Jeotgalibacillus salarius sp. nov., isolated from a marine saltern, and reclassification of *Marinibacillus marinus* and *Marinibacillus campisalis* as *Jeotgalibacillus marinus* comb. nov. and *Jeotgalibacillus campisalis* comb. nov., respectively

Jung-Hoon Yoon,¹ So-Jung Kang,¹ Peter Schumann²
and Tae-Kwang Oh¹

Correspondence
Jung-Hoon Yoon
jhyoon@kribb.re.kr

¹Korea Research Institute of Bioscience and Biotechnology (KRIBB), PO Box 115, Yusong, Taejeon, Republic of Korea

²DSMZ-Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH, Mascheroder Weg 1B, D-38124 Braunschweig, Germany

A Gram-variable, motile and rod-shaped bacterial strain, ASL-1^T, was isolated from a marine saltern located on the coast of the Yellow Sea, Korea. A neighbour-joining phylogenetic tree based on 16S rRNA gene sequences showed that strain ASL-1^T clustered with *Jeotgalibacillus alimentarius* YKJ-13^T and that this cluster joined the clade comprising the type strains of two *Marinibacillus* species. Strain ASL-1^T exhibited 16S rRNA gene sequence similarity values of 97.3% to *J. alimentarius* YKJ-13^T and 96.5% to the type strains of *Marinibacillus marinus* and *Marinibacillus campisalis*. The chemotaxonomic properties of strain ASL-1^T were similar to those of one or two of the genera *Jeotgalibacillus* and *Marinibacillus*. The peptidoglycan type was A1 α linked directly through L-lysine as the diamino acid. Strain ASL-1^T contained MK-7 as the predominant menaquinone with the presence of a significant amount of MK-8. The predominant fatty acid was anteiso-C_{15:0}. The DNA G+C content was 42.9 mol%. Differential phenotypic properties, together with the phylogenetic and genetic distinctiveness, revealed that strain ASL-1^T could be differentiated from *J. alimentarius* and the two *Marinibacillus* species. On the basis of the data presented, strain ASL-1^T represents a novel species within the genus *Jeotgalibacillus*, for which the name *Jeotgalibacillus salarius* sp. nov. is proposed. The type strain is ASL-1^T (=KCTC 13257^T=CCUG 56751^T). It is also proposed that *Marinibacillus marinus* and *Marinibacillus campisalis* be reclassified as *Jeotgalibacillus marinus* comb. nov. (type strain 581^T=DSM 1297^T=ATCC 29841^T=CCUG 28884^T=CIP 103308^T=LMG 6930^T) and *Jeotgalibacillus campisalis* comb. nov. (type strain SF-57^T=KCCM 41644^T=JCM 11810^T), respectively.

The genus *Jeotgalibacillus* was created by Yoon *et al.* (2001b) with the description of *Jeotgalibacillus alimentarius* as the sole recognized species of the genus. The genus *Jeotgalibacillus* is characterized chemotaxonomically by having cell-wall peptidoglycan based on L-lysine as the diamino acid, MK-7 and MK-8 as the predominant menaquinones and major amounts of the fatty acid iso-C_{15:0}. *J. alimentarius* was isolated from a Korean traditional fermented seafood, jeotgal. The genus *Jeotgalibacillus* is most phylogenetically closely related to the genus *Marinibacillus* (Yoon *et al.*, 2001b, 2004). The genus *Marinibacillus* was proposed by Yoon *et al.* (2001b) by the reclassification of

Bacillus marinus (Rüger & Richter, 1979; Rüger, 1983) and subsequently, another species, *Marinibacillus campisalis* (Yoon *et al.*, 2004), was described. Members of the genus *Marinibacillus* have cell-wall peptidoglycan based on L-lysine as the diamino acid, MK-7 as the predominant menaquinone and anteiso-C_{15:0} as the predominant fatty acid (Yoon *et al.*, 2001b, 2004). In this study, we describe a bacterial strain, ASL-1^T, which was isolated from a marine saltern in Korea. This isolate was phylogenetically related to the genera *Jeotgalibacillus* and *Marinibacillus* on the basis of 16S rRNA gene sequence comparisons. The aim of the present work was to determine the exact taxonomic position of strain ASL-1^T by using a polyphasic characterization and to re-evaluate the taxonomic status of the genera *Jeotgalibacillus* and *Marinibacillus*.

The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain ASL-1^T is EU874389.

Strain ASL-1^T was isolated by means of the standard dilution plating technique at 30 °C on marine agar 2216 (MA; Difco) supplemented with 8 % (w/v) NaCl. *J. alimentarius* YKJ-13^T, *Marinibacillus marinus* DSM 1297^T and *M. campisalis* SF-57^T were used as reference strains for DNA–DNA hybridization and/or phenotypic characterization. The morphological, physiological and biochemical characteristics of strain ASL-1^T were investigated using routine cultivation on MA at 30 °C. Cell morphology was examined by using light microscopy (E600; Nikon) and transmission electron microscopy. Flagellation was determined using a Philips CM-20 transmission electron microscope with cells from exponentially growing cultures. For this purpose, the cells were negatively stained with 1 % (w/v) phosphotungstic acid and the grids were examined after being air-dried. Growth under anaerobic conditions was determined after incubation in a Forma anaerobic chamber on MA and on MA supplemented with potassium nitrate (0.1 %, w/v), both of which had been prepared anaerobically under a nitrogen atmosphere. The pH range for growth was determined in marine broth 2216 (MB; Difco), adjusted to various pH values (pH 4.5–9.5, at intervals of 0.5 pH units) by the addition of HCl or Na₂CO₃. Growth in the absence of NaCl was investigated using trypticase soy broth prepared according to the formula of the Difco medium except that NaCl was excluded. Growth in the absence of NaCl and in the presence of 0.5, 1.0, 2.0 and 3.0 % (w/v) NaCl was investigated by using trypticase soy broth, using supplementation with 0.45 % (w/v) MgCl₂·6H₂O or 0.06 % (w/v) KCl, prepared according to the formula of the Difco medium except that NaCl was excluded. Growth at various NaCl concentrations (2.0–20.0 %, w/v, at increments of 1.0 %) was investigated in MB. Growth at various temperatures (4, 10, 15, 20, 25, 28, 30, 35, 37, 40 and 45 °C) was measured on MA. Catalase and oxidase activities and hydrolysis of casein, starch and Tweens 20, 40, 60 and 80 were determined as described by Cowan & Steel (1965). Hydrolysis of hypoxanthine, tyrosine and xanthine was tested on MA using the substrate concentrations described by Cowan & Steel (1965). Hydrolysis of aesculin, gelatin and urea and nitrate reduction were investigated as described previously (Lányi, 1987) with the modification that artificial seawater was used for the preparation of media. The artificial seawater 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 (Bruns *et al.*, 2001). H₂S production was tested as described previously (Bruns *et al.*, 2001). Susceptibility to antibiotics was investigated on MA plates by using antibiotic discs with the following concentrations: polymyxin B (100 U), streptomycin (50 µg), penicillin G (20 U), chloramphenicol (100 µg), ampicillin (10 µg), cephalothin (30 µg), gentamicin (30 µg), novobiocin (5 µg), tetracycline (30 µg), kanamycin (30 µg), lincomycin (15 µg), oleandomycin (15 µg), neomycin (30 µg) and carbenicillin (100 µg). Acid production from carbohydrates was tested as described by Leifson (1963). Enzyme

activities were determined by using the API ZYM system (bioMérieux) with the modification that the cells used to inoculate the API ZYM strip were suspended in artificial seawater and the strip was incubated for 8 h.

Cell biomass for DNA extraction and for the analyses of cell-wall peptidoglycan and isoprenoid quinones was obtained from cultures grown in MB at 30 °C. Chromosomal DNA was isolated and purified according to the method described by Yoon *et al.* (1996), with the exception that RNase T1 was used in combination with RNase A to minimize the contamination of RNA. The 16S rRNA gene was amplified by PCR using two universal primers, 5'-GAGTTTGATCCTGGCTCAG-3' and 5'-AGAAAGGAGGTGATCCAGCC-3', as described previously (Yoon *et al.*, 1998). Sequencing of the amplified 16S rRNA gene and phylogenetic analysis were performed as described by Yoon *et al.* (2003). Preparation of cell walls and determination of peptidoglycan structure were carried out by using methods described by Schleifer & Kandler (1972), MacKenzie (1987) and Groth *et al.* (1996). Isoprenoid quinones were analysed as described by Komagata & Suzuki (1987) using reversed-phase HPLC and a YMC ODS-A (250 × 4.6 mm) column. For cellular fatty acid analysis, cell mass of strain ASL-1^T and *J. alimentarius* YKJ-13^T was harvested from MA plates after cultivation for 3 days at 30 °C. The fatty acids were extracted and fatty acid methyl esters were prepared according to the standard protocol of the MIDI/Hewlett Packard Microbial Identification System (Sasser, 1990). The DNA G+C content was determined by using the method of Tamaoka & Komagata (1984) with the modification that DNA was hydrolysed using nuclease P1 (Sigma) and the resultant nucleotides were analysed by using reversed-phase HPLC. DNA–DNA hybridization was performed fluorometrically using the method of Ezaki *et al.* (1989) with photobiotin-labelled DNA probes and microdilution wells. Hybridization was performed with five replications for each sample. The highest and lowest values obtained in each sample were excluded, and the means of the remaining three values were quoted as DNA–DNA relatedness values.

Morphological, cultural, physiological and biochemical characteristics of strain ASL-1^T are given in the species description (see below) or are shown in Table 1. The almost-complete 16S rRNA gene sequence of strain ASL-1^T determined in this study comprised 1507 nt, representing approximately 96 % of the *Escherichia coli* 16S rRNA gene sequence. In the phylogenetic tree based on the neighbour-joining algorithm, strain ASL-1^T clustered with *J. alimentarius* YKJ-13^T with a bootstrap resampling value of 95.1 %, and this cluster joined the clade comprising two *Marinibacillus* species with a bootstrap resampling value of 99.5 % (Fig. 1). The same topology was also found in the trees constructed using the maximum-likelihood and maximum-parsimony algorithms (Fig. 1). Strain ASL-1^T exhibited a 16S rRNA gene sequence similarity value of 97.3 % to *J. alimentarius* YKJ-13^T and relatively high

Table 1. Differential phenotypic characteristics of *Jeotgalibacillus salarius* and the type strains of *Jeotgalibacillus* and *Marinibacillus* species

Species: 1, *J. salarius* sp. nov.; 2, *J. alimentarius* (data from Yoon *et al.*, 2001b and this study); 3, *M. marinus* (Rüger, 1983; Yoon *et al.*, 2001b; this study); 4, *M. campisalis* (Yoon *et al.*, 2004; this study). +, Positive reaction; –, negative reaction; w, weakly positive reaction; v, variable reaction; ND, not determined. All species were rod-shaped and positive for motility, catalase, hydrolysis of aesculin and casein, acid production from D-fructose, D-glucose, maltose, sucrose and trehalose, and susceptibility to carbenicillin, cephalothin, chloramphenicol, gentamicin, neomycin, oleandomycin and penicillin G. All species were negative for hydrolysis of hypoxanthine, xanthine, tyrosine and urea, and acid production from L-arabinose, lactose, L-rhamnose, *myo*-inositol and D-sorbitol, susceptibility to polymyxin B, and activity of alkaline phosphatase, lipase (C14), leucine arylamidase, valine arylamidase, cystine arylamidase, trypsin, α -chymotrypsin, acid phosphatase, α -galactosidase, β -glucuronidase, β -glucosidase, *N*-acetyl- β -glucosaminidase, α -mannosidase and α -fucosidase.

Characteristic	1	2	3	4
Spore shape	Ellipsoidal	Round	Round or slightly ellipsoidal	Round or ellipsoidal
Spore position	Subterminal	Terminal or subterminal	Terminal or subterminal	Terminal or subterminal
Swollen sporangia	Slight	+	– or slight	Slight
Flagella type	Peritrichous	Peritrichous	Peritrichous	Single polar
Gram staining	v	v	+	+ or v
Anaerobic growth	–	+	–	–
Oxidase	+	+	–	–
Nitrate reduction	–	+	–	+
Growth at 20 % NaCl	–	w	–	–
Optimum growth temperature (°C)	30	30–35	12–23	30
Growth at:				
5 °C	+	–	+	+
45 °C	–	+	–	–
Hydrolysis of:				
Gelatin	–	+	+	–
Starch	–	–	–	+
Tween 80	w	+	–	–
Acid production from:				
Cellobiose	w	–	–	+
D-Galactose	+	+	–	–
Mannitol	+	+	–	+
D-Mannose	–	–	+	–
Melezitose	+	+	ND	w
Melibiose	–	+	–	+
Raffinose	–	+	–	–
D-Ribose	+	+	ND	–
D-Xylose	–	–	+	–
Susceptibility to antibiotics*				
Streptomycin	+	+	–	+
Ampicillin	+	+	–	+
Novobiocin	+	+	–	–
Tetracycline	+	–	–	–
Kanamycin	+	+	–	+
Lincomycin	+	+	–	–
Enzyme activity (API ZYM)*				
Esterase (C4)	+	+	–	–
Esterase lipase (C8)	+	+	–	w
Naphthol-AS-BI-phosphohydrolase	–	–	+	w
β -Galactosidase	–	+	–	+
α -Glucosidase	–	+	–	–
Predominant menaquinone(s)	MK-7, MK-8	MK-7, MK-8	MK-7	MK-7, MK-8
Predominant fatty acid	anteiso-C _{15:0}	iso-C _{15:0}	anteiso-C _{15:0}	anteiso-C _{15:0}
DNA G + C content (mol%)	42.9	44	39.3 ± 0.5	41.8

*Data for the type strains of reference species were from this study.

Fig. 1. Neighbour-joining phylogenetic tree based on 16S rRNA gene sequences showing the positions of *J. salarius* ASL-1^T and some other related taxa. Bootstrap values (expressed as percentages of 1000 replications) of >50% are shown at branch points. Filled circles indicate that the corresponding nodes were also recovered in the trees generated with the maximum-likelihood and maximum-parsimony algorithms. *Paenibacillus polymyxa* NCDO 1774^T was used as an outgroup. Bar, 0.01 substitutions per nucleotide position.

similarity values (96.5%) to the type strains of the two *Marinibacillus* species. It exhibited 16S rRNA gene sequence similarity values less than 94.2% to other species used in the phylogenetic analysis.

The total hydrolysate of the peptidoglycan (4 M HCl, 16 h at 100 °C) of strain ASL-1^T contained the amino acids alanine, glutamic acid and lysine in the approximate ratio 1.6:1.2:1.0. The partial hydrolysate contained the peptides L-Ala-D-Glu and L-Lys-D-Ala in addition to the amino acids. From these data, it was concluded that strain ASL-1^T has the peptidoglycan type A1 α , L-Lys-direct, as described by Schleifer & Kandler (1972). The predominant menaquinone detected in strain ASL-1^T was MK-7 (approx. 75%); a significant amount of MK-8 (approx. 21%) was also detected. The cellular fatty acid profile of strain ASL-1^T is shown in Table 2, together with those of *J. alimentarius* YKJ-13^T analysed in this study and two *Marinibacillus* species analysed previously (Yoon *et al.*, 2001b, 2004). Strain ASL-1^T had large amounts of branched and unsaturated fatty acids; the major components (each constituting >10% of total fatty acids) were anteiso-C_{15:0}, C_{16:1} ω 7c alcohol, anteiso-C_{17:0}, iso-C_{16:0} and iso-C_{14:0}. This fatty acid profile of strain ASL-1^T was more similar to those of the type strains of two *Marinibacillus* species than to that of *J. alimentarius* YKJ-13^T, in that anteiso-C_{15:0} was the predominant fatty acid (Tables 1 and 2). The DNA G + C content of strain ASL-1^T was 42.9 mol%.

The cell-wall peptidoglycan types (L-Lys-direct) of strain ASL-1^T and the genera *Jeotgalibacillus* and *Marinibacillus* were found to be identical (Yoon *et al.*, 2001b, 2004). The

Table 2. Cellular fatty acid compositions (%) of *Jeotgalibacillus* and *Marinibacillus* species

Strains: 1, ASL-1^T (*J. salarius* sp. nov.); 2, *J. alimentarius* YKJ-13^T (data from this study); 3, *M. marinus* DSM 1297^T (Yoon *et al.*, 2001b); 4, *M. campisalis* SF-57^T (Yoon *et al.*, 2004). Fatty acids that represent <0.5% in all strains were omitted. —, Not detected.

Fatty acid	1	2	3	4
Straight-chain fatty acid				
C _{14:0}	0.2	0.3	—	0.8
C _{15:0}	1.1	1.0	—	1.1
C _{16:0}	0.5	0.5	1.5	0.9
Unsaturated fatty acid				
C _{16:1} ω 7c alcohol	12.6	6.7	2.6	12.3
C _{16:1} ω 11c	0.7	1.0	—	1.9
Branched fatty acid				
iso-C _{14:0}	10.8	4.2	5.3	14.1
iso-C _{15:0}	9.4	46.3	22.2	2.5
anteiso-C _{15:0}	35.9	15.8	47.7	49.8
iso-C _{16:0}	12.0	6.3	5.1	5.2
iso-C _{17:1} ω 10c	0.3	2.3	—	—
iso-C _{17:0}	1.7	7.6	2.6	—
anteiso-C _{17:0}	12.2	5.8	10.7	7.4
Summed feature*				
4	2.4	1.9	2.3	3.9

*Summed features represent groups of two or three fatty acids that cannot be separated by GLC with the MIDI system. Summed feature 4 contains iso-C_{17:1} and/or anteiso-C_{17:1}.

genus *Jeotgalibacillus* was distinguished from the genus *Marinibacillus*, in which a significant amount of MK-8 is absent and the predominant fatty acid is anteiso-C_{15:0} (Yoon *et al.*, 2001b). However, the second *Marinibacillus* species, *M. campisalis*, was found to contain a significant amount of MK-8, although it formed a coherent cluster with *M. marinus* in the phylogenetic tree based on 16S rRNA gene sequences and contained anteiso-C_{15:0} as the predominant fatty acid (Yoon *et al.*, 2004). Strain ASL-1^T formed a coherent phylogenetic cluster with *J. alimentarius* and contained a significant amount of MK-8, but contained anteiso-C_{15:0} as the predominant fatty acid, which is characteristic of the genus *Marinibacillus*. Because of the data given above, the taxonomic status of the genera *Jeotgalibacillus* and *Marinibacillus* might have to be re-evaluated by considering the phylogenetic and chemotaxonomic data. The isoprenoid quinone profiles of strain ASL-1^T and members of the two genera were similar in that the predominant menaquinone was MK-7, although strain ASL-1^T, *J. alimentarius* and *M. campisalis* contained significant amounts of MK-8 (approx. 20–35%). The intrageneric differences in fatty acid profiles have been reported for members of some related genera (Yoon *et al.*, 2001a; Hanada *et al.*, 2002; Hua *et al.*, 2007; Nam *et al.*, 2008). Taking into account these data, it is likely to be more reasonable that the genera *Jeotgalibacillus* and

Marinibacillus should be integrated into one genus, *Jeotgalibacillus*. Accordingly, it is proposed that *M. marinus* and *M. campisalis* be reclassified as members of the genus *Jeotgalibacillus* and strain ASL-1^T be considered as a member of the genus *Jeotgalibacillus*.

Strain ASL-1^T exhibited a mean DNA–DNA relatedness value of 13 % with respect to *J. alimentarius* YKJ-13^T. Strain ASL-1^T could be distinguished from *J. alimentarius* and the two *Marinibacillus* species by differences in several phenotypic characteristics, including spore shape, anaerobic growth, nitrate reduction, hydrolysis of and acid production from several substrates, activity of some enzymes and susceptibility to antibiotics (Table 1). The phylogenetic and genetic distinctiveness and the differential phenotypic properties of strain ASL-1^T are sufficient to categorize it as a member of a species that is separate from *J. alimentarius* and the two *Marinibacillus* species (Wayne *et al.*, 1987; Stackebrandt & Goebel, 1994). On the basis of the data presented, strain ASL-1^T represents a novel species of the genus *Jeotgalibacillus*, for which the name *Jeotgalibacillus salarius* sp. nov. is proposed.

Description of *Jeotgalibacillus salarius* sp. nov.

Jeotgalibacillus salarius (sa.la'ri.us. L. masc. adj. *salarius* of salt).

Cells are Gram-variable and rod-shaped (0.4–0.7 × 1.3–8.5 µm). Cells longer than 10.0 µm occasionally occur. Subterminal ellipsoidal endospores are observed in slightly swollen sporangia. Motile by means of peritrichous flagella. Colonies on MA are circular to irregular, raised, glistening, smooth, light-yellow in colour and 2.0–3.0 mm in diameter after 2 days incubation at 30 °C. The optimal growth temperature is 30 °C; growth occurs at 4 and 40 °C, but not at 45 °C. The optimal pH for growth is between 7.0 and 8.0; growth occurs at pH 6.0, but not at pH 5.5. Optimal growth occurs in the presence of 2 % (w/v) NaCl; growth occurs at 0–18 % (w/v) NaCl. Mg²⁺ ions are required for growth. Anaerobic growth does not occur on MA or on MA supplemented with nitrate. Catalase- and oxidase-positive. Nitrate reduction is negative. Aesculin and casein are hydrolysed and Tween 80 is weakly hydrolysed, but gelatin, starch, hypoxanthine, xanthine, tyrosine and urea are not. Acid is produced from D-fructose, D-galactose, D-glucose, maltose, D-mannitol, melezitose, D-ribose, sucrose and trehalose and weakly produced from cellobiose, but not from L-arabinose, myo-inositol, lactose, D-mannose, melibiose, L-rhamnose, raffinose, D-sorbitol or D-xylose. Esterase (C4) and esterase lipase (C8) are present, but alkaline phosphatase, lipase (C14), leucine arylamidase, valine arylamidase, cystine arylamidase, trypsin, α-chymotrypsin, acid phosphatase, naphthol-AS-BI-phosphohydrolase, α-galactosidase, β-galactosidase, β-glucuronidase, α-glucosidase, β-glucosidase, N-acetyl-β-glucosaminidase, α-mannosidase and α-fucosidase are absent. Susceptible to ampicillin, carbenicillin, cephalothin, chloramphenicol, gentamicin, kanamycin, lincomycin, neomycin, novobiocin, oleandomycin, penicillin G, streptomycin and tetracycline, but not to polymyxin B. The peptidoglycan type is A1α (L-Lys-direct). The predominant menaquinone is MK-7; a significant amount of MK-8 is also present. Major fatty acids (>10 % of total fatty acids) are anteiso-C_{15:0}, C_{16:1}ω7c alcohol, anteiso-C_{17:0}, iso-C_{16:0} and iso-C_{14:0}. The DNA G+C content of the type strain is 42.9 mol% (determined by HPLC).

cin, lincomycin, neomycin, novobiocin, oleandomycin, penicillin G, streptomycin and tetracycline, but not to polymyxin B. The peptidoglycan type is A1α (L-Lys-direct). The predominant menaquinone is MK-7; a significant amount of MK-8 is also present. Major fatty acids (>10 % of total fatty acids) are anteiso-C_{15:0}, C_{16:1}ω7c alcohol, anteiso-C_{17:0}, iso-C_{16:0} and iso-C_{14:0}. The DNA G+C content of the type strain is 42.9 mol% (determined by HPLC).

The type strain, ASL-1^T (=KCTC 13257^T=CCUG 56751^T), was isolated from sediment of a marine saltern located on the coast of the Yellow Sea, Korea.

Description of *Jeotgalibacillus marinus* (Rüger and Richter 1979) comb. nov.

Jeotgalibacillus marinus (ma.ri'nus. L. masc. adj. *marinus* of the sea, marine).

Basonym: *Bacillus globisporus* subsp. *marinus* Rüger and Richter 1979 (Approved Lists 1980).

Marinibacillus marinus (Rüger and Richter 1979) Yoon *et al.* 2001 is another homotypic synonym.

The description is the same as those given by Rüger & Richter (1979), Rüger (1983), Rüger *et al.* (2000) and Yoon *et al.* (2001b). Additional characteristics for the type strain determined in this study are as follows. Naphthol-AS-BI-phosphohydrolase is present, but alkaline phosphatase, esterase (C4), esterase lipase (C8), lipase (C14), leucine arylamidase, valine arylamidase, cystine arylamidase, trypsin, α-chymotrypsin, acid phosphatase, α-galactosidase, β-galactosidase, β-glucuronidase, α-glucosidase, β-glucosidase, N-acetyl-β-glucosaminidase, α-mannosidase and α-fucosidase are absent. Susceptible to carbenicillin, cephalothin, chloramphenicol, gentamicin, neomycin, oleandomycin and penicillin G, but not to ampicillin, kanamycin, lincomycin, novobiocin, polymyxin B, streptomycin or tetracycline.

The type strain is strain 581^T (=DSM 1297^T=ATCC 29841^T=CCUG 28884^T=CIP 103308^T=LMG 6930^T).

Description of *Jeotgalibacillus campisalis* Yoon *et al.* 2004 comb. nov.

Jeotgalibacillus 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).

Basonym: *Marinibacillus campisalis* Yoon *et al.* 2004.

The description is the same as that given by Yoon *et al.* (2004). Additional characteristics determined in this study are as follows. β-Galactosidase is present and esterase lipase (C8) and naphthol-AS-BI-phosphohydrolase are weakly present, but alkaline phosphatase, esterase (C4), lipase (C14), leucine arylamidase, valine arylamidase, cystine arylamidase, trypsin, α-chymotrypsin, acid phosphatase, α-galactosidase, β-glucuronidase, α-glucosidase, β-glucosi-

dase, *N*-acetyl- β -glucosaminidase, α -mannosidase and α -fucosidase are absent. Susceptible to ampicillin, carbenicillin, cephalothin, chloramphenicol, gentamicin, kanamycin, neomycin, oleandomycin, penicillin G and streptomycin, but not to lincomycin, novobiocin, polymyxin B or tetracycline.

The type strain is strain SF-57^T (=KCCM 41644^T=JCM 11810^T).

Acknowledgements

This work was supported by the 21C Frontier program of Microbial Genomics and Applications (grant MG05-0401-2-0) from the Ministry of Science and Technology (MOST) of the Republic of Korea.

References

- 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 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.
- Groth, I., Schumann, P., Weiss, N., Martin, K. & Rainey, F. A. (1996). *Agrococcus jenensis* gen. nov., sp. nov., a new genus of actinomycetes with diaminobutyric acid in the cell wall. *Int J Syst Bacteriol* **46**, 234–239.
- Hanada, S., Liu, W. T., Shintani, T., Kamagata, Y. & Nakamura, K. (2002). *Tetrasphaera elongata* sp. nov., a polyphosphate-accumulating bacterium isolated from activated sludge. *Int J Syst Evol Microbiol* **52**, 883–887.
- Hua, N.-P., Kanekiyo, A., Fujikura, K., Yasuda, H. & Naganuma, T. (2007). *Halobacillus profundus* sp. nov. and *Halobacillus kuroshimensis* sp. nov., moderately halophilic bacteria isolated from a deep-sea methane cold seep. *Int J Syst Evol Microbiol* **57**, 1243–1249.
- Komagata, K. & Suzuki, K. (1987). Lipids and cell-wall analysis in bacterial systematics. *Methods Microbiol* **19**, 161–207.
- Lányi, 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.
- MacKenzie, S. L. (1987). Gas chromatographic analysis of amino acids as the *N*-heptafluorobutyl isobutyl esters. *J Assoc Off Anal Chem* **70**, 151–160.
- Nam, J.-H., Bae, W. & Lee, D.-H. (2008). *Oceanobacillus caeni* sp. nov., isolated from a *Bacillus*-dominated wastewater treatment system in Korea. *Int J Syst Evol Microbiol* **58**, 1109–1113.
- 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 no. 1. Newark, DE: MIDI Inc.
- Schleifer, K. H. & Kandler, O. (1972). Peptidoglycan types of bacterial cell walls and their taxonomic implications. *Bacteriol Rev* **36**, 407–477.
- Stackebrandt, E. & Goebel, B. M. (1994). Taxonomic note: a place for DNA-DNA reassociation and 16S rRNA sequence analysis in the present species definition in bacteriology. *Int J Syst Bacteriol* **44**, 846–849.
- Tamaoka, J. & Komagata, K. (1984). Determination of DNA base composition by reversed-phase high-performance liquid chromatography. *FEMS Microbiol Lett* **25**, 125–128.
- Wayne, L. G., Brenner, D. J., Colwell, R. R., Grimont, P. A. D., Kandler, O., Krichevsky, M. I., Moore, L. H., Moore, W. E. C., Murray, R. G. E. & 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 intraspecific phylogenetic analysis of the genus *Nocardioides* and related taxa based on 16S rRNA gene sequences. *Int J Syst Bacteriol* **48**, 187–194.
- Yoon, J.-H., Kang, S.-S., Lee, K.-C., Kho, Y. H., Kang, K. H. & Park, Y.-H. (2001a). *Planomicrobium koreense* gen. nov., sp. nov., a bacterium isolated from the Korean traditional fermented seafood jeotgal, and transfer of *Planococcus okeanoikoites* (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., 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.
- Yoon, J.-H., Kang, K. H. & Park, Y.-H. (2003). *Psychrobacter jeotgali* sp. nov., isolated from jeotgal, a traditional Korean fermented seafood. *Int J Syst Evol Microbiol* **53**, 449–454.
- Yoon, J.-H., Kim, I.-G., Schumann, P., Oh, T.-K. & Park, Y.-H. (2004). *Marinibacillus campisalis* sp. nov., a moderate halophile isolated from a marine solar saltern in Korea, with emended description of the genus *Marinibacillus*. *Int J Syst Evol Microbiol* **54**, 1317–1321.