Primorskyibacter sedentarius gen. nov., sp. nov., a novel member of the class *Alphaproteobacteria* from shallow marine sediments

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Two Gram-negative, aerobic, non-pigmented, non-motile, rod-shaped bacteria, strains KMM 9015 and KMM 9018^T, were isolated from a sample of shallow sediment collected from the Sea of Japan. An analysis of the nearly complete 16S rRNA gene sequences showed that the isolates were very close to each other phylogenetically (99.9% sequence similarity) and their close relatives were *Marinovum algicola* FF3^T (95.8 and 95.9%, respectively) and members of the genera *Leisingera* (95.7–95.1 and 95.8–95.2%), *Phaeobacter* (95.0–94.2 and 95.1–94.2%) and *Thalassobius* (96.3–94.8 and 96.2–94.7%) of the class *Alphaproteobacteria*. In phylogenetic trees based on 16S rRNA gene sequences, strains KMM 9015 and KMM 9018^T were positioned as a distinct phylogenetic line adjacent to *Marinovum algicola*. The major isoprenoid quinone was Q-10, the polar lipids consisted of phosphatidylcholine, phosphatidylethanolamine, phosphatidylglycerol, diphosphatidylglycerol and an unknown lipid and the major fatty acid was C_{18:1}ω7c, followed by 11-methyl C_{18:1}ω7c, in both strains. The DNA G+C contents of strains KMM 9015 and KMM 9018^T were 60.2 and 61.9 mol%, respectively. Based on distinctive phenotypic characteristics and phylogenetic analysis, strains KMM 9015 and KMM 9018^T represent a novel species in a novel genus, for which the name *Primorskyibacter sedentarius* gen. nov., sp. nov. is proposed. The type strain of *Primorskyibacter sedentarius* is strain KMM 9018^T (=NRIC 0784^T =JCM 16874^T).

Shallow marine environments are significant as natural harbours of unusual micro-organisms that are capable of dwelling under the peculiar conditions provided by the seashore habitat. The *Roseobacter* clade (order *Rhodobacterales*, class *Alphaproteobacteria*) comprises a large group of bacteria (Garrrity *et al.*, 2005, 2006) that are probably one of the most significant components of microbial communities that colonize shallow marine waters and sediments (Buchan *et al.*, 2005). In this study, we report the isolation and phenotypic and phylogenetic characterization of two novel strains, designated KMM

9015 and KMM 9018^T, that were found during a study of bacteria inhabiting shallow sediments of the Sea of Japan. Phylogenetic analysis of 16S rRNA gene sequences revealed that the novel isolates were closely related to members of the *Roseobacter* clade, including the genera *Marinovum*, *Leisingera*, *Phaeobacter* and *Thalassobius*, where they formed a separate line adjacent to *Marinovum algicola*. Based on distinctive phenotypic characteristics and phylogenetic distance, a novel genus and species are described to accommodate strains KMM 9015 and KMM 9018^T.

Strains KMM 9015 and KMM 9018^T were isolated from the same shallow sediment sample, collected from Peter the Great Bay, Sea of Japan, Russia (42° 40.108' N 131° 12.983' E), as described previously (Romanenko *et al.*, 2003). The strains were grown aerobically on marine 2216 agar (MA) or in marine broth (MB) and were stored at –80 °C in MB supplemented with 30% (v/v) glycerol. Motility was determined by the hanging drop method as described by

Abbreviations: Bchl, bacteriochlorophyll; FAME, fatty acid methyl ester.

The GenBank/EMBL/DDBJ accession numbers for the 16S rRNA gene sequences of strains KMM 9015 and KMM 9018^T are AB550559 and AB550558, respectively.

Two supplementary figures are available with the online version of this paper.

Gerhardt *et al.* (1994). Cells were observed by oil-immersion phase-contrast microscopy (AX70; Olympus) using 2-day cultures grown on MA at 25 °C. Gram staining, oxidase and catalase, hydrolysis of gelatin, casein, DNA and Tweens 20, 40 and 80 and production of H₂S from thiosulfate were tested according to standard methods (Smibert & Krieg, 1994). Acid production from carbohydrates was examined using oxidation/fermentation medium as described by Leifson (1963). Requirement for and tolerance of NaCl were tested on artificial seawater (ASW)-based medium using various concentrations of NaCl in the range 0–20 %, supplemented with (l⁻¹) 10.0 g Bacto peptone, 2.0 g yeast extract, 0.028 g FeSO₄ and 15.0 g agar. ASW was prepared as described by Bruns *et al.* (2001) and contained (per litre distilled water) 23.6 g NaCl, 4.53 g MgCl₂·6H₂O, 3.9 g Mg₂SO₄·7H₂O, 0.64 g KCl and 1.3 g CaCl₂·2H₂O. In addition, strains were tested for growth on the above medium containing NaCl alone without any of the sea salts components, MgCl₂, Mg₂SO₄, KCl and CaCl₂. The ability to grow in the presence of organic substrates as sole carbon and energy sources was tested for 3 weeks on ASW-based medium supplemented with (l⁻¹) 2 g NH₄Cl, 0.5 g yeast extract and 0.4 % carbon source. Growth was considered as negative if it was equal to or less than that in the negative control to which no carbon source had been added. Growth at 4–45 °C and pH 4.0–13.0 and antibiotic resistance were studied as described previously (Romanenko *et al.*, 2003, 2005). In addition, biochemical tests were carried out using API ZYM, API 32GN and API 20NE test kits (bioMérieux) according to the manufacturer's instructions, except that the cultures were suspended in ASW. Production of bacteriochlorophyll (Bchl) *a* was tested spectrophotometrically in methanolic extracts of cells grown on MA and in MB in the dark as described by Lafay *et al.* (1995). For polar lipid and fatty acid analyses, strains KMM 9015 and KMM 9018^T were cultivated on MA at 28 °C for 3 days, and lipids were extracted using the extraction method of Folch *et al.* (1957). Two-dimensional TLC of polar lipids was carried out on silica gel 60 F₂₅₄ plates (10 × 10 cm; Merck) using chloroform/methanol/water (65:25:4, by vol.) for the first direction and chloroform/methanol/acetic acid/water (80:12:15:4, by vol.) for the second (Collins & Shah, 1984). Fatty acid methyl esters (FAMES) were prepared according to the procedure of the Microbial Identification System (MIDI) (Sasser, 1990). Analysis of FAMES was performed using a GC-17A chromatograph (Shimadzu) equipped with a capillary column (30 m × 0.25 mm i.d.) coated with Supelcowax-10 and SPB-5 phases (Supelco). Identification of FAMES was accomplished by determining equivalent chain-length values and comparing the retention times of the samples to those of standards. In addition, FAMES were analysed using a GLC-MS Shimadzu GC-MS model QP5050 (column MDM-5S; temperature program from 140 to 250 °C, at a rate of 2 °C min⁻¹). Cells for respiratory lipoquinone analysis were obtained from MB cultures grown at 25 °C. Isoprenoid quinones were analysed as described by Collins & Shah (1984). Methanol/2-propanol

(2:1, v/v) was used as the 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). DNA–DNA hybridization between strains KMM 9015 and KMM 9018^T was carried out by the method of Ezaki *et al.* (1989). The 16S rRNA gene sequences of strains KMM 9015 and KMM 9018^T, containing 1438 and 1436 nt, respectively, were determined as described by Shida *et al.* (1997). The sequences obtained were compared with 16S rRNA gene sequences retrieved from the EMBL/GenBank/DBJ databases by using the FASTA program (Pearson & Lipman, 1988). Phylogenetic analysis of 16S rRNA gene sequences was performed using the software package MEGA4 (Tamura *et al.*, 2007) after multiple alignment of the data by CLUSTAL_X (version 1.83; Thompson *et al.*, 1997). Phylogenetic trees were constructed by the neighbour-joining and maximum-parsimony methods and distances were calculated according to Kimura's two-parameter model. The robustness of phylogenetic trees was estimated by bootstrap analysis of 1000 replicates.

Comparative 16S rRNA gene sequence analysis showed that the novel strains KMM 9015 and KMM 9018^T were closely related to each other, with a sequence similarity of 99.9 %. Their closest phylogenetic neighbours were the type strains of *Marinovum algicola* (95.8 and 95.9 % sequence identity, respectively), *Leisingera methylohalidivorans* (95.7 and 95.8 %), *Phaeobacter gallaeciensis* (94.9 and 95.0 %) and *Thalassobius mediterraneus* (96.3 and 96.2 %). Different treeing algorithms [neighbour-joining (Fig. 1) and maximum-parsimony (Supplementary Fig. S1, available in IJSEM Online)] positioned strains KMM 9015 and KMM 9018^T within the *Roseobacter* lineage of the class *Alphaproteobacteria* as a separate branch adjacent to *Marinovum algicola* [formerly *Roseobacter algicola* and *Ruegeria algicola* (Lafay *et al.*, 1995; Uchino *et al.*, 1998, 1999); reclassified by Martens *et al.* (2006)]. The low values of sequence similarity to related alphaproteobacteria demonstrated that strains KMM 9015 and KMM 9018^T could be representatives of a novel genus. The DNA–DNA relatedness between strains KMM 9015 and KMM 9018^T was found to be 71 %, supporting their assignment to the same species (Wayne *et al.*, 1987). Physiological, biochemical and chemotaxonomic characteristics of strains KMM 9015 and KMM 9018^T are given in Tables 1 and 2, Supplementary Fig. S2 and the genus and species descriptions. Strains KMM 9015 and KMM 9018^T were phenotypically identical, being Gram-negative, strictly aerobic, oxidase- and catalase-positive, non-fermentative, heterotrophic, non-motile, rod-shaped bacteria that were enlarged at one pole due to the budding process (Fig. 2). It should be mentioned that strains KMM 9015 and KMM 9018^T could grow at a relatively narrow range of pH 6.5–9.5. Both strains gave negative results for carbon source assimilation in API 32GN and API 20NE tests, but they could grow on D-glucose and most carbohydrates, organic and amino acids when they were tested by a conventional method applying

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 isolates KMM 9015 and KMM 9018^T and related genera of the class *Alphaproteobacteria*. Phylogenetic analysis was performed using the software package MEGA4 (Tamura *et al.*, 2007) after multiple alignment of the data by CLUSTAL_X (version 1.83; Thompson *et al.*, 1997). Bootstrap values based on 1000 replications are given as percentages at branching points; numbers indicate percentages greater than 70 %. Bar, 0.01 substitutions per nucleotide position.

ASW-based medium (Table 1). Chemotaxonomically, the major isoprenoid quinone was Q-10 and the polar lipids consisted of phosphatidylcholine, phosphatidylethanolamine, phosphatidylglycerol and an unknown lipid in both strains (Supplementary Fig. S2). Fatty acid analysis revealed a high content of C_{18:1}ω7c (86.85 and 85.79 %) followed by 11-methyl C_{18:1}ω7c (5.48 and 5.69 %) in both strains (Table 2).

The chemotaxonomic properties of strains KMM 9015 and KMM 9018^T (ubiquinone Q-10, the predominance of C_{18:1}ω7c, the presence of phosphatidylcholine, phosphatidylethanolamine and phosphatidylglycerol and DNA G + C contents of 60.2–61.9 mol%) are in agreement with those reported for phylogenetically related genera of the *Roseobacter* clade, class *Alphaproteobacteria*. Strains KMM 9015 and KMM 9018^T can be distinguished from their phylogenetic relatives by the presence of diphosphatidylglycerol and the identity of the hydroxy fatty acids present in trace amounts. In addition, unlike *Marinovum algicola*, strains KMM 9015 and KMM 9018^T contained C_{16:0} and a small amount of C_{17:0} (Table 2). The phylogenetic distinctiveness found for strains KMM 9015 and KMM 9018^T was supported by a combination of phenotypic characteristics that differentiate them from closely related bacteria. The two isolates could be distinguished from their closest relatives in non-motility (except *Thalassobius mediterraneus*), cellular morphology and cell division by budding, pigmentation, the ability to hydrolyse DNA, aesculin (except *Marinovum algicola*) and Tween 80 and carbon source utilization. Based on their distinctive phenotypic characteristics and phylogenetic distance, strains KMM 9015 and KMM 9018^T are considered to represent a novel genus and species, for which the name *Primorskyibacter sedentarius* gen. nov., sp. nov. is proposed.

Description of *Primorskyibacter* gen. nov.

Primorskyibacter (Pri.mor'sky.i.bac'ter. N.L. n. *Primorsky-yos* Primorsky Kray, a Far-Eastern region of the Russian Federation, where the first strains were isolated; N.L. masc. n. *bacter* rod; N.L. masc. n. *Primorskyibacter* rod isolated from Primorsky Kray).

Gram-negative, strictly aerobic, oxidase- and catalase-positive, rod-shaped bacteria that are enlarged at one pole due to cell division by budding. Chemo-organoheterotrophic. Sodium ions are essential for growth. The predominant isoprenoid quinone is Q-10. Polar lipids include phosphatidylcholine, phosphatidylethanolamine, phosphatidylglycerol, diphosphatidylglycerol and an unknown lipid. The major fatty acid is C_{18:1}ω7c, followed by 11-methyl C_{18:1}ω7c. Known strains have been isolated from marine environments. On the basis of 16S rRNA gene sequence analysis, the genus represents a separate branch within the *Alphaproteobacteria* closely related to the genera *Marinovum*, *Leisingera*, *Phaeobacter* and *Thalassobius*. The type species of the genus is *Primorskyibacter sedentarius*.

Description of *Primorskyibacter sedentarius* sp. nov.

Primorskyibacter sedentarius (se.den.ta'ri.us. L. masc. adj. *sedentarius* sedentary, non-motile).

In addition to the properties given in the genus description, the species is characterized as follows. Cells are 1.2–1.5 μm in diameter and 2.5–3.5 μm long. Non-motile. Produces whitish, opaque, smooth and shiny colonies with regular edges, 2–3 mm in diameter, on MA. Bchl *a* is not produced. Growth occurs at 0.5–8 % NaCl (w/v) and is optimal in 3–5 % NaCl. Grows in/on basal medium containing NaCl alone without any of the

Table 1. Differential characteristics of strains KMM 9015 and KMM 9018^T (*Primorskyibacter sedentarius* gen. nov., sp. nov.) and related members of the class *Alphaproteobacteria*

Strains: 1 and 2, KMM 9015 and KMM 9018^T (data from the present study); 3, *Marinovum algicola* DSM 10251^T (data from Martens *et al.*, 2006; Ruiz-Ponte *et al.*, 1998; Lafay *et al.*, 1995; Labrenz *et al.*, 1999); 4, *Leisingera methylohalidivorans* DSM 14336^T (Schaefer *et al.*, 2002; Vandecandelaere *et al.*, 2008); 5, *Leisingera aquimarina* CCUG 55860^T (Vandecandelaere *et al.*, 2008); 6, *Phaeobacter inhibens* DSM 16374^T (Martens *et al.*, 2006; Vandecandelaere *et al.*, 2008); 7, *Phaeobacter gallaeciensis* CIP 105210^T (Ruiz-Ponte *et al.*, 1998; Martens *et al.*, 2006); 8, *Phaeobacter daeponensis* TF-218^T (Yoon *et al.*, 2007; Vandecandelaere *et al.*, 2008); 9, *Thalassobius mediterraneus* CIP 108400^T (Arahal *et al.*, 2005); 10, *Thalassobius gelatinovorans* CECT 4357^T (Arahal *et al.*, 2005; Rüger & Höfle, 1992). w, Weak reaction; NG, no growth; ND, no data available.

Characteristic	1 and 2	3	4	5	6	7	8	9	10
Pigmentation*	WH	BG/PH	—	DBG/P	BR	BR	—	—	BG/BR
Bchl <i>a</i>	—	—	—	ND	—	—	—	ND	ND
Motility	—	+	+	+	+	+	+	—	+
Growth at:									
4 °C	+	—	+	+	+	—	+	—	+
37 °C	+	+	—	+	—	+	+	+	+
>37 °C	+	+	—	—	—	ND	+	—	+
Nitrate reduction	—	—	—	—	—	—	+	—	+
Utilization of:									
Glucose	+	+	—	—	+	+	+	+	—
Rhamnose	+	—	—	ND	—	—	ND	ND	—
Maltose	+	+	—	—	+	+	—	W	+
Acetate	+	—	—	ND	+	+	+	+	+
Citrate	+	+	—	—	+	—	+	+	—
Leucine	—	—	—	ND	+	+	+	W	+
L-Tyrosine	+	ND	—	—	+	—	+	—	+
Hydrolysis of:									
DNA	+	—	—	—	—	—	—	ND	ND
Aesculin	+	+	—	—	—	ND	—	ND	ND
Gelatin	—	+	—	W	—	—	—	—	+
Tween 80	+	—	—	—	—	—	—	NG	W
Starch	—	W	+	—	—	—	—	—	—
DNA G + C content (mol%)	60.2, 61.9†	60	60.5	61.4	55.7	57.6–58.0‡	64.9	57	59

*BG, Beige; BR, brown; DBG, dark beige; P, pink; PH, pinkish; WH, whitish; —, not pigmented.

†Data for KMM 9015 and KMM 9018^T, respectively.

‡Range of values for four strains, including the type strain (Ruiz-Ponte *et al.*, 1998).

sea salts components MgCl₂, KCl, CaCl₂ and MgSO₄. Grows at 4–39 °C, with optimum growth at 25–30 °C; weak growth at 40 °C, and no growth above 40 °C. The pH range for growth is 6.5–9.5, with optimum growth at pH 7.5–8.5. Negative for hydrolysis of casein, gelatin, chitin and starch and H₂S production. Positive for hydrolysis of DNA, Tweens 80, 40 and 20 and L-tyrosine. On L-tyrosine-containing medium, brown diffusible pigments are produced and a clearance zone is formed. No acid production from D-glucose, maltose, D-galactose, sucrose, lactose, D-mannose, cellobiose, D-xylose, L-arabinose, L-rhamnose, melibiose, D-ribose, fructose, L-sorbose, raffinose, N-acetylglucosamine, glycerol, *myo*-inositol or D-mannitol. In API 20NE strips, positive for the PNPG test and aesculin hydrolysis and negative for nitrate reduction, indole production, glucose acidification under anaerobic conditions, gelatin hydrolysis, arginine dihydrolase, urease and assimilation of D-glucose, L-arabinose, D-mannose, D-mannitol, N-acetylglucosamine, maltose, D-gluconate,

caprate, adipate, L-malate, citrate and phenylacetate. In ID32 GN strips, negative for assimilation of L-rhamnose, N-acetylglucosamine, D-ribose, inositol, sucrose, maltose, itaconic acid, suberic acid, sodium malonate, sodium acetate, lactic acid, L-alanine, potassium 5-ketogluconate, glycogen, 3-hydroxybenzoic acid, L-serine, D-mannitol, D-glucose, salicin, melibiose, L-fucose, D-sorbitol, L-arabinose, propionic acid, capric acid, valeric acid, trisodium citrate, L-histidine, potassium 2-ketogluconate, 3-hydroxybutyric acid, 4-hydroxybenzoic acid and L-proline. In API ZYM tests, positive for alkaline phosphatase, esterase (C4), esterase lipase (C8), leucine arylamidase, acid phosphatase and α-glucosidase, weakly positive for naphthol-AS-BI-phosphohydrolase and negative for lipase (C14), valine arylamidase, cystine arylamidase, trypsin, α-chymotrypsin, N-acetyl-β-glucosaminidase, α-galactosidase, β-galactosidase, β-glucuronidase, β-glucosidase, α-mannosidase and α-fucosidase. Positive for utilization of D-glucose, maltose, L-rhamnose, L-arabinose, sucrose, fructose, raffinose, cellobiose, D-mannitol,

Table 2. Fatty acid and polar lipid profiles of strains KMM 9015 and KMM 9018^T and related members of the class *Alphaproteobacteria*

Strains: 1, KMM 9015; 2, KMM 9018^T (data in columns 1 and 2 from the present study); 3, *Marinovum algicola* DSM 10251^T (Martens *et al.*, 2006); 4, *Leisingera methylohalidivorans* DSM 14336^T (Schaefer *et al.*, 2002); 5, *Leisingera aquimarina* CCUG 55860^T (Vandecastelaere *et al.*, 2008); 6, *Phaeobacter inhibens* DSM 16374^T (Martens *et al.*, 2006); 7, *Phaeobacter gallaeciensis* CIP 105210^T (Martens *et al.*, 2006); 8, *Phaeobacter daeponensis* TF-218^T (Yoon *et al.*, 2007); 9, *Thalassobius mediterraneus* CIP 108400^T (Arahal *et al.*, 2005); 10, *Thalassobius gelatinovorans* CECT 4357^T (Arahal *et al.*, 2005). Data for fatty acids are percentages of the total fatty acid content (–, not detected/not reported); polar lipids are indicated as present or absent. ND, No data available; ECL, equivalent chain length.

Component	1	2	3	4	5	6	7	8	9	10
Fatty acid										
C _{10:0} 3-OH	–	–	1.15	1.83	2.0	1.71	1.86	1.7	1.9	1.5
C _{12:0} 3-OH	–	–	1.64	2.27	2.1	1.59	1.27	2.6	–	5.8
C _{12:1} 3-OH	0.52	0.57	–	–	–	–	–	–	4.0	–
C _{14:1}	–	–	–	2.27	–	2.19	2.14	–	–	–
iso-C _{14:1} E	–	–	–	–	11.6	–	–	–	–	–
C _{10:0}	–	–	–	–	–	–	–	–	–	3.5
C _{12:0}	–	–	–	–	–	–	–	1.2	–	3.1
C _{16:0}	3.09	3.34	–	5.08	3.5	3.83	3.79	8.6	3.0	2.9
C _{16:0} 2-OH	–	–	–	6.97	4.2	3.10	3.90	5.6	–	–
C _{17:0}	0.95	1.52	–	–	–	–	–	0.6	–	–
C _{18:1} ω7c	86.85	85.79	86.74	70.27	71.6	73.77	75.51	57.7	84.6	68.8
C _{18:1} ω9c	–	–	0.84	2.54	–	0.76	0.89	–	–	–
11-Methyl C _{18:1} ω7c	5.48	5.69	3.17	6.86	–	7.45	6.60	16.6	–	7.5
C _{18:0}	2.92	2.81	2.73	0.97	–	3.14	2.57	2.4	1.1	1.9
cyclo C _{19:0}	–	–	–	–	–	–	–	–	–	2.3
ECL 11.798	–	–	–	–	2.7	–	–	2.3	3.6	–
Unknown	–	–	2.58	–	–	–	–	–	–	–
Polar lipid										
Phosphatidylcholine	+	+	+	–	ND	+	+	+	ND	ND
Phosphatidylethanolamine	+	+	+	+	ND	+	+	+	ND	ND
Phosphatidylglycerol	+	+	+	+	ND	+	+	+	ND	ND
Diphosphatidylglycerol	+	+	–	–	ND	–	–	–	ND	ND
Unknown aminolipid(s)	–	–	+	+	ND	+	+	+	ND	ND
Unknown phospholipid(s)	–	–	+	+	ND	+	+	+	ND	ND
Unknown lipid(s)	+	+	+	+	ND	+	+	+	ND	ND

ornithine, L-tyrosine, L-asparagine, citrate, acetate, fumarate and malate as carbon and energy sources, weakly positive for utilization of D-galactose, D-mannose, glycerol, inositol, L-arginine and L-α-alanine and negative for utilization of

Fig. 2. Phase-contrast micrograph displaying cell morphology of strain KMM 9018^T grown on MA for 2 days at 25 °C. Bar, 10 μm.

DL-leucine, DL-β-phenylalanine, DL-lysine, L-methionine and aminoacetic acid. Utilization of L-xylose is strain-dependent (type strain positive). Detailed fatty acid and polar lipid compositions are listed in Table 2. Susceptible to (amount per disc) ampicillin (10 μg), benzylpenicillin (10 U), carbenicillin (100 μg), gentamicin (10 μg), rifampicin (5 μg), streptomycin (30 μg), vancomycin (30 μg), nalidixic acid (30 μg), ofloxacin (5 μg), oxacillin (10 μg), neomycin (30 μg), oleandomycin (15 μg), erythromycin (15 μg), cephazolin (30 μg), cephalexin (30 μg), tetracycline (30 μg) and chloramphenicol (30 μg); resistant to kanamycin (30 μg), lincomycin (15 μg) and polymyxin (300 U). The DNA G+C content is 60.2–61.9 mol% (thermal denaturation method).

The type strain is strain KMM 9018^T (=NRIC 0784^T =JCM 16874^T), isolated from a sample of shallow sediment collected from the Sea of Japan, Russia. A second strain of the species, KMM 9015, was isolated from the same sample.

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