Marivita cryptomonadis gen. nov., sp. nov. and *Marivita litorea* sp. nov., of the family *Rhodobacteraceae*, isolated from marine habitats

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Two strictly aerobic, Gram-negative, rod-shaped bacteria containing photosynthesis-related genes, designated strains CL-SK44^T and CL-JM1^T, were isolated from a culture of the marine phytoplankton *Cryptomonas* sp. and coastal seawater from Korea, respectively. Phylogenetic analysis of 16S rRNA gene sequences revealed that the two strains were related to members of the genera *Thalassobius* (95.3–96.7 % similarity), *Pelagibaca* (95.3–96.0 %) and *Donghicola* (95.6 %) in the family *Rhodobacteraceae*. However, the two novel strains did not form a robust clade with any species of the *Roseobacter* clade, forming a distinct clade. The major polar lipids of the strains were phosphatidylcholine, phosphatidylglycerol, phosphatidylethanolamine, diphosphatidylglycerol, an unidentified aminolipid and an unidentified lipid, profiles that were distinguishable from those of the related genera examined. Although the level of 16S rRNA gene sequence similarity between strains CL-SK44^T and CL-JM1^T was very high (99.1 %), DNA–DNA relatedness between the strains was 13 %, suggesting that they represent genomically distinct species. In addition, the two strains could be differentiated based on the presence of a minor polar lipid, on the hydrolysis of gelatin and the utilization of carbon sources. Based on the data from the present study, strains CL-SK44^T and CL-JM1^T are considered to represent separate novel species of a new genus of the family *Rhodobacteraceae*, for which the names *Marivita cryptomonadis* gen. nov., sp. nov. (type species) and *Marivita litorea* sp. nov. are proposed. The type strains of *Marivita cryptomonadis* and *Marivita litorea* are CL-SK44^T (=KCCM 90070^T=JCM 15447^T) and CL-JM1^T (=KCCM 90071^T=JCM 15446^T), respectively.

The *Roseobacter* clade within the family *Rhodobacteraceae* is a major group in the class *Alphaproteobacteria* (Garrity *et al.*, 2005). At the time of writing, the *Roseobacter* clade comprises more than 39 genera (see List of Prokaryotic Names with Standing in Nomenclature, <http://www.bacterio.cict.fr>). Members of the *Roseobacter* clade are physiologically diverse (Buchan *et al.*, 2005); one of their distinct characteristics is aerobic anoxygenic phototrophy. Aerobic anoxygenic phototrophs were discovered by Shiba *et al.* (1979). The first described aerobic anoxygenic

phototrophs of the *Roseobacter* clade were *Roseobacter litoralis* and *Roseobacter denitrificans*, both of which contain bacteriochlorophyll *a* (Shiba, 1991). Several members containing bacteriochlorophyll *a* or genes for the photosynthetic apparatus, namely the *pufL* and *pufM* genes, which code for proteins of the photosynthetic reaction centre, have since been discovered in members of the *Roseobacter* clade (e.g. *Dinoroseobacter shibae*, *Roseovarius mucosus*, *Staleya guttiformis* and *Thalassobacter stenotrophicus*; Oz *et al.*, 2005; Biebl *et al.*, 2005a, b; Yi & Chun, 2006). In the present study, two bacteria containing the *pufL* and *pufM* genes were isolated from marine habitats and subjected to a polyphasic taxonomic analysis.

A clonal culture of the marine phytoplankton *Cryptomonas* sp. CR-MAL01 was established and maintained as described in Yih *et al.* (2004). An aliquot (100 µl) of the culture in the exponential phase was taken and spread on a marine agar 2216 (MA; Difco) plate, which was then incubated at 20 °C for 1 week. Bacterial strain CL-SK44^T

The GenBank/EMBL/DDBJ accession numbers for the 16S rRNA gene sequences of strains CL-SK44^T and CL-JM1^T are EU512919 and EU512918, respectively.

Two-dimensional thin-layer chromatograms of the polar lipids of strains CL-SK44^T and CL-JM1^T, a neighbour-joining tree derived from 16S rRNA gene sequences for strains CL-SK44^T, CL-JM1^T and most members in the family *Rhodobacteraceae*, and a table giving the cellular fatty acid composition of strains CL-SK44^T, CL-JM1^T and other phylogenetically related genera in the family *Rhodobacteraceae* are available with the online version of this paper.

was isolated and subsequently purified on MA at 20 °C four times.

Strain CL-JM1^T was isolated from coastal seawater of the east coast of Korea; an aliquot (100 µl) of seawater was taken and spread on MA, which was then incubated at 30 °C for 1 week. Strain CL-JM1^T was subsequently purified on MA at 30 °C four times. The two novel strains were maintained on MA at 30 °C as growth of strain CL-SK44^T was faster at 30 than at 20 °C. The two strains were also maintained in marine broth 2216 (MB; Difco) supplemented with 30 % (v/v) glycerol at –80 °C.

For 16S rRNA gene amplification by PCR, DNA was extracted from a single colony by a boiling method (Englen & Kelley, 2000). The crude extracts served as the DNA template for PCRs, which included *Taq* DNA polymerase (Bioneer) and primers 27F and 1492R (Lane, 1991). The PCR product was purified by using the AccuPrep PCR purification kit (Bioneer) and direct sequence determination of the purified 16S rRNA gene was performed with an Applied Biosystems automated sequencer (ABI 3730XL) at MacroGen, Seoul, Korea. The almost-complete 16S rRNA gene sequences of strains CL-SK44^T (1376 nt) and CL-JM1^T (1369 nt) were obtained and compared with available 16S rRNA gene sequences in the GenBank database by using BLASTN searches (Altschul *et al.*, 1990). The sequences of strains CL-SK44^T and CL-JM1^T were aligned manually with those of species in the family *Rhodobacteraceae*, obtained from the GenBank and Ribosomal Database Project II (Cole *et al.*, 2007) databases, by using known 16S rRNA gene secondary-structure information. Phylogenetic trees were obtained by use of the neighbour-joining (Saitou & Nei, 1987) and maximum-parsimony (Fitch, 1971) methods. An evolutionary distance matrix for the neighbour-joining method was generated according to the model of Jukes & Cantor (1969). The robustness of the tree topologies was assessed by bootstrap analyses based on 1000 replications for the neighbour-joining and maximum-parsimony methods. Alignment analysis was performed by using the jPHYDIT program (Jeon *et al.*, 2005) and phylogenetic analyses were carried out by using MEGA4 (Tamura *et al.*, 2007). Levels of genomic DNA–DNA relatedness were determined by dot-blot hybridization (Kim *et al.*, 2007b). Pre-hybridization, hybridization and detection were performed by using a DIG labelling and detection kit (Roche Molecular Biochemicals) according to the manufacturer's instructions. The experiment was repeated on different days.

Morphological and physiological tests were performed as follows. Gram-staining was conducted as described by Smibert & Krieg (1994). Motility of the cells was observed via the hanging-drop method (Suzuki *et al.*, 2001). Cell morphology and presence of flagellum were assessed by using transmission electron microscopy (EX2; JEOL). Anaerobic growth was checked on MA and ZOF medium (Lemos *et al.*, 1985) supplemented with agar (1.5 %) by using the GasPak anaerobic system (BBL) at 30 °C for

15 days. Poly-β-hydroxybutyrate granules were observed by epifluorescence microscopy (BX60; Olympus) after Nile blue A staining (Ostle & Holt, 1982).

Bacteriochlorophyll *a* production was determined in 90 % acetone extracts by using an Ultraspec 2000 spectrophotometer (Pharmacia Biotech) for cells that had been grown in MB or a defined medium (Biebl *et al.*, 2005b) either in the light (~10 µE m⁻² s⁻¹) or in the dark for 7 days at 30 °C. Attempts to induce bacteriochlorophyll *a* expression were further performed for cells that had been grown in a different defined medium (Yoon *et al.*, 2004) either in the light (~40 µE m⁻² s⁻¹), in the dark or under a light (~40 µE m⁻² s⁻¹; 12 h)/dark (12 h) cycle for 14–21 days at 30 °C. The presence of photosynthetic reaction centre genes, *pufL* and *pufM*, was determined by using PCR amplification with specific primers (Allgaier *et al.*, 2003) for strains CL-SK44^T and CL-JM1^T. *Porphyrobacter donghaensis* SW-132^T (=KCTC 12229^T; Yoon *et al.*, 2004) served as a positive control. Furthermore, the presence of *bch* genes (i.e. *bchL* and *bchX*) coding for enzymes in the bacteriochlorophyll biosynthetic pathway was determined by using PCR amplification with specific primers (Oz *et al.*, 2005) for the above strains. The PCR products for the *pufL* and *pufM* genes (~1500 nt) and the *bchL* and *bchX* genes (~350 nt) were cloned by using the pGEM Easy TA vector (Promega) and were sequenced to clarify identities.

The temperature range for growth was examined on the basis of colony formation on MA incubated at temperatures ranging from 5 to 45 °C, by using increments of 5 °C, and at 33 °C. The pH range (pH 5–11, increments of 1 pH unit) for growth was determined by assessing changes in OD₆₀₀ over the incubation period (up to 9 days) in MB at 30 °C. The final pH was adjusted by using 1 M NaOH and 1 M HCl solutions. The tolerances of strains CL-SK44^T and CL-JM1^T to sea salts (Sigma) or NaCl were determined by assessing changes in OD₆₀₀ in synthetic ZoBell broth (per litre distilled water: 5 g Bacto peptone, 1 g yeast extract and 0.1 g ferric citrate; Yi & Chun, 2004) with concentrations of 0–10 % (increments of 1 %) and 15 % (w/v) sea salts or NaCl at 30 °C.

Oxidase and catalase tests were performed according to the protocols described by Smibert & Krieg (1994). Amylase and nitrate reductase activities and degradation of Tweens 40 and 80 were determined according to Hansen & Sørheim (1991). Other enzyme activities were assayed by using API ZYM and API 20NE kits (bioMérieux) according to the manufacturer's instructions, except that the cell suspension was prepared by using artificial seawater (per litre distilled water: 24 g NaCl, 10.9 g MgCl₂·6H₂O, 4 g Na₂SO₄, 1.5 g CaCl₂·2H₂O, 0.7 g KCl, 0.2 g NaHCO₃, 0.1 g KBr, 0.027 g H₃BO₃, 0.03 g SrCl₂·6H₂O and 0.003 g NaF; Lyman & Fleming, 1940). Carbon utilization was tested by using the basal broth medium supplemented with yeast extract (per litre distilled water: 23.6 g NaCl, 0.64 g KCl, 4.53 g MgCl₂·6H₂O, 5.94 g MgSO₄·7H₂O, 1.3 g

CaCl₂ · 2H₂O, 0.2 g NaNO₃, 0.2 g NH₄Cl and 0.05 g yeast extract; Bruns *et al.*, 2001) containing 0.4 % carbon source. Strains CL-SK44^T and CL-JM1^T were incubated for 4 weeks, and carbon utilization was scored as negative when growth rate was equal to or less than that in the negative control with no carbon source. Growth rate was measured by assessing changes in OD₆₀₀.

Polar lipids were extracted by using the procedures described by Minnikin *et al.* (1984) and were identified by two-dimensional TLC followed by spraying with appropriate detection reagents (Komagata & Suzuki, 1987). The fatty acid methyl esters in whole cells of strains CL-SK44^T and CL-JM1^T grown on MA at 30 °C for 4 days were analysed by GC according to the instructions of the Microbial Identification System (MIDI) at the Korean Culture Center of Microorganisms (KCCM) in Seoul, Korea. The quinone system was determined according to Minnikin *et al.* (1984) and was analysed by HPLC as described by Collins (1985), by using *Cucumibacter marinus* CL-GR60^T (Hwang & Cho, 2008) as a reference. The DNA G + C content was analysed by HPLC (HP 100; Hewlett Packard) analysis of deoxyribonucleosides as described by Mesbah *et al.* (1989), after DNA extraction according to the method of Marmur (1961). Lambda phage DNA was used as a standard.

The level of 16S rRNA gene sequence similarity between strains CL-SK44^T and CL-JM1^T was 99.1 %. Phylogenetic analyses based on 16S rRNA gene sequences showed that strains CL-SK44^T and CL-JM1^T belonged to the *Roseobacter* clade in the family *Rhodobacteraceae* (Fig. 1). Strains CL-SK44^T and CL-JM1^T showed 95.3–96.7 % 16S rRNA gene sequence similarity to members of the genus *Thalassobius*, 95.3–96.0 % to members of the genus *Pelagibaca*, 95.6 % to members of the genus *Donghicola* and 87.0–95.3 % to the type strains of other type species of genera in the family *Rhodobacteraceae*. In spite of a high level of sequence similarity between the novel strains and the type strains of species of the genus *Thalassobius*, the novel strains did not form a robust clade with the genus *Thalassobius* or with any other recognized species in the family *Rhodobacteraceae*, but instead formed a distinct clade in the neighbour-joining and maximum-parsimony phylogenetic trees (Fig. 1 and Supplementary Fig. S1 in IJSEM Online). The level of DNA–DNA relatedness between strains CL-SK44^T and CL-JM1^T was on average 13 %, which was much lower than the level accepted as delineating separate species (Vandamme *et al.*, 1996). Based on these results, the novel strains are considered to represent two separate species in a new genus within the family *Rhodobacteraceae*.

Cells of strains CL-SK44^T and CL-JM1^T were Gram-negative, motile rods approximately 0.4–1.2 × 1.9–3.5 µm and 0.3–0.9 × 1.0–3.5 µm in size, respectively. The two strains were strictly aerobic and contained poly-β-hydroxybutyrate granules (Table 1). The *pufL* and *pufM* genes and the *bchL* and *bchX* genes were detected in both strains CL-

SK44^T and CL-JM1^T (data not shown). However, bacteriochlorophyll *a* was not detected in either strain. It is not uncommon that strains containing the *pufL* and *pufM* genes do not produce bacteriochlorophyll *a* (Allgaier *et al.*, 2003; Kim *et al.*, 2007a), probably as a result of inappropriate culture conditions employed (Biebl *et al.*, 2006). Other phenotypic characteristics of the two novel strains are given in the genus and species descriptions below and in Table 1. Most biochemical characteristics tested were similar between strains CL-SK44^T and CL-JM1^T except gelatin hydrolysis (Table 1). However, carbon source utilization patterns were significantly (six of 19 tested sources) different between the two novel strains.

The polar lipid profile of strain CL-SK44^T comprised phosphatidylcholine, phosphatidylglycerol, phosphatidylethanolamine, an unidentified aminolipid, diphosphatidylglycerol and an unidentified lipid (see Supplementary Fig. S2 in IJSEM Online). A similar polar lipid profile was detected for strain CL-JM1^T except for the presence of an additional unidentified lipid (Supplementary Fig. S2). The fatty acid profiles were generally similar between the two strains (Supplementary Table S1); the predominant fatty acids were C_{18:1ω7c} (73.5–76.1 % of the total) and 11-methyl C_{18:1ω7c} (9.0–11.4 %). The two strains had ubiquinone 10 as a major isoprenoid quinone. The DNA G + C contents of strains CL-SK44^T and CL-JM1^T were 58.6 and 61.0 mol%, respectively (Table 1).

In addition to the phylogenetic divergence of strains CL-SK44^T and CL-JM1^T from members of related genera in the family *Rhodobacteraceae*, several phenotypic and chemotaxonomic characteristics could be used to differentiate these novel strains from other related genera. Strains CL-SK44^T and CL-JM1^T could be differentiated from members of their phylogenetically closest genus *Thalassobius* by an inability to grow at 37 °C and utilization of certain carbon sources (i.e. acetate, L-arginine, citrate and succinate; Table 1). Several phenotypic characteristics (e.g. the presence of motility, inability to grow at 37 °C, inability to reduce nitrate and utilization of certain carbon sources) could be used to differentiate strains CL-SK44^T and CL-JM1^T from members of the genera *Donghicola*, *Oceanicola* and *Pelagibaca* (Table 1). The presence of an unidentified lipid and the absence of an unidentified phospholipid distinguished strains CL-SK44^T and CL-JM1^T from members of the genus *Sulfitobacter* (Table 1). Several phenotypic characteristics (e.g. the presence of motility, inability to grow at 37 °C and utilization of certain carbon sources) and chemotaxonomic characteristics (e.g. polar lipids or DNA G + C contents) differentiated strains CL-SK44^T and CL-JM1^T from members of the genera *Marinovum*, *Oceanibulbus* and *Pseudoruegeria* (Table 1). Based on data collected using a polyphasic approach, strains CL-SK44^T and CL-JM1^T are considered to represent separate novel species of a new genus, for which the names *Marivita cryptomonadis* gen. nov., sp. nov. and *Marivita litorea* sp. nov. are proposed, respectively.

Fig. 1. Neighbour-joining tree derived from 16S rRNA gene sequences for strains CL-SK44^T, CL-JM1^T and related members in the family Rhodobacteraceae; *Alteromonas marina* SW-47^T served as the outgroup. Bootstrap values (based on 1000 resamplings) are shown at branch points (only values >60% are shown). Solid circles indicate that the corresponding nodes were also recovered in the maximum-parsimony tree. Bar, 0.02 nt substitutions per site.

Description of *Marivita* gen. nov.

Marivita (Ma.ri.vi'ta. L. neut. n. *mare* the sea; L. fem. n. *vita* life; N.L. fem. n. *Marivita* sea life).

Cells are Gram-negative rods. Motile by means of a polar flagellum. Growth is strictly aerobic. Oxidase- and catalase-positive. Photosynthesis-related genes are present. The major polar lipids are phosphatidylcholine, phosphatidylglycerol, phosphatidylethanolamine, diphosphatidylglycerol, an unidentified aminolipid and an unidentified lipid. The predominant cellular fatty acids are C_{18:1}ω7c and 11-methyl C_{18:1}ω7c. The isoprenoid quinone is ubiquinone 10. The G+C content of the DNA is 58.6–61.0 mol%. Phylogenetically, the genus is a member of the family Rhodobacteraceae. The type species is *Marivita cryptomonadis*.

Description of *Marivita cryptomonadis* sp. nov.

Marivita cryptomonadis (cryp.to.mo.na'dis. N.L. gen. n. *cryptomonadis* of the generic name of the *Cryptomonas* sp. from which the type strain was isolated).

Displays the following properties in addition to those given in the genus description. After 5 days on MA plates at 30 °C, colonies are creamy and approximately 1 mm in diameter. Cells are approximately 0.4–1.2 μm wide and 1.9–3.5 μm long. Grows at 15–35 °C (optimum, 30 °C) and pH 6–10 (optimum, pH 7–9). Growth occurs at sea salt concentrations of 2–10% (w/v) (optimum, 3–5%), but no growth occurs in media containing NaCl as the only salt. Cells contain poly-β-hydroxybutyrate granules. Amylase is not produced. Tweens 40 and 80 are hydrolysed. Nitrate is not reduced to nitrite. Positive for the

Table 1. Selected differential characteristics between strains CL-SK44^T and CL-JM1^T and related taxa in the family *Rhodobacteraceae*

Taxa: 1, strain CL-SK44^T; 2, strain CL-JM1^T; 3, *Thalassobius gelatinovorans* (data from Rüger & Höfle, 1992; Arahall *et al.*, 2005); 4, *Thalassobius aestuarii* (Yi & Chun, 2006); 5, *Thalassobius mediterraneus* (Arahall *et al.*, 2005); 6, *Donghicola eburneus* (Yoon *et al.*, 2007a); 7, *Oceanicola* (Cho & Giovannoni, 2004; Gu *et al.*, 2007; Lin *et al.*, 2007); 8, *Sulfitobacter* (Pukall *et al.*, 1999; Labrenz *et al.*, 2000; Ivanova *et al.*, 2004; Park *et al.*, 2007; Yoon *et al.*, 2007b); 9, *Pelagibaca bermudensis* (Cho & Giovannoni, 2006); 10, *Marinovum algicola* (Lafay *et al.*, 1995; Martens *et al.*, 2006); 11, *Oceanibulbus indolifex* (Wagner-Döbler *et al.*, 2004); 12, *Pseudoruegeria aquimaris* (Yoon *et al.*, 2007c). +, Positive; −, negative; v, variable; w, weakly positive; NA, data not available.

Characteristic	1	2	3	4	5	6	7	8	9	10	11	12
Cell morphology	Rod-shaped	Rod-shaped	Coccoid to rod-shaped	Ovoid	Coccoid to rod-shaped	Coccoid or rod-shaped	Short rod-shaped	Rod-shaped	Short rod-shaped or ovoid	Ovoid rod-shaped	Irregular rod-shaped	Rod-shaped
Colony colour	Creamy	Creamy	Beige	Creamy	Non-pigmented	Ivory	Faint-yellowish, cream whitish	Slightly yellowish, greyish yellow, beige, creamy	Creamy	Beige, pinkish beige	Whitish	Greyish yellow
Motility	+	+	+	−	−	−	−	v	−	+	−	−
Growth at:												
4 °C	−	−	+	−	−	−	v	v	−	−	−	−
37 °C	−	−	+	NA*	+	+	+	v	+	+	−	+
Nitrate reduction	−	−	+	−	−	+	v	v	+	−	−	−
Hydrolysis of:												
Starch	−	−	−	−	−	−	−	v	NA	w	−	−
Gelatin	+	−	+	+	−	−	−	v	+	+	−	−
Poly-β-hydroxybutyrate	+	+	+	+	+	NA	+	+	−	−	+	NA
Utilization of:												
Acetate	−	−	+	+	+	+	+	v	NA	v	−	+
L-Arginine	−	−	+	+	+	NA	v	NA	+	v	NA	NA
Cellobiose	+	−	−	−	−	+	v	v	+	−	NA	+
Citrate	−	−	+	+	+	−	+	v	+	+	+	+
D-Fructose	−	−	+	−	+	+	v	v	+	+	NA	+
D-Galactose	+	−	NA	−	NA	+	+	v	−	−	NA	+
D-Glucose	+	−	v	+	+	+	v	v	+	+	+	+
myo-Inositol	−	−	+	−	+	NA	v	NA	−	NA	NA	NA
Lactose	+	−	−	−	−	NA	v	+	NA	−	NA	NA
D-Mannitol	−	−	+	−	+	NA	v	v	+	v	+	NA
D-Mannose	−	−	NA	−	NA	+	v	v	+	−	NA	+
Succinate	−	−	+	+	+	+	v	v	+	−	+	+
Sucrose	−	−	+	−	+	−	v	v	+	NA	NA	+
Trehalose	+	−	−	−	NA	−	v	v	+	+	−	+
Major polar lipids†	PC, PG, PE, DPG, AL, L	PC, PG, PE, DPG, AL, L	NA	NA	NA	NA	NA	PC, PG, PE, DPG, AL, PL	NA	PC, PG, PE, AL, PL, L	PC, PG, PE, DPG, AL	PG, PE, DPG, PL, GL
DNA G + C content (mol%)	58.6	61.0	59	61	57	59.7	64.7–71.5	55.0–63.7	65.4	60	60.1	67.0

*Growth occurred at 35 °C but not at 40 °C (Yi & Chun, 2006).

†AL, an unidentified aminolipid; DPG, diphosphatidylglycerol; GL, an unidentified glycolipid; L, an unidentified lipid PC, phosphatidylcholine; PE, phosphatidylethanolamine; PG, phosphatidylglycerol; PL, an unidentified phospholipid.

following enzyme activities as tested with the API ZYM system: alkaline phosphatase, acid phosphatase and leucine arylamidase. Weakly positive for esterase (C4), esterase lipase (C8), naphthol-AS-BI-phosphohydrolase and valine arylamidase, but negative for *N*-acetyl- β -glucosaminidase, α -chymotrypsin, cystine arylamidase, α -fucosidase, α -galactosidase, β -galactosidase, α -glucosidase, β -glucosidase, β -glucuronidase, lipase (C14), α -mannosidase and trypsin. Positive for the following enzyme activities as tested with the API 20NE system: aesculin hydrolysis, β -galactosidase (PNPG) and gelatinase. Negative for indole production, nitrate reductase and urease. Utilizes L-arabinose, D-cellobiose, D-galactose, D-glucose, lactose, trehalose and xylose, but not acetate, L-arginine, citrate, D-fructose, glycerol, *myo*-inositol, D-mannitol, D-mannose, L-ornithine, L-rhamnose, D-salicin, sorbitol, succinate or sucrose as sole carbon source.

The type strain, CL-SK44^T (=KCCM 90070^T=JCM 15447^T), was isolated from a culture of the marine phytoplankton *Cryptomonas* sp.

Description of *Marivita litorea* sp. nov.

Marivita litorea (li.to're.a. L. fem. adj. *litorea* of the shore).

Displays the following properties in addition to those given in the genus description. After 5 days on MA plates at 30 °C, colonies are creamy and approximately 1 mm in diameter. Cells are approximately 0.3–0.9 μ m wide and 1.0–3.5 μ m long. Grows at 15–33 °C (optimum, 30 °C) and pH 6–10 (optimum, pH 7–8). Growth occurs at sea salt concentrations of 1–10 % (w/v) (optimum, 3–5 %), but no growth occurs in media containing NaCl as the only salt. Cells contain poly- β -hydroxybutyrate granules. Amylase is not produced. Tweens 40 and 80 are hydrolysed. Nitrate is not reduced to nitrite. Positive for the following enzyme activities as tested with the API ZYM system: esterase lipase (C8) and leucine arylamidase. Weakly positive for alkaline phosphatase, acid phosphatase, esterase (C4), naphthol-AS-BI-phosphohydrolase and valine arylamidase, but negative for *N*-acetyl- β -glucosaminidase, α -chymotrypsin, cystine arylamidase, α -fucosidase, α -galactosidase, β -galactosidase, α -glucosidase, β -glucosidase, β -glucuronidase, lipase (C14), α -mannosidase and trypsin. Positive for the following enzyme activities as tested with the API 20NE system: aesculin hydrolysis and β -galactosidase (PNPG). Negative for gelatinase, indole production, nitrate reductase and urease. Acetate, L-arabinose, L-arginine, cellobiose, citrate, D-fructose, D-galactose, D-glucose, glycerol, *myo*-inositol, lactose, D-mannitol, D-mannose, L-ornithine, L-rhamnose, D-salicin, sorbitol, succinate, sucrose, trehalose and xylose are not utilized as sole carbon source. In addition to the polar lipids listed in the genus description, a minor amount of an additional unidentified lipid is present.

The type strain, CL-JM1^T (=KCCM 90071^T=JCM 15446^T), was isolated from coastal seawater of Korea.

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