Marinibacillus campisalis sp. nov., a moderate halophile isolated from a marine solar saltern in Korea, with emended description of the genus *Marinibacillus*

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A Gram-positive, motile, round to ellipsoidal, endospore-forming, rod-shaped bacterial strain, SF-57^T, was isolated from a marine solar saltern in Korea. This organism grew between 4 and 39 °C, with optimum growth at 30 °C. Strain SF-57^T grew in the presence of 0.5–15.0 % NaCl, with optimum growth at 2–3 % NaCl. The peptidoglycan type of strain SF-57^T was A1 α linked directly through L-Lys. In strain SF-57^T, menaquinone-7 (MK-7) was the predominant isoprenoid quinone and anteiso-C_{15:0} was the major fatty acid. The DNA G + C content was 41.8 mol%. Phylogenetic analyses based on 16S rRNA gene sequences showed that strain SF-57^T formed a coherent cluster with *Marinibacillus marinus*, with a bootstrap resampling value of 100 %. The level of 16S rRNA gene sequence similarity between strain SF-57^T and *M. marinus* DSM 1297^T was 98.9 %. The mean DNA–DNA relatedness level between strain SF-57^T and the type strain of *M. marinus* was 20.6 %. Based on phenotypic properties, phylogenetic analyses and genomic data, strain SF-57^T merits placement in the genus *Marinibacillus* as a representative of a novel species, for which the name *Marinibacillus campisalis* sp. nov. is proposed. The type strain is SF-57^T (=KCCM 41644^T=JCM 11810^T).

Bacillus species belonging to rRNA group 2 have been differentiated from other *Bacillus* species by their type of cell wall peptidoglycan and endospore shape, as well as by phylogenetic inference (Ash *et al.*, 1991; Rheims *et al.*, 1999; Stackebrandt *et al.*, 1987). Such observations have suggested that rRNA group 2 *Bacillus* species may be members of genera other than the genus *Bacillus* (Farrow *et al.*, 1994; Rheims *et al.*, 1999; Yoon *et al.*, 2001a). Differential taxonomic data have recently permitted reassignment of some rRNA group 2 *Bacillus* species to other existing genera or to new genera. *Bacillus globisporus*, *Bacillus psychrophilus*

and *Bacillus pasteurii* have been transferred to the genus *Sporosarcina*, and *Bacillus marinus* has been reclassified as a member of a new genus, *Marinibacillus* (Yoon *et al.*, 2001a, b). Recently, a round to ellipsoidal, endospore-forming Gram-positive rod (strain SF-57^T) was isolated from a marine solar saltern, Baekryung Island, Korea. This organism was phylogenetically related to *Bacillus* rRNA group 2, particularly to the genera *Marinibacillus* and *Jeotgalibacillus*, based on 16S rRNA gene sequence comparisons. Accordingly, the aim of the present study was to determine the exact taxonomic position of strain SF-57^T using a combination of phenotypic properties, detailed phylogenetic analyses based on 16S rRNA gene sequences and genomic relatedness.

Strain SF-57^T was isolated by the standard dilution plating technique on marine agar 2216 (MA; Difco). *Marinibacillus marinus* DSM 1297^T, used as a reference strain, was obtained from the Deutsche Sammlung von Mikroorganismen und

Published online ahead of print on 30 January 2004 as DOI 10.1099/ij.s.0.02779-0.

The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of *Marinibacillus campisalis* SF-57^T is AY190535.

A phylogenetic tree is available as supplementary material in IJSEM Online.

Zellkulturen (DSMZ), Braunschweig, Germany. Cell mass of strain SF-57^T for analyses of cell wall and menaquinones was obtained from cultures grown in marine broth 2216 (MB; Difco) at 30 °C. For DNA extraction, strain SF-57^T and *M. marinus* DSM 1297^T were cultivated in MB at 30 °C. For fatty acid methyl ester analysis, cell mass of strain SF-57^T was obtained from agar plates after cultivation for 3 days at 30 °C on MA. Cell morphology was observed with a Nikon light microscope. Flagellum type was examined using TEM with cells from exponentially growing cultures. Gram reaction was determined using the bioMérieux Gram Stain kit according to the manufacturer's instructions. Growth at various NaCl concentrations was investigated in MB. The pH range for growth was determined in MB adjusted to various pH values (pH 4.5–9.5 at intervals of 0.5 pH units). Growth at various temperatures was measured on MA at 4–50 °C. Growth under anaerobic conditions was determined by incubation in an anaerobic chamber on MA that had been prepared anaerobically. All physiological tests were performed at 30 °C, except for temperature range determinations. Oxidase activity was determined by examining oxidation of 1% (w/v) *p*-aminodimethylaniline oxalate. Catalase activity was determined by bubble production in a 3% (v/v) H₂O₂ solution. Hydrolysis of casein, starch and Tween 80, and urease activity were determined as described by Cowan & Steel (1965). Hydrolysis of aesculin and gelatin, and nitrate reduction were studied as described previously (Lanyi, 1987) with a modification that artificial sea water was used instead of distilled water. 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). Hydrolysis of birchwood xylan (Sigma) was determined on solid marine salts basal medium (Baumann & Baumann, 1981) containing 0.5% (w/v) xylan as sole carbon source. H₂S production was tested as described previously (Bruns *et al.*, 2001). Hydrolysis of hypoxanthine, tyrosine and xanthine was tested on MA plates using substrate concentrations described previously (Cowan & Steel, 1965). Acid production from carbohydrates was determined as described by Leifson (1963).

Preparation of cell wall samples and determination of peptidoglycan structure were carried out using the methods described by Schleifer (1985) and Schleifer & Kandler (1972), except that TLC on cellulose sheets was used instead of paper chromatography. GC-MS analysis of amino acid derivatives was performed as described by MacKenzie (1987). Menaquinones were analysed as described by Komagata & Suzuki (1987) using reversed-phase HPLC. For quantitative analysis of cellular fatty acid compositions, a loopful of cell mass was harvested and fatty acid methyl esters were prepared by the standard protocol of the MIDI/Hewlett Packard Microbial Identification system (Sasser, 1990). Chromosomal DNA was isolated and purified according to a method described previously (Yoon *et al.*, 1996), except that ribonuclease T1 was used with ribonuclease A. DNA 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.

The 16S rRNA gene was amplified by PCR using two universal primers as described previously (Yoon *et al.*, 1998). The PCR product was purified with a QIAquick PCR purification kit (Qiagen). Sequencing of the purified 16S rRNA gene was performed using an ABI PRISM BigDye Terminator cycle sequencing ready reaction kit (Applied Biosystems) as recommended by the manufacturer. The purified sequencing reaction mixtures were electrophoresed automatically on an Applied Biosystems model 377 automatic DNA sequencer. Alignment of sequences was carried out with CLUSTAL W software (Thompson *et al.*, 1994). Gaps at the 5' and 3' ends of the alignment were omitted from further analyses. Phylogenetic analyses were performed as described by Yoon *et al.* (2001b). DNA–DNA hybridization was performed fluorometrically by the method of Ezaki *et al.* (1989) using photobiotin-labelled DNA probes and microdilution wells. Hybridization reactions were replicated five times for each sample. Of the values obtained, the highest and lowest values in each sample were excluded and the remaining three measurements were used to calculate the mean relatedness value.

Strain SF-57^T was motile by means of a single polar flagellum. This flagellation pattern differed from the peritrichous pattern exhibited by members of the genus *Jeotgalibacillus* and *M. marinus* (Rüger, 1983; Yoon *et al.*, 2001b). Phenotypic properties of strain SF-57^T are shown in Table 1 or are given in the species description (see below). As shown in Table 1, some differences are observed between strain SF-57^T and *M. marinus*.

Strain SF-57^T did not contain any diaminopimelic acid as the diagnostic diamino acid in the cell wall peptidoglycan. The cell wall of strain SF-57^T contained peptidoglycan directly cross-linked with L-lysine as the diagnostic diamino acid. Accordingly, the peptidoglycan type of SF-57^T was concluded to be A1 α , based directly on L-Lys, as described by Schleifer & Kandler (1972). Dinitrophenylated cell walls of strain SF-57^T contained only DNP-lysine. This peptidoglycan type has also been found in the genera *Marinibacillus* and *Jeotgalibacillus* among members of the *Bacillus* rRNA group 2 (Rüger *et al.*, 2000; Yoon *et al.*, 2001b). The predominant menaquinone found in strain SF-57^T was menaquinone-7 (MK-7) (approx. 76%) and minor amounts of MK-8 (approx. 20%) were detected. Whereas the level of MK-7 in the type strain of *M. marinus* was 87%, the amount of this menaquinone in the genus *Jeotgalibacillus* was 62% (Yoon *et al.*, 2001b). Strain SF-57^T has a cellular fatty acid profile containing large amounts of branched and unsaturated fatty acids; the major fatty acid was anteiso-C_{15:0}. This cellular fatty acid profile of strain SF-57^T was more similar to that of the genus *Marinibacillus* than to that of the genus *Jeotgalibacillus* (Table 2). The cellular fatty acid profile of the genus *Marinibacillus* is characterized by the predominance of

Table 1. Phenotypic characteristics of strain SF-57^T and *M. marinus*

+, Positive reaction; –, negative reaction; w+, weakly positive reaction; v, variable reaction. Both species were rods and positive for growth at 5 °C, motility and catalase. Both species were negative for anaerobic growth, growth without NaCl, decomposition of urea, and acid production from L-arabinose, lactose, D-raffinose, L-rhamnose and D-sorbitol. Data in parentheses are for the type strain of *M. marinus*.

Characteristic	Strain SF-57 ^T	<i>Marinibacillus marinus</i> *
Spore shape	Round or ellipsoidal	Round or slightly ellipsoidal
Spore position	Terminal or subterminal	Terminal or subterminal
Swollen sporangia	Slight	– or slight
Gram staining	+ or v	+
Flagellum type	Single polar	Peritrichous
Cytochrome oxidase	–	v (–)
Nitrate reduction	+	v (–)
H ₂ S production	–	v (+)
Decomposition of:		
Aesculin	+	v (+)
Casein	+	v (+)
Gelatin	–	v (+)
Hypoxanthine	–	(–)
Starch	+	–
Tween 80	–	(–)
Tyrosine	–	(–)
Xanthine	–	(–)
Acid production from:†		
D-Glucose	+	v (+)
Maltose	+	v (+)
D-Trehalose	+	v (+)
D-Cellobiose	+	–
D-Xylose	–	v (+)
D-Mannitol	+	–
D-Mannose	–	v (+)
Sucrose	+	–
Growth at:		
7 % NaCl	+	v (w+)
10 % NaCl	+	–
Growth at:		
30 °C	+	v (+)
37 °C	+	–
Optimum growth temperature (°C)	30	12–23
Maximum growth temperature (°C)	39	30
DNA G + C content (mol%)	41.8	36.9–41.6

*Data from Rüger & Richter (1979), Rüger (1983), Rüger *et al.* (2000) and Yoon *et al.* (2001b).

†Isomer type of sugar (D or L) for *M. marinus* is unknown.

anteiso-C_{15:0}, whereas the genus *Jeotgalibacillus* is characterized by the predominance of iso-C_{15:0} (Table 2). Noteworthy differences were also found between strain SF-57^T and the type strain of *M. marinus* in the proportions of some fatty acids, particularly iso-C_{14:0}, iso-C_{15:0} and C_{16:1}ω7c alcohol (Table 2). The DNA G + C content of strain SF-57^T was 41.8 mol%.

An almost-complete 16S rRNA gene sequence of strain SF-57^T comprising 1506 nt (approx. 96 % of the *Escherichia*

coli 16S rRNA gene sequence) was determined directly after PCR amplification. Phylogenetic trees based on 16S rRNA gene sequences showed that strain SF-57^T was closely related to the genera *Marinibacillus* and *Jeotgalibacillus*. In the tree generated using the neighbour-joining algorithm, strain SF-57^T and *M. marinus* formed a coherent cluster supported by bootstrap analysis at a confidence level of 100 % (the phylogenetic tree is available as supplementary material in IJSEM Online). This cluster joined to the evolutionary lineage of *Jeotgalibacillus alimentarius*; this

Table 2. Cellular fatty acid profiles (%) of strain SF-57^T, *M. marinus* DSM 1297^T and *J. alimentarius* KCCM 80002^T*

Fatty acid	Strain SF-57 ^T	<i>M. marinus</i> DSM 1297 ^T *	<i>J. alimentarius</i> KCCM 80002 ^T *
Straight-chain fatty acids:			
C _{14:0}	0.8	ND	0.7
C _{15:0}	1.1	ND	1.1
C _{16:0}	0.9	1.5	3.9
C _{18:0}	ND	ND	3.4
Branched fatty acids:			
iso-C _{14:0}	14.1	5.3	2.1
iso-C _{15:0}	2.5	22.2	47.6
anteiso-C _{15:0}	49.8	47.7	15.2
iso-C _{16:0}	5.2	5.1	1.9
iso-C _{17:0}	ND	2.6	6.5
anteiso-C _{17:0}	7.4	10.7	4.6
iso-C _{17:1} ω10c			3.8
Unsaturated fatty acids:			
C _{16:1} ω7c alcohol	12.3	2.6	5.2
C _{16:1} ω11c	1.9	ND	1.2
Summed feature 4†	3.9	2.3	2.3

ND, Not detected.

*Data from Yoon *et al.* (2001b).

†Summed feature 4 contained one or more of following fatty acids: iso-C_{17:1} I and/or ante-C_{17:1} B, which could not be separated by GLC with the MIDI system.

relationship was supported by a bootstrap resampling value of 98.6 %. A similar phylogenetic relationship between strain SF-57^T, *M. marinus*, *J. alimentarius* and other members of *Bacillus* rRNA group 2 was also observed in trees generated with maximum-likelihood and maximum-parsimony algorithms (data not shown). The level of 16S rRNA gene sequence similarity between strain SF-57^T and *M. marinus* DSM 1297^T was 98.9 %. Strain SF-57^T exhibited 95.9 % 16S rRNA gene sequence similarity to *J. alimentarius* KCCM 80002^T and less than 94.1 % similarity to other species used in the phylogenetic analyses. The mean level of DNA–DNA relatedness between strain SF-57^T and *M. marinus* DSM 1297^T was 20.6 %, when each of their DNAs was separately used as labelled DNA probe. These data indicate that strain SF-57^T is a member of a genomic species that is distinct from *M. marinus* (Wayne *et al.*, 1987).

Strain SF-57^T exhibited closest phylogenetic affiliation to *M. marinus* according to 16S rRNA gene sequence analyses (phylogenetic tree available in IJSEM Online). The chemotaxonomic traits of strain SF-57^T are most similar to those of the genus *Marinibacillus* (Yoon *et al.*, 2001b). Therefore, both phylogenetic and chemotaxonomic results clearly indicate that strain SF-57^T belongs to the genus *Marinibacillus*. The levels of DNA–DNA relatedness, together with some differing phenotypic properties and phylogenetic distinctiveness, justify separation of strain SF-57^T from

M. marinus, the single species of the genus *Marinibacillus* (Wayne *et al.*, 1987). Therefore, on the basis of phenotypic, chemotaxonomic and phylogenetic data, and genomic distinctiveness, strain SF-57^T should be classified as a representative of a novel species in the genus *Marinibacillus*; the name *Marinibacillus campisalis* sp. nov. is proposed.

Description of *Marinibacillus campisalis* sp. nov.

Marinibacillus campisalis (cam.pi.sa'lis. L. n. *campus* field; L. gen. n. *salis* of salt; N.L. gen. n. *campisalis* of the field of salt).

Cells are rods, 1.3–1.6 × 2.5–4.0 µm. Gram-positive, but Gram-variable in older cultures. Round to ellipsoidal endospores lie centrally or subterminally in slightly swollen sporangia. Colonies are smooth, glistening, circular to slightly irregular, flat to raised, light orange–yellow in colour and 2–3 mm in diameter after 3 days incubation on marine agar 2216. Growth occurs at 4 °C; maximum growth temperature is 39 °C. Optimal pH for growth is 7.0–8.0; no growth occurs at pH 4.5. Optimal growth occurs in the presence of 2–3 % (w/v) NaCl. Growth occurs in the presence of 15 % NaCl, but not 16 % NaCl. Xylan is not hydrolysed. Acid is produced from D-fructose and melibiose, and weakly produced from D-melezitose. Acid is not produced from adonitol, D-galactose, *myo*-inositol, D-ribose or stachyose. Other characteristics are given in Table 1. The peptidoglycan type is A1α (L-Lys direct). The predominant menaquinone is MK-7. The major fatty acid is anteiso-C_{15:0}.

The type strain, SF-57^T (=KCCM 41644^T=JCM 11810^T), was isolated from a marine solar saltern in Korea. Its DNA G + C content is 41.8 mol% (determined by HPLC).

Emended description of the genus *Marinibacillus*

The description of the genus *Marinibacillus* is as given by Yoon *et al.* (2001b) but with the following amendments. Motile by means of single polar flagellum or peritrichous flagella. Starch hydrolysis is variable. Growth at 37 °C is variable. Growth in the presence of 10 % NaCl is variable. The DNA G + C content is 36.9–41.8 mol%.

Acknowledgements

This work was supported by the 21C Frontier programme of Microbial Genomics and Applications (grant MG02-0401-001-1-0-0) and the NRL research programme (grant M10104000294-01J000012811) from the Ministry of Science and Technology (MOST) of the Republic of Korea and by the research fund of Probiotic Corporation of Korea.

References

Ash, C., Farrow, J. A. E., Wallbanks, S. & Collins, M. D. (1991). Phylogenetic heterogeneity of the genus *Bacillus* as revealed by comparative analysis of small-subunit-ribosomal RNA sequences. *Lett Appl Microbiol* 13, 202–206.

- Baumann, L. & Baumann, P. (1981). The marine Gram-negative eubacteria; genera *Photobacterium*, *Beneckea*, *Alteromonas*, *Pseudomonas*, and *Alcaligenes*. In *The Prokaryotes*, pp. 1302–1330. Edited by M. P. Starr, H. Stolp, H. G. Trüper, A. Balows & H. G. Schlegel. Berlin: Springer.
- Bruns, A., Rohde, M. & Berthe-Corti, L. (2001). *Muricauda ruestringensis* gen. nov., sp. nov., a facultatively anaerobic, appendaged bacterium from German North Sea intertidal sediment. *Int J Syst Evol Microbiol* 51, 1997–2006.
- Cowan, S. T. & Steel, K. J. (1965). *Manual for the Identification of Medical Bacteria*. London: Cambridge University Press.
- Ezaki, T., Hashimoto, Y. & Yabuuchi, E. (1989). Fluorometric deoxyribonucleic acid-deoxyribonucleic acid hybridization in microdilution 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.
- Farrow, J. A. E., Wallbanks, S. & Collins, M. D. (1994). Phylogenetic interrelationships of round-spore-forming bacilli containing cell walls based on lysine and the non-spore-forming genera *Caryophanon*, *Exiguobacterium*, *Kurthia*, and *Planococcus*. *Int J Syst Bacteriol* 44, 74–82.
- Komagata, K. & Suzuki, K. I. (1987). Lipid and cell-wall analysis in bacterial systematics. *Methods Microbiol* 19, 161–206.
- 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. *K Fysiogr Sallsk Lund Forh* 16, 45–56.
- MacKenzie, S. L. (1987). Gas chromatographic analysis of amino acids as the *N*-heptafluorobutyl isobutyl esters. *J Assoc Off Anal Chem* 70, 151–160.
- Rheims, H., Frühling, A., Schumann, P., Rohde, M. & Stackebrandt, E. (1999). *Bacillus silvestris* sp. nov., a new member of the genus *Bacillus* that contains lysine in its cell wall. *Int J Syst Bacteriol* 49, 795–802.
- Rüger, H.-J. (1983). Differentiation of *Bacillus globisporus*, *Bacillus marinus* comb. nov., *Bacillus aminovorans*, and *Bacillus insolitus*. *Int J Syst Bacteriol* 33, 157–161.
- Rüger, H. J. & Richter, G. (1979). *Bacillus globisporus* subsp. *marinus* subsp. nov. *Int J Syst Bacteriol* 29, 196–203.
- Rüger, H. J., Fritze, D. & Spröer, C. (2000). New psychrophilic and psychrotolerant *Bacillus marinus* strains from tropical and polar deep-sea sediments and emended description of the species. *Int J Syst Evol Microbiol* 50, 1305–1313.
- Sasser, M. (1990). Identification of bacteria by gas chromatography of cellular fatty acids. *Technical Note 101*. Newark, DE: MIDI.
- Schleifer, K. H. (1985). Analysis of the chemical composition and primary structure of murein. *Methods Microbiol* 18, 123–156.
- Schleifer, K. H. & Kandler, O. (1972). Peptidoglycan types of bacterial cell walls and their taxonomic implications. *Bacteriol Rev* 36, 407–477.
- Stackebrandt, E., Ludwig, W., Weizenegger, M., Dorn, S., McGill, T. J., Fox, G. E., Woese, C. E., Schubert, W. & Schleifer, K.-H. (1987). Comparative 16S rRNA oligonucleotide analyses and murein types of round-spore-forming bacilli and non-spore-forming relatives. *J Gen Microbiol* 133, 2523–2529.
- Tamaoka, J. & Komagata, K. (1984). Determination of DNA base composition by reversed-phase high-performance liquid chromatography. *FEMS Microbiol Lett* 25, 125–128.
- Thompson, J. D., Higgins, D. G. & Gibson, T. J. (1994). CLUSTAL W: improving the sensitivity of progressive multiple sequence alignment through sequence weighting, position-specific gap penalties and weight matrix choice. *Nucleic Acids Res* 22, 4673–4680.
- 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. & Park, Y.-H. (1998). Inter- and intra-specific phylogenetic analysis of the genus *Nocardioidea* and related taxa based on 16S rDNA sequences. *Int J Syst Bacteriol* 48, 187–194.
- Yoon, J.-H., Lee, K.-C., Weiss, N., Kho, Y. H., Kang, K. H. & Park, Y.-H. (2001a). *Sporosarcina aquimarina* sp. nov., a bacterium isolated from seawater in Korea, and transfer of *Bacillus globisporus* (Larkin and Stokes 1967), *Bacillus psychrophilus* (Nakamura 1984) and *Bacillus pasteurii* (Chester 1898) to the genus *Sporosarcina* as *Sporosarcina globispora* comb. nov., *Sporosarcina psychrophila* comb. nov. and *Sporosarcina pasteurii* comb. nov., and emended description of the genus *Sporosarcina*. *Int J Syst Evol Microbiol* 51, 1079–1086.
- Yoon, J.-H., Weiss, N., Lee, K.-C., Lee, I.-S., Kang, K. H. & Park, Y.-H. (2001b). *Jeotgalibacillus alimentarius* gen. nov., sp. nov., a novel bacterium isolated from jeotgal with L-lysine in the cell wall, and reclassification of *Bacillus marinus* Rüger 1983 as *Marinibacillus marinus* gen. nov., comb. nov. *Int J Syst Evol Microbiol* 51, 2087–2093.