Postechiella marina gen. nov., sp. nov., isolated from seawater

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A Gram-staining-negative, strictly aerobic, non-motile, yellow-pigmented bacterium, designated strain M091^T, was isolated from seawater at Damupo beach in Pohang, Republic of Korea, and investigated using a polyphasic taxonomic approach. The novel strain grew optimally at 25 °C, pH 7.0–8.0, and in the presence of 3 % (w/v) NaCl. In a phylogenetic analysis based on 16S rRNA gene sequences, strain M091^T formed a lineage within the family *Flavobacteriaceae* that was distinct from the most closely related genera of *Flaviramulus* (95.1 % sequence similarity), *Algibacter* (94.9–93.9 %), *Mariniflexile* (94.8–94.2 %), *Winogradskyella* (94.8–93.2 %), *Lacinutrix* (94.7–93.8 %) and *Tamlana* (94.7–92.9 %). The polar lipid profile of the novel strain comprised phosphatidylethanolamine, two unidentified aminolipids, one unidentified phospholipid and seven unidentified lipids. The predominant cellular fatty acids were iso-C_{15:0} (20.5 %), iso-C_{17:0} 3-OH (15.4 %), iso-C_{15:0} 3-OH (12.4 %), C_{15:0} (10.9 %) and iso-C_{15:1} G (9.9 %). The genomic DNA G+C content of strain M091^T was 34.4 mol% and the major respiratory quinone was MK-6. Based on phenotypic and genotypic data, strain M091^T represents a new genus and novel species in the family *Flavobacteriaceae*, for which the name *Postechiella marina* gen. nov., sp. nov. is proposed. The type strain of the type species is M091^T (=KCTC 23537^T=JCM 17630^T).

The family *Flavobacteriaceae* was first proposed by Jooste (1985) and subsequently described and emended by Bernardet *et al.* (1996, 2002). This family is one of the major phylogenetic lineages within the phylum *Bacteroidetes* (Garrity & Holt, 2001). At the time of writing, the family comprised more than 90 recognized genera (<http://www.bacterio.cict.fr/>). Many members of this family were isolated from various marine environments and Antarctic habitats (Bowman *et al.*, 1997, 1998; Bowman, 2000; Bowman & Nichols, 2002, 2005; Cho & Giovannoni, 2004; Nedashkovskaya *et al.*, 2004; Nichols *et al.*, 2005; Pinhassi *et al.*, 2006). These bacteria are known to play an important role in the uptake and degradation of complex dissolved and particulate organic matter in marine ecosystems (Kirchman, 2002). In the course of investigations of bacterial diversity in seawater, a novel yellow-pigmented bacterium, designated strain M091^T, was isolated from a seawater sample collected at Damupo beach in Pohang, Korea. On the basis of phylogenetic analysis, strain M091^T formed a distinct cluster closely related to members of the genera *Flaviramulus*,

Algibacter, *Mariniflexile*, *Winogradskyella*, *Lacinutrix* and *Tamlana* of the phylum *Bacteroidetes*. The taxonomic characterization of strain M091^T, using a polyphasic approach, is described in this report.

Strain M091^T was isolated from seawater collected at Damupo beach in Pohang, Republic of Korea (36° 1' 55.01" N 129° 34' 50.98" E), by using a standard serial dilution plating technique on marine agar 2216 (MA; Difco). The strain was initially grown at 25 °C for 5 days and then routinely maintained on MA, with subculture every 3 days, under aerobic conditions at 25 °C. The strain was also stored at –80 °C in marine broth (MB; Difco) supplemented with 20 % (v/v) glycerol.

In the phenotypic and chemotaxonomic comparisons, *Flaviramulus basaltis* DSM 18180^T (Einen & Øvreås, 2006), *Algibacter lectus* KCTC 12103^T (Nedashkovskaya *et al.*, 2004), *Algibacter mikhailovii* KCTC 12710^T (Nedashkovskaya *et al.*, 2007), *Mariniflexile gromovii* KCTC 12570^T (Nedashkovskaya *et al.*, 2006), *Mariniflexile fucanivorans* DSM 18792^T (Barbeyron *et al.*, 2008), *Tamlana crocina* KCTC 12721^T (Lee, 2007), *Tamlana agarivorans* KCTC 22176^T (Yoon *et al.*, 2008), *Gaetbulibacter saemankumensis* KCTC 12379^T (Jung *et al.*, 2005), *Gaetbulibacter marinus* KCCM 42380^T (Yang & Cho, 2008), *Yeosuana aromativorans* KCCM 42019^T (Kwon

The GenBank accession number for the 16S rRNA gene sequence of strain M091^T is HQ336487.

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

et al., 2006) and strains representing six members of the genus *Winogradskyella* [*W. thalassocola* (Nedashkovskaya *et al.*, 2005), *W. epiphytica* (Nedashkovskaya *et al.*, 2005), *W. eximia* (Nedashkovskaya *et al.*, 2005), *W. rapida* (Pinhassi *et al.*, 2009), *W. arenosi* (Romanenko *et al.*, 2009) and *W. echinorum* (Nedashkovskaya *et al.*, 2009)] were used for reference.

Genomic DNA of strain M091^T was extracted and purified with an Exgene genomic extraction kit (GeneAll Biotechnology) before the nearly-complete 16S rRNA gene sequence was amplified using the bacterial universal primers 27F and 1492R (Weisburg *et al.*, 1991). The PCR product was purified with an Expin DNA purification kit (GeneAll Biotechnology) and then ligated into a T-Blunt vector (SolGent) according to the vector manufacturer's instructions. The ligation product was transformed into competent *Escherichia coli* DH5 α cells. The cloned 16S rRNA gene sequence was then sequenced on an automated sequencer (ABI3730XL; Applied Biosystems) at Macrogen Co. Ltd. The almost-complete 16S rRNA gene sequence (1444 bp) of strain M091^T was obtained and compared with the 16S rRNA gene sequences available in GenBank. The BLAST program (<http://www.ncbi.nlm.nih.gov/blast/>) was used to determine the approximate phylogenetic affiliation of the novel strain while the CLUSTAL_X software (Thompson *et al.*, 1997) was used to align the sequences of closely related organisms. Sequence similarity values were computed using the EzTaxon server (<http://www.eztaxon.org/>; Chun *et al.*, 2007). Gaps at the 5' and 3' ends and ambiguous bases were removed from the alignments using BioEdit (Hall, 2007). Phylogenetic trees, each based on comparison of 1283 bp from each strain, were constructed using the neighbour-joining, maximum-parsimony and maximum-likelihood algorithms and the MEGA 5 software package (Kumar *et al.*, 2008), with bootstrap values based on 1000 replications (Felsenstein, 1985). Evolutionary distance matrices were calculated according to the Kimura two-parameter model (Kimura, 1983).

The phylogenetic analyses based on 16S rRNA gene sequences indicated that strain M091^T should be placed within the family *Flavobacteriaceae* of the phylum *Bacteroidetes*, although the novel strain appeared distinct from any recognized species in the family *Flavobacteriaceae* (Fig. 1). In the neighbour-joining (Fig. 1) and maximum-parsimony trees (see Fig. S1, available in IJSEM Online), strain M091^T joined the phylogenetic lineage of *F. basaltis* H35^T, albeit with a low bootstrap value (32%). In the maximum-likelihood tree (Fig. S2), however, the novel strain formed a phyletic clade with members of the genus *Winogradskyella*. In the pairwise comparisons of 16S rRNA gene sequences, strain M091^T appeared most closely related to *F. basaltis* H35^T (95.1% sequence similarity; Eien & Øvreås, 2006), followed by *A. mikhailovii* LMG 23988^T (94.9%; Nedashkovskaya *et al.*, 2007), *M. fucanivorans* SW5^T (94.8%; Barbeyron *et al.*, 2008), *W. thalassocola* KMM 3907^T (94.7%; Nedashkovskaya *et al.*, 2005), *L. algicola* AKS293^T (94.7%; Nedashkovskaya *et al.*, 2008) and *T. agarivorans* JW-26^T (94.7%; Yoon *et al.*, 2008).

Cells of strain M091^T grown aerobically on MA at 25 °C for 5 days were used for the examination of colony morphology, size and colour. Cell morphology and size were explored under a light microscope (FDX-35; Nikon), and in a transmission electron microscope (JEM-1010; JEOL), using the methods described by Jeon *et al.* (2004). Gliding motility was investigated using phase-contrast light microscopy and the hanging drop method described by Bernardet *et al.* (2002).

The following tests were performed on strain M091^T and the reference strains. The optimal temperature and temperature range for growth were tested on MA at 4, 10, 15, 20, 25, 30, 35, 37 and 42 °C. NaCl requirement and tolerance were determined on synthetic Zobell agar medium (ZoBell, 1941) that contained 5 g Bacto peptone, 1 g yeast extract, 0.1 g ferric citrate and 15 g Bacto agar per litre modified artificial seawater; the modified artificial seawater contained (l⁻¹): 0–100 g NaCl, 5.94 g MgSO₄·7H₂O, 4.53 g MgCl₂·6H₂O, 0.64 g KCl and 1.3 g CaCl₂. The pH range for growth was determined in marine broth 2216 (MB, Difco) that was adjusted to pH values between 4.0 and 11.0 (at intervals of 0.5 pH unit), with HCl or NaOH, after sterilization. Gram staining was determined by using the bioMérieux Gram stain kit according to the manufacturer's instructions. To detect flexirubin-type pigments, cell mass was subjected to KOH testing, as described by Bernardet *et al.* (2002). Anaerobic growth was assessed on MA incubated in a GasPak anaerobic system (BBL) for up to 20 days at 25 °C. Catalase and oxidase activities were determined using standard methods (Tindall *et al.*, 2007). The degradation of agar, starch and carboxymethylcellulose were tested according to the methods of Smibert & Krieg (1994). Casein hydrolysis was determined according to the method of Norris *et al.* (1985) while hydrolysis of chitin and Tweens 20, 40, 60 and 80 was determined according to Baumann & Baumann (1981). DNase activity was determined with DNase test agar (Difco). Antibiotic sensitivity was explored by using the disc diffusion method and antibiotic discs (Oxoid) containing ampicillin (10 µg), carbenicillin (100 µg), chloramphenicol (30 µg) erythromycin (15 µg), gentamicin (10 µg), kanamycin (30 µg), lincomycin (15 µg), nalidixic acid (30 µg), neomycin (30 µg), novobiocin (5 µg), oleandomycin (15 µg), penicillin (10 U), polymyxin B (300 µg), rifampicin (5 µg), streptomycin (25 µg) or tetracycline (30 µg). The results were interpreted as described in the guidelines of the Clinical and Laboratory Standards Institute (CLSI, 2003). API 20E, API 20NE and API ZYM kits (bioMérieux), with incubation at 25 °C for 5 days, 5 days and 12 h, respectively, were used to explore other phenotypic characteristics and enzyme activities of strain M091^T and the reference strains. Acid production from carbohydrates and the oxidation of different carbon sources were assessed using API 50CH kits (bioMérieux) and GN2 MicroPlates (Biolog) according to the manufacturers' instructions. All commercial kits were inoculated with bacterial suspensions containing 3% (w/v) sea salts. The detailed results of the morphological, physiological and

Fig. 1. Neighbour-joining phylogenetic tree based on 16S rRNA gene sequences, showing the relationship of strain M091^T with representative members of the family *Flavobacteriaceae*. Bootstrap percentages (>50%) based on 1000 replicates are shown at branch points. *Flavobacterium aquatile* ATCC 11947^T was used as an outgroup. Bar, 0.01 substitution per nucleotide position.

biochemical tests are given in the genus and species descriptions and in Table 1.

For cellular fatty acid analysis, cells of strain M091^T and the reference strains were grown aerobically on MA at 25 °C for 3 days. Fatty acid methyl esters were obtained by saponification, methylation, and extraction according to the standard protocol of version 6.1 of the Sherlock Microbial Identification System (MIDI). Fatty acids were separated on a gas chromatograph (7890A; Agilent) and identified using version 6.0 of the TSBA database. The major respiratory quinone of strain M091^T was analysed as described previously (Minnikin *et al.*, 1984; Komagata & Suzuki, 1987). Polar lipids were extracted according to the procedures described by Minnikin *et al.* (1984) and separated by two-dimensional TLC using silica gel 60 F₂₅₄ plates (Merck). Individual polar lipids were identified by spraying with the appropriate detection reagents and by co-migration with authentic standards

(Sigma) (Komagata & Suzuki, 1987). The G + C content of the genomic DNA of strain M091^T was determined by using the thermal denaturation method (Marmur & Doty, 1962), an Ultrospec 2100 spectrophotometer (Pharmacia Biotech) and, as a control, DNA from *E. coli* K-12.

The major cellular fatty acids of strain M091^T were iso-C_{15:0} (20.5%), iso-C_{17:0} 3-OH (15.4%), iso-C_{15:0} 3-OH (12.4%), C_{15:0} (10.9%) and iso-C_{15:1} G (9.9%). Such a fatty acid profile is characteristic of members of the family *Flavobacteriaceae* (Bernardet *et al.*, 2002). Although, overall, the reference strains grown under the same conditions showed similar fatty acid profiles, the respective proportions of several fatty acids could be used to differentiate strain M091^T from all of its closest phylogenetic neighbours (Table 2). The major respiratory quinone of strain M091^T was menaquinone-6 (MK-6), as seen in all recognized members of the family *Flavobacteriaceae*

Table 1. Phenotypic characteristics that differentiate strain M091^T from phylogenetically related genera in the family Flavobacteriaceae

Taxa: 1, strain M091^T; 2, *F. basaltis* DSM 18180^T (data from Einen & Øvreås, 2006); 3, *Algibacter* [*A. lectus* KCTC 12103^T (Nedashkovskaya *et al.*, 2004) and *A. mikhailovii* KCTC 12710^T (Nedashkovskaya *et al.*, 2007)]; 4, *Mariniflexile* [*M. fucanivorans* DSM 18792^T (Barbeyron *et al.*, 2008) and *M. gromovii* KCTC 12570^T (Nedashkovskaya *et al.*, 2006)]; 5, *Tamlana* [*T. agarivorans* KCTC 22176^T (Yoon *et al.*, 2008) and *T. crocina* KCTC 12721^T (Lee, 2007)]; 6, *Gaetbulibacter* [*G. saemankumensis* KCTC 12379^T (Jung *et al.*, 2005) and *G. marinus* KCCM 42380^T (Yang & Cho, 2008)]; 7, *Y. aromativorans* KCCM 42019^T (Kwon *et al.*, 2006); 8, *Winogradskyella* [*W. thalassocola* (Nedashkovskaya *et al.*, 2005), *W. epiphytica* (Nedashkovskaya *et al.*, 2005), *W. eximia* (Nedashkovskaya *et al.*, 2005), *W. poriferorum* (Lau *et al.*, 2005), *W. rapida* (Pinhassi *et al.*, 2009), *W. arenosi* (Romanenko *et al.*, 2009), *W. echinorum* (Nedashkovskaya *et al.*, 2009), *W. exilis* (Ivanova *et al.*, 2010), *W. pacifica* (Kim & Nedashkovskaya, 2010) and *W. lutea* (Yoon *et al.*, 2011)]. All data for taxa 1, 2, 3, 4 and 5 are from this study except those on respiratory quinones, DNA G + C contents and acid production from carbohydrates, which were from the literature. +, Positive; −, negative; w, weakly positive; ND, not determined; v, variable.

Characteristic	1	2	3	4	5	6	7	8
Flexirubin-type pigments	−	−	−	−	v	−	−	−
Gliding motility	−	−	+	+	−	v	−	+
Nitrate reduction	−	−	v	−	v	v	−	−
Acetoin production	−	w	−	v	v	−	ND	−
H ₂ S production	−	+	−	−	−	−	−	v
Oxidase	−	−	+	−	−	v	−	+
Acid production from carbohydrates	−	+	+	+	−	+	−	v
Hydrolysis of:								v
Agar	+	−	+	−	v	−	−	v
DNA	+	+	v	+	+	−	ND	v
Gelatin	−	+	+	v	−	−	+	+
Starch	+	+	+	−	−	v	−	v
Tween 80	−	+	−	v	−	−	ND	v
Assimilation of:								
Glucose	+	−	+	+	v	+	+	v
Arabinose	−	+	−	−	v	−	ND	+
Mannitol	−	−	+	v	−	−	ND	v
Maltose	−	+	+	−	+	+	+	v
Gluconate	−	−	−	v	v	−	ND	−
Malic acid	−	+	v	−	v	−	ND	v
Enzyme activity:							ND	
Valine arylamidase	+	+	+	+	−	+	ND	v
Trypsin	−	−	v	−	−	v	ND	v
α-Chymotrypsin	−	−	+	+	v	v	ND	v
Naphthol-AS-BI-phosphohydrolase	+	−	+	+	+	v	ND	v
β-Galactosidase	+	−	+	−	v	−	+	v
α-Glucosidase	+	−	−	v	−	v	ND	v
N-Acetyl-β-glucosaminidase	−	−	−	v	−	v	ND	v
Susceptibility to:			−					
Ampicillin	+	+	−	+	v	−	ND	v
Nalidixic acid	+	−	v	−	−	ND	ND	ND
Novobiocin	−	+	+	+	+	ND	ND	ND
Penicillin	−	+	+	−	v	+	ND	−
Streptomycin	−	+	−	−	−	−	ND	−
Respiratory quinone(s)	MK-6	MK-6	MK-6	MK-6	MK-6	MK-6	MK-5, MK-6	MK-6
DNA G + C content (mol%)	34.4	31.4	31.0–35.1	34.5–35.7	36.2–36.8	34.7–38.1	51.4	30.2–36.3

(Bernardet & Nakagawa, 2006). The polar lipid profile of strain M091^T comprised phosphatidylethanolamine, two unidentified aminolipids, one unidentified phospholipid and seven unidentified lipids (Fig. S3). Although the major polar lipids of strain M091^T were similar to those of *F. basaltis* DSM 18180^T (both containing phosphatidylethanolamine and the unidentified lipids L1 and L2), some of the unidentified polar lipids found in the novel strain

(PL, AL1, AL2 and L3–L7) were not detected in *F. basaltis* DSM 18180^T and, conversely, three unidentified lipids found in *F. basaltis* DSM 18180^T (AL, L3 and L4) were not seen in the novel strain. The genomic DNA G + C content of strain M091^T, 34.4 mol%, was close to corresponding values reported for *M. fucanivorans* DSM 18792^T (34.5 mol%; Barbeyron *et al.*, 2008) and *A. mikhailovii* KCTC 12710^T (35.1 mol%; Nedashkovskaya *et al.*, 2007) and

Table 2. Cellular fatty acid composition (%) of strain M091^T and phylogenetically related genera in the family *Flavobacteriaceae*

Taxa: 1, strain M091^T; 2, *F. basaltis* DSM 18180^T; 3, *Algibacter* (*A. lectus* KCTC 12103^T and *A. mikhailovii* KCTC 12710^T); 4, *Mariniflexile* (*M. fucanivorans* DSM 18792^T and *M. gromovii* KCTC 12570^T); 5, *Tamlana* (*T. agarivorans* KCTC 22176^T and *T. crocina* KCTC 12721^T); 6, *Gaetbulibacter* (*G. saemankumensis* KCTC 12379^T and *G. marinus* KCCM 42380^T); 7, *Y. aromativorans* KCCM 42019^T; 8, *Winogradskyella* (*W. thalassocola* KCTC 12221^T, *W. epiphytica* KCTC 12220^T, *W. eximia* KCTC 12219^T, *W. rapida* CCUG 56098^T, *W. arenosi* JCM 15527^T and *W. echinorum* KCTC 22026^T). All data are from this study. Fatty acids amounting to <1.0% of the total fatty acids in all strains are not shown. tr, Trace amount (<1.0%); –, not detected.

Fatty acid	1	2	3	4	5	6	7	8
Straight-chain								
C _{15:0}	10.9	10.6	12.3–14.4	4.5–14.9	9.4–18.2	2.1–3.5	6.1	tr–6.8
C _{16:0}	4.1	1.2	1.2–1.9	1.0–2.5	1.1–1.4	1.1–1.6	1.1	tr–2.1
Branched								
iso-C _{14:0}	tr	1.1	tr	1.3–1.9	0–1.1	1.3–2.1	2.7	tr–2.3
iso-C _{15:0}	20.5	16.3	10.6–10.8	19.8	19.6–26.9	21.4–21.5	24.1	7.8–25.3
iso-C _{15:1} G	9.9	20.3	12.1–20.3	7.3–17.6	13.5–15.9	10.3–3.9	8.7	7.7–14.6
iso-C _{16:0}	1.0	tr	tr	1.5–2.3	1.1–1.5	tr–1.7	3.3	tr–5.6
iso-C _{16:1} H	–	–	tr	tr–3.3	0–1.0	tr	2.1	tr–3.3
anteiso-C _{15:0}	4.1	6.4	11.9–13.9	7.0–9.5	4.5–5.3	5.2–9.7	9.3	7.8–14.1
anteiso-C _{15:1} A	tr	2.4	1.5–1.6	tr–1.2	1.1–1.6	1.4–3.2	tr	2.3–4.9
iso-C _{17:1} ω9c	–	–	–	–	–	0–1.4	–	0–1.5
Unsaturated								
C _{14:1} ω5c	–	–	–	–	0–1.5	–	–	0–1.2
C _{15:1} ω6c	2.0	1.9	4.1–5.2	2.4–6.3	4.0–7.2	tr	1.4	0–1.9
C _{17:1} ω6c	1.2	tr	2.6–3.5	tr–2.2	2.3–2.5	tr–1.0	tr	tr–1.1
C _{18:1} ω5c	1.7	1.0	1.1	tr–1.3	–	tr	tr	tr–2.8
Hydroxy								
C _{15:0} 2-OH	tr	1.6	1.9	1.7–1.8	1.1–1.3	tr–1.8	1.7	1.5–2.9
C _{17:0} 2-OH	tr	1.4	2.0–2.4	1.6–2.5	1.2–2.7	1.7–3.2	2.0	2.6–7.6
C _{15:0} 3-OH	2.1	3.2	2.9–3.0	1.9–3.6	1.6–3.7	tr	1.7	0–1.4
C _{16:0} 3-OH	2.8	1.2	2.1–2.6	tr–1.5	tr–4.0	tr–1.1	tr	0–1.3
C _{17:0} 3-OH	1.2	–	1.8	0–1.2	0–1.4	0.58	–	–
iso-C _{15:0} 3-OH	12.4	13.2	9.7–10.4	5.8–6.2	5.3–5.7	6.0–7.4	3.9	2.6–13.9
iso-C _{16:0} 3-OH	4.8	5.9	3.3–3.4	5.2–7.7	2.2–8.5	2.5–8.4	9.6	6.1–20.3
iso-C _{17:0} 3-OH	15.4	13.4	12.3–13.6	8.5–14.2	14.4–18.6	9.8–16.9	10.5	6.9–12.7
C _{18:0} 10-methyl, TBSA	–	–	1.1	–	–	–	–	–
Summed feature*								
3	8.4	5.3	6.3–6.5	7.5–8.5	4.7–5.2	2.9–10.7	8.1	2.0–4.7
9	–	–	–	0–1.5	tr	0–2.0	3.7	1.6–2.7

*Summed features are groups of two or three fatty acids that cannot be separated by GLC using the MIDI system. Summed feature 3 comprised C_{16:1}ω6c and/or C_{16:1}ω7c. Summed feature 9 comprised C_{16:0} 10-methyl and/or iso-C_{17:1}ω9c.

slightly higher than the value, of 31 mol%, reported for *F. basaltis* DSM 18180^T (Einen & Øvreås, 2006).

The results of the phylogenetic analysis based on the 16S rRNA gene sequence of strain M091^T were supported by a combination of phenotypic and chemotaxonomic characteristics (Tables 1 and 2). Strain M091^T could be clearly differentiated from *F. basaltis* by its oxidase, naphthol-AS-BI-phosphohydrolase and β-galactosidase activities, its ability to assimilate glucose and hydrolyse agar, its susceptibility to nalidixic acid, and its inability to generate acids from carbohydrates or produce acetoin or H₂S. Its α-glucosidase activity, ability to hydrolyse starch, susceptibility to nalidixic acid and its lack of gliding motility distinguished strain M091^T from members of the genera *Algibacter*,

Mariniflexile and *Tamlana*. Strain M091^T could be differentiated from members of the genera *Gaetbulibacter* and *Winogradskyella* by its β-glucosidase activity and ability to hydrolyse agar and DNA. Strain M091^T could also be clearly distinguished from its closest phylogenetic neighbours by its fatty acid profile and the proportions of several fatty acids (Table 2). Based on the phenotypic and phylogenetic data, strain M091^T represents a novel species of a new genus in the family *Flavobacteriaceae*, for which the name *Postechiella marina* gen. nov., sp. nov. is proposed.

Description of *Postechiella* gen. nov.

Postechiella (Pos.te.chi'el.la. N.L. dim. fem. n. *Postechiella* arbitrarily developed from the acronym POSTECH formed

from the initial letters of the Pohang University of Science and Technology, where the initial taxonomic studies on this genus were conducted).

Cells are Gram-staining-negative, non-flagellated, strictly aerobic, yellow-pigmented and rod-shaped. Gliding motility is absent. Oxidase- and catalase-positive. Cells produce non-diffusible carotenoid pigments but flexirubin pigments are absent. Cellular fatty acids are dominated by iso-C_{15:0}, iso-C_{17:0} 3-OH, iso-C_{15:0} 3-OH, C_{15:0} and iso-C_{15:1} G. The major respiratory quinone is MK-6. The polar lipids are phosphatidylethanolamine, two unidentified aminolipids, one unidentified phospholipid and seven unidentified lipids. The genus is a member of the family *Flavobacteriaceae*, phylum *Bacteroidetes*. The type species is *Postechiella marina*.

Description of *Postechiella marina* sp. nov.

Postechiella marina (ma.ri'na. L. fem. adj. *marina* of or belonging to the sea, marine).

In addition to the characteristics described for the genus above, the species is distinguished by the following properties. Cells are non-motile rods measuring 0.5–0.7 µm in diameter and 1.0–2.5 µm in length. After incubation for 3 days, colonies on MA are circular, convex, entire, smooth, yellow-coloured and 1.0–5.0 mm in diameter. Growth occurs at 4–30 °C (optimum, 25 °C), at pH 6.0–9.0 (optimum between pH 7.0 and pH 8.0), and with 1.0–5.0 % (w/v) NaCl (optimum, 3.0 %). Agar, DNA, starch, Tween 20, Tween 40 and Tween 60 are hydrolysed but casein, carboxymethylcellulose and Tween 80 are not. In API 20E tests, glucose is oxidized but mannitol, inositol, sorbitol, rhamnose, sucrose, melibiose, amygdalin and arabinose are not. Negative result in tests for arginine dihydrolase, lysine decarboxylase, ornithine decarboxylase, tryptophan deaminase and urease activities and for acetoin, indole and H₂S production. In API 20NE tests, aesculin is hydrolysed, β-galactosidase activity is present and glucose and mannose are assimilated but arabinose, mannitol, N-acetyl-D-glucosamine, maltose, gluconate, caprate, adipate, malate, citrate and phenylacetate are not assimilated. Nitrate is not reduced. Negative result in tests for indole production, glucose acidification, gelatin hydrolysis and arginine dihydrolase and urease activities. Positive result, in API ZYM tests, for alkaline phosphatase, esterase (C4), esterase lipase (C8), leucine arylamidase, valine arylamidase, cystine arylamidase, acid phosphatase, naphthol-AS-BI-phosphohydrolase, β-galactosidase and α-glucosidase activities but negative for lipase (C14), trypsin, α-chymotrypsin, α-galactosidase, β-glucuronidase, β-glucosidase, N-acetyl-β-glucosaminidase, α-mannosidase and α-fucosidase activities. Acid is only produced aerobically, in API 50CH tests, from aesculin-ferric citrate and 5-ketogluconate. α-Cyclodextrin, dextrin, glycogen, cellobiose, D-galactose, gentiobiose, α-D-glucose, α-lactose, maltose, D-mannose, trehalose, acetic acid, D-glucosaminic acid, D-glucuronic acid, D-saccharic acid, L-alanyl glycine, L-asparagine, L-aspartic acid, L-glutamic acid, L-threonine, DL-α-glycerol phosphate, glucose 1-phosphate and glucose 6-phosphate (but none of the other carbon sources included in

the GN2 MicroPlate) are oxidized as sole carbon sources. Sensitive to ampicillin (10 µg), carbenicillin (100 µg), chloramphenicol (30 µg), erythromycin (15 µg), lincomycin (15 µg), nalidixic acid (30 µg), oleandomycin (15 µg), rifampicin (5 µg) and tetracycline (30 µg), but resistant to gentamicin (10 µg), kanamycin (30 µg), neomycin (30 µg), novobiocin (5 µg), penicillin (10 IU), polymyxin B (300 µg) and streptomycin (25 µg).

The type strain, M091^T (=KCTC 23537^T=JCM 17630^T), was isolated from seawater collected at Damupo beach in Pohang, Korea. The DNA G + C content of the type strain is 34.4 mol%.

Acknowledgements

This work was supported by the 21C Frontier Microbial Genomics and Applications Centre Program, Ministry of Education, Science & Technology, Republic of Korea.

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