Virgibacillus koreensis sp. nov., a novel bacterium from a salt field, and transfer of *Virgibacillus picturae* to the genus *Oceanobacillus* as *Oceanobacillus picturae* comb. nov. with emended descriptions

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A novel *Virgibacillus* strain, BH30097^T, was isolated from a salt field near Tae-an-Gun on the Yellow Sea in Korea. Cells were Gram-positive rods and bore ellipsoidal endospores in terminal positions. The optimum pH and temperature for growth of this organism were pH 7 and 25 °C, respectively. The main respiratory quinone was MK-7 and the major cellular fatty acids were anteiso-C_{15:0} and iso-C_{16:0}. Analysis based on 16S rRNA gene sequence data revealed that the isolate formed an evolutionary lineage distinct from other *Virgibacillus* species. Levels of sequence similarity between the isolate and other *Virgibacillus* species ranged from 93.8 to 96.7 %. DNA–DNA relatedness values between strain BH30097^T and a phylogenetically closely related strain, *Virgibacillus halodenitrificans* KCTC 3790^T, were less than 24 %. On the basis of morphological, physiological and chemotaxonomic characteristics, 16S rRNA gene sequence comparison and DNA–DNA hybridization, a novel species, *Virgibacillus koreensis* sp. nov., is proposed, with the type strain BH30097^T (= KCTC 3823^T = JCM 12387^T). It is also proposed that *Virgibacillus picturae* be transferred to the genus *Oceanobacillus* as *Oceanobacillus picturae* comb. nov. based on its 16S rRNA gene sequences and other taxonomic characteristics.

Aerobic, rod-shaped, spore-forming, moderately halophilic bacteria have been isolated from various environments. They were originally assigned to the genus *Bacillus* but subsequently reclassified into several genera such as *Halobacillus* (Spring *et al.*, 1996), *Gracilibacillus* (Wainø *et al.*, 1999), *Virgibacillus* (Heyndrickx *et al.*, 1999), *Filobacillus* (Schlesner *et al.*, 2001), *Oceanobacillus* (Lu *et al.*, 2001), *Lentibacillus* (Yoon *et al.*, 2002) and *Pontibacillus* (Lim *et al.*, 2005) based on 16S rRNA gene sequence comparisons and chemotaxonomic characteristics.

The genus *Virgibacillus* was first proposed by Heyndrickx *et al.* (1998) based on polyphasic data from amplified rDNA restriction analysis (ARDRA), fatty acid profiles, SDS-PAGE patterns of whole-cell proteins and phenotypic

characterization, and its description was later emended by Heyrman *et al.* (2003). Members of the genus *Virgibacillus* bear oval to ellipsoidal endospores, are motile, Gram-positive rods and have DNA G + C contents ranging from 36 to 43 mol% (Heyrman *et al.*, 2003). The halotolerant bacterium *Bacillus salexigens* (Garabito *et al.*, 1997) was transferred to the new genus *Salibacillus* as *Salibacillus salexigens* (Wainø *et al.*, 1999). Arahall *et al.* (2000) later proposed the reclassification of *Bacillus marismortui* as *Salibacillus marismortui*. Subsequently, Heyrman *et al.* (2003) proposed on the basis of genotypic and phenotypic data that *Virgibacillus* and *Salibacillus* should be combined in a single genus. Following the Rules of the Bacteriological Code (Lapage *et al.*, 1992), the species of *Salibacillus* were transferred to *Virgibacillus* as *Virgibacillus salexigens* and *Virgibacillus marismortui*. Recently, *Bacillus halodenitrificans*, first described by Denariáz *et al.* (1989), was transferred to the genus *Virgibacillus* as *Virgibacillus halodenitrificans* (Yoon *et al.*, 2004). The genus *Virgibacillus* comprises eight species at the time of writing.

We isolated a novel bacterium, strain BH30097^T, from a salt field. The morphological, biochemical and phylogenetic

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The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain BH30097^T is AY616012.

A photomicrograph showing sporangia and vegetative cells of the type strain of *Virgibacillus koreensis* is available as supplementary material in IJSEM Online.

distinctiveness of the isolate is described, and we consider that it should be assigned to a novel species of the genus *Virgibacillus*. As part of our study of this novel isolate, it became apparent that *Virgibacillus picturae* is closer to the genus *Oceanobacillus* than to *Virgibacillus* based on a phylogenetic analysis of their 16S rRNA gene sequences. *V. picturae* was described by Heyrman *et al.* (2003); at that time, Heyrman *et al.* (2003) studied the polyphasic characteristics of *Virgibacillus picturae*, but did not describe its phylogenetic relationship to the genus *Oceanobacillus*. The genus *Oceanobacillus*, with the single species *Oceanobacillus iheyensis*, was first described by Lu *et al.* (2001), and *Oceanobacillus oncorhynchi* was subsequently proposed by Yumoto *et al.* (2005). Therefore, to clarify the taxonomic position of *V. picturae*, we examined its phenotypic and chemotaxonomic characteristics, 16S rRNA gene sequences and phylogenetic relationships.

Strain BH30097^T was isolated from a salt field near Taean-Gun on the Yellow Sea in Korea on a nutrient agar containing artificial sea water (ASW) including 7% NaCl. The isolate and reference strains, such as *V. halodenitrificans* KCTC 3790^T and related *Virgibacillus* and *Oceanobacillus* species, were cultured on marine agar 2216 (Difco) for 48 h at 30 °C.

Cell morphology was examined by light microscopy and motility was determined with an optical microscope using the hanging drop technique (Skerman, 1967). The flagellum type was determined using transmission electron microscopy using cells from the exponential phase of growth, in which cells were negatively stained with 1% (w/v) phosphotungstic acid and air-dried and the grids were examined using a transmission electron microscope (Philips). Anaerobic growth was recorded in an anaerobic chamber on marine agar. Growth experiments were performed using screw-capped tubes and growth was estimated by monitoring the OD₆₀₀. The ability to grow with different added salt concentrations (0–25% w/v NaCl) was tested with nutrient broth (Difco) as the basal medium. Growth at different temperatures was observed in trypticase soy broth at 10, 15, 20, 25, 30, 35, 40, 45 and 50 °C. Growth experiments at different pH values were performed using 10 ml trypticase soy broth adjusted to pH 6.0–10.0 (Sorokin, 2005); 100 mM Na₂HPO₄/NaH₂PO₄ buffer (pH 6.0–8.0) and 100 mM NaHCO₃/Na₂CO₃ buffer (pH 9.0–10.0) were used. This experiment was performed based on the methods of Yumoto *et al.* (1998). API 20E and API 50CHB systems (bioMérieux) were used for physiological and biochemical characterization. All suspension media were supplemented with 7% (w/v) NaCl. All API tests were performed in accordance with the manufacturer's recommendations (bioMérieux). Catalase activity was determined by bubble production from 3% (v/v) H₂O₂, and oxidase activity was determined using 1% (w/v) tetramethyl-*p*-phenylene-diamine.

Cells of the isolate were Gram-positive rods, motile by means of peritrichous flagella, that formed chains and/or

filaments (see Supplementary Fig. S1 in IJSEM Online); ellipsoidal endospores formed in terminal positions (Supplementary Fig. S1). Strain BH30097^T formed circular, low-convex, smooth, semi-translucent and cream-coloured colonies. The isolate grew anaerobically and at an NaCl concentration of 0.5–20%; optimum growth was at 5–10% (w/v) NaCl. The isolate grew at between 10 and 45 °C, but not at 50 °C; optimum growth was observed at 25 °C. Strain BH30097^T grew at pH 5.5–9.0, with an optimum at pH 7.0. The isolate tested positive for aesculin hydrolysis, β-galactosidase, oxidase and catalase activities and acid production from amygdalin, L-arabinose, cellobiose, aesculin, D-fructose, maltose and D-xylose. It gave negative results for nitrate reduction, indole production, D-glucose acidification, arginine hydrolysis, urease, gelatin hydrolysis and acid production from N-acetylglucosamine, D-arabinose, galactose, L-fucose, glycerol, glycogen, *myo*-inositol, 5-keto-D-gluconate, mannitol, D-mannose, D-melibiose, L-rhamnose and D-turanose.

For total cellular fatty acid analysis, cells were cultured on trypticase soy agar for 48 h at 30 °C and the fatty acids were extracted following the procedures for the Microbial Identification System (MIDI, Inc.), as described previously (Lee *et al.*, 1996; Yang *et al.*, 1993). Isoprenoid quinones were extracted with chloroform/methanol (2:1, v/v), and purified by TLC on Merck Kieselgel 60 F₂₅₄ plates (20 × 20 cm, 0.5 mm thickness) using petroleum ether/diethyl ether (9:1, v/v) as the solvent. The identity of the quinones was determined by HPLC, as described by Shin *et al.* (1996). Diaminopimelic acid (DAP) isomers were determined using the method of Komagata & Suzuki (1987). Extraction and analysis of polar lipids by two-dimensional TLC were performed according to the methods of Komagata & Suzuki (1987).

Whole-cell fatty acid profiles for strain BH30097^T and related *Virgibacillus* and *Oceanobacillus* species are shown in Table 1. Major fatty acids (>1%) in strain BH30097^T were anteiso-C_{15:0} (43.42%), iso-C_{16:0} (14.42%), iso-C_{14:0} (8.32%), anteiso-C_{17:0} (7%), iso-C_{15:0} (6.13%), C_{16:0} (5.91%), C_{15:0} (5.08%), C_{16:1ω7c} alcohol (3.35%), C_{16:1ω11c} (2.24%) and C_{14:0} (1.81%). This profile was similar to those of members of the genus *Virgibacillus*. The major menaquinone and DAP isomer in the cell-wall peptidoglycan of strain BH30097^T were MK-7 and *meso*-DAP, respectively. Cells of strain BH30097^T and *O. iheyensis* KCTC 3954^T contained diphosphatidylglycerol, phosphatidylglycerol and unidentified phospholipids. An unknown aminophospholipid that gave a positive reaction to ninhydrin spraying, reported for some *Virgibacillus* species by Heyrman *et al.* (2003), was not detected in strain BH30097^T or *O. iheyensis* KCTC 3954^T.

DNA was extracted and purified by a modification of the method of Marmur (1961). The DNA G+C content was determined using the reversed-phase HPLC method described by Tamaoka & Komagata (1984). The DNA G+C

Table 1. Whole-cell fatty acid composition of strain BH30097^T and related *Virgibacillus* and *Oceanobacillus* species

Strains: 1, BH30097^T; 2, *V. halodenitrificans* KCTC 3790^T; 3, *V. pantothenicus* KCTC 3539^T; 4, *V. proomii* KCTC 3822^T; 5, *V. salexigens* KCTC 3844^T; 6, *V. marismortui* KCTC 3845^T; 7, *V. carmonensis* KCTC 3819^T; 8, *V. necropolis* KCTC 3820^T; 9, *V. picturae* KCTC 3821^T; 10, *O. iheyensis* KCTC 3954^T; 11, *O. oncorhynchi* R-2^T (data from Yumoto *et al.*, 2005). tr, Trace amount; –, not detected. The positions of double bonds can be located by counting from the methyl (ω) end of the carbon chain; *cis* and *trans* isomers are indicated by the suffixes *c* and *t*.

Fatty acid	1	2	3	4	5	6	7	8	9	10	11
Saturated											
C _{14:0}	1·81	tr	tr	tr	tr	tr	tr	tr	tr	4·83	tr
C _{15:0}	5·08	tr	tr	tr	tr	tr	tr	0·78	tr	0·78	tr
C _{16:0}	5·91	1·06	1·27	4·00	5·08	1·80	1·03	1·61	0·88	14·28	2·1
Unsaturated											
C _{16:1} ω 7 <i>c</i> alcohol	3·35	3·05	–	–	0·91	1·13	6·53	2·41	3·08	–	–
C _{16:1} ω 11 <i>c</i>	2·24	0·40	–	–	0·58	0·64	0·63	1·01	0·25	–	–
Branched											
iso-C _{14:0}	8·32	7·44	2·33	2·44	4·18	2·89	3·32	2·23	8·82	7·15	1·1
iso-C _{15:0}	6·13	2·36	7·06	15·13	33·99	39·02	5·73	3·84	2·88	31·60	22·7
anteiso-C _{15:0}	43·42	51·8	55·30	38·49	30·50	33·93	58·29	67·85	53·14	25·29	49·3
iso-C _{16:0}	14·42	11·76	7·16	7·31	8·42	4·33	6·42	4·16	10·35	7·53	3·2
iso-C _{17:0}	tr	tr	2·00	6·33	5·61	5·63	0·90	0·87	tr	3·78	4·3
anteiso-C _{17:0}	7·00	19·52	23·95	24·93	9·29	8·55	11·13	12·19	14·33	4·49	18·0
Summed features*											
SF3	tr	–	–	–	–	–	4·98	2·1	–	–	–
SF4	tr	1·58	–	–	tr	0·74	–	–	1·12	–	–
SF7	–	–	–	–	–	–	–	–	4·42	–	–

*Summed features represent groups of two or three fatty acids that can not be separated by GLC with the MIDI system. SF3, C_{16:1} ω 7*c* and/or iso-C_{15:0} 2-OH; SF4, iso-C_{15:0} 2-OH and/or C_{16:1} ω 7*t*; SF7, C_{18:1} ω 7*c*, C_{18:1} ω 9*t* and/or C_{18:1} ω 12*t*.

contents of BH30097^T and *V. halodenitrificans* KCTC 3790^T were 41 and 38 mol%, respectively.

Two universal primers (9F and 1492R) described by Stackebrandt & Liesack (1993) were used for PCR amplification of the 16S rRNA gene, and the amplified PCR product was purified using a QIAquick PCR purification kit (Qiagen). The purified 16S rRNA gene was then sequenced using an ABI Prism BigDye Terminator cycle sequencing ready reaction kit (Applied Biosystems), with an automatic DNA sequencer (model 377; Applied Biosystems). Nearly complete 16S rRNA gene sequences (1435 bp) were determined for BH30097^T and aligned with those of representatives from the genus *Virgibacillus* and related taxa using CLUSTAL W software (Thompson *et al.*, 1994). A phylogenetic tree was constructed using the neighbour-joining method (Saitou & Nei, 1987) based on distance matrix data. Evolutionary distances were calculated using the Jukes & Cantor (1969) model. The PHYLIP software package (Felsenstein, 1993) was used for all the analyses. The topology of the phylogenetic tree was evaluated using a bootstrap analysis (Felsenstein, 1985) of the neighbour-joining method based on 1000 replications.

The primary structures of the 16S rRNA gene sequence of strain BH30097^T were compared with those of closely

related reference strains. A phylogenetic tree, based on *K*_{nuc} values (Fig. 1), indicated that strain BH30097^T belonged to the genus *Virgibacillus*. Strain BH30097^T was phylogenetically most closely related to *V. halodenitrificans* KCTC 3790^T (96·7% 16S rRNA gene sequence similarity). Levels of sequence similarity between strain BH30097^T and other *Virgibacillus* species ranged from 93·8 to 96·0%. These values fell within the range that generally can be used to define a novel species (Rossello-Mora & Amann, 2001; Stackebrandt *et al.*, 2002).

DNA–DNA hybridization was carried out by fluorometric hybridization in microdilution wells using biotinylated DNA (Ezaki *et al.*, 1989). We chose two reference strains, *V. halodenitrificans* KCTC 3790^T and *Virgibacillus carmonensis* KCTC 3819^T, for the DNA–DNA hybridization experiments, *V. halodenitrificans* KCTC 3790^T because it was the strain most closely related to BH30097^T and *V. carmonensis* KCTC 3819^T as the type species of the genus. As shown in Table 2, DNA–DNA reassociation values between strain BH30097^T and the two reference strains were less than 28%, and that between the two reference strains was less than 33%. As such, the 16S rRNA gene sequence data comparison and DNA–DNA hybridization results demonstrated that strain BH30097^T was most closely related to the genus

Fig. 1. Neighbour-joining tree showing the phylogenetic position of strain BH30097^T with other *Virgibacillus* species and related taxa based on 16S rRNA gene sequences. Bootstrap values from 1000 resamplings are indicated. Bar, 0.1 accumulated changes per nucleotide.

Virgibacillus but was not a member of any recognized *Virgibacillus* species.

The genus *Virgibacillus* is phylogenetically related to the genera *Lentibacillus* (Yoon *et al.*, 2002; Namwong *et al.*, 2005) and *Oceanobacillus* (Lu *et al.*, 2001). *Oceanobacillus* currently comprises two species, *O. iheyensis* (Lu *et al.*, 2001) and *O. oncorhynchi* (Yumoto *et al.*, 2005). In our study, we found that *V. picturae* was linked to the genus *Oceanobacillus* with a bootstrap resampling value of 68.9% (Fig. 1). In the phylogenetic tree constructed using the neighbour-joining algorithm, the genus *Oceanobacillus* (including *V.*

picturae) formed a distinct clade with *Virgibacillus* and *Lentibacillus* (Fig. 1). A phylogenetic tree was also constructed using the maximum-likelihood method (Saitou & Nei, 1987) based on distance matrix data. Evolutionary distances were calculated using the Jukes & Cantor (1969) model. The topology of the phylogenetic tree constructed using the maximum-likelihood algorithm was similar to that of the tree constructed using the neighbour-joining algorithm (data not shown). There are currently not enough taxonomic data to distinguish *Virgibacillus* from *Oceanobacillus* (Tables 1 and 2). They have similar chemotaxonomic characteristics, such as their major menaquinone (MK-7), cellular fatty acids (anteiso-C_{15:0}) and polar lipids (Table 3). In their fatty acid profiles, genera related to the genus *Bacillus* have anteiso-C_{15:0} as the major cellular fatty acid. *V. picturae* and the two *Oceanobacillus* species also had anteiso-C_{15:0} as the major fatty acid. Clear differences in the amounts of iso-C_{15:0}, iso-C_{16:0}, anteiso-C_{17:0} and C_{16:0} among *V. picturae* and *O. iheyensis* and *O. oncorhynchi* were observed. *V. picturae* grew at pH 7.0–10.0, and *O. iheyensis* and *O. oncorhynchi* respectively grew at pH 6.5–10.0 and pH 9.0–10.0. These results showed they are facultatively alkaliphilic bacteria, an important characteristic of the genus *Oceanobacillus*. On the basis of the morphological, physiological and chemotaxonomic characteristics presented and 16S rRNA gene sequence comparisons, it is proposed that *Virgibacillus picturae* be transferred to the genus *Oceanobacillus* as *Oceanobacillus picturae* comb. nov.

Distinctive characteristics of the novel isolate and species of the genera *Virgibacillus* and *Oceanobacillus*, taken from previous studies (Arahal *et al.*, 1999, 2000; Denariáz *et al.*, 1989; Heyndrickx *et al.*, 1998, 1999; Heyrman *et al.*, 2003; Lu *et al.*, 2001; Wainø *et al.*, 1999; Yoon *et al.*, 2004; Yumoto *et al.*, 2005), are given in Table 3.

Description of *Virgibacillus koreensis* sp. nov.

Virgibacillus koreensis (ko.re.en'sis. N.L. masc. adj. *koreensis* for Korea, where the type strain was isolated).

Cells are Gram-positive, rod-shaped (0.5–0.7 × 2.0–7.0 µm) and motile by means of peritrichous flagella. Ellipsoidal spores are formed in terminal positions. Colonies are circular, low-convex, smooth, semi-translucent and cream-coloured on marine agar. The type strain grows in an anaerobic chamber at 37 °C. The temperature range for growth is 10–45 °C (optimal at 25 °C). The pH range for growth is 5.5–9.0 (optimal at pH 7.0). No growth occurs with NaCl concentrations of more than 20%, while optimal growth occurs with a NaCl concentration of 5–10%. Positive for aesculin hydrolysis, β-galactosidase, oxidase and catalase activities and acid production from amygdalin, L-arabinose, cellobiose, aesculin, D-fructose, maltose and D-xylose. Negative for nitrate reduction, indole production, glucose acidification, arginine hydrolysis, urease, gelatin hydrolysis and acid production from N-acetylglucosamine, D-arabinose, galactose, L-fucose, glycerol, glycogen, myo-inositol, 5-keto-D-gluconate, mannitol, D-mannose,

Table 2. DNA–DNA reassociation values for isolate BH30097^T, *V. halodenitrificans* KCTC 3790^T and *V. carmonensis* KCTC 3819^T

Strain	Reassociation (%) with labelled DNA from:		
	BH30097 ^T	KCTC 3790 ^T	KCTC 3819 ^T
BH30097 ^T	100	24	28
<i>V. halodenitrificans</i> KCTC 3790 ^T	21	100	33
<i>V. carmonensis</i> KCTC 3819 ^T	24	29	100

Table 3. Distinctive phenotypic characteristics of strain BH30097^T and related *Virgibacillus* and *Oceanobacillus* species

Strains/species: 1, BH30097^T; 2, *V. halodenitrificans*; 3, *V. pantothenicus*; 4, *V. proomii*; 5, *V. salexigens*; 6, *V. marismortui*; 7, *V. carmonensis*; 8, *V. necropolis*; 9, *V. picturae*; 10, *O. iheyensis*; 11, *O. oncorhynchi*. +, Positive; –, negative; v, variable; w, weakly positive; NT, not tested. Data were taken from this study and from Arahall *et al.* (1999, 2000), Denariáz *et al.* (1989), Heyndrickx *et al.* (1998, 1999), Heyman *et al.* (2003), Lu *et al.* (2001), Wainø *et al.* (1999), Yoon *et al.* (2004) and Yumoto *et al.* (2005). All species contain MK-7 as the major menaquinone.

Characteristic	1	2	3	4	5	6	7	8	9	10	11
Pigmentation	–	–	–	–	–	–	Pink	–	–	–	–
Chains of cells	–	+	+	+	+	+	–	+	–	–	–
Sporangia:*											
Spore shape	E	E	ES	ES	E	E	ES	E	ES	E	E
Spore position	T	TS	TS	TS	CST	TS	S	CST	T	TS	S
Anaerobic growth	+	+	+	+	–	–	–	–	–	–	+
Temperature range (°C)	10–45	10–45	15–50	15–50	15–45	15–> 50	10–40	10–40	5–40	15–42	15–40
Growth in NaCl at:											
0.5 %	W	–	+	W	–	–	–	W	W	+	+
25 %	–	W	–	–	W	+	–	–	–	–	–
Hydrolysis of:											
Gelatin	–	+	+	V	+	+	–	W	W	–	–
Aesculin	+	–	+	+	+	+	W	–	W	+	NT
H ₂ S production	–	–	–	–	+	–	–	–	–	–	NT
Acid production from:											
N-Acetylglucosamine	–	+	+	+	W	+	–	W	W	W	–
Amygdalin	+	–	+	–	W	–	–	–	–	–	–
D-Arabinose	–	–	+	–	–	–	–	–	–	–	–
Galactose	–	+	–	+	W	–	–	–	W	–	–
D-Glucose	W	+	–	+	W	+	–	W	W	+	+
D-Fructose	+	+	–	+	W	+	–	W	W	+	+
L-Fucose	–	–	+	–	–	–	–	–	–	–	–
Glycerol	–	W	+	–	–	W	–	W	W	+	–
Glycogen	–	–	–	V	–	–	–	–	W	–	–
myo-Inositol	–	–	–	+	–	–	–	–	–	–	–
5-Keto-D-gluconate	–	W	–	–	–	–	W	W	–	–	–
Mannitol	–	W	–	–	–	–	–	–	W	W	–
D-Mannose	–	+	–	+	W	+	–	W	W	+	+
D-Melibiose	–	–	–	–	–	–	–	–	W	–	+
L-Rhamnose	–	–	+	V	–	–	–	–	–	W	–
D-Trehalose	W	+	+	+	–	–	–	W	W	–	+
D-Turanose	–	–	+	–	–	–	–	–	W	W	–
Polar lipids†	PG, DPG, PLs	PG, DPG, PLs	PG, DPG, PE, PLs, APL	PG, DPG, PE, PLs, APL	PG, DPG, PLs	PG, DPG, PE, PLs, APL	PG, DPG, PLs	PG, DPG, PLs	PG, DPG, PLs	PG, DPG, PLs	NT
DNA G + C content (mol%)	41	38	37–38	37	36–40	39–43	40	37	40	36	38.5

*Spore shape: E, ellipsoidal; s, spherical. Spore position: T, terminal; s, subterminal; C, central.

†PG, Phosphatidylglycerol; DPG, diphosphatidylglycerol; PE, phosphatidylethanolamine; PLs, unidentified phospholipids; APL, unknown aminophospholipid.

D-melibiose, L-rhamnose and D-turanose. The DNA G+C content is 41 mol%, the major isoprenoid quinone is MK-7 and the major cellular fatty acids are anteiso-C_{15:0} and iso-C_{16:0}. The cell-wall peptidoglycan contains *meso*-DAP.

The type strain, BH30097^T (= KCTC 3823^T = JCM 12387^T), was isolated from a salt field near Taean-Gun on the Yellow Sea in Korea.

Emended description of genus *Oceanobacillus* Lu *et al.* 2002

Oceanobacillus (O.ce.a.no.ba.cil'lus. Gr. n. *okeanos* the ocean; L. dim. n. *bacillus* a small rod; N.L. masc. n. *Oceanobacillus* the ocean bacillus/rod).

Gram-positive, spore-forming rods, motile by means of peritrichous flagella. Ellipsoidal spores are subterminal or terminal within swollen sporangia. Obligately aerobic or facultatively anaerobic, obligately or facultatively alkaliphilic and grow at 0–22% (w/v) NaCl. Catalase and oxidase reactions are positive. Growth occurs at 5–42 °C. The predominant cellular fatty acid is anteiso-C_{15:0}. The major isoprenoid quinone is MK-7. The DNA G+C content is 35.8–40 mol%. The type species is *Oceanobacillus iheyensis*.

Description of *Oceanobacillus picturae* (Heyrman *et al.* 2003) comb. nov.

Oceanobacillus picturae (pic.tu'rae. L. gen. n. *picturae* pertaining or belonging to a painting).

Basonym: *Virgibacillus picturae* Heyrman *et al.* 2003.

The description matches that given by Heyrman *et al.* (2003). The type strain is strain LMG 19492^T (= DSM 14867^T = KCTC 3821^T).

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