Report on 24 unrecorded bacterial species of Korea belonging to the phylum *Firmicutes*

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As an outcome of the study on the bacterial species diversity in Korea, we report 24 unrecorded bacterial species of Korea belonging to the phylum Firmicutes. The unrecorded species excavated through this study were assigned to 12 different genera of 7 families, namely *Bacillus*, *Halobacillus*, *Lysinibacillus* and *Thalassobacillus* of *Bacillaceae*, *Brevibacillus* and *Paenibacillus* of *Paenibacillaceae*, *Viridibacillus* of *Planococcaceae*, *Salinicoccus* and *Staphylococcus* of *Staphylococcaceae*, *Enterococcus* of *Enterococcaceae*, *Lactobacillus* of *Lactobacillaceae*, and *Lactococcus* of *Streptococcaceae*, respectively. The bacterial isolates were obtained from various ecosystems in Korea. The isolates were identified based on 16S rRNA gene sequences, and those exhibiting at least 99% sequence similarity with known bacterial species but never reported in Korea were selected as unrecorded species. The selected isolates were subjected to further taxonomic characterization including the analysis of cell shape and fine structure using electron microscope, colony color and shapes, enzyme activities and carbon source utilization. The descriptive information on the 24 unrecorded species are provided.

Keywords: Bacillales, Firmicutes, Lactobacillales, unrecorded bacterial species

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INTRODUCTION

The phylum Firmicutes encompasses broad bacterial taxa that have Gram positive cell walls and low DNA G + C contents (Dworkin *et al.*, 2006; De Vos *et al.*, 2009). Firmicutes can be isolated from virtually everywhere, i.e. soil, fresh or marine aquatic environment, air, and plant or animal hosts. Recent studies indicate that Firmicutes constitutes a major portion of human and mouse gut microbiome (Ley *et al.*, 2006). The phylum current-

ly contains three classes, namely Bacilli, Clostridia and Erysipelotrichia (De Vos *et al.*, 2009). The class Bacilli includes endospore-forming groups and lactic acid producing groups, Clostridia includes endospore forming or non-forming anaerobic groups and anoxygenic phototrophic groups, and Erysipelotrichia includes non-motile, non-spore-forming and aerobic groups. *Bacillus, Clostridium, Lactobacillus* and *Paenibacillus* are large membered genera, each containing more than 100 validly described species (List of Prokaryotic Names with Standing in Nomenclature, http://www.bacterio.net). Firmicutes includes industrially important groups as well as causative agents of various diseases. Lactic acid bacteria are the representative probiotic bacteria, and thus one of the most industrially important bacterial groups (Tannock, 2005). *Bacillus* and *Paenibacillus* are known as two important taxa that exhibit plant growth promoting potential, and thus can be used as agricultural agents (McSpadden Gardner, 2004). In contrast, species of *Bacillus* (anthrax, food poisoning), *Clostridium* (tetanus, food poisoning, gas gangrene), *Enterococcus* (urinary tract infection), *Listeria* (listerosis), *Streptococcus* (pneumonia, meningitis, dental caries) and *Staphylococcus* (scalded skin syndrome) are some examples of medically significant bacteria of Firmicutes (Dworkin *et al.*, 2006).

In this study, bacteria belonging to Firmicutes were isolated from various sources such as ginseng cultivation soil, mud, salted fish and shrimp, guts of insects, plant root, freshwater and seawater. Through the phylogenetic analysis using 16S rRNA gene sequences, we recovered a total of 23 species that could be recognized as unrecorded species in Korea.

MATERIALS AND METHODS

Bacterial strains were isolated as pure cultures from diverse environmental sources including soil, mud, freshwater, seawater, salted fish and shrimp, plant root, guts of insects. Diverse culture media including R2A, marine agar 2216, nutrient agar, Luria agar and tryptic soy agar were used to isolate diverse groups of bacteria belonging to Firmicutes, and the inoculated plates were incubated at 25-30°C for 2-5 days. The designation of strains, source of isolation and culture media are summarized in Table 1. All strains were purified as single colonies and stored as 10-20% glycerol suspension – 80°C as well as lyophilized ampoules.

Bacterial DNA extraction, PCR amplification and 16S rRNA gene sequencing were performed using the standard procedures described elsewhere. The 16S rRNA gene sequences of the strains assigned to the phylum Firmicutes were selected for subsequent analysis. The selected strains were identified using the EzTaxon-e server (Kim *et al.*, 2012). The cutoff value of 98.7% sequence similarity was employed for identification. Phylogenetic trees were generated by using neighbor-joining (Saitou and Nei, 1987), maximum-likelihood (Felsenstein, 1981) and maximum-parsimony (Kluge and Farris, 1969) algorithms that are programmed in MEGA 6.0 (Tamura *et al.*, 2013). The robustness of the phylogenetic trees was confirmed by bootstrap analyses based on 1000 random replicates.

Colony morphology of the strains was observed on

agar plates with a magnifying glass after cells grew up to stationary phase. Cellular morphology and cell size were examined by either transmission electron microscopy or scanning electron microscopy (Fig. 1). Gram staining was performed using a Gram-staining kit or the standard procedures. Biochemical characteristics were tested by using API 20NE galleries (bioMérieux) according to the manufacturer's instructions.

RESULTS AND DISCUSSION

From diverse sources, a total of 26 bacterial strains belonging to Firmicutes were obtained. All isolates could be assigned to 24 different species based on 16S rRNA gene sequence similarity. The taxonomic composition and identification results of the isolates are summarized in Table 1. The isolates could be assigned to 11 different genera of 7 families, namely Bacillus (5 species), Halobacillus (1 species), Lysinibacillus (1 species) and Thalassobacillus (1 species) of Bacillaceae, Brevibacillus (1 species) and Paenibacillus (5 species) of Paenibacillaceae, Viridibacillus (1 species) of Planococcaceae, Salinicoccus (1 species) and Staphylococcus (2 species) of Staphylococcaceae, Enterococcus (3 species) of Enterococcaceae, Lactobacillus (2 species) of Lactobacillaceae, and Lactococcus (1 species) of Streptococcaceae, respectively. The families Bacillaceae, Paenibacillaceae, Planococcaceae and Staphylococcaceae belong to the Order Bacillales, whereas the remaining three families belong to the order Lactobacillales (Figs. 2-4). Both orders belong to the class Bacilli.

Soil and water are common habitats for the members of Firmicutes (Dworkin et al., 2006; De Vos et al., 2009). In contrast, not much is known on the other habitats. In this study, five strains belonging to Bacillus, Enterococcus and Lactobacillus were obtained from insect guts. Although there have been only a handful of reports on new species of those genera from insect gut, for example Bacillus oleronius (Kuhnik et al., 1996), Bacillus trypoxylicola (Aizawa et al., 2010), Enterococcus diestrammenae (Kim et al., 2013) and Lactobacillus apis (Killer et al., 2014), this study confirms that members of Firmicutes can be a major constituent in the gut microflora of insects. This finding is in line with a report that members of Firmicutes, Bacillus in particular, are known to form a significant portion of gut microbial community of soil invertebrates (König, 2006).

Two strains were recovered from salted marine animals in this study, namely one identified as *Halobacillus kuroshimensis*, and the other as *Salinicoccus siamensis*. This can be considered natural since the members of both genera are inhabitants of marine environment (Spring, 2010; Ventosa, 2010), although it is not clear whether the

Family	Genus	Family Genus Strain code		S NIBR ID ^a Identification sim	Sequence similarity (%)	Isolation source	Medium ^b	Growth temperature
	Bacillus	RS3-5 B DE L 1 4 DE L 2 2 J27 J29	NIBRBA000113942 NIBRBA0000114025 NIBRBA0000114028 NIBRBA0000114104 NIBRBA0000114104 NIBRBA0000114105	B. acidiceler CBD 119 ^T B. aryabhattai B8W22 ^T B. aerophilus 28K ^T B. infriensis SMC 4352-2 ^T B. infantis SMC 4352-1 ^T	99.9 99.7 100 100	Soil Insect gut Insect gut Seawater Seawater	R2A LA LA MA MA	30°C 25°C 25°C 25°C
Bacillaceae	Lysinibacillus Thalassobacillus	WR-M2W MA19 HME8790 KYW872	NIBRBA0000113998 NIBRBA0000113967 NIBRBA0000114093 NIBRBA0000114104	L. fusiformis AMNH732 ^T L. fusiformis AMNH732 ^T T. devorans DSM16966 ^T T. devorans DSM16966 ^T	99.7 100 99.4 99.9	Soil Soil Mud Seawater	MA MA MA MA	25°C 25°C 30°C 25°C
	Halobacillus	PM1	NIBRBA0000114056	H. kuroshimensis IS-Hb7 ^T	99.4	Salted anchovy	MA	25°C
Enterococcaceae	Enterococcus	OR L 1 6 OR L 2 3 MR1	NIBRBA000114027 NIBRBA0000114026 NIBRBA0000114031	E. plantarum CCM 7889 ^T E. quebecensis CCRI-16985 ^T E. asini ATCC 700915 ^T	7.99 7.99 8.99	Insect gut Insect gut Insect gut	LA LA R2A	25°C 25°C 25°C
Lactobacillaceae	Lactobacillus	IK 36 HY M 2 2	NIBRBA0000113962 NIBRBA0000114033	L. aquaticus IMCC 1736 ^T L. kuunkeei YH-15 ^T	100 99.7	Freshwater Insect gut	PCA MRSA	25°C 25°C
Paenibacillaceae	Paenibacillus	H4-2-1 H RS5-1 Rk5-7 B MS5-14 MK5-2	NIBRBA000113934 NIBRBA000113946 NIBRBA0000113946 NIBRBA0000113948 NIBRBA0000113948 NIBRBA0000113949	P. glycanilyticus DS-1 ^T P. massiliensis 2301065 ^T P. peoriae DSM8320 ^T P. timonensis 230 1032 ^T P. xylanexedens B22a ^T	9.99 8.99 7.99 7.99	Soil Soil Soil Soil	R2A R2A R2A MA MA	30°C 30°C 30°C 30°C
	Brevibacillus	UEJ4-1 D	NIBRBA0000113940	B. laterosporus DSM25 ^T	99.5	Soil	R2A	30°C
Planococcaceae	Viridibacillus	CT1-1	NIBRBA0000113860	V. arenosi LMG 22166 ^T	99.8	Roof of Pteridium sp.	TSA	30°C
	Salinicoccus	SJ2-6	NIBRBA0000114061	S. siamensis $PN1-2^{T}$	99.5	Salted shrimp	MA	25°C
Staphylococcaceae	Staphylococcus	ES05-9M-1-MA CNS5-1	NIBRBA0000113917 NIBRBA0000113957	S. warneri ATCC 27836 ^T S. nepalensis CW1 ^T	100 99.9	Seawater Soil	MA NA	25°C 30°C
Streptococcaceae	Lactococcus	OR Y 1 1	NIBRBA0000114037	L. garvieae ATCC 29156 ^T	7.99	Insect gut	TSYA	25°C
^a Identification number ^b LA, Luria agar; MA, r	by the National Institut nannitol agar; PCA, pla	^a Identification number by the National Institute of Biological Resources (NIBR) ^b LA, Luria agar; MA, mannitol agar; PCA, plate count agar; MRSA, MRSA aga	es (NIBR). MRSA agar; TSA, tryptic soy	^a Identification number by the National Institute of Biological Resources (NIBR). ^b LA, Luria agar; MA, mannitol agar; PCA, plate count agar; MRSA, MRSA agar; TSA, tryptic soy agar; TSYA, tryptic soya agar.				

Table 1. List of strains belonging to the phylum Firmicutes and their taxonomic assignment based on 16S rRNA gene analysis.

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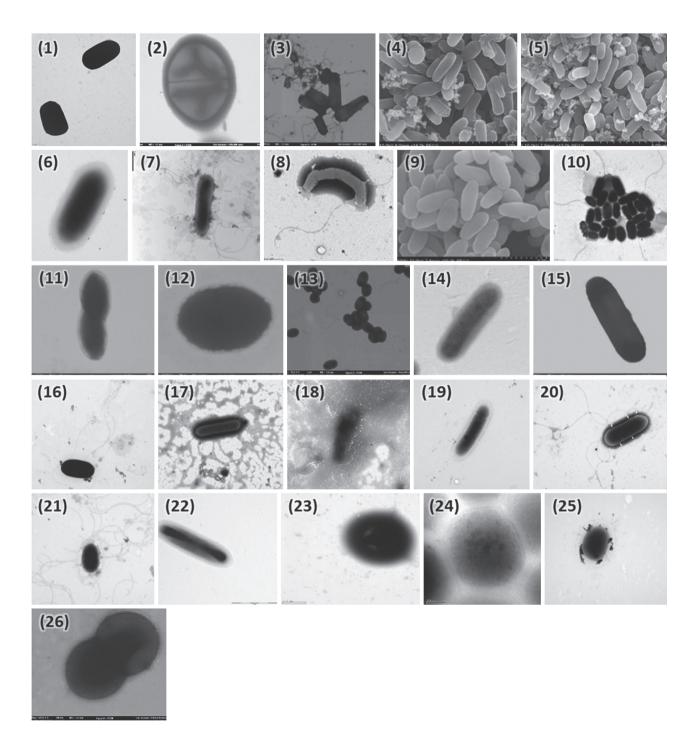


Fig. 1. Transmission electron micrographs or scanning electron micrographs of cells of the strains isolated in this study. Strains: 1. RS3-5 B; 2. DE L 1 4; 3. DE L 2 2; 4. J27; 5. J29; 6. WR-M2W; 7. MA19; 8. HME8790; 9. KYW872; 10. PM1; 11. OR L 1 6; 12. OR L 2 3; 13. MR1; 14. IK36; 15. HY M 2 2; 16. H4-2-1 H; 17. RS5-1; 18. Rk5-7 B; 19. MS5-14; 20. MK5-2; 21. UEJ4-1 D; 22. CT1-1; 23. SJ2-6; 24. ES05-9M-1-MA; 25. CNS5-1; 26. OR Y 1 1.

strains were originated from applied salt or the animal bodies.

Through this study, the diversity of bacterial species belonging to Firmicutes whose presence in Korean peninsula has not been previously reported was unveiled. Accordingly, the following 24 species are reported as unrecorded species in Korea.

Description of Bacillus acidiceler RS3-5 B

Cells are Gram-staining-positive, non-flagellated, non-

pigmented and rod shaped. Colonies are irregular, lobate, smooth and white colored after 2 days on R2A at 30°C. Based on API 20NE, positive for urease, esculin hydrolysis, gelatinase and β -galactosidase, but negative for oxidase, nitrate reduction, indole production, glucose fermentation and arginine dihydrolase. D-Glucose, Larabinose, D-mannose, D-mannitol, D-maltose, potassium gluconate and adipic acid are utilized. Does not utilize capric acid, malic acid, trisodium citrate and phenylacetic acid. Strain RS3-5 B (=NIBRBA0000113942) was isolated from soil of ginseng cultivation field, Anseong, Korea.

Description of Bacillus aryabhattai DE L 1 4

Cells are Gram-staining-positive, non-flagellated, nonpigmented, and oval shaped. Colonies are circular, raised, entire and cream colored after 2 days on LA at 25°C. Based on API 20NE, positive for esculin hydrolysis, gelatinase and β -galactosidase, but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase and urease. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain DE L 1 4 (=NIBRBA0000) was isolated from gut of insect, Seoul, Korea.

Description of Bacillus aerophilus DE L 2 2

Cells are Gram-staining-positive, non-flagellated, nonpigmented, and rod shaped. Colonies are circular, raised, entire and white colored after 2 days on LA at 25°C. Based on API 20NE, positive for esculin hydrolysis, gelatinase and β -galactosidase, but negative for nitrate reduction, indole production, glucose fermentation, arginine, dihydrolase and urease. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic

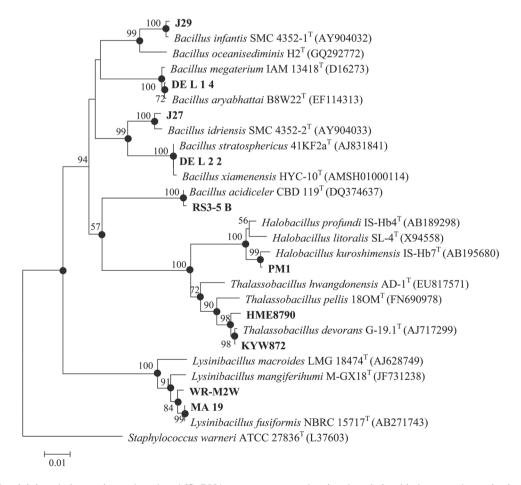


Fig. 2. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences, showing the relationship between the strains isolated in this study and their relatives of the family *Bacillaceae*. Bootstrap values (>50%) are shown at nodes. Filled circles indicate the nodes recovered by three other treeing methods including maximum likelihood, maximum parsimony, and neighbor joining. Bar, 0.01 substitutions per nucleotide position.

acid. Strain DE L 2 2 (=NIBRBA0000) was isolated from gut of insect, Soeul, Korea.

Description of Bacillus idriensis J27

Cells are Gram-staining-negative, non-flagellated, non-pigmented, and coccus shaped. Colonies are opaque, round, smooth, convex and cream colored after 3 days on MA at 25°C. Based on API 20NE, positive for glucose fermentation, esculin hydrolysis and gelatinase, but negative for nitrate reduction, indole production, arginine dihydrolase, urease, and β -galactosidase. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Oxidase activity is positive. Strain J27 (=NIBRBA0000) was isolated from seawater, Gwangyang, Korea.

Description of Bacillus infantis J29

Cells are Gram-staining-negative, non-flagellated, nonpigmented, and rod shaped. Colonies are opaque, round, smooth, convex and shell pink colored after 3 days on MA at 25°C. Based on API 20NE, positive for esculin hydrolysis, gelatinase and β -galactosidase, but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase and urease. D-Glucose, Dmannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate and malic acid are utilized. Does not utilize L-arabinose, capric acid, adipic acid, trisodium citrate, and phenylacetic acid. Oxidase activity is positive. Strain J29 (=NIBRBA0000) was isolated from seawater, Gwangyang, Korea.

Description of Lysinibacillus fusiformis WR-M2W

Cells are Gram-staining-positive, non-flagellated, nonpigmented, and rod-shaped. Colonies are irregular, smooth, glistening and pale-yellow colored after 3 days of incubation on MA at 25°C. Negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis, gelatinase, and β -galactosidase in API 20NE. Capric acid, malic acid, phenylacetic acid are utilized. Strain WR-M2W (= NIBRBA 0000113998) was isolated from soil, Wando, Korea.

Description of Lysinibacillus fusiformis MA19

Cells are Gram-staining-positive, flagellated, non-pigmented, and rod-shaped. Colonies are circular, and graycolored after 2 days of incubation on MA at 25°C. Based on API 20NE, positive for urease and gelatinase and, but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, esculin hydrolysis, and β -galactosidase. *N*-acetyl-glucosamine, gluconate and malic acid are utilized. Strain MA19 (=NIBRBA 0000113967) was isolated from soil, Gwanak Mountain, Seoul, Korea.

Description of Thalassobacillus devorans HME8790

Cells are Gram-staining-positive, flagellated, non-pigmented, and rod-shaped. Colonies are circular, convex, entire and white-colored after 2 days of incubation on MA at 30°C. Based on API 20NE, positive for nitrate reduction, esculin hydrolysis, gelatinase, and β -galactosidase, but negative for glucose fermentation, indole production, arginine dihydrolase, and urease. Strain HME8790 (=NIBRBA0000114093) was isolated from mud, Shinan, Korea.

Description of Thalassobacillus devorans KYW872

Cells are Gram-staining-negative, non-flagellated, non-pigmented, and rod-shaped. Colonies are opaque, round, smooth, convex, and cream-colored after 2 days of incubation on MA at 25°C. Negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease esculin hydrolysis, gelatinase, and β -galactosidase in API 20NE. Strain KYW872 (=NIBR BA0000114114) was isolated from seawater, Gwangyang, Korea.

Description of Halobacillus kuroshimensis PM1

Cells are Gram-staining-positive, non-flagellated, nonpigmented, and rod-shaped. Colonies are circular, raised, entire and pale yellow colored after 2 days on MA at 25 °C. Based on API 20NE, positive for esculin hydrolysis, gelatin hydrolysis, and β -galactosidase, but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, and urease. Potassium gluconate is utilized. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, Dmaltose, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain PM1 (= NIBRBA 0000114056) was isolated from salted anchovies, Korean fermented food.

Description of Enterococcus plantarum OR L 16

Cells are Gram-staining-positive, non-flagellated, nonpigmented and oval-shaped. Colonies are circular, raised, entire and translucent after 2 days of incubation on LA at 25°C. Based on API 20NE, positive for esculin hydrolysis, but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, gelatinase and β -galactosidase. Does not utilize Dglucose, L-arabinose, D-mannose, D-mannitol, *N*-acetylglucosamine, D-maltose, potassium gluconate, capric

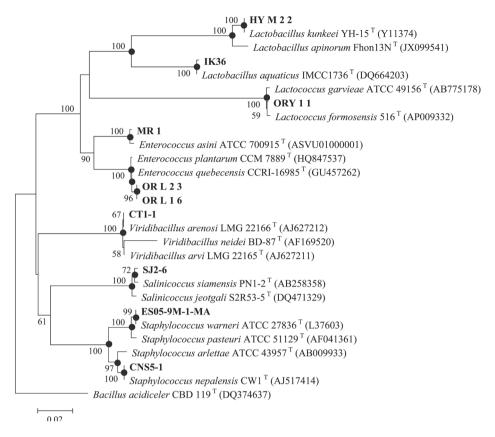


Fig. 3. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences, showing the relationship between the strains isolated in this study and their relatives of the family *Enterococcaceae*, *Lactobacillaceae*, *Planococcaceae*, *Staphylococcaceae*, and *Streptococcaceae*. Bootstrap values (>50%) are shown at nodes. Filled circles indicate the nodes recovered by three other treeing methods including maximum likelihood, maximum parsimony, and neighbor joining. Bar, 0.02 substitutions per nucleotide position.

acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. Strain OR L 1 6 (= NIBRBA0000114027) was isolated from gut of insect, Seoul, Korea.

Description of Enterococcus quebecensis OR L 2 3

Cells are Gram-staining-positive, non-flagellated, nonpigmented and oval-shaped. Colonies are circular, raised, entire and translucent after 2 days of incubation on LA at 25°C. Based on API 20NE, positive for esculin hydrolysis, but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, gelatinase and β -galactosidase. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetylglucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. Strain OR L 2 3 (= NIBRBA0000114026) was isolated from gut of insect, Seoul, Korea.

Description of Enterococcus asini MR1

Cells are Gram-staining-positive, non-flagellated, nonpigmented and oval-shaped. Colonies are circular, raised, entire and translucent after 2 days of incubation on R2A at 25°C. Based on API 20NE, positive for nitrate reduction, glucose fermentation, arginine dihydrolase, esculin hydrolysis and β -galactosidase, but negative for indole production, urease and gelatinase. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. Strain MR1 (=NIBRBA0000114031) was isolated from gut of insect, Seoul, Korea.

Description of Lactobacillus aquaticus IK36

Cells are Gram-staining-positive, non-flagellated, nonpigmented and rod shaped. Colonies are circular, smooth and white colored after 5 days of incubation on PCA at 25°C. Based on API 20NE, positive for arginine dihydrolase, urease and esculin hydrolysis, but negative for nitrate reduction, indole production, glucose fermentation, gelatinase and β -galactosidase. D-Mannose is utilized. Does not utilize D-glucose, L-arabinose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and

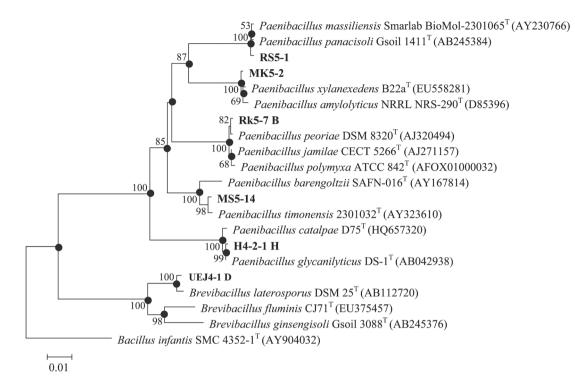


Fig. 4. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences, showing the relationship between the strains isolated in this study and their relatives of the family *Paenibacillaceae*. Bootstrap values (>50%) are shown at nodes. Filled circles indicate the nodes recovered by three other treeing methods including maximum likelihood, maximum parsimony, and neighbor joining. Bar, 0.01 substitutions per nucleotide position.

phenylacetic acid. Strain IK36 (= NIBRBA0000113962) was isolated from freshwater, Incheon, Korea.

Description of Lactobacillus kuunkeei HY M 2 2

Cells are Gram-staining-positive, non-flagellated, nonpigmented and rod shaped. Colonies are circular, raised, entire and white colored after 2 days of incubation on MRSA at 25°C. Negative for nitrate reduction, indole production, arginine dihydrolase, urease, esculin hydrolysis, glucose fermentation, gelatinase and β -galactosidase. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. Strain HY M 2 2 (= NIBRBA0000114033) was isolated from gut of insect, Seoul, Korea.

Description of Paenibacillus glycaniyticus H4-2-1 H

Cells are Gram-staining-negative, flagellated, non-pigmented, and rod-shaped. Colonies are circular, entire, smooth, and pink colored after 2 days of incubation on R2A at 30°C. Based on API 20NE, positive for esculin hydrolysis and β -galactosidase, but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease and gelatinase. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose and potassium gluconate are utilized. Does not utilize capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. Strain H4-2-1_H (=NIBRBA0000113934) was isolated from ginseng cultivation soil, Geumsan, Korea.

Description of Paenibacillus massiliensis RS5-1

Cells are Gram-staining-negative, flagellated, non-pigmented, and rod-shaped. Colonies are rhizoid, undulate, smooth and white colored after 2 days of incubation on R2A at 30°C. Based on API 20NE, positive for nitrate reduction, but negative for indole production, glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis, gelatinase and β -galactosidase. D-Mannose and D-mannitol are utilized. Does not utilize D-Glucose, Larabinose, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. Strain RS5-1 (= NIBRBA 0000113946) was isolated from ginseng cultivation soil, Anseong, Korea.

Description of Paenibacillus peoriae Rk5-7 B

Cells are Gram-staining-negative, non-flagellated, nonpigmented, and rod-shaped. Colonies are circular, convex, and yellow-colored after 3 days of incubation on VXG at 25°C. Based on API 20NE, positive for glucose fermentation, esculin hydrolysis, gelatinase, and β -galactosidase, but negative for nitrate reduction, indole production, arginine dihydrolase, and urease. D-Glucose, L-arabinose, D-mannose, D-mannitol and D-maltose are utilized. Does not utilize *N*-acetyl-glucosamine, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid Strain Rk5-7_B (=NIBRBA0000113947) was isolated from ginseng cultivation soil, Anseong, Korea.

Description of Paenibacillus timonensis MS5-14

Cells are Gram-staining-negative, non-flagellated, nonpigmented, and rod-shaped. Colonies are punctiform, entire, smooth and white-colored after 2 days of incubation on MA at 30°C. Based on API 20NE, positive for esculin hydrolysis and β -galactosidase, but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease and gelatinase. D-Glucose, L-arabinose, D-mannose, *N*-acetyl-glucosamine, D-maltose and potassium gluconate are utilized. Does not utilize D-mannitol, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain MS5-14 (=NIBRBA0000113948) was isolated from ginseng cultivation soil, Anseong, Korea.

Description of Paenibacillus xylanexedens MK5-2

Cells are Gram-staining-negative, flagellated, non-pigmented, and rod-shaped. Colonies are circular, entire, smooth and light yellow-colored after 2 days of incubation on MA at 30°C. Based on API 20NE, positive for nitrate reduction, esculin hydrolysis and β -galactosidase, but negative for indole production, glucose fermentation, arginine dihydrolase, urease and gelatinase. D-Glucose, L-arabinose, D-mannitol, *N*-acetyl-glucosamine and Dmaltose are utilized. Does not utilize D-mannose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. Strain MK5-2 (= NIBRBA0000113949) was isolated from ginseng cultivation soil, Anseong, Korea.

Description of Brevibacillus laterosporus UEJ4-1 D

Cells are Gram-staining-negative, flagellated, non-pigmented, and short rod-shaped. Colonies are circular, entire, smooth, and white-colored after 2 days of incubation on R2A at 30°C. Based on API 20NE, positive for nitrate reduction, esculin hydrolysis and gelatinase, but negative for indole production, glucose fermentation, arginine dihydrolase, urease and β -galactosidase. D-Glucose, D-mannose, D-mannitol, *N*-acetyl-glucosamine and D-maltose are utilized. Does not L-arabinose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. Strain UEJ4-1_ D (=NIBRBA0000113940) was isolated from ginseng cultivation soil, Anseong, Korea.

Description of Viridibacillus arenosi CT1-1

Cells are Gram-staining-positive, non-flagellated, nonpigmented and rod shaped. Colonies are irregular and ivory colored after 2 days of incubation on TSA at 30°C. Based on API 20NE, positive for nitrate reduction and urease, but negative for indole production, arginine dihydrolase, esculin hydrolysis, glucose fermentation, gelatinase and β -galactosidase. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. Strain CT1-1 (= NIBRBA0000113860) was isolated from root of *Ptheridium*.

Description of Salinicoccus siamensis SJ2-6

Cells are Gram-staining-positive, non-flagellated, nonpigmented, and coccus-shaped. Colonies are circular, raised, entire and orange colored after 2 days on MA at 25°C. Based on API 20NE, positive for nitrate reduction and glucose fermentation, but negative for indole production, arginine dihydrolase, urease, esculin hydrolysis, gelatin hydrolysis, and β -galactosidase. D-Glucose, Dmannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, malic acid and trisodium citrate are utilized. Does not utilize L-arabinose, D-mannose, adipic acid, and phenylacetic acid. Strain SJ2-6 (= NIBR BA0000114061) was isolated from salted shrimp, Korean fermented food.

Description of Staphylococcus warneri ES05-9M-1-MA

Cells are Gram-staining-positive, non-flagellated, nonpigmented, and coccoid-shaped. Colonies are circular, entire, smooth and beige colored after 4 days of incubation on MA at 25°C. Based on API 20NE, positive for nitrate reduction and urease, but negative for indole production, glucose fermentation, arginine dihydrolase, esculin hydrolysis, gelatinase and β -galactosidase. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetylglucosamine, D-maltose and potassium gluconate are not utilized. Strain ES05-9M-1-MA (= NIBRBA0000113917) was isolated from seawater, Pohang, Korea.

Description of Staphylococcus nepalensis CNS5-1

Cells are Gram-staining-positive, non-flagellated, nonpigmented, and coccoid-shaped. Colonies are circular, entire, smooth and beige colored after 2 days of incubation on NA at 30°C. Based on API 20NE, positive for nitrate reduction, urease, esculin hydrolysis, and β -galactosidase, but negative for indole production, glucose fermentation, arginine dihydrolase and gelatinase. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose and potassium gluconate are utilized. Strain CNS5-1 (=NIBRBA0000113957) was isolated from a soil sample, Anseong, Korea.

Description of Lactococcus garvieae OR Y 1 1

Cells are Gram-staining-positive, non-flagellated, nonpigmented and coccus shaped. Colonies are circular, raised, entire and white colored after 2 days of incubation on TSYA at 25°C. Based on API 20NE, positive for glucose fermentation, arginine dihydrolase, esculin hydrolysis, and β -galactosidase, but negative for nitrate reduction, indole production, urease and gelatinase. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. Strain OR Y 1 1 (=NIBR BA0000114037) was isolated from gut of insect, Seoul, Korea.

ACKNOWLEDGEMENTS

This study was supported by the research grant 'The Survey of Korean Indigenous Species' from the National Institute of Biological Resources of the Ministry of Environment in Korea.

References

- Aizawa, T., M. Urai, N. Iwabuchi, M. Nakajima and M. Sunairi. 2010. *Bacillus trypoxylicola* sp. nov., xylanase-producing alkaliphilic bacteria isolated from the guts of Japanese horned beetle larvae (*Trypoxylus dichotomus septentrionalis*). Int. J. Syst. Evol. Microbiol. 60:61-66.
- De Vos, P., G.M. Garrity, D. Jones, N.R. Krieg, W. Ludwig, F.A. Rainey, K.-H. Schleifer and W.B. Whitman (editors). 2009. Bergey's Manual of Systematic Bacteriology, 2nd edn, vol. 3, The Firmicutes. New York: Springer.
- Dworkin, M., S. Falkow, E. Rosenberg, K.-H. Schleifer and E. Stackebrandt (editors). 2006. The Prokaryotes, 3rd edn, vol. 3. New York: Springer.
- Felsenstein, J. 1981. Evolutionary trees from DNA sequences: a maximum likelihood approach. J. Mol. Evol. 17: 368-376.
- Killer, J., S. Dubná, I. Sedláček and P. Švec. 2014. Lactobacillus apis sp. nov., from the stomach of honeybees (Apis mellifera), having an in vitro inhibitory effect on the causative agents of American and European foulbrood. Int. J. Syst. Evol. Microbiol. 64:152-157.

- Kim, J.Y., N.R. Shin, H.K. Na, D.W. Hyun, T.W. Whon, P.S. Kim, J.H. Yun and J.W. Bae. 2013. *Enterococcus diestrammenae* sp. nov., isolated from the gut of *Diestrammena coreana*. Int. J. Syst. Evol. Microbiol. 63:4540-4545.
- Kim, O.S., Y.J. Cho, K. Lee, S.H. Yoon, M. Kim, H. Na, S.C. Park, Y.S. Jeon, J.H. Lee, H. Yi, S. Won and J. Chun. 2012. Introducing EzTaxon-e: a prokaryotic 16S rRNA gene sequence database with phylotypes that represent uncultured species. Int. J. Syst. Evol. Microbiol. 62:716-721.
- Kluge, A.G. and J.S. Farris. 1969. Quantitative phyletics and the evolution of anurans. Syst. Zool. 18:1-32.
- König, H. 2006. *Bacillus* species in the intestine of termites and other soil invertebrates. J. Appl. Microbiol. 101:620-627.
- Kuhnigk, T., E.M. Borst, A. Breunig, H. König, M.D. Collins, R.A. Hutson and P. Kämpfer. 1995. *Bacillus oleronius* sp. nov., a member of the hindgut flora of the termite Reticulitermes santonensis (Feytaud). Can. J. Microbiol. 41:699-706.
- Ley, R.E., D.A. Peterson and J.I. Gordon. 2006. Ecological and evolutionary forces shaping microbial diversity in the human intestine. Cell 124:837-848.
- McSpadden Gardner, B.B. 2004. Ecology of *Bacillus* and *Paenibacillus* spp. in agricultural systems. Phytopathology 94:1251-1258.
- Saitou, N. and M. Nei. 1987. The neighbor-joining method: a new method for reconstructing phylogenetic trees. Mol. Biol. Evol. 4:406-425.
- Spring, S. 2009. Genus IX. *Halobacillus* Spring, Ludwig, Márquez, Ventosa and Schleifer 1996, 495^{VP}. In Bergey's Manual of Systematic Bacteriology, 2nd edn, vol. 3, The Firmicutes, pp. 164-168. Edited by De Vos, P., Garrity, G., Jones, D., Krieg, N. R., Ludwig, W., Rainey, F. A., Schleifer, K.-H., and Whitman, W. B. New York: Springer.
- Tamura, K., G. Stecher, D. Peterson, A. Filipski and S. Kumar. 2013. MEGA6: molecular evolutionary genetics analysis version 6.0. Mol. Biol. Evol. 30:2725-2729.
- Tannock, G. (editor) 2005. Probiotics and Prebiotics: Scientific Aspects (1st ed.). Caister Academic Press.
- Ventosa, A. 2009. Genus IV. Salinicoccus Ventosa, Márquez, Ruiz-Berraquerro and Kocur 1990b, 320^{VP} (Effective publication: Ventosa, Márquez, Ruiz-Berraquerro and Kocur 1990a, 32). In Bergey's Manual of Systematic Bacteriology, 2nd edn, vol. 3, The Firmicutes, pp. 426-429. Edited by De Vos, P., Garrity, G., Jones, D., Krieg, N. R., Ludwig, W., Rainey, F. A., Schleifer, K.-H., and Whitman, W. B. New York: Springer.

Submitted: May 21, 2015 Revised: July 15, 2015 Accepted: July 27, 2015