***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.**

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A moderately halophilic, round-endospore-forming bacterium (strain YKJ-13^T) was isolated from jeotgal, a traditional Korean fermented seafood, and studied by a polyphasic taxonomic approach. This organism was related to the phylogenetic clade comprising members of *Bacillus* rRNA group 2 and formed a cluster with *Bacillus marinus* with a bootstrap fidelity value of 93.6%. The peptidoglycan type was A1 α linked directly through L-Lys. Based on cell morphology, peptidoglycan type and phylogeny, strain YKJ-13^T, together with *B. marinus*, is considered to be a member of *Bacillus* rRNA group 2. Strain YKJ-13^T was also characterized by having MK-7 and MK-8 as the predominant menaquinones and iso-C_{15:0} as the major fatty acid. The DNA G+C content was 44 mol%. Strain YKJ-13^T exhibited a 16S rDNA similarity value of 95.7% with *B. marinus* DSM 1297^T, its closest phylogenetic relative. Levels of 16S rDNA similarity between strain YKJ-13^T and other *Bacillus* spp. were less than 94.2%. Therefore, on the basis of the data presented, the name *Jeotgalibacillus alimentarius* gen. nov., sp. nov. is proposed for strain YKJ-13^T (= KCCM 80002^T = JCM 10872^T). It is also proposed that *B. marinus* be reclassified in *Marinibacillus* gen. nov. as *Marinibacillus marinus* comb. nov.

Keywords: *Jeotgalibacillus alimentarius*, *Bacillus marinus*, *Marinibacillus marinus*, *Bacillus* rRNA group 2, jeotgal

INTRODUCTION

Jeotgal, one of the representative traditional foods of Korea, is prepared through blending of various kinds of seafoods, including seawater and other ingredients, and becomes palatable through proper preservation. Preliminary studies on the microbiology of jeotgal have demonstrated the presence of a variety of bacterial strains; the majority of the isolates were Gram-positive or -variable, endospore-forming bacilli. Considering their halotolerant or halophilic physiological properties, most of bacterial isolates appear to have originated from seafoods and seawater. Among many bacilli from jeotgal, a round-endospore-forming,

moderately halophilic bacterium (strain YKJ-13^T) was studied in this report.

Formation of round endospores is a typical characteristic of organisms assigned to *Bacillus* rRNA group 2, which are characterized by having L-lysine or D-ornithine at position 3 of the peptide subunit of the peptidoglycan (Rheims *et al.*, 1999; Stackebrandt *et al.*, 1987). *Bacillus* species belonging to this group form the radiation of a cluster distinct from members of other rRNA groups of the genus *Bacillus* (Ash *et al.*, 1991; Stackebrandt *et al.*, 1987). However, it should be noted that this group also consists of a phylogenetic jumble with some non-*Bacillus*-type organisms, such as the genera *Caryophanon*, *Planococcus*, *Filibacter* and *Sporosarcina* (Clausen *et al.*, 1985; Farrow *et al.*, 1992, 1994; Stackebrandt *et al.*, 1987). On the basis of these properties, it has been recognized that the L-

The GenBank accession number for the 16S rDNA sequence of strain YKJ-13^T is AF281158.

lysine- and D-ornithine-containing bacilli belonging to rRNA group 2 may have to be taxonomically re-evaluated (Farrow *et al.*, 1994; Rheims *et al.*, 1999).

In the present work, the morphological, phenotypic and phylogenetic characteristics of strain YKJ-13^T are described in order to unravel its exact taxonomic status. This organism has taxonomic properties indicative of rRNA group 2 bacilli. Results of 16S rDNA sequence comparison showed that strain YKJ-13^T is phylogenetically most closely related to *Bacillus marinus*, with formation of a coherent cluster. *B. marinus* was later elevated to species rank by Rüger (1983) with strains that had originally been described as *Bacillus globisporus* subsp. *marinus* by Rüger & Richter (1979). This species has been known to produce round-spore-forming cells and contain lysine in the cell wall (Rüger, 1983; Claus & Berkeley, 1986). Nevertheless, *B. marinus* had rarely been included within *Bacillus* rRNA group 2 because of the lack of chemotaxonomic data, e.g. the cell wall murein type and menaquinone type (Ash *et al.*, 1991; Rheims *et al.*, 1999). Moreover, the 16S rDNA sequence of *B. marinus*, which would have been an important criterion for grouping this species within rRNA group 2, was not available until a recent publication by Rüger *et al.* (2000). In the study of Rüger *et al.* (2000), it was also shown that the type strain of *B. marinus* has a cell wall peptidoglycan type linked directly through L-lysine. The objective of the present study was to determine the exact taxonomic status of *B. marinus* as well as that of strain YKJ-13^T. On the basis of results presented, it is proposed that strain YKJ-13^T should be classified as *Jeotgalibacillus alimentarius* gen. nov., sp. nov., and *B. marinus* should be reclassified in *Marinibacillus* gen. nov. as *Marinibacillus marinus* comb. nov.

METHODS

Bacterial strains and culture conditions. Strain YKJ-13^T was isolated from jeotgal, a traditional Korean fermented seafood, by a dilution plating technique on marine agar (Difco). *B. marinus* DSM 1297^T, used as a reference strain, was obtained from Deutsche Sammlung von Mikroorganismen und Zellkulturen (DSMZ), Braunschweig, Germany. Cell mass for analyses of the cell wall and menaquinones and for DNA extraction was obtained from marine broth (Difco) culture grown at 30 °C for strain YKJ-13^T or 20 °C for *B. marinus* DSM 1297^T. Strains were cultivated on a horizontal shaker at 150 r.p.m. and the broth cultures were checked for purity microscopically before being harvested by centrifugation. For fatty acid methyl ester analysis, cell mass of strain YKJ-13^T and *B. marinus* DSM 1297^T was obtained after growth for 3 d at 30 °C on marine agar.

Morphological characterization. The morphologies of colonies and cells grown on marine agar were examined. Cell micromorphology was observed using phase-contrast microscopy and transmission electron microscopy. Flagellum type was determined using transmission electron microscopy with cells from an exponentially growing culture. For transmission electron microscopic observation, cells were negatively stained with 1 % (w/v) phosphotungstic acid and,

after air-drying, the grids were examined with a model CM-20 transmission electron microscope (Philips).

Physiological characterization. All physiological tests were performed at 30 °C, except for the study of temperature range for growth. Oxidase activity was determined by examining oxidation of 1 % *p*-aminodimethylaniline oxalate. Catalase activity was determined by bubble formation in a 3 % (v/v) hydrogen peroxide solution. Hydrolysis of aesculin and nitrate reduction were determined as described previously (Lanyi, 1987). Hydrolyses of casein, gelatin, starch and Tween 80, and urease activity were determined as described by Cowan & Steel (1965). Hydrolyses of hypoxanthine, tyrosine and xanthine were performed on marine agar with concentration of substrates described previously (Cowan & Steel, 1965). Acid production from carbohydrates was determined as described by Leifson (1963). Growth under anaerobic conditions was determined after incubation in an anaerobic chamber with marine agar that was anaerobically prepared. Growth at various NaCl concentrations was investigated on marine agar or in marine broth. Growth at various temperatures was measured on marine agar or in marine broth at 4–55 °C.

Isolation of DNA. Chromosomal DNA was isolated and purified according to a previously described method (Yoon *et al.*, 1996), with the exception that ribonuclease T1 was used together with ribonuclease A.

Chemotaxonomic characterization. Preparation of the cell wall 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 fatty acid methyl esters were prepared and identified according to the instructions of the Microbial Identification System (MIDI).

DNA base composition. The 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.

16S rDNA sequencing and phylogenetic analysis. 16S rDNA 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 rDNA 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 using an Applied Biosystems model 310 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 analysis. Phylogenetic trees were inferred using three tree-making algorithms, i.e. the neighbour-joining (Saitou & Nei, 1987), maximum-likelihood (Felsenstein, 1981) and maximum-parsimony (Kluge & Farris, 1969) methods in the PHYLIP package (Felsenstein, 1993). Evolutionary distance matrices for the neighbour-joining method were calculated with the algorithm of Jukes & Cantor (1969) with the DNADIST program. The stability of relationships was assessed by a bootstrap analysis based on 1000 resamplings of the neighbour-joining dataset using the programs SEQBOOT and CONSENSE of the PHYLIP package.

RESULTS

Morphology

Most cells of strain YKJ-13^T were rods measuring 1.0–1.2 × 2.0–4.0 µm in 3 d culture on marine agar at 30 °C; however, longer rods were often observed. Cells were Gram-variable and motile by means of peritrichous flagella. Round spores were located subterminally or terminally in swollen sporangia. After

incubation on marine agar, colonies were smooth, glistening, irregular, flat-raised and orange-yellow in colour.

Cultural and physiological characteristics

Strain YKJ-13^T grew optimally at 30–35 °C. Growth occurred at 10 and 45 °C, but not at 4 or 50 °C. It grew optimally at pH 7.0–8.0 and no growth was

Table 1. Differential phenotypic characteristics of strain YKJ-13^T and *B. marinus*

+, Positive reaction; –, negative reaction; w+, weakly positive reaction; v, variable reaction. Both species were rod-shaped, produced round spores (terminal or subterminal), had peritrichous flagella and were positive for motility, catalase, decomposition of aesculin and gelatin, and acid production from glucose, fructose, maltose, sucrose and trehalose. Both species were negative for decomposition of starch and urea, and acid production from adonitol, arabinose, cellobiose, rhamnose and sorbitol.

Characteristic	Strain YKJ-13 ^T	<i>B. marinus</i> *
Swollen sporangia	+	– or slightly
Gram staining	v	+
Pigment	+	–
Anaerobic growth	+	–
Cytochrome oxidase	+	v (–)
Nitrate reduction	+	v (–)
Decomposition of:		
Casein	+	v (+)
Hypoxanthine	–	–†
Tween 80	+	–†
Tyrosine	–	–†
Xanthine	–	–†
Acid production from:		
Lactose	–	v (+)
Xylose	–	v (+)
Galactose	+	–
Mannitol	+	–
Mannose	–	+
Melibiose	+	–
Raffinose	+	–
Growth in NaCl at:		
0 %	–	–
7 %	+	v (w+)
10 %	+	–
20 %	w+	–
21 %	–	–
Growth at (°C):		
5	–	+
10	+	+
30	+	v (+)
37	+	–
Optimum growth temperature (°C)	30–35	12–23
Maximum growth temperature (°C)	45–50	25–30
Peptidoglycan type	L-Lys-direct	L-Lys-direct†
Predominant menaquinone	MK-7, MK-8	MK-7†
Major fatty acid	iso-C _{15:0}	anteiso-C _{15:0} †
G + C content (mol %)	44	37–42

* Data from Rüger & Richter (1979), Rüger (1983) and Rüger *et al.* (2000), except where indicated. Data in parentheses are for the type strain of *B. marinus* from Rüger & Richter (1979), Rüger (1983) or Rüger *et al.* (2000).

† Data are for *B. marinus* DSM 1297^T obtained from this study.

Table 2. Cellular fatty acid profiles of strain YKJ-13^T and *B. marinus* DSM 1297^T on marine agar

Strain	Fatty acid composition (%)*														Summed feature 5†
	i-C _{14:0}	C _{14:0}	i-C _{15:0}	ai-C _{15:0}	C _{15:0}	C _{16:1 ω7c} alcohol	C _{16:1 ω11c}	i-C _{16:0}	C _{16:0}	i-C _{17:1 ω10c}	i-C _{17:0}	ai-C _{17:0}	C _{18:0}		
Strain YKJ-13 ^T	2.1	0.7	47.6	15.2	1.1	5.2	1.2	1.9	3.9	3.8	6.5	4.6	3.4	2.8	
<i>B. marinus</i>	5.3	ND	22.2	47.7	ND	2.6	ND	5.1	1.5	ND	2.6	10.7	ND	2.3	
DSM 1297 ^T															

ND, Not detected.

^{*} i, iso; ai, anteiso.[†] Summed feature 5 represents iso-C_{17:1} I and/or anteiso-C_{17:1} B, which could not be separated by GLC with the MIDI system. **Fig. 1.** Neighbour-joining tree showing the phylogenetic position of strain YKJ-13^T, some *Bacillus* spp. and representatives of some other taxa based on 16S rDNA sequences. Bar, 0.01 substitution per nucleotide position. Bootstrap values (expressed as percentages of 1000 replications) greater than 50% are shown at the branch points.

observed at pH values below 6.0. Strain YKJ-13^T grew optimally in the presence of 3–12% (w/v) NaCl. It grew in the presence of 19% (w/v) NaCl and weakly in the presence of 20% NaCl. Growth did not occur in the presence of more than 21% (w/v) NaCl. Strain YKJ-13^T grew under anaerobic conditions on marine agar. Strain YKJ-13^T showed catalase and oxidase activities, but no urease activity. Aesculin, casein, gelatin and Tween 80 were hydrolysed; no hydrolysis of hypoxanthine, starch, tyrosine or xanthine was observed. Nitrate was reduced to nitrite. Phenotypic properties of strain YKJ-13^T are summarized in Table 1, together with those of *B. marinus*.

Chemotaxonomic characteristics and DNA base composition

No diaminopimelic acid was found as the diagnostic amino acid in the cell wall hydrolysate of strain YKJ-13^T. The cell wall of strain YKJ-13^T contained a directly cross-linked peptidoglycan with L-lysine as the diagnostic diamino acid. On the basis of this result, it was concluded that the peptidoglycan type of strain YKJ-13^T is A1 α , based directly on L-Lys, as described by Schleifer & Kandler (1972). Dinitrophenylated cell walls of strain YKJ-13^T contained only ϵ -DNP-lysine, thus confirming the above-mentioned type. *B. marinus* DSM 1297^T had a directly cross-linked peptidoglycan based on L-lysine as the diamino acid. The α -carboxyl group of D-glutamic acid was substituted by a glycine residue. This result also has recently been proven by Rüger *et al.* (2000). To our knowledge, this type has not been found in any other organism up to now. Strain YKJ-13^T contained MK-7 (62%) as the predominant menaquinone and also a significant amount of MK-8 (35%). *B. marinus* DSM 1297^T contained a large proportion of MK-7 (87%). The cellular fatty acid profile of strain YKJ-13^T was characterized by the predominance of iso-C_{15:0} (47.6%) followed by anteiso-C_{15:0} (15.2%), whereas *B. marinus* DSM 1297^T was characterized by the predominance of anteiso-C_{15:0} (47.7%) and the occurrence of significant amounts of iso-C_{15:0} (22.2%) and anteiso-C_{17:0} (10.7%) (Table 2). The DNA G + C content of strain YKJ-13^T was 44 mol %.

Phylogenetic analysis

The 16S rDNA of strain YKJ-13^T was directly sequenced after PCR amplification and its almost complete nucleotide sequence was determined. This sequence comprised 1508 nt, representing approximately 96% of the *Escherichia coli* 16S rRNA sequence. In the tree-based neighbour-joining algorithm, strain YKJ-13^T was phylogenetically related to members of *Bacillus* rRNA group 2 and formed a coherent cluster with *B. marinus* DSM 1297^T (Fig. 1). The clustering fidelity between strain YKJ-13^T and *B. marinus* DSM 1297^T was supported by bootstrap analysis at a confidence level of 93.6%. The relationship between this cluster and the cluster comprising members of *Bacillus* rRNA group 2 was supported by a relatively high bootstrap

resampling value of 91.8%. The phylogenetic relationship between strain YKJ-13^T, *B. marinus* and members of *Bacillus* rRNA group 2 was also found in trees generated by the maximum-likelihood and maximum-parsimony algorithms. Strain YKJ-13^T showed the highest degree of relatedness to *B. marinus* DSM 1297^T, sharing 95.7% 16S rDNA similarity. Sequence similarity values of 16S rDNA from strain YKJ-13^T with 16S rDNA from the type strains of *Bacillus* species belonging to rRNA group 2 were in the range 92.4–93.9%. Strain YKJ-13^T exhibited levels of 16S rDNA similarity of less than 94.2% with the type strains of other *Bacillus* species that had known 16S rDNA sequences.

DISCUSSION

Many bacilli have been recently isolated from jeotgal. In the course of characterizing these strains, one isolate (strain YKJ-13^T) has attracted our attention because of its morphological characteristic of forming round endospores and its moderately halophilic physiology. 16S rDNA sequence analysis showed that strain YKJ-13^T was phylogenetically related to the radiation of a cluster comprising members of *Bacillus* rRNA group 2, with the formation of a coherent cluster with *B. marinus* (Fig. 1). Strain YKJ-13^T contained L-lysine at position 3 of the cell wall peptidoglycan, which is characteristic of *Bacillus* rRNA group 2 (Rheims *et al.*, 1999; Stackebrandt *et al.*, 1987). Strain YKJ-13^T had MK-7 and MK-8 as the predominant menaquinones and iso-C_{15:0} as the major fatty acid. Among the rRNA group 2 bacilli, some species, such as *Bacillus sphaericus* and *Bacillus silvestris*, have been found to contain iso-C_{15:0} as the major fatty acid (Rheims *et al.*, 1999; Shida *et al.*, 1997). On the basis of these data, strain YKJ-13^T is considered to be a member of *Bacillus* rRNA group 2. Results showed that the type strain of *B. marinus* had MK-7 as the predominant menaquinone and L-lysine at position 3 of the peptide subunit of the peptidoglycan. *B. marinus* has already been known to form round endospores (Rüger, 1983; Claus & Berkeley, 1986). Accordingly, *B. marinus* must also be a member of *Bacillus* rRNA group 2.

16S rDNA sequence comparison showed that strain YKJ-13^T and the type strain of *B. marinus* exhibited the closest phylogenetic relationship, with 95.7% similarity. There were some physiological differences between strain YKJ-13^T and *B. marinus*, such as the ability to grow anaerobically, and NaCl and growth temperature tolerances (Table 1). Whereas *B. marinus* showed slight growth at 7% NaCl and no growth at 10% NaCl, strain YKJ-13^T grew at 20% NaCl (Table 1). Strain YKJ-13^T is a mesophile growing at 10 and 45 °C with an optimum of 30–35 °C, whereas *B. marinus* is a psychrophile showing a growth range of 5–30 °C, with an optimum of 12–23 °C (Table 1). Some chemotaxonomic properties are important for distinguishing strain YKJ-13^T from *B. marinus*. It is noteworthy that the fatty acid profile of strain YKJ-13^T differed from that of *B. marinus* DSM 1297^T.

Strain YKJ-13^T and *B. marinus* DSM 1297^T showed a distinct difference in the amounts of iso-C_{15:0} and anteiso-C_{15:0} they contained (Table 2). Strain YKJ-13^T could be distinguished from the type strain of *B. marinus* by menaquinone composition. The menaquinone profile of strain YKJ-13^T was characterized by the predominance of MK-7 (62%) followed by MK-8 (35%), whereas *B. marinus* DSM 1297^T has 87% MK-7 and no MK-8. This menaquinone profile of strain YKJ-13^T has not been found in other bacilli belonging to rRNA group 2 (Rheims *et al.*, 1999). *B. marinus* DSM 1297^T has a unique peptidoglycan structure that has not been found in any other organism. On the basis of these data, particularly chemotaxonomic data, strain YKJ-13^T and *B. marinus* should be distinguished as members of different genera in *Bacillus* rRNA group 2.

The taxonomic status of the rRNA group 2 bacilli has recently been discussed. It has been recognized that *Bacillus* species belonging to this group should be taxonomically distinguished from *Bacillus* rRNA group 1, including *Bacillus subtilis*, the type species of this genus, and all *meso*-diaminopimelic acid-containing bacilli by micromorphology, phylogeny and cell wall composition (Farrow *et al.*, 1994). Therefore, the L-lysine- and D-ornithine-containing bacilli of rRNA group 2 may be in need of taxonomic re-evaluation to transfer them into several new genera or existing genera. Since no proposal about taxonomic reclassification of the rRNA group 2 bacilli has been forwarded, Rheims *et al.* (1999) proposed that any strain worthy of species rank within rRNA group 2, exhibiting taxonomic properties that would identify this taxon as a member of the genus *Bacillus*, should still be described as a species of this genus. However, there is no longer any reason to delay taxonomic re-evaluation of the rRNA group 2 bacilli. Recently, *B. globisporus*, *Bacillus psychrophilus* and *Bacillus pasteurii*, which belong to rRNA group 2, together with one novel isolate, were transferred to the genus *Sporosarcina* (Yoon *et al.*, 2001). Accordingly, it appears to be more appropriate that strain YKJ-13^T and *B. marinus* be placed within two other genera, not the genus *Bacillus*.

Therefore, the creation of a new genus and species, *Jeotgalibacillus alimentarius* gen. nov., sp. nov., for strain YKJ-13^T and the reclassification of *B. marinus* (Rüger 1983) in a new genus, *Marinibacillus* gen. nov., as *Marinibacillus marinus* comb. nov. are proposed.

Description of *Jeotgalibacillus* gen. nov.

Jeotgalibacillus (Je.ot.ga.li.ba.cil'lus. Korean n. *jeotgal* jeotgal, traditional Korean food; Gr. n. *baktron* rod; N.L. masc. n. *Jeotgalibacillus* rod from jeotgal).

Rod-shaped bacterium. Round endospores are observed in swollen sporangia. Catalase- and oxidase-positive. Urease-negative. Nitrate is reduced to nitrite. Cell wall peptidoglycan contains L-lysine at position 3 of the peptide subunit. Predominant menaquinones

are MK-7 and MK-8. Major fatty acid is iso-C_{15:0}. DNA G+C content is 44 mol% (determined by HPLC). Type species is *Jeotgalibacillus alimentarius*.

Description of *Jeotgalibacillus alimentarius* sp. nov.

Jeotgalibacillus alimentarius (a.li.men.ta'ri.us. L. adj. *alimentarius* relating to food).

Gram-variable, facultatively anaerobic rods of 1.0–1.2 × 2.0–4.0 µm; longer rods are often observed. Round endospores lie subterminally or terminally in swollen sporangia. Motile by means of peritrichous flagella. Colonies are smooth, glistening, irregular, flat to raised and orange-yellow in colour on marine agar. Grows in the presence of 19% NaCl and weakly in the presence of 20% NaCl. Growth occurs at 10 and 45 °C, but not at 4 or 50 °C. Optimal growth temperature is 30–35 °C. Optimal pH for growth is pH 7.0–8.0 and no growth is observed at pH 6.0. Catalase- and oxidase-positive. Urease-negative. Aesculin, casein, gelatin and Tween 80 are hydrolysed; no hydrolysis of hypoxanthine, starch, tyrosine or xanthine is observed. Nitrate is reduced to nitrite. Acid is produced from D-ribose, D-fructose, D-mannitol, melibiose, D-melezitose, D-glucose, D-galactose, sucrose, maltose, D-trehalose and D-raffinose. Acid is not produced from D-sorbitol, *myo*-inositol, D-xylose, L-arabinose, D-mannose, adonitol, L-rhamnose, D-cellobiose, stachyose or lactose. Peptidoglycan type is A1α (L-Lys-direct). Predominant menaquinones are MK-7 and MK-8. Major fatty acid is iso-C_{15:0}. DNA G+C content is 44 mol% (determined by HPLC). Isolated from jeotgal, traditional Korean fermented seafood. Type strain is strain YKJ-13^T (= KCCM 80002^T = JCM 10872^T).

Description of *Marinibacillus* gen. nov.

Marinibacillus (Ma.ri.ni.ba.cil'lus. L. adj. *marinus* of the sea; Gr. n. *baktron* rod; M.L. masc. n. *Marinibacillus* rod of the sea).

The description is the same as that given by Rüger (1983) and Rüger *et al.* (2000). Additional chemotaxonomic characters found in this study are as follows: cell wall peptidoglycan contains L-lysine at position 3 of the peptide subunit; the predominant menaquinone is MK-7; and the major fatty acid is anteiso-C_{15:0}. Type species is *Marinibacillus marinus*.

Description of *Marinibacillus marinus* comb. nov. (basonym *Bacillus marinus* Rüger 1983)

The species description is as given above for the genus. Type strain is DSM 1297^T.

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