Maritalea porphyrae sp. nov., isolated from a red alga (*Porphyra yezoensis*), and transfer of *Zhangella mobilis* to *Maritalea mobilis* comb. nov.

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Three Gram-negative, motile, aerobic bacteria were isolated from cultures of the marine red alga *Porphyra yezoensis*. Phylogenetic analysis based on 16S rRNA gene sequences revealed that the novel strains were closely related to *Maritalea myrionectae* CL-SK30^T (97.9% 16S rRNA gene sequence similarity) and *Zhangella mobilis* E6^T (96.2%). 16S rRNA gene sequence similarity between *Z. mobilis* E6^T and *M. myrionectae* CL-SK30^T was 97.9%. The DNA G + C contents of the isolates (49.4–50.0 mol%) were similar to those of *M. myrionectae* DSM 19524^T (52.3 mol%) and *Z. mobilis* JCM 15144^T (50.3 mol%). From these results, it was difficult to differentiate the genus *Zhangella* from the genus *Maritalea*. DNA–DNA hybridization demonstrated that the isolates belonged to a single species. The isolates could also be distinguished from *M. myrionectae* and *Z. mobilis* on the basis of chemotaxonomic and phenotypic features, including fatty acid composition (particularly C_{16:1ω7c}), growth with 6–9% (w/v) NaCl, carbon utilization, oxidation patterns and so on. A novel species of the genus *Maritalea* is proposed to accommodate the three isolates, with the name *Maritalea porphyrae* sp. nov. The type strain is LCM-3^T (=LMG 25872^T=NBRC 107169^T). Furthermore, it is proposed that *Zhangella mobilis* should be transferred from the genus *Zhangella* to the genus *Maritalea*, with the name *Maritalea mobilis* comb. nov. (type strain E6^T=CGMCC 1.7002^T=JCM 15144^T).

The family *Hyphomicrobiaceae* is a member of the order *Rhizobiales* within the class *Alphaproteobacteria* and at the time of writing consists of 18 genera (Garrity *et al.*, 2005; Lee *et al.*, 2005; Hwang & Cho, 2008; Hwang *et al.*, 2009; Xu *et al.*, 2009). Most of the species belonging to this family have been isolated from various non-marine habitats, such as soil and freshwater (Garrity *et al.*, 2005). Recently, *Cucumibacter marinus*, *Maritalea myrionectae* and *Zhangella mobilis* have been isolated from marine environments, such as coastal seawater and a marine ciliate culture (Hwang & Cho, 2008; Hwang *et al.*, 2009; Xu *et al.*, 2009). *M. myrionectae* and *Z. mobilis* were separately proposed as novel species, each in a different genus, on the

basis of DNA G + C content differentiating them from *C. marinus* (Hwang & Cho, 2008; Hwang *et al.*, 2009; Xu *et al.*, 2009). However, as the descriptions of *M. myrionectae* and *Z. mobilis* were published at about the same time, their biochemical and physiological traits were not compared and the distinction between them at the genus level has remained unclarified. During a study on the bacterial flora associated with the red alga *Porphyra yezoensis*, several strains, including LCM-3^T, SCM-20 and SNM-9, were isolated. Phylogenetic analysis based on 16S rRNA gene sequences indicated that strains LCM-3^T, SCM-20 and SNM-9 belonged to a novel species that was phylogenetically related to *M. myrionectae* and *Z. mobilis*. The aim of this study was to characterize these three isolates and consider the reclassification of *Z. mobilis*.

Thalli of *P. yezoensis* were cultured in sterile modified half-strength SWM-III medium (Ogata, 1970) at 17 °C for 1 week and then the thalli and used media were incubated

The GenBank/EMBL/DDBJ accession numbers for the 16S rRNA gene sequences of strains LCM-3^T, SCM-20 and SNM-9 are AB583774, AB583775 and AB583776, respectively.

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

on marine agar 2216 (MA; Difco) at 20 °C for 2 weeks. Twenty colonies were randomly selected from each plate and purified by three subcultivations on MA at 20 °C. Strain LCM-3^T was isolated from a thallus surface and strains SCM-20 and SNM-9 were isolated from two different samples of used medium. *M. myrionectae* DSM 19524^T and *Z. mobilis* JCM 15144^T were also genetically, phenotypically and chemotaxonomically characterized in this study. All strains were maintained on MA at 30 °C and stored at -80 °C in marine broth 2216 (MB; Difco) containing 20 % (v/v) glycerol.

DNA was prepared by the method of Johnson (1981). The 16S rRNA genes of strains LCM-3^T, SCM-20 and SNM-9 were amplified using the universal primers 27F and 1492R (Weisburg *et al.*, 1991). The almost-complete 16S rRNA gene sequences (approximately 1357 bp, corresponding to positions 45–1404, *Escherichia coli* ATCC 11775^T) were determined using four sequencing primers, 27F, 800F, 760R and 1492R (Satomi *et al.*, 1997) using an automated DNA sequencer (model 3100; Applied Biosystems). The sequences were compared with those in the public databases using the BLASTN algorithm (Altschul *et al.*,

1990) and were aligned with related sequences using CLUSTAL_X (Thompson *et al.*, 1997). Phylogenetic trees were constructed using three methods of analysis. A neighbour-joining tree was constructed using MEGA version 4 (Tamura *et al.*, 2007) with distances calculated according to Kimura's two-parameter model (Kimura, 1980). Alignment gaps and ambiguous bases were not taken into consideration and the complete deletion option was used. Bootstrap analysis was performed with 1000 replications. Maximum-likelihood and maximum-parsimony trees were constructed using PHYLIP version 3.69 (Felsenstein, 2009).

The neighbour-joining phylogenetic tree (Fig. 1) shows that the three isolates belonged to a cluster in the family Hyphomicrobiaceae that also contained *M. myrionectae* CL-SK30^T and *Z. mobilis* E6^T, which was supported by a high bootstrap value (100 %). The cluster was also recovered in the maximum-likelihood and maximum-parsimony trees. Thus the phylogenetic analysis indicated that the three isolates and *Z. mobilis* E6^T belonged to the genus *Maritalea*. 16S rRNA gene sequence similarity among the three isolates was 100 % and was 97.9 and 96.2 % between the isolates and *M. myrionectae* CL-SK30^T

Fig. 1. Neighbour-joining phylogenetic tree based on 16S rRNA gene sequences showing the relationships of *Maritalea porphyrae* sp. nov. and *Maritalea mobilis* comb. nov. with closely related taxa in the family Hyphomicrobiaceae. Bootstrap values (>50 %) based on 1000 replications are shown at branch nodes. Filled circles indicate that the corresponding nodes were recovered in the trees generated using the maximum-parsimony and maximum-likelihood algorithms. Open circles indicate that the corresponding nodes were recovered in the tree generated using the maximum-likelihood algorithm ($P < 0.01$). *Escherichia coli* ATCC 11775^T was used as an outgroup. Bar, 0.02 % sequence divergence.

and *Z. mobilis* E6^T, respectively. 16S rRNA gene sequence similarity between *Z. mobilis* E6^T and *M. myrionectae* CL-SK30^T was 97.9 %.

The G + C content of the DNA was measured using HPLC (Tamaoka & Komagata, 1984). DNA–DNA hybridization was performed using the microplate hybridization method (Ezaki *et al.*, 1989) and photobiotin-labelled DNA from strain LCM-3^T, *M. myrionectae* DSM 19524^T and *Z. mobilis* JCM 15144^T. DNA–DNA relatedness was calculated as the mean of triplicate measurements. The G + C content and DNA–DNA relatedness are shown in Table 1. The DNA G + C contents of the three isolates were 49.4–50.0 mol%. These values were similar to those of *M. myrionectae* DSM 19524^T (52.3 mol%) and *Z. mobilis* JCM 15144^T (50.3 mol%) but more than 10 mol% lower than that of *C. marinus* CL-GR60^T (62.9 mol%) (Hwang & Cho, 2008); thus, a distinct genetic difference at the genus level between *C. marinus* CL-GR60^T and the strains tested in this study was confirmed (Stackebrandt & Liesack, 1993). DNA–DNA relatedness between strain LCM-3^T and strains SCM-20 and SNM-9 was high (92.0–98.2 %), which indicated that the three isolates belonged to the same species (Wayne *et al.*, 1987). On the other hand, strain LCM-3^T was clearly shown to belong to a species different from those of *M. myrionectae* DSM 19524^T (6.9 % DNA–DNA relatedness) and *Z. mobilis* JCM 15144^T (6.4 %). Between *M. myrionectae* DSM 19524^T and *Z. mobilis* JCM 15144^T, 28.7–29.6 % DNA–DNA relatedness was observed, which suggested that these two strains belonged to different species.

Unless otherwise indicated, cultivation for the following tests was conducted at 30 °C on MA or in MB for 3 days. Cell morphology, including flagellum and bud formation, was observed by transmission electron microscopy (JEM-1200EX II; JEOL), with cells negatively stained with 1.0 % (w/v) uranyl acetate (Supplementary Fig. S1, available in IJSEM Online). Gram-staining (Merck), motility and gliding motility (Bowman, 2000) were observed by light microscopy (BX50; Olympus). Poly-β-hydroxybutyrate granules were stained with Nile blue A and observed by epifluorescence microscopy (Ostle & Holt, 1982). Bacteriochlorophyll *a* was extracted with acetone/methanol (7:2, v/v) (Biebl *et al.*, 2005) and the absorption spectrum was determined using a

Hitachi U-2000A spectrophotometer. Colony morphology and pigmentation were observed on MA. The following phenotypic tests were determined after incubation at 30 °C for 2 weeks. Aerobic growth was determined on MA using the AnaeroPack system (Mitsubishi Gas Chemical). Growth at 0–45 °C (at intervals of 5 °C) was determined on MA for 2 weeks. Growth at pH 4.0–10.0 (at intervals of one pH unit) was determined in MB with the pH adjusted with solutions of NaOH and HCl (both 1 M). After autoclaving, the pH of medium subsamples was measured and the medium was adjusted with filter-sterilized solutions as necessary. Growth with 0–10 (at intervals of 1 %) and 15 % (w/v) NaCl was determined on a medium made with NaCl-free artificial seawater (ASW; containing 1^{−1} distilled water: 30 g NaCl, 0.7 g KCl, 5.3 g MgSO₄·7H₂O, 10.8 g MgCl₂·6H₂O, 1.3 g CaSO₄·2H₂O) and (1^{−1}) 5.0 g peptone and 1.0 g yeast extract. Oxidase and catalase activities were assayed using oxidase reagent (bioMérieux) and 3 % H₂O₂, respectively. Methyl red and Voges–Proskauer reactions were determined on VP-MR medium (Nissui Pharmaceutical). H₂S production was determined with SIM medium (Eiken Chemical). Hydrolysis of agar, alginate, DNA, starch and Tweens 20, 40 and 80 was determined using MA as the basal medium (Sawabe *et al.*, 1995). Other biochemical tests were carried out using the API 20 NE, API ZYM and API 50 CH systems (bioMérieux), according to the manufacturer's instructions except that cells were suspended in 75 % ASW. The results with API 20 NE and API ZYM were recorded after 2 weeks and 1 day, respectively. Carbon utilization tests (API 50 CH) were conducted with basal medium broth supplemented with 0.025 % (w/v) yeast extract (Baumann *et al.*, 1972) and recorded after 3 weeks. Acid production tests (API 50 CH) were performed using a medium containing equal amounts of CHB/E medium (bioMérieux) and ASW and were recorded after 1 week. Antibiotic susceptibility was tested with the diffusion plate assay, using MA and commercial antibiotics (Eiken Chemical, Becton Dickinson) or filter-paper discs impregnated with various antibiotics. Susceptibility was recorded for zone diameters above 10 mm after incubation at 30 °C for 2 weeks (Alain *et al.*, 2008).

The main phenotypic features of the three isolates and *Z. mobilis* JCM 15144^T, such as Gram-negative, rod-shaped

Table 1. DNA G + C content of and DNA–DNA relatedness between the isolates and their closest phylogenetic neighbours

Strain	DNA G + C content (mol%)	Hybridization (%) with biotinylated DNA from:		
		1	4	5
1. <i>M. porphyrae</i> sp. nov. LCM-3 ^T	49.6	100.0	7.6	6.4
2. <i>M. porphyrae</i> sp. nov. SCM-20	50.0	92.0	7.0	7.9
3. <i>M. porphyrae</i> sp. nov. SNM-9	49.4	98.2	9.9	9.6
4. <i>M. myrionectae</i> DSM 19524 ^T	52.3	6.9	100.0	29.6
5. <i>M. mobilis</i> comb. nov. JCM 15144 ^T	50.3	6.4	28.7	100.0

cells, motility, aerobic growth and oxidase and catalase activities, corresponded with those of the genus *Maritalea*. Table 2 shows the phenotypic features that differentiated the isolates, *M. myrionectae* DSM 19524^T and *Z. mobilis* JCM 15144^T. The isolates were phenotypically similar to each other and showed differences in only 11 traits (utilization and acid production of 10 carbon compounds). Between species, strain LCM-3^T was most phenotypically similar to *M. myrionectae* DSM 19524^T and *Z. mobilis* JCM 15144^T was most phenotypically similar to *M. myrionectae* DSM 19524^T, but the differences, such as conditions for growth, carbon utilization, oxidation patterns and so on, were observed (Table 2).

Polar lipids were extracted after cultivation on MA at 30 °C for 72 h, according to the method described by Minnikin *et al.* (1984). After two-dimensional TLC, lipids were identified by spraying with the appropriate detection reagents (Minnikin *et al.*, 1984; Komagata & Suzuki, 1987). Isoprenoid quinones were extracted after incubation for 3 days in MB with chloroform/methanol (2:1, v/v) and were analysed by HPLC (Akagawa-Matsushita *et al.*, 1992). Methyl esters of cellular fatty acids were prepared using cells cultured on MA at 30 °C for 72 h, according to Ikemoto *et al.* (1978) with 5 % HCl in methanol at 100 °C for 3 h. The fatty acids were analysed using a gas chromatograph equipped with a flame-ionization detector (GC-2010; Shimadzu) and a capillary column (Omegawax 320; Supelco) and were identified by comparing the sample retention times with those of a standard (Supelco). Furthermore, the major fatty acids (>1 % of the total) were identified with GC-MS (GC-17A, QP-5000; Shimadzu) after formation of oxazoline derivatives (Yu *et al.*, 1989).

The polar lipid profiles of the three isolates, *M. myrionectae* DSM 19524^T and *Z. mobilis* JCM 15144^T are shown in Supplementary Fig. S2. The major polar lipids of all strains were an unidentified amino lipid, two unidentified glycolipids, phosphatidylglycerol and an unidentified lipid (L4). The minor polar lipids of all strains were phosphatidylethanolamine and three unidentified lipids (L1, L2 and L3). Diphosphatidylglycerol was detected in all strains, but was present in lesser amounts in the novel isolates in comparison with *M. myrionectae* DSM 19524^T and *Z. mobilis* JCM 15144^T. An unidentified phospholipid was detected only in *M. myrionectae* DSM 19524^T and *Z. mobilis* JCM 15144^T and two unidentified lipids (L5 and L6) were detected only in the isolates. The major isoprenoid quinone of all strains was ubiquinone-10 (Q-10), which is characteristic of many members in the class *Alphaproteobacteria* (Martens *et al.*, 2006; Alain *et al.*, 2008). The cellular fatty acid compositions are shown in Table 3. The predominant fatty acid in all strains was C_{18:1}ω7c (68.8–74.6 % in the isolates, 71.5 % in *M. myrionectae* DSM 19524^T and 70.3 % in *Z. mobilis* JCM 15144^T). The presence of C_{18:1}ω7c is a typical trait of members of the class *Alphaproteobacteria* (Alain *et al.*, 2008). All strains contained moderate amounts of C_{16:0}, C_{18:0} and 11-methyl C_{18:1}ω7c, but the proportions of 11-methyl C_{18:1}ω7c were lower in the isolates (5.3–6.7 %)

Table 2. Phenotypic characteristics that distinguish the novel strains from their closest phylogenetic neighbours

Strains: 1, *Maritalea porphyrae* sp. nov. LCM-3^T; 2, *M. porphyrae* sp. nov. SCM-20; 3, *M. porphyrae* sp. nov. SNM-9; 4, *M. myrionectae* DSM 19524^T; 5, *M. mobilis* comb. nov. JCM 15144^T. +, Positive; –, negative; R, resistant; S, susceptible.

Characteristic	<i>M. porphyrae</i> sp. nov.				
	1	2	3	4	5
Growth at/with:					
5 °C	–	–	–	+	–
pH 9.0	–	–	–	+	+
6–9 % NaCl	–	–	–	+	+
10 % NaCl	–	–	–	–	+
Hydrolysis of:					
DNA	–	–	–	+	+
Tween 80	+	+	+	–	–
Enzymes (API ZYM)					
β-Galactosidase	–	–	–	+	+
α-Glucosidase	–	–	–	+	+
N-Acetyl-β-glucosaminidase	–	–	–	–	+
Utilization of (API 50 CH):					
D-Arabinose	–	+	–	–	+
L-Arabinose	–	+	+	+	–
Ribose	+	–	+	+	+
D-Xylose	+	+	+	+	–
Fructose	+	+	+	–	+
Rhamnose	–	–	–	+	–
Mannitol	+	+	+	–	–
Sorbitol	+	+	+	–	–
Amygdalin	+	–	+	+	+
Maltose	+	+	+	+	–
Melibiose	+	+	+	–	–
Sucrose	–	+	–	–	–
Trehalose	–	+	–	–	–
Turanose	+	+	+	–	–
D-Lyxose	–	–	–	+	+
L-Fucose	–	+	+	+	+
D-Arabitol	+	+	+	–	–
2-Ketogluconate	–	+	+	+	+
Acid from (API 50 CH):					
D-Arabinose	–	–	–	–	+
L-Arabinose	+	–	–	+	+
D-Xylose	+	+	+	+	–
Rhamnose	–	–	–	+	–
Mannitol	+	+	+	–	–
Sorbitol	+	+	+	–	–
N-Acetylglucosamine	+	+	+	–	–
Cellobiose	+	+	+	–	+
Lactose	–	–	+	–	–
Melibiose	+	+	+	–	+
Gentiobiose	–	+	+	–	+
D-Arabitol	+	+	+	–	–
Susceptibility to:					
Norfloracin (10 µg)	S	S	S	S	R

Table 3. Cellular fatty acid compositions of the novel strains and their closest phylogenetic neighbours

Strains: 1, *M. porphyrae* sp. nov. LCM-3^T; 2, *M. porphyrae* sp. nov. SCM-20; 3, *M. porphyrae* sp. nov. SNM-9; 4, *M. myrionectae* DSM 19524^T; 5, *M. mobilis* comb. nov. JCM 15144^T. ECL, Equivalent chain-length; ND, not detected.

Fatty acid (%)	1	2	3	4	5
C _{16:0}	4.4	4.2	6.2	4.1	3.0
C _{17:0}	0.9	0.7	1.3	1.2	2.2
C _{18:0}	5.3	5.0	5.0	7.3	5.5
C _{16:1} ω7c	7.1	7.5	8.5	0.5	0.6
C _{18:1} ω7c	72.0	74.6	68.8	71.5	70.3
11-Methyl C _{18:1} ω7c	6.7	5.3	6.5	13.9	13.1
anteiso-C _{15:0}	0.6	0.6	0.7	0.9	1.1
Unknown ECL 19.380	ND	ND	ND	ND	1.4

in comparison with *M. myrionectae* DSM 19524^T (13.9%) and *Z. mobilis* JCM 15144^T (13.1%). In contrast, the proportions of C_{16:1}ω7c were higher in the isolates (7.1–8.5%) in comparison with *M. myrionectae* DSM 19524^T (0.5%) and *Z. mobilis* JCM 15144^T (0.6%).

In conclusion, the 16S rRNA gene sequence analysis and DNA G+C contents demonstrated that the three isolates and *Z. mobilis* should be considered as members of the genus *Maritalea*. Furthermore, strains LCM-3^T, SCM-20 and SNM-9 should be assigned as representatives of a novel species, with the name *Maritalea porphyrae* sp. nov. We also propose the transfer of *Zhangella mobilis* to another novel species of the genus *Maritalea*, with the name *Maritalea mobilis* comb. nov.

Description of *Maritalea porphyrae* sp. nov.

Maritalea porphyrae (por.phy'ra.e. N.L. gen. n. *porphyrae* of *Porphyra*, from *Porphyra yezoensis*, the scientific name of the red alga from which the species was first isolated).

Cells are Gram-negative-staining rods, approximately 0.42 µm wide and 1.58 µm long ($n=30$) with a single polar flagellum. Gliding motility is not observed. Bud formation, poly-β-hydroxybutyrate accumulation and bacteriochlorophyll *a* are absent. Colonies on MA are circular, convex, entire, creamy and approximately 0.4 mm in diameter ($n=30$). Growth is aerobic. Grows at 10–40 °C (optimum 30 °C), but not at 5 or 45 °C, at pH 5.0–8.0 (optimum pH 7.0), but not at pH 4.0 or 9.0, and with 1–5% (w/v) NaCl (optimum 2% NaCl), but not with 0 or 6% NaCl. Positive for oxidase, catalase and nitrate reduction, but negative for methyl red and Voges–Proskauer tests and H₂S and indole production. Hydrolyses Tween 80, aesculin and gelatin, but does not hydrolyse agar, alginate, DNA, starch or Tweens 20 or 40. With API ZYM, the type strain is positive in tests for alkaline phosphatase, esterase, esterase lipase, lipase, leucine arylamidase, valine arylamidase, cystine arylamidase, trypsin, chymotrypsin, acid phosphatase and naphthol-AS-BI-phosphohydrolase, but gives a negative result for

α- and β-galactosidase, β-glucuronidase, α- and β-glucosidase, N-acetyl-β-glucosaminidase, α-mannosidase and α-fucosidase. With API 50 CH, the type strain is positive for utilization of glycerol, ribose, D-xylose, galactose, glucose, fructose, mannose, mannitol, sorbitol, N-acetylglucosamine, amygdalin, arbutin, aesculin, salicin, cellobiose, maltose, melibiose, glycogen, gentiobiose, turanose, D-arabitol and 5-ketogluconate, but negative for utilization of erythritol, D-arabinose, L-arabinose, L-xylose, adonitol, methyl β-D-xylopyranoside, sorbose, rhamnose, dulcitol, inositol, methyl α-D-mannopyranoside, methyl α-D-glucopyranoside, lactose, sucrose, trehalose, inulin, melezitose, raffinose, starch, xylitol, D-lyxose, D-tagatose, D-fucose, L-fucose, L-arabitol, gluconate and 2-ketogluconate. With API 50 CH, the type strain produces acid from glycerol, L-arabinose, D-xylose, galactose, glucose, mannose, mannitol, sorbitol, N-acetylglucosamine, aesculin, ferric citrate, salicin, cellobiose, maltose, melibiose, sucrose, trehalose, turanose, D-lyxose, D-fucose, L-fucose and D-arabitol, but not from erythritol, D-arabinose, ribose, L-xylose, adonitol, methyl β-D-xylopyranoside, fructose, sorbose, rhamnose, dulcitol, inositol, methyl α-D-mannopyranoside, methyl α-D-glucopyranoside, amygdalin, arbutin, lactose, inulin, melezitose, raffinose, starch, glycogen, xylitol, gentiobiose, D-tagatose, L-arabitol, gluconate, 2-ketogluconate or 5-ketogluconate. Susceptible to (µg per disc unless otherwise stated) chloramphenicol (30), erythromycin (15), gentamicin (10), tetracycline (30), norfloxacin (10), ampicillin (10), novobiocin (30), neomycin (30), penicillin G (10 U), rifampicin (5), vancomycin (30), carbenicillin (100) and ciprofloxacin (5), but resistant to nalidixic acid (30), streptomycin (10), kanamycin (30) and polymyxin B (300 U). The major polar lipids are an unidentified amino lipid, two unidentified glycolipids, phosphatidylglycerol and an unidentified lipid. The isoprenoid quinone is Q-10. The major cellular fatty acids are C_{18:1}ω7c, C_{16:1}ω7c, 11-methyl C_{18:1}ω7c, C_{18:0} and C_{16:0}.

The type strain, LCM-3^T (=LMG 25872^T=NBRC 107169^T), was isolated from the surface of a thallus of the red alga *P. yezoensis*. Other strains are SCM-20 (=LMG 25873=NBRC 107170) and SNM-9 (=LMG 25874=NBRC 107171). The DNA G+C content of the type strain is 49.6 mol%.

Description of *Maritalea mobilis* comb. nov.

Maritalea mobilis (mo'bi.lis. L. fem. adj. *mobilis* motile, pertaining to the motility of the type strain).

Basonym: *Zhangella mobilis* Xu *et al.* 2009.

The description of *Maritalea mobilis* is the same as that for *Zhangella mobilis* (Xu *et al.*, 2009). The type strain is E6^T (=CGMCC 1.7002^T=JCM 15144^T), isolated from coastal seawater of Tianjin, China.

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