CO₂ was determined after incubation for 1 week on MA using an AnaeroPack (Mitsubishi Gas Chemical Co.). Formation of H₂S from thiosulfate and from cysteine was tested using a lead acetate paper strip. Acid production from carbohydrates was examined using the oxidation/fermentation medium of Leifson (1963) for marine bacteria. The ability of strain KMM 3900^T to grow in the presence of organic substrates as sole carbon and energy sources was tested for 4 weeks on artificial seawater (ASW)-based medium supplemented with 2 g NH₄Cl l⁻¹, 0.5 g yeast extract l⁻¹ and 0.4 % carbon source. ASW contained (per litre distilled water): 24 g NaCl, 4.9 g MgCl₂, 3.9 g Na₂SO₄, 1.1 g CaCl₂, 0.66 g KCl, 0.2 g NaHCO₃, 0.096 g KBr, 0.026 g H₃BO₃, 0.024 g SrCl₂ and 0.003 g NaF. Requirements for organic growth factors and sodium ions were tested on the basal medium of Baumann & Baumann (1981) supplemented with 0.1 % glycerol, 0.1 % potassium acetate or 0.1 % potassium succinate and in basal medium in which sodium salts had been replaced by equimolar amounts of potassium salts. Requirement for and tolerance of NaCl were tested on ASW-based medium using 0–20 % NaCl, supplemented with (l⁻¹) 10.0 g Bacto peptone, 2.0 g yeast extract, 0.028 g FeSO₄ and 15.0 g agar. Growth at 4–42 °C and pH 4.0–12.0 and antibiotic resistance were studied as described previously (Romanenko *et al.*, 2003, 2004). In addition, biochemical tests were carried out using API ZYM, API 20NE and API 20E test kits (bioMérieux) according to the manufacturer's instructions, except that the culture was suspended in ASW.

For polar lipid and fatty acid analyses, strain KMM 3900^T was cultivated on MA at 28 °C for 3 days and lipids were extracted using the chloroform/methanol extraction method of Bligh & Dyer (1959). Polar lipids were analysed as described by Vaskovsky & Terekhova (1979). Two-dimensional TLC of polar lipids was carried out using chloroform/methanol/benzene/28 % NH₄OH (65:30:10:6, by vol.) for the first dimension and chloroform/methanol/benzene/acetone/acetic acid/water (70:30:10:5:4:1, by vol.) for the second one. Non-specific detection of lipids on the TLC plate was conducted with 10 % H₂SO₄ in methanol at 180 °C. Amino group-containing lipids were determined with ninhydrin, phospholipids with molybdate reagent, glycolipids with anthrone spray and choline lipids with Dragendorff's reagent. Fatty acid methyl esters were obtained by alkaline methanolysis (15 % NaOH/methanol). The resultant fatty acid methyl esters were extracted by hexane and analysed using a GLC-MS Hewlett Packard model 6890 gas chromatograph equipped with an HP 5 MS 5 % phenyl methyl siloxane capillary column (30 m × 250 µm × 0.25 µm) and connected to a Hewlett Packard model 5973 mass spectrometer. Cellular biomass of strain KMM 3900^T for respiratory lipoquinone analysis was obtained from an MB culture grown at 25 °C. Isoprenoid quinones were extracted using chloroform/methanol (2:1, v/v), purified by preparative TLC (silica gel 60 Adamant; Fluka) and analysed by HPLC (Agilent 1100 Series)

using a reversed-phase column (Hypersil ODS 5 µm; 40 × 250 mm). Methanol/2-propanol (65:35) was used as a mobile phase and quinones were detected at 270 nm. The DNA base composition was determined as described by Marmur & Doty (1962) and Owen *et al.* (1969). The 16S rRNA gene sequence of strain KMM 3900^T (1519 nt) was determined as described by Shida *et al.* (1997). The sequence obtained was compared with 16S rRNA gene sequences retrieved from the EMBL/GenBank/DDBJ databases by using the FASTA program (Pearson & Lipman, 1988). Phylogenetic trees based on 16S rRNA gene sequences were constructed by the neighbour-joining and maximum-parsimony methods using the MEGA 4 package (Tamura *et al.*, 2007) and by the maximum-likelihood method using the PHYLIP package (version 3.5c; Felsenstein, 1989) after multiple alignment of data by CLUSTAL_X (version 1.83; Thompson *et al.*, 1997). Distances were calculated according to Kimura's two-parameter model. The robustness of phylogenetic trees was estimated by bootstrap analysis of 1000 replicates for the neighbour-joining and maximum-parsimony trees and of 100 replicates for the maximum-likelihood tree.

Cultural, physiological and metabolic properties of strain KMM 3900^T are listed in Table 1 and in the genus and species descriptions. Analysis of respiratory lipoquinones revealed ubiquinone Q-8 to be the major compound. Polar lipids included phosphatidylcholine, phosphatidylethanolamine, phosphatidylglycerol and diphosphatidylglycerol and two unknown phospholipids (Supplementary Fig. S1, available in IJSEM Online). Q-8 was reported as the major isoprenoid quinone for members of the related genera *Reinekea* (Romanenko *et al.*, 2004) and *Kangiella* (Yoon *et al.*, 2004b). The presence of phosphatidylethanolamine, phosphatidylglycerol and diphosphatidylglycerol is in line with the polar lipids found in *Marinobacter hydrocarbonoclasticus* (Spröer *et al.*, 1998) and some other marine gammaproteobacteria (Romanenko *et al.*, 2003, 2004, 2005b). *Reinekea marinisedimentorum* differed from strain KMM 3900^T in the absence of phosphatidylcholine and the presence of phosphatidylinositol in its lipid composition. Unlike the novel bacterium KMM 3900^T, *Marinobacter hydrocarbonoclasticus* strains did not contain phosphatidylcholine in their polar lipids and contained Q-9 as the major ubiquinone (Spröer *et al.*, 1998) (Table 1). Polar lipid and ubiquinone profiles have been not reported for *Spongiibacter marinus* (Graeber *et al.*, 2008) or *Alcanivorax borkumensis* (Yakimov *et al.*, 1998; Fernández-Martínez *et al.*, 2003) and polar lipids have not been reported for *Kangiella* species (Yoon *et al.*, 2004b). The fatty acid composition of strain KMM 3900^T was characterized by a large amount of iso-C_{15:0}, followed by C_{16:1ω7c} and C_{16:0}. The detailed fatty acid composition was as follows: C_{12:0} 3-OH (3.5 %), C_{13:0} (3.9 %), C_{14:0} (1.2 %), iso-C_{15:0} (39.5 %), C_{16:1ω7c} (30.4 %), C_{16:0} (10.7 %), iso-C_{17:0} (6.9 %) and iso-C_{18:0} (2.8 %).

The chemotaxonomic properties of strain KMM 3900^T (ubiquinone Q-8 and predominance of iso-C_{15:0}) are

Table 1. Differential characteristics of strain KMM 3900^T (*Marinicella litoralis* gen. nov., sp. nov.) and related gammaproteobacteria

Taxa: 1, KMM 3900^T (data from the present study); 2, *Kangiella* (Yoon *et al.*, 2004b); 3, *Reinekea marinisedimentorum* (Romanenko *et al.*, 2004); 4, *Spongiibacter marinus* (Graeber *et al.*, 2008); 5, *Alcanivorax borkumensis* (Yakimov *et al.*, 1998; Fernández-Martínez *et al.*, 2003); 6, *Marinobacter hydrocarbonoclasticus* (unless indicated, data from Gauthier *et al.*, 1992; Spröer *et al.*, 1998; Yoon *et al.*, 2003); 7, *Microbulbifer hydrolyticus* (González *et al.*, 1997; Yoon *et al.*, 2004a; Tang *et al.*, 2008). +, Positive; –, negative; w, weak reaction; v, variable reaction between species or strains; ND, no data available.

Characteristic	1	2	3	4	5	6	7
Motility	–	–	+	+	–	+	–
Growth at 4 °C	–	v	+	–	+	–	–
Maximum growth temperature (°C)	35	43–48	37	40	35	43–45*	41
NaCl range for growth (% w/v)	1–5	0.5–13	0.5–5	1–7	1–12.5	0.5–18.5*	0.6–6
Tolerance of 10 % NaCl	–	+	–	–	+	+	–
Nitrate reduction	–	–	+	ND	+	+	–
Carbohydrate utilization	–	–	+	+	–	–	+
Hydrolysis of:							
Aesculin	–	–	–	ND	–	–	+
Gelatin	+	+	–	ND	–	–	+
Starch	–	–	–	ND	–	–	+
Tween 80	+	+	w	+	+	+	+
Tyrosine	–	+	–	ND	ND	ND	ND
Casein	w	+	–	ND	ND	–*	+
DNA	+	ND	ND	ND	ND	–*	ND
Urea	–	–	–	ND	–	v	ND
Enzyme activity (API ZYM)							
Alkaline phosphatase	+	+	+	+	ND	+	ND
Esterase (C4)	–	+	–	–	ND	+	ND
Esterase lipase (C8)	+	+	–	+	ND	+	ND
Lipase (C14)	–	–	–	–	ND	–	ND
Leucine arylamidase	+	+	+	+	ND	+	ND
Valine arylamidase	–	+	–	–	ND	w	ND
Trypsin	w	+	–	–	ND	–	ND
α-Chymotrypsin	–	–	–	–	ND	–	ND
Cystine arylamidase	–	–	–	–	ND	–	ND
Acid phosphatase	–	v	–	+	ND	+	ND
Naphthol-AS-BI-phosphohydrolase	+	+	+	+	ND	+	ND
N-Acetyl-β-glucosaminidase	–	–	–	+	ND	+	–
Major ubiquinone	Q-8	Q-8	Q-8	ND	ND	Q-9	Q-8
Main fatty acids	iso-C _{15:0} , C _{16:0} , C _{16:1ω7c}	iso-C _{15:0}	C _{16:0} , C _{16:1ω7c} , C _{18:1ω7c}	C _{17:1ω8} , C _{17:0} , C _{18:1ω7}	C _{16:0} , C _{16:1ω7c} , C _{18:1ω7c}	C _{18:1ω9c} , C _{16:0} , C _{16:1ω9c}	iso-C _{15:0} , C _{16:0}
DNA G + C content (mol%)	43.8	44	51.1	69.1	53–54	55.7–57.5	57.7

*Data obtained in the present study for *Marinobacter hydrocarbonoclasticus* strains DSM 8798^T (Gauthier *et al.*, 1992), DSM 50418 (type strain of *Pseudomonas nautica*; Baumann *et al.*, 1983; Spröer *et al.*, 1998) and VT8 (type strain of *Marinobacter aquaeolei*; Nguyen *et al.*, 1999; Márquez & Ventosa, 2005).

similar to those reported for *Kangiella* species (Yoon *et al.*, 2004b) and *Microbulbifer hydrolyticus* (González *et al.*, 1997; Tang *et al.*, 2008; Yoon *et al.*, 2004a). However, strain KMM 3900^T differed significantly from *Kangiella* species and *Microbulbifer hydrolyticus* in the absence of iso-C_{11:0}, iso-C_{17:1}, iso-C_{17:0} and iso-C_{11:0} 3-OH and from *Kangiella* species in the presence of C_{16:1ω7c} and the absence of iso-C_{17:0} 3-OH. *Reinekea marinisedimentorum* contained the fatty acids C_{16:0} and C_{16:1ω7c} but differed from strain KMM 3900^T in the absence of iso-C_{15:0}. In

contrast to strain KMM 3900^T, strains of *Alcanivorax borkumensis* (Yakimov *et al.*, 1998; Fernández-Martínez *et al.*, 2003) and *Marinobacter hydrocarbonoclasticus* (Gauthier *et al.*, 1992; Spröer *et al.*, 1998; Nguyen *et al.*, 1999; Márquez & Ventosa, 2005) contain C_{18:1} as a predominant fatty acid and do not contain branched fatty acids, and *Spongiibacter marinus* HAL40b^T (Graeber *et al.*, 2008) is characterized by the abundance of C_{17:1} and the presence of C_{11:0} 3-OH. Therefore, we can conclude that the combination of iso-C_{15:0}, C_{16:1ω7c} and C_{16:0} as

predominant fatty acids makes the fatty acid composition of strain KMM 3900^T unique compared with those of its phylogenetic relatives, including members of the genera *Reinekea*, *Kangiella* and *Spongiibacter* and *Alcanivorax borkumensis*, *Microbulbifer hydrolyticus* and *Marinobacter hydrocarbonoclasticus*.

The DNA G+C content of 43.8 mol% determined for strain KMM 3900^T was close to the G+C contents found for *Kangiella* species (44 mol%), but clearly distinguished it from *Spongiibacter marinus* (69.1 mol%), *Reinekea mariniseditentorum* (51.1 mol%), *Alcanivorax borkumensis* (53–54 mol%) and *Marinobacter hydrocarbonoclasticus* (55.7–57.5 mol%) (Table 1). Comparative 16S rRNA gene sequence analysis showed that the novel marine isolate was affiliated to the *Gammaproteobacteria* on a separate branch adjacent to the members of the genera *Reinekea* and *Kangiella* (Fig. 1). The same relationships were also evident from 16S rRNA gene sequence dendrograms generated with the maximum-parsimony and maximum-likelihood algorithms (Supplementary Figs S2 and S3). Strain KMM 3900^T was remotely related to representatives of *Reinekea*, *Kangiella*, *Spongiibacter*, *Alcanivorax*, *Marinobacter*, *Microbulbifer*, *Granulosicoccus* and *Methylostratum*, displaying 85–87% 16S rRNA gene sequence similarity. The highest sequence similarity (96.9%) was obtained with the 16S rRNA gene sequence of gammaproteobacterium N2yML2 (GenBank accession no. EF629832), which was found among the bacterial associates of an aquacultured sponge, *Mycale laxissima* (Mohamed *et al.*, 2008). It is interesting to note that the novel strain KMM 3900^T clustered with members of *Reinekea* and *Kangiella*, which have been isolated from Pacific coastal marine environments. The presence of isolate N2yML2 recovered from an aquacultured sponge specimen in this cluster may indicate that similar strains are common inhabitants of coastal environments. The very low sequence similarities (<88%) and

distant relationships between strain KMM 3900^T and other described genera suggested that the strain represents a novel genus and species within the *Gammaproteobacteria*.

The isolated phylogenetic position of strain KMM 3900^T was supported by its unique physiological and biochemical properties. Novel isolate KMM 3900^T was Gram-negative, aerobic, non-fermentative, heterotrophic, stenohaline, greyish–yellowish-pigmented, non-motile and rod-shaped (Supplementary Fig. S4). Strain KMM 3900^T required sodium ions for growth and also complex proteinaceous compounds, including peptone, casein, gelatin or meat extract. Strain KMM 3900^T exhibited proteolytic and lipolytic enzymes in routine and API ZYM tests, as described in Table 1 and the species description. Strain KMM 3900^T was characterized by some phenotypic traits, such as lack of motility, growth temperature of 5–35 °C with an optimum at 25–28 °C and no growth at 4 °C, a narrow range of NaCl concentration for growth, 1–5%, with optimum growth at 2–3%, and utilization of a restricted number of carbon sources, which have been reported as characteristic for many coastal marine bacteria. As seen from Table 1, strain KMM 3900^T differed phenotypically from *Kangiella* species in the maximum temperature for growth (35 °C compared with 43–48 °C for *Kangiella*), the NaCl range that supported growth (1–5% compared with 0.5–13%) and the absence of tyrosine hydrolysis, esterase (C4) and valine arylamidase and from *Reinekea mariniseditentorum* in its lack of motility, its maximum temperature for growth (35 °C compared with 37 °C), the absence of nitrate reduction, carbohydrate utilization and positive reactions for hydrolysis of gelatin and casein and esterase lipase (C8) activity. Strain KMM 3900^T could be distinguished from *Spongiibacter marinus*, *Alcanivorax borkumensis*, *Marinobacter hydrocarbonoclasticus* and *Microbulbifer hydrolyticus* by minimum and maximum growth temperatures, salinity range for growth

Fig. 1. Neighbour-joining phylogenetic tree based on 16S rRNA gene sequences available from the GenBank/EMBL/DBJ databases (accession numbers in parentheses) showing the relationship of strain KMM 3900^T and related members of the *Gammaproteobacteria*. Phylogenetic analysis was performed using the software package MEGA 4 (Tamura *et al.*, 2007) after multiple alignment of data by CLUSTAL_X (version 1.83; Thompson *et al.*, 1997). Bootstrap values (>70%) based on 1000 replications are given as percentages at branching points. Bar, 0.02 substitutions per nucleotide position.

and metabolic properties (Table 1). On the basis of phenotypic and phylogenetic evidence, it is proposed to classify strain KMM 3900^T within a novel genus and species, *Marinicella litoralis* gen. nov., sp. nov.

Description of *Marinicella* gen. nov.

Marinicella (Ma.ri.ni.cel'la. L. adj. *marinus* of the sea; L. n. *cella* a chamber, a cell; N.L. fem. n. *Marinicella* a cell from the sea).

Gram-negative, aerobic, oxidase- and catalase-positive, rod-shaped bacteria. Chemo-organoheterotrophic. Not capable of photoautotrophic growth with CO₂. Sodium ions are essential for growth. The predominant isoprenoid quinone is Q-8. Polar lipids include phosphatidylcholine, phosphatidylethanolamine, phosphatidylglycerol, diphosphatidylglycerol and unknown phospholipids. The major fatty acids are iso-C_{15:0}, C_{16:0} and C_{16:1}ω7c. The DNA G+C content of the type strain of the type species is 43.8 mol% (thermal denaturation method). On the basis of 16S rRNA gene sequence analysis, the genus represents a separate branch within the *Gammaproteobacteria*, related to the genera *Reinekea*, *Kangiella*, *Spongiibacter*, *Alcanivorax* and *Microbulbifer*. The type species of the genus is *Marinicella litoralis*. The only known strain was isolated from a marine environment.

Description of *Marinicella litoralis* sp. nov.

Marinicella litoralis (li.to.ra'lis. L. fem. adj. *litoralis* of the seashore).

In addition to properties given in the genus description, the species is characterized as follows. Cells are 0.4–0.6 µm in diameter and 1.8–4.5 µm long. Non-motile. Produces greyish–yellowish-pigmented, transparent, smooth, shiny colonies with regular edges, 2–3 mm in diameter, on MA. Abundant growth is observed on/in MA or MB supplemented with casein hydrolysate and media containing natural or artificial seawater, supplemented with 0.5 % (w/v) peptone, tryptone or meat hydrolysate. No growth on basal medium supplemented with 0.1 % glycerol, 0.1 % potassium acetate or 0.1 % potassium succinate or on basal medium when sodium salts have been replaced by equimolar amounts of potassium salts. No growth when D-glucose or a mixture of amino acids (L-alanine, L-asparagine, L-arginine, L-phenylalanine, L-lysine, L-leucine, L-valine and L-histidine) is added. NaCl is required for growth; growth occurs at 1–5 % NaCl (w/v) and is optimal in 2–3 %. Grows well in/on peptone media containing NaCl alone without addition of any sea-salt components (MgCl₂, KCl, CaCl₂, NaNO₃, K₂HPO₄, KCl, NaSO₄, NaHCO₃, NaF or FeSO₄). The temperature range for growth is 5–35 °C with an optimum of 25–28 °C. No growth at 4 °C or above 35 °C. The pH range for growth is 6.0–11.0, with an optimum at pH 8.5–9.5. Negative for H₂S production. Positive for hydrolysis of gelatin, DNA and Tweens 20, 40 and 80. Casein is hydrolysed within

3–5 days. Does not degrade CM-cellulose, agar, chitin or starch. On L-tyrosine-containing medium, does not produce melanin-like pigments or clearance zones. No acid production is observed from D-glucose, maltose, sucrose, lactose, D-galactose, D-mannose, cellobiose, D-xylose, L-arabinose, L-rhamnose, D-sorbitol or D-mannitol under aerobic or anaerobic conditions. According to API 20NE tests, positive for gelatin hydrolysis and negative for nitrate reduction, indole production, glucose acidification under anaerobic conditions, arginine dihydrolase, urease production, aesculin hydrolysis, PNPG test and assimilation of D-glucose, D-mannitol, maltose, L-arabinose, D-mannose, N-acetylglucosamine, D-gluconate, caprate, adipate, L-malate, citrate and phenylacetate. In API 20E tests, positive for gelatin hydrolysis and negative for ONPG, arginine dihydrolase, lysine decarboxylase, ornithine decarboxylase, H₂S production, urease, tryptophan deaminase, indole production, acetoin production, trisodium citrate utilization and oxidation and fermentation of D-glucose, D-mannitol, inositol, D-sorbitol, L-rhamnose, sucrose, melibiose, amygdalin and D-arabinose. Does not grow on D-glucose, maltose, sucrose, D-xylose, D-galactose, N-acetylglucosamine, lactose, melibiose, raffinose, L-rhamnose, L-arabinose, D-ribose, D-mannose, cellobiose, glycerol, acetate, glutamic acid, DL-methionine, D-mannitol, citrate, L-alanine, L-asparagine, L-arginine, L-phenylalanine, L-valine or L-lysine. According to API ZYM tests, positive for alkaline phosphatase, esterase lipase (C8), leucine arylamidase and naphthol-AS-BI-phosphohydrolase, weakly positive for trypsin and negative for esterase (C4), lipase (C14), valine arylamidase, cystine arylamidase, α-chymotrypsin, acid phosphatase, N-acetyl-β-glucosaminidase, α-galactosidase, β-galactosidase, α-glucosidase, β-glucuronidase, β-glucosidase, α-mannosidase and α-fucosidase. In addition to the major fatty acids, contains smaller amounts of C_{12:0} 3-OH, C_{13:0}, C_{14:0}, iso-C_{17:0} and iso-C_{18:0}. Susceptible to (content per disc) ampicillin (10 µg), benzylpenicillin (10 U), carbenicillin (100 µg), gentamicin (10 µg), lincomycin (15 µg), oleandomycin (15 µg), rifampicin (5 µg), streptomycin (30 µg), vancomycin (30 µg), kanamycin (30 µg), nalidixic acid (30 µg), neomycin (30 µg), ofloxacin (5 µg), polymyxin (300 U), erythromycin (15 µg), cephazolin (30 µg), cephalixin (30 µg) and chloramphenicol (30 µg) and resistant to oxacillin (10 µg) and tetracycline (30 µg).

The type strain, strain KMM 3900^T (=NRIC 0758^T =JCM 16154^T), was isolated from a coastal seawater sample collected from the Sea of Japan, Russia.

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