Planococcus maritimus sp. nov., isolated from sea water of a tidal flat in Korea

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Two Gram-positive, motile cocci, strains TF-9^T and TF-16, were isolated from sea water of a tidal flat in Korea. Phylogenetic analysis based on 16S rDNA sequences showed that the strains fall within the radiation of the cluster comprising *Planococcus citreus* and *Planococcus kocurii*, and this cluster joined the clade comprising *Planomicrobium* species and *Planococcus alkanoclasticus* and *Planococcus psychrophilus* with a high bootstrap resampling value. Strains TF-9^T and TF-16 contained MK-8, MK-7 and MK-6 as the predominant menaquinones. The major fatty acid was anteiso-C_{15:0}. The DNA G + C contents of strains TF-9^T and TF-16 were respectively 48 and 49 mol%. The level of 16S rDNA identity between strains TF-9^T and TF-16 was 98.9%. Strain TF-9^T and TF-16 respectively exhibited levels of 16S rDNA identity of 97.2–98.4 and 96.9–99.5% to the type strains of *Planococcus kocurii*, *Planococcus citreus* and *Planococcus antarcticus*. The mean level of DNA–DNA relatedness between strains TF-9^T and TF-16 was 36.7%. Strains TF-9^T and TF-16 respectively exhibited levels of DNA–DNA relatedness of 7.1–43.4 and 3.5–80.9% to *Planococcus citreus* DSM 20549^T, *Planococcus kocurii* DSM 20747^T and *Planococcus antarcticus* DSM 14505^T. On the basis of the phenotypic, phylogenetic and genomic data, strain TF-9^T (=KCCM 41587^T=JCM 11543^T) should be placed as a novel species of the genus *Planococcus*, for which the name *Planococcus maritimus* sp. nov. is proposed, and strain TF-16 should be classified as a member of *Planococcus citreus*.

The genus *Planococcus* was first proposed by Migula (1894) to accommodate motile cocci. However, the name *Planococcus* was not validly published for many years. The first species, *Planococcus citreus*, was proposed by Kocur *et al.* (1970) and the second, *Planococcus kocurii*, was proposed by Hao & Komagata (1985). Two further species, *Planococcus okeanokoites* (Nakagawa *et al.*, 1996) and *Planococcus mcmeekinii* (Junge *et al.*, 1998), were then added to the

genus. Recently, on the basis of some differential taxonomic data, the latter two species were transferred to a new genus *Planomicrobium*, which was created with the newly isolated strain *Planomicrobium koreense* JG-07^T (Yoon *et al.*, 2001). Subsequently, three more *Planococcus* species have been described: *Planococcus alkanoclasticus* (Engelhardt *et al.*, 2001), *Planococcus antarcticus* and *Planococcus psychrophilus* (Reddy *et al.*, 2002). In this study, we describe two bacterial strains, TF-9^T and TF-16, isolated from sea water of a tidal flat of the Yellow Sea in Korea. The two strains were found to be phylogenetically related to the genera *Planococcus* and *Planomicrobium*. Accordingly, the aim of the present study was to determine the exact taxonomic positions of strains TF-9^T and TF-16 with a combination of phenotypic properties, phylogeny based on 16S rDNA sequence and genomic relatedness.

Strains TF-9^T and TF-16 were isolated by the dilution

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Abbreviation: ITS, internally transcribed spacer.

The GenBank accession numbers for the 16S rDNA sequences of strains TF-9^T and TF-16 are respectively AF500007 and AF500008 and for the 16S–23S rDNA ITS sequences of strains TF-9^T and TF-16 they are AF500009 and AF500010.

Detailed results of DNA–DNA relatedness experiments are available as supplementary material in IJSEM Online.

plating technique on marine agar 2216 (MA) (Difco) at 30 °C. *Planococcus citreus* DSM 20549^T, *Planococcus kocurii* DSM 20747^T and *Planococcus antarcticus* DSM 14505^T were used as reference strains for some analyses. Cell biomass of strains TF-9^T and TF-16 for menaquinone and cell-wall analyses and for DNA extraction was obtained from marine broth 2216 (MB) (Difco) cultures at 30 °C. Cell biomass for polar lipid analysis was produced in a liquid medium (IFO medium no. 326) that contained (l⁻¹) 10 g peptone, 2 g yeast extract, 1 g MgSO₄·7H₂O and 30 g NaCl. For fatty acid methyl ester (FAME) analysis, cell mass of strains TF-9^T and TF-16 was obtained from agar plates after 2 days cultivation at 30 °C on MA.

Flagellation was examined with transmission electron microscopy using cells from an exponentially growing culture as described previously (Yoon *et al.*, 2001). Gram reaction was determined using the bioMérieux Gram Stain kit according to the manufacturer's instructions. Catalase and oxidase activities were determined as described by Cowan & Steel (1965) after cultivation for 3 days. Hydrolysis of casein, starch and Tween 80 and production of urease was determined as described by Cowan & Steel (1965). Hydrolysis of aesculin and nitrate reduction were determined as described previously (Lanyi, 1987). Hydrolysis of hypoxanthine, tyrosine and xanthine was performed on MA plates with concentration of substrates described previously (Cowan & Steel, 1965). Hydrolysis of gelatin was studied as by Cowan & Steel (1965) with the modification that artificial sea water was used. The artificial sea water contained (l⁻¹ distilled water) 23.6 g NaCl, 0.64 g KCl, 4.53 g MgCl₂·6H₂O, 5.94 g MgSO₄·7H₂O and 1.3 g CaCl₂·2H₂O (Levring, 1946). Acid production from carbohydrates was determined as described by Leifson (1963). Other characteristics were investigated as described by Yoon *et al.* (2003).

Preparation of cell walls and determination of peptidoglycan structure were carried out by the methods described by Schleifer & Kandler (1972), with the modification that TLC on cellulose sheets was used instead of paper chromatography. Menaquinones were analysed as described previously (Komagata & Suzuki, 1987) using reversed-phase HPLC. For quantitative analysis of cellular fatty acid compositions, a loop of cell mass was harvested and FAMES were prepared and identified following the instructions of the Microbial Identification System (MIDI). Polar lipids were extracted using the procedures described by Minnikin *et al.* (1984) and identified by two-dimensional TLC followed by spraying with appropriate detection reagents (Komagata & Suzuki, 1987). Chromosomal DNA was isolated and purified according to the method described previously (Yoon *et al.*, 1996), with the exception that ribonuclease T1 was used together with ribonuclease A. The G+C content was determined by the method of Tamaoka & Komagata (1984). DNA was hydrolysed and the resultant nucleotides were analysed by reversed-phase HPLC.

16S rDNA was amplified by PCR using two universal primers as described previously (Yoon *et al.*, 1998). Sequencing of the amplified 16S rDNA and phylogenetic analysis were performed as described by Yoon *et al.* (2003). Sequencing of the 16S–23S rDNA internally transcribed spacer (ITS) was performed as described previously (Yoon *et al.*, 1997). DNA–DNA hybridization was performed fluorometrically by the method of Ezaki *et al.* (1989) using photobiotin-labelled DNA probes and microdilution wells. Hybridization was performed with five replications for each sample. Of the values obtained, the highest and lowest values in each sample were excluded and the mean of the remaining three values was used as the DNA relatedness value.

Morphological, physiological and biochemical characteristics are given in Table 1 or the species description. The cell wall of strains TF-9^T and TF-16 contained the amino acids lysine, glutamic acid and alanine. Accordingly, the peptidoglycan type of strains TF-9^T and TF-16 was A4 α , based on L-Lys–D-Glu, as described by Schleifer & Kandler (1972). The menaquinones detected in strains TF-9^T and TF-16 were MK-8 (54 and 54 %, respectively), MK-7 (28 and 25 %) and MK-6 (18 and 21 %). Strains TF-9^T and TF-16 contained anteiso-C_{15:0} as the major fatty acid and significant amounts of iso-C_{16:0} and iso-C_{14:0} (Table 2). The cellular phospholipids found in strains TF-9^T and TF-16 were phosphatidylethanolamine, phosphatidylglycerol and diphosphatidylglycerol. The genomic DNA G+C contents of strains TF-9^T and TF-16 were respectively 48 and 49 mol%.

The 16S rDNA sequences of strains TF-9^T and TF-16 determined in this study respectively comprised 1507 and 1506 nucleotides, representing 96 % of the *Escherichia coli* 16S rRNA sequence. Phylogenetic analyses based on three tree-making algorithms showed that strains TF-9^T and TF-16 fall within the evolutionary radiation enclosed by the genus *Planococcus* (a neighbour-joining tree is shown in Fig. 1). The level of 16S rDNA identity between strains TF-9^T and TF-16 was 98.9 %. Strains TF-9^T and TF-16 respectively exhibited levels of 16S rDNA identity of 97.2–98.4 and 96.9–99.5 % to the type strains of *Planococcus citreus*, *Planococcus kocurii* and *Planococcus antarcticus*. Strains TF-9^T and TF-16 exhibited levels of 16S rDNA identity of 96.8–97.4 % to the type strains of *Planococcus alkanoclasticus* and *Planococcus psychrophilus* and of 97.4–98.0 % to the type strains of *Planomicrobium* species. The 16S–23S ITS regions of strains TF-9^T and TF-16 were respectively 188 and 185 bp long. Strain TF-9^T exhibited levels of 16S–23S ITS identity of 94.5 and 78.5 % to *Planococcus citreus* DSM 20549^T and *Planococcus kocurii* DSM 20747^T, respectively, and strain TF-16 exhibited levels of 16S–23S ITS identity of 100 and 81.6 % to *Planococcus citreus* DSM 20549^T and *Planococcus kocurii* DSM 20747^T. Strains TF-9^T and TF-16 exhibited two independent levels of DNA–DNA relatedness of 37.0 and 36.3 %. Levels of DNA–DNA relatedness between strain

Table 1. Differential phenotypic properties of strains TF-9^T and TF-16 and *Planococcus* species

Strain/species: 1, strain TF-9^T; 2, strain TF-16; 3, *Planococcus citreus* (data from Hao & Komagata, 1985); 4, *Planococcus kocurii* (Hao & Komagata, 1985); 5, *Planococcus antarcticus* (Reddy *et al.*, 2002). +, Positive; –, negative; V, variable; ND, not determined. All strains or species are cocci and are positive for Gram stain, motility, catalase and growth in the absence of NaCl. All strains or species are negative for spore formation, oxidase, urease, nitrate reduction, hydrolysis of aesculin and starch and acid production from D-cellobiose and lactose.

Characteristic	1	2	3	4	5
Growth in:					
15 % NaCl	+	+	+	–	–
17 % NaCl	+	–	ND	ND	–
Max. temperature for growth (°C)	41	43	ND	ND	30
Hydrolysis of gelatin	+	–	+	V	+
Acid production from:					
D-Glucose	+	–	+	V	+
D-Mannitol	+	–	–	–	ND
Melibiose	–	+	–	–	ND
Predominant menaquinones	MK-8, MK-7, MK-6	MK-8, MK-7, MK-6	MK-8, MK-7	MK-8, MK-7	MK-7, MK-8
DNA G+C content (mol%)	48	49	48–51	40–43	42

TF-9^T and *Planococcus citreus* DSM 20549^T, *Planococcus kocurii* DSM 20747^T and *Planococcus antarcticus* DSM 14505^T were 7.1–43.4 %. Strain TF-16 exhibited levels of

DNA–DNA relatedness of 80.9 % to *Planococcus citreus* DSM 20549^T and 3.5–5.7 % to *Planococcus kocurii* DSM 20747^T and *Planococcus antarcticus* DSM 14505^T (levels of DNA–DNA relatedness are available as supplementary material in IJSEM Online).

Table 2. Cellular fatty acid profiles of strains TF-9^T and TF-16 and the type strains of *Planococcus citreus* and *Planococcus kocurii*

Strains: 1, TF-9^T; 2, TF-16; 3, *Planococcus citreus* DSM 20549^T (data from Yoon *et al.*, 2001); 4, *Planococcus kocurii* DSM 20747^T (Yoon *et al.*, 2001). Values are percentages of total fatty acids. –, Not detected.

Fatty acid	1	2	3	4
Straight-chain fatty acids:				
C _{15:0}	3.1	4.0	6.7	7.2
C _{16:0}	0.8	0.7	–	1.4
C _{17:0}	2.5	2.2	2.3	–
Branched fatty acids:				
iso-C _{14:0}	13.1	21.6	8.8	13.1
iso-C _{15:0}	9.5	6.4	–	5.1
anteiso-C _{15:0}	30.6	26.1	52.1	40.9
iso-C _{16:0}	18.5	17.7	8.1	7.2
iso-C _{17:0}	3.1	1.4	–	1.7
anteiso-C _{17:0}	4.4	2.6	5.2	2.6
iso-C _{17:1} ω10c	0.8	0.5	–	2.5
iso-C _{18:0}	2.1	1.3	–	–
Unsaturated fatty acids:				
C _{16:1} ω7c alcohol	8.9	13.1	9.8	11.4
C _{16:1} ω11c	0.7	1.1	2.5	2.5
Hydroxy fatty acids:				
C _{16:0} 2-OH	0.8	–	–	–
Summed feature 4*	1.3	1.3	4.5	4.5

*Summed feature 4 represents iso-C_{17:1} I and/or anteiso-C_{17:1} B, which could not be separated by GLC with the MIDI system.

The genus *Planococcus* has recently been dissected into two genera, *Planococcus* and *Planomicrobium*, on the basis of menaquinone profiles and phylogenetic data as well as cellular morphology (Yoon *et al.*, 2001). This classification indicates that cellular morphology may be important for determining the taxonomic status of organisms that are phylogenetically related to the genera *Planococcus* and *Planomicrobium*, although cells of *Planomicrobium mcmee-kinii* are cocci or short rods in old cultures. Since the proposal of Yoon *et al.* (2001), the additional *Planococcus* species *Planococcus alkanoclasticus*, *Planococcus antarcticus* and *Planococcus psychrophilus* have been described (Engelhardt *et al.*, 2001; Reddy *et al.*, 2002). However, cells of *Planococcus alkanoclasticus* and *Planococcus psychrophilus* are rods, unlike other *Planococcus* species (Engelhardt *et al.*, 2001; Reddy *et al.*, 2002). Moreover, with the recent description of the genus *Planomicrobium*, it is apparent that *Planococcus alkanoclasticus* and *Planococcus psychrophilus* fall within the evolutionary radiation comprising *Planomicrobium* species, not *Planococcus* species (Engelhardt *et al.*, 2001) (Fig. 1). This cluster joins the clade comprising *Planococcus* species with a high bootstrap resampling value (Engelhardt *et al.*, 2001) (Fig. 1). Accordingly, it is very likely that *Planococcus alkanoclasticus* and *Planococcus psychrophilus* can be considered as members of the genus *Planomicrobium*.

Strains TF-9^T and TF-16 fall within the radiation of the cluster comprising *Planococcus citreus*, *Planococcus kocurii* and *Planococcus antarcticus*. This cluster was differentiated from the phylogenetic clade comprising *Planomicrobium*

Fig. 1. Neighbour-joining tree based on 16S rDNA sequences showing the positions of strains TF-9^T and TF-16, *Planococcus* species, *Planomicrobium* species and representatives of some other taxa. Bar, 0.01 substitutions per nucleotide position. Bootstrap values (expressed as percentages of 1000 replications) greater than 50% are shown at branch points.

species and *Planococcus alkanoclasticus* and *Planococcus psychrophilus* by a high bootstrap resampling value (Fig. 1). Cells of strains TF-9^T and TF-16 were observed to be cocci in all growth phases, as shown for *Planococcus citreus*, *Planococcus kocurii* and *Planococcus antarcticus*. The cellular fatty acid patterns of strains TF-9^T and TF-16 are similar to those of members of the genus *Planococcus* (Table 2). Strains TF-9^T and TF-16 have an identical cell-wall peptidoglycan type (L-Lys–D-Glu) to *Planococcus* species, whereas *Planomicrobium* species, except *Planomicrobium koreense*, have cell-wall peptidoglycan based on L-Lys–D-Asp (Yoon *et al.*, 2001). Strains TF-9^T and TF-16 were found to have menaquinone profiles that differed slightly from those of *Planococcus* species (Yoon *et al.*, 2001). The two strains are characterized by the predominance of MK-8, followed by MK-7 and MK-6, whereas *Planococcus* species have similar amounts of MK-7 and MK-8 (Hao & Komagata, 1985). The menaquinone profile of strains TF-9^T and TF-16 is more similar to that of *Planomicrobium koreense* than those of *Planococcus* species (Yoon *et al.*, 2001). Menaquinones may not be a key marker for differentiating the genera *Planococcus* and *Planomicrobium*. These data indicate that there is heterogeneity or cross-over in the properties of the genera *Planococcus* and *Planomicrobium*, e.g. the cell-wall peptidoglycan type in *Planomicrobium koreense* and the menaquinone pattern in strains TF-9^T and TF-16. Accordingly, the primary evidence for differentiating the two genera appears to be morphology and phylogenetic analysis based on 16S rDNA sequences.

Strains TF-9^T and TF-16 are similar in most morphological and physiological characteristics except some properties such as acid production from carbohydrates and temperature for growth (Table 1). There are 16 nucleotide differences (1.1% difference) in the 16S rDNA sequences of strains TF-9^T and TF-16 (Fig. 1). The DNA relatedness between the two strains is less than 70%, indicating a level of DNA relatedness appropriate for defining a species in current bacterial systematics (Wayne *et al.*, 1987). Accordingly, strains TF-9^T and TF-16 are considered as members of different species of the genus *Planococcus*. The DNA–DNA

relatedness result indicates that strain TF-16 belongs to *Planococcus citreus*. The 16S–23S ITS sequence analysis also supports a close genetic relatedness between strain TF-16 and *Planococcus citreus*. Strain TF-9^T is differentiated from *Planococcus citreus* and *Planococcus kocurii* as well as from strain TF-16 by comparison of 16S rDNA and 16S–23S ITS sequences. Levels of DNA–DNA relatedness provide decisive evidence that strain TF-9^T is genetically different from *Planococcus citreus*, *Planococcus kocurii* and *Planococcus antarcticus* (Wayne *et al.*, 1987). Therefore, on the basis of differences in some phenotypic characteristics and genetic distinctiveness, strain TF-9^T should be placed in the genus *Planococcus* as a novel species, for which the name *Planococcus maritimus* sp. nov. is proposed.

Description of *Planococcus maritimus* sp. nov.

Planococcus maritimus (ma.ri'ti.mu.s. L. masc. adj. *maritimus* living near the sea).

Cells are cocci, 1.0–1.4 µm in diameter on MA. Motile by means of a single polar flagellum. Strictly aerobic. Colonies are smooth, glistening, low-convex, circular and yellow to orange in colour and 2.0–3.0 mm in diameter after 3 days cultivation at 30 °C on MA. Growth occurs at 4 and 41 °C but not at above 42 °C. Optimal growth temperature is 30 °C. Optimal pH for growth is 6.0–8.0. Growth occurs weakly at pH 5.0 but not at 4.5. Grows in the presence of 0–17% (w/v) NaCl. Optimal growth occurs in the presence of 2% (w/v) NaCl. Casein is hydrolysed. Hypoxanthine, Tween 80, tyrosine and xanthine are not hydrolysed. Acid is produced from D-fructose and D-ribose but not from adonitol, L-arabinose, D-galactose, maltose, D-mannose, D-melezitose, *myo*-inositol, D-raffinose, L-rhamnose, D-sorbitol, stachyose, sucrose, D-trehalose or D-xylose. The DNA G+C content of the type strain is 48 mol%. Other characteristics are given in Table 1.

The type strain, strain TF-9^T (=KCCM 41587^T=JCM 11543^T), was isolated from sea water of a tidal flat of the Yellow Sea in Korea.

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References

- Cowan, S. T. & Steel, K. J. (1965). *Manual for the Identification of Medical Bacteria*. London: Cambridge University Press.
- Engelhardt, M. A., Daly, K., Swannell, R. P. J. & Head, I. M. (2001). Isolation and characterization of a novel hydrocarbon-degrading, Gram-positive bacterium, isolated from intertidal beach sediment, and description of *Planococcus alkanoclasticus* sp. nov. *J Appl Microbiol* **90**, 237–247.
- Ezaki, T., Hashimoto, Y. & Yabuuchi, E. (1989). Fluorometric deoxyribonucleic acid-deoxyribonucleic acid hybridization in micro-dilution wells as an alternative to membrane filter hybridization in which radioisotopes are used to determine genetic relatedness among bacterial strains. *Int J Syst Bacteriol* **39**, 224–229.
- Hao, M. V. & Komagata, K. (1985). A new species of *Planococcus*, *P. kocurii* isolated from fish, frozen foods, and fish curing brine. *J Gen Appl Microbiol* **31**, 441–455.
- Junge, K., Gosink, J. J., Hoppe, H.-G. & Staley, J. T. (1998). *Arthrobacter*, *Brachybacterium* and *Planococcus* isolates identified from antarctic sea ice brine. Description of *Planococcus mcmeekinii*, sp. nov. *Syst Appl Microbiol* **21**, 306–314.
- Kocur, M., Páčová, Z., Hodgkiss, W. & Martinec, T. (1970). The taxonomic status of the genus *Planococcus* Migula 1894. *Int J Syst Bacteriol* **20**, 241–248.
- Komagata, K. & Suzuki, K. (1987). Lipids and cell-wall analysis in bacterial systematics. *Methods Microbiol* **19**, 161–203.
- Lanyi, B. (1987). Classical and rapid identification methods for medically important bacteria. *Methods Microbiol* **19**, 1–67.
- Leifson, E. (1963). Determination of carbohydrate metabolism of marine bacteria. *J Bacteriol* **85**, 1183–1184.
- Levring, T. (1946). Some culture experiments with *Ulva* and artificial seawater. *Kungl Fysiografiska Sällsk Lund Förhandlingar* **16**, 45–56.
- Migula, W. (1894). Über ein neues system der bakterien. *Arb Bakteriell Inst Karlsruhe* **1**, 235–238.
- Minnikin, D. E., O'Donnell, A. G., Goodfellow, M., Alderson, G., Athalye, M., Schaal, A. & Parlett, J. H. (1984). An integrated procedure for the extraction of bacterial isoprenoid quinones and polar lipids. *J Microbiol Methods* **2**, 233–241.
- Nakagawa, Y., Sakane, T. & Yokota, A. (1996). Emendation of the genus *Planococcus* and transfer of *Flavobacterium okeanokoites* Zobell and Upham 1944 to the genus *Planococcus* as *Planococcus okeanokoites* comb. nov. *Int J Syst Bacteriol* **46**, 866–870.
- Reddy, G. S. N., Prakash, J. S. S., Vairamani, M., Prabhakar, S., Matsumoto, G. I. & Shivaji, S. (2002). *Planococcus antarcticus* and *Planococcus psychrophilus* spp. nov. isolated from cyanobacterial mat samples collected from ponds in Antarctica. *Extremophiles* **6**, 253–261.
- Schleifer, K. H. & Kandler, O. (1972). Peptidoglycan types of bacterial cell walls and their taxonomic implications. *Bacteriol Rev* **36**, 407–477.
- Tamaoka, J. & Komagata, K. (1984). Determination of DNA base composition by reverse-phase high-performance liquid chromatography. *FEMS Microbiol Lett* **25**, 125–128.
- Wayne, L. G., Brenner, D. J., Colwell, R. R. & 9 other authors (1987). International Committee on Systematic Bacteriology. Report of the ad hoc committee on reconciliation of approaches to bacterial systematics. *Int J Syst Bacteriol* **37**, 463–464.
- Yoon, J.-H., Kim, H., Kim, S.-B., Kim, H.-J., Kim, W. Y., Lee, S. T., Goodfellow, M. & Park, Y.-H. (1996). Identification of *Saccharomonospora* strains by the use of genomic DNA fragments and rRNA gene probes. *Int J Syst Bacteriol* **46**, 502–505.
- Yoon, J.-H., Lee, S. T., Kim, S.-B., Goodfellow, M. & Park, Y.-H. (1997). Inter- and intraspecific genetic analysis of the genus *Saccharomonospora* with 16S to 23S ribosomal DNA (rDNA) and 23S to 5S rDNA internally transcribed spacer sequences. *Int J Syst Bacteriol* **47**, 661–669.
- Yoon, J.-H., Lee, S. T. & Park, Y.-H. (1998). Inter- and intraspecific phylogenetic analysis of the genus *Nocardioides* and related taxa based on 16S rDNA sequences. *Int J Syst Bacteriol* **48**, 187–194.
- Yoon, J.-H., Kang, S.-S., Lee, K.-C., Lee, E. S., Kho, Y. H., Kang, K. H. & Park, Y.-H. (2001). *Planomicrobium koreense* gen. nov., sp. nov., a bacterium isolated from the Korean traditional fermented seafood jeotgal, and transfer of *Planococcus okeanokoites* (Nakagawa *et al.* 1996) and *Planococcus mcmeekinii* (Junge *et al.* 1998) to the genus *Planomicrobium*. *Int J Syst Evol Microbiol* **51**, 1511–1520.
- Yoon, J.-H., Kim, I.-G., Shin, D.-Y., Kang, K. H. & Park, Y.-H. (2003). *Microbulbifer salipaludis* sp. nov., a moderate halophile isolated from a Korean salt marsh. *Int J Syst Evol Microbiol* **53**, 53–57.