A report of 43 unrecorded bacterial species within the phyla Bacteroidetes and Firmicutes isolated from various sources from Korea in 2019

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In 2019, 43 bacterial strains were isolated from food, soil, marine environments, human, and animals related sources from the Republic of Korea. Based on the analysis of 16S rRNA gene sequence, these isolates were allocated to the phyla Bacteroidetes and Firmicutes as unrecorded species in Korea. The 10 Bacteroidetes strains were classified into the families Bacteroidaceae, Chitinophagaceae, Cytophagaceae, Flavobacteriaceae, and Prolisibacteriaceae (of the orders Bacteroidales, Chitinophagales, Cytophagales, Flavobacteriales, and Marinilabiliales, respectively). The 33 Firmicutes strains belonged to the families Bacillaceae, Paenibacillaceae, Planococcaceae, Staphylococcaceae, Clostridiaceae, Lachnospiraceae, Peptostreptococcaceae, Enterococcaceae, Lactobacillaceae, Leuconostocaceae, and Streptococcaceae (of the orders Bacillales, Clostridiales, and Lactobacillales). These unrecorded bacteria were determined based on taxonomic criterion (> 98.7%; 16S rRNA gene sequence similarity). In addition, their phylogenetic affiliation, as well as cell and colony morphologies, staining reactions, and physiological and biochemical properties were investigated. Therefore, we report 43 isolates as unrecorded species, and described basic features, isolation source, and locations of these strains.

Keywords: 16S rRNA gene, Bacteroidetes, Firmicutes, unrecorded species

INTRODUCTION

The bacteria belonging to phyla Bacteroidetes and Firmicutes can be found from diverse natural habitats, as well as human and animal gastrointestinal tracts (Haaken et al., 2008; García-López et al., 2019). Bacteroidetes are all Gram-stain-negative heterotrophs, mainly rod-shaped, and do not form endospores (Krieg et al., 2010). They are known to play important roles in the biogeochemical processes such as the decomposition of peptides and polysaccharides (Russell et al., 2014; Hahnke et al., 2016). Meanwhile, most Firmicutes contains Gram-stain-positive, chemo-organotrophic bacteria (a few are anoxygenic photoheterotrophs), and are phenotypically diverse (spherical, straight, curved or helical rods or filaments; with or without flagella; and with or without heat-resistant endospores) (De Vos et al., 2009). Members of this taxon include some extremophilic and lactic acid bacteria that may be useful in the food and pharmaceutical industries (Sharmin et al., 2013; Kim et al., 2016; Na-
har et al., 2018). In addition, the phyla Bacteroidetes and Firmicutes are reported to be the most dominant bacteria in the human gut, and the ratio between them is considered to be the most important in microbiome studies (Ley et al., 2006; Koliada et al., 2017).

In 2019, a total of 193 unrecorded species were isolated from various samples, of which 43 belong to the phyla Bacteroidetes and Firmicutes. In this study, we report these species and describe their characteristics.

**Materials and Methods**

The unrecorded bacteria were isolated from soil, marine environment, food, human, and animal samples in Korea. Several agar media [Reasoner’s 2A agar (R2A), Mueller-Hinton agar (MHA), nutrient agar (NA), tryptic soy agar (TSA), all from Difco] were used for isolation of soil and marine bacteria. MRS agar was used for isolation of lactic acid bacteria. Anaerobe basal, blood, chocolate and marine bacteria. MRS agar was used for isolation of anaerobic bacteria in human and animal samples. These isolates were cultured at 25, 30 or 37°C for 2–5 days. All bacterial strains were stored in cryogenic tubes with 10% (v/v) glycerol stock at −80°C and by freeze-drying. The bacterial identification and phylogenetic investigation of 43 isolates were performed by using 16S rRNA gene sequence analysis. The 16S rRNA gene sequences of 43 isolates were obtained according to Janda and Abbott (2007) using universal primers (Lane, 1991) and those of the nearest strains were retrieved from the EzBioCloud (Yoon et al., 2017). These sequences were aligned using the SILVA Incremental Aligner (Pruesse et al., 2012). Further phylogenetic analysis was performed by using the software package MEGA software v.7.0 (Kumar et al., 2016). Phylogenetic reconstructions were produced using the neighbor-joining, maximum-parsimony, and maximum-likelihood methods (Fitch, 1971; Felsenstein, 1981; Saitou and Nei, 1987). The statistical reliability was evaluated by bootstrapping analysis of 1000 replicates according to Felsenstein (1985). Colony color and shape were observed on agar plates according to Alexander and Strete (2001). Cell size and shape were determined by transmission electron microscopy. Gram-staining was performed using a gram stain kit or standard procedures from Magee et al. (1975). Biochemical characteristics were tested by using API 20A or API 20NE galleries (bioMérieux) according to the manufacturer’s instructions. Cytochrome oxidase test was assessed according to Brown (2007).

**Results and Discussion**

Of the 43 bacterial strains isolated in 2019, 10 isolates were identified as belonging to the phylum Bacteroidetes. The isolated strains in the phylum Bacteroidetes were Gram-stain-negative and rod-shaped (strain SS28 was cocci) (Fig. 1). Most cells were positive for aesculin hydrolysis (strain LPB0329 was negative) and oxidase activity (strains LPB0329, FS31, and F-49 were negative). Ten bacterial strains (strains LPB0329, SO92, FS31, BT243, F-49, HMF9403, SS28, HMF6110, HMF6096, and HMF6964) were most closely related to following species (sequence similarity value), respectively: Bacteroides fragilis (99.6%), Arachidobacter rhizphaerae (98.9%), Chitinophaga cymbidii (98.9%), Parasegetibacter luojensis (99.8%), Dyadobacter jianguoensis (99.9%), Aquatilaela lipolytica (100%), Chryseobacterium luteum (99.7%), Chryseobacterium ureilyticum (99.8%), Empedobacter brevis (100%), and Mangrovibacterium marium (99.7%). These isolates formed a monophyletic clade with their most closely related type strain in the phylogenetic trees (Fig. 2).

The remaining 33 isolates were assigned to the phylum Firmicutes. These bacteria were distributed in the orders Bacillales, Lactobacillales, and Clostridiales of the classes Bacilli and clostridia; 21 strains for the order Bacillales, eight strains for the order Lactobacillales, and four strains for order Clostridiales. Unrecorded bacterial strains in the phylum Firmicutes were revealed through highest sequence similarity with the 16S rRNA gene of the following species (sequence similarity value): Bacillus halotolerans (99.9%), Bacillus proteolyticus (100%), Bacillus sporothermodurans (99.1%), Bacillus salaceticus (98.9%), Cytobacillus depressus (98.7%), Domibacillus mangrovi (99.4%), Halobacillus litoralis (99.7%), Jeotgalibacillus terrae (99.0%), Oceanobacillus luteolus (99.8%), Oceanobacillus sojae (99.9%), Virgibacillus proomii (100%), Brevisbacillus halotolerans (99.8%), Paenibacillus barengoltzii (98.7%), Paenibacillus laioningsis (99.6%), Paenibacillus stellifer (99.5%), Paenibacillus zeae (99.1%), Chryseomicrobium palamuruense (99.8%), Lysinibacillus pakistanensis (100%), Solibacillus cecembensis (99.7%), Staphylococcus cohnii subsp. urealyticus (99.9%), Staphylococcus succinus subsp. succinus (100%), Clostridium sardiniense (99.9%), Lactimispora celerecrescens (99.6%), Paeniclostridium sordellii (99.7%), Romboutsia hominis (99.2%), Caterlicoccus marimammalium (99.9%), Vagococcus lutrae (99.9%), Lactiplantibacillus plantarum (100%), Lactobacillus sakei subsp. sakei (100%), Leuconostoc gelidium subsp. gasicomitatum (100%), Streptococcus infantis (99.2%), Streptococcus oralis subsp. dentisani (99.3%), and Streptococcus rubneri (98.9%). Additionally, the phylogenetic positions of this isolates were presented in Figures 3, 4, and 5. Most strains were Gram-stain-positive, but some others were Gram-stain-negative. Cells were rods or cocci-shaped (Fig. 1). Other physiological and biochemical
Fig. 1. Transmission electron micrographs of cells. Strains: 1, LPB0329; 2, SO92; 3, FS31; 4, BT243; 5, F-49; 6, HMF9403; 7, SS28; 8, HMF6110; 9, HMF6096; 10, HMF6964; 11, R20; 12, 19D1S38; 13, LPB0288; 14, CAU 1601; 15, LPB0313; 16, BT246; 17, JBTF-M5; 18, LPB0275; 19, 19D1F21; 20, DN10; 21, 19D1C9; 22, LPB0284; 23, N17; 24, BT366; 25, BT245; 26, CAU 1600; 27, BSSK_R2A22; 28, FS120; 29, CAU 1604; 30, D5-19; 31, NC2; 32, CAU 1557; 33, CAU 1563; 34, CAU 1572; 35, CAU 1562; 36, LPB0311; 37, LPB0214; 38, YG19; 39, AM8; 40, AM13; 41, LPB0309; 42, LPB0308; 43, LPB0307.
characteristics are shown in the description section. The additional characteristics (morphological, physiological, and biochemical) are described below. Here, 43 strains isolated from various sources from Korea are reported as unrecorded species of the phyla Bacteroidetes and Firmicutes.

**Description of Bacteroides fragilis LPB0329**

Gram-stain-negative, anaerobic, non-flagellated, rod-shaped bacterium (0.6–0.9 μm wide, 1.9–2.0 μm long). Colonies grown on anaerobe basal agar are cream, circular, entire, and convex. Oxidase activity is negative. In the API 20A test, cells are positive for urease activity; and acidification of D-glucose, D-mannitol, D-lactose, sucrose,
Fig. 3. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences, showing the relationship between the isolates and their relatives of the family *Bacillaceae*. Bootstrap values (>70%) are shown. Filled circles indicate that both maximum-likelihood and maximum-parsimony trees obtained the same node arrangement, while empty circles indicate either only maximum-likelihood or maximum-parsimony obtained the same corresponding nodes. *Escherichia coli* ATCC 11775T (X80725) was used as an outgroup. Bar, 0.02 substitutions per nucleotide position.
d-maltose, d-xylose, L-arabinose, d-mannose, d-melezitose, d-raffinose, and d-sorbitol, but negative for indole production; hydrolysis of aesculin and gelatin; and acidification of salicin, glycerol, d-cellobiose, d-rhamnose, and d-trehalose. Strain LPB0329 (=NIBRBAC00050336) was isolated from an animal intestine sample (mouse) collected from Daejeon, Republic of Korea (36°23’56.5”N, 127°23’39.8”E).

Fig. 4. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences, showing the relationship between the isolates and their relatives of the families Paenibacillaceae, Planococcaceae and Staphylococcaceae. Bootstrap values (>70%) are shown. Filled circles indicate that both maximum-likelihood and maximum-parsimony trees obtained the same node arrangement, while empty circles indicate either only maximum-likelihood or maximum-parsimony obtained the same corresponding nodes. Escherichia coli ATCC 11775T (X80725) was used as an outgroup. Bar, 0.02 substitutions per nucleotide position.
**Description of *Arachidicoccus rhizosphaerae* SO92**

Gram-stain-negative, aerobic, non-flagellated, rod-shaped bacterium (0.6–0.7 μm wide, 1.5–1.7 μm long). Colonies grown on R2A are creamy white, circular, smooth, convex, and opaque. Oxidase activity is posi-
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<th>Phylum</th>
<th>Order</th>
<th>Family</th>
<th>Strain ID</th>
<th>NIBR ID</th>
<th>Most closely related species</th>
<th>Similarity (%)</th>
<th>Isolation source</th>
<th>Medium</th>
<th>Incubation condition</th>
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<td>BHI</td>
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Table 1. Taxonomic affiliation and isolation information of the isolates belonging to the phyla Bacteroidetes and Firmicutes.
tive. In the API 20NE test, cells are positive for aesculin hydrolysis; β-galactosidase activity; and assimilation of d-glucose, l-arabinose, d-mannose, d-mannitol, N-acetyl-glucosamine, and d-maltose, but negative for nitrate reduction; indole production; glucose fermentation; activity of arginine dihydrolase and urease; gelatin hydrolysis; and assimilation of potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain F-49 (= NIBRBAC000503373) was isolated from a soil sample collected from Daejeon, Republic of Korea (36°22′33.4″N, 127°20′33.8″E).

**Description of Chitinophaga cymbidii FS31**

Gram-stain-negative, aerobic, non-flagellated, rod-shaped bacterium (0.6–0.7 μm wide, 1.7–1.8 μm long). Colonies grown on R2A are pale yellow, circular, convex, smooth, and opaque. Oxidase activity is negative. In the API 20NE test, cells are positive for nitrate reduction; indole production; aesculin hydrolysis; β-galactosidase activity; and assimilation of d-glucose, l-arabinose, d-mannose, N-acetyl-glucosamine, and d-maltose, but negative for glucose fermentation; activity of arginine dihydrolase and urease; gelatin hydrolysis; and assimilation of potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain FS31 (= NIBRBAC000503298) was isolated from a soil sample collected from Suncheon, Republic of Korea (36°51′27.2″N, 128°27′28.6″E).

**Description of Parasegetibacter luojiensis BT243**

Gram-stain-negative, aerobic, non-flagellated, short rod-shaped bacterium (0.6–0.8 μm wide, 0.7–1.3 μm long). Colonies grown on R2A are yellow, circular, convex, and smooth. Oxidase activity is positive. In the API 20NE test, cells are positive for nitrate reduction; hydrolysis of aesculin and gelatin; and β-galactosidase activity, but negative for nitrate reduction; indole production; glucose fermentation; activity of arginine dihydrolase and urease; and assimilation of 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 BT243 (= NIBRBAC000502993) was isolated from a soil sample collected from Suncheon, Republic of Korea (35°00′06.4″N, 127°30′28.5″E).

**Description of Dyadobacter jiangsuensis F-49**

Gram-stain-negative, aerobic, non-flagellated, rod-shaped bacterium (0.8–0.9 μm wide, 1.3–1.5 μm long). Colonies grown on R2A are light yellow, circular, convex, and undulate. Oxidase activity is negative. In the API 20NE test, cells are positive for aesculin hydrolysis; activity of urease and β-galactosidase; and assimilation of d-glucose, d-mannose, N-acetyl-glucosamine, and d-maltose, but negative for nitrate reduction; indole production; glucose fermentation; arginine dihydrolase activity; gelatin hydrolysis; and assimilation of l-arabinose, d-mannitol, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain F-49 (= NIBRBAC000503373) was isolated from a soil sample collected from Yeongju, Republic of Korea (36°51′27.2″N, 128°27′28.6″E).

**Description of Chryseobacterium ureilyticum HMF6110**

Gram-stain-negative, facultative anaerobic, non-flagellated, rod-shaped bacterium (0.5–0.6 μm wide, 1.6–1.8 μm long). Colonies grown on R2A are light yellow, circular, convex, and smooth. Oxidase activity is positive. In the API 20NE test, cells are positive for indole production; urease activity; and hydrolysis of aesculin and gelatin; but negative for nitrate reduction; glucose fermentation; activity of arginine dihydrolase and β-galactosidase;
and assimilation of 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 HMF6110 (= NIBRBAC000503111) was isolated from a seawater sample collected from Jeju, Republic of Korea (33°29′50.0″N, 126°27′06.1″E).

Description of *Empedobacter brevis* HMF6096

Gram-stain-negative, facultative anaerobic, non-flagellated, rod-shaped bacterium (0.4–0.6 μm wide, 0.8–1.0 μm long). Colonies grown on R2A agar are pale yellow, circular, convex, and smooth. Oxidase activity is positive. In the API 20NE test, cells are positive for indole production; hydrolysis of aesculine and gelatin; and assimilation of N-acetyl-glucosamine, but negative for nitrate reduction; glucose fermentation; activity of arginine dihydrolase; urease; and assimilation of D-glucose, L-arabinose, D-mannose, D-mannitol, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain HMF6096 (= NIBRBAC000503110) was isolated from a seawater sample collected from Jeju, Republic of Korea (33°29′50.0″N, 126°27′06.1″E).

Description of *Mangrovibacterium marinum* HMF6964

Gram-stain-negative, facultative anaerobic, non-flagellated, long rod-shaped bacterium (0.3–0.4 μm wide, 2.5–5.0 μm long). Colonies grown on marine agar are pale pink, circular, convex, and smooth. Oxidase activity is positive. In the API 20NE test, cells are positive for aesculine hydrolysis; and β-galactosidase, but negative for nitrate reduction; indole production; glucose fermentation; activity of arginine dihydrolase and urease; gelatin hydrolysis; and assimilation of 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 HMF6964 (= NIBRBAC000503117) was isolated from a sediment sample of seashore collected from Shinan, Republic of Korea (34°51′39.4″N, 126°08′28.4″E).

Description of *Bacillus halotolerans* 19D1S38

Gram-stain-positive, facultative anaerobic, flagellated, long rod-shaped bacterium (0.7–0.8 μm wide, 3.2–3.5 μm long). Colonies grown on mueller hinton agar are brown, circular, and flat. Oxidase activity is negative. In the API 20NE test, cells are positive for nitrate reduction; hydrolysis of aesculine and gelatin; β-galactosidase activity; and assimilation of D-glucose, L-arabinose, D-mannose, D-mannitol, N-acetyl-glucosamine, D-maltose, potassium gluconate, adipic acid, malic acid, trisodium citrate, and phenylacetic acid, but negative for indole production; glucose fermentation; activity of arginine dihydrolase and urease; and assimilation of capric acid. Strain 19D1S38 (= NIBRBAC000503265) was isolated from a sediment sample collected from Jeongseon, Republic of Korea (37°22′56.8″N, 128°40′01.2″E).

Description of *Bacillus proteolyticus* LPB0288

Gram-stain-positive, aerobic, flagellated, rod-shaped bacterium (0.7–0.8 μm wide, 1.8–2.0 μm long). Colonies grown on R2A agar are white, irregular, lobate, and flat. Oxidase activity is positive. In the API 20NE test, cells are positive for urease activity; hydrolysis of aesculine and gelatin; and assimilation of D-glucose, N-acetyl-glucosamine, D-maltose, potassium gluconate, malic acid, and trisodium citrate, but negative for nitrate reduction; indole production; glucose fermentation; activity of arginine dihydrolase and β-galactosidase; and assimilation of L-arabinose, D-mannose, D-mannitol, capric acid, adipic acid, and phenylacetic acid. Strain LPB0288 (= NIBRBAC000503338) was isolated from a seashore sand sample collected from Gangneung, Republic of Korea (37°44′54.0″N, 128°58′26.0″E).

Description of *Bacillus sporothermodurans* CAU 1601

Gram-stain-positive, aerobic, flagellated, rod-shaped bacterium (0.8–0.9 μm wide, 2.2–2.7 μm long). Colonies grown on nutrient agar are cream, circular, convex, smooth, and opaque. Oxidase activity is positive. In the API 20NE test, cells are positive for urease activity; hydrolysis of aesculine and gelatin; and assimilation of D-glucose, D-mannitol, N-acetyl-glucosamine, and potassium gluconate, but negative for nitrate reduction; indole production; glucose fermentation; activity of arginine dihydrolase and β-galactosidase; and assimilation of L-arabinose, D-mannose, D-mannitol, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain CAU 1601 (= NIBRBAC000503250) was isolated from a sand sample collected from Jeju, Republic of Korea (33°14′00.9″N, 126°22′30.7″E).

Description of *Bacillus salacetis* LPB0313

Gram-stain-positive, aerobic, flagellated, rod-shaped bacterium (0.7–0.8 μm wide, 1.9–2.2 μm long). Colonies grown on marine agar are cream, circular, entire, and convex. Oxidase activity is positive. In the API 20NE test, cells are positive for aesculine hydrolysis; and β-galactosidase activity, but negative for nitrate reduction; indole production; glucose fermentation; activity of arginine dihydrolase and urease; gelatin hydrolysis; and assimilation of D-glucose, L-arabinose, D-mannose, D-mannitol, N-ace-
tyl-glucosamine, d-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain LPB0313 (= NIBRBC000503350) was isolated from a tidal flat sample collected from Taean, Republic of Korea (36°29'21.0"N, 126°20'00.1"E).

**Description of Cytobacillus depressus R20**

Gram-stain-positive, aerobic, flagged, rod-shaped bacterium (0.5–0.6 μm wide, 1.3–1.5 μm long). Colonies grown on R2A agar are light yellow and circular. Oxidase activity is positive. In API 20NE test, nitrate reduction; urease activity; and gelatin hydrolysis, but negative for indole production; glucose fermentation; aesculin hydrolysis; activity of arginine dihydrolase and urease; and assimilation of trisodium citrate, and phenylacetic acid. Strain R20 (= NIBRBC000503217) was isolated from a soil sample collected from Jeongseon, Republic of Korea (37°15'38.4"N, 128°36'28.7"E).

*Bacillus depressus* was reclassified as *Cytobacillus depressus* (Patel and Gupta, 2020).

**Description of Domibacillus mangrove BT246**

Gram-stain-positive, aerobic, non-flagellated, rod-shaped bacterium (1.3–1.6 μm wide, 2.8–3.9 μm long). Colonies grown on R2A agar are white, circular, and smooth. Oxidase activity is negative. In the API 20NE test, cells are positive for nitrate reduction; urease activity; gelatin hydrolysis; and assimilation of d-gluconate and d-maltose, but negative for indole production; glucose fermentation; activity of arginine dihydrolase and β-galactosidase; aesculin hydrolysis; and assimilation of 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 BT246 (= NIBRBC000502996) was isolated from a soil sample collected from Uijeongbu, Republic of Korea (37°45'15.6"N, 127°02'16.4"E).

**Description of Halobacillus litoralis JBTF-M5**

Gram-stain-positive, aerobic, non-flagellated, rod-shaped bacterium (0.5–0.8 μm wide, 0.8–1.3 μm long). Colonies grown on marine agar are light yellow, circular, slightly convex, and glistening. Oxidase activity is negative. In the API 20NE test, cells are positive for hydrolysis of aesculin and gelatin; and β-galactosidase activity, but negative for nitrate reduction; indole production; glucose fermentation; activity of arginine dihydrolase and urease; and assimilation of 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 JBTF-M5 (= NIBRBC000503334) was isolated from a tidal flat sample collected from Hwaseong, Republic of Korea (37°09’48.0”N, 126°37’01.0”E).

**Description of Jeotgalibacillus terrae LPB0275**

Gram-stain-positive, aerobic, flagged, rod-shaped bacterium (0.6–0.7 μm wide, 1.0–1.2 μm long). Colonies grown marine agar are yellow orange, circular, entire, and convex. Oxidase activity is negative. In the API 20NE test, cells are positive for glucose fermentation; β-galactosidase activity; and assimilation of trisodium citrate, but negative for nitrate reduction; indole production; activity arginine dihydrolase and urease; hydrolysis of aesculin and gelatin; and assimilation of d-glucose, l-arabinose, d-mannose, d-mannitol, N-acetyl-glucosamine, d-maltose, potassium gluconate, capric acid, adipic acid, malic acid, and phenylacetic acid. Strain LPB0275 (= NIBRBC000503344) was isolated from a soil sample collected from Seoul, Republic of Korea (37°35’05.6”N, 127°01’36.3”E).

**Description of Oceanobacillus luteolus 19D1F21**

Gram-stain-positive, aerobic, non-flagellated, rod-shaped bacterium (0.6–0.7 μm wide, 2.0–2.2 μm long). Colonies grown on Mueller Hinton agar are cream, circular, undulate, raised, and glistening. Oxidase activity is negative. In the API 20NE test, cells are positive for hydrolysis of aesculin and gelatin, but negative for nitrate reduction; indole production; glucose fermentation; activity of arginine dihydrolase, urease, and β-galactosidase; and assimilation of 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 19D1F21 (= NIBRBC000503261) was isolated from a soil sample collected from Jeongseon, Republic of Korea (37°22’41.2”N, 127°31’20.0”E).

**Description of Oceanobacillus sojae DN10**

Gram-stain-positive, aerobic, non-flagellated, rod-shaped bacterium (0.5–0.7 μm wide, 1.7–1.9 μm long). Colonies grown on R2A agar are white, circular, entire, and convex. Oxidase activity is positive. In the API 20NE test, cells are positive for glucose fermentation; urease activity; aesculin hydrolysis; and assimilation of d-glucose, d-mannose, malic acid, and trisodium citrate, but negative for nitrate reduction; indole production; activity of arginine dihydrolase and β-galactosidase; gelatin hydrolysis; and assimilation of l-arabinose, d-mannitol, N-acetyl-glucosamine, d-maltose, potassium gluconate, capric acid, adipic acid,
adipic acid, and phenylacetic acid. Strain DN10 (= NIBRBAC000503400) was isolated from a sample of pickled perilla leaves in soy sauce collected from Anseong, Republic of Korea (37°00'39.2"N, 127°15'50.8"E).

**Description of Virgibacillus promii 19D1C9**

Gram-stain-positive, facultative anaerobic, flagellated, rod-shaped bacterium (0.3–0.5 μm wide, 2.0–2.7 μm long). Colonies grown on mueller hinton agar are cream, circular, undulate, and convex. Oxidase activity is positive. In the API 20NE test, cells are positive for hydrolysis of aesculin and gelatin; and assimilation of d-glucose, N-acetyl-glucosamine, d-maltose and potassium gluconate, but negative for nitrate reduction; indole production; glucose fermentation; activity of arginine dihydrolase, urease, and β-galactosidase; and assimilation of l-arabinose, d-mannose, d-mannitol, capric acid, malic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain 19D1C9 (= NIBRBAC000503257) was isolated from a soil sample collected from Jeongseon, Republic of Korea (37°22'56.8"N, 128°40'01.2"E).

**Description of Brevibacillus halotolerans LPB0284**

Gram-stain-negative, aerobic, non-flagellated, rod-shaped bacterium (0.7–0.9 μm wide, 2.6–2.9 μm long). Colonies grown on R2A are white, irregular, rhizoid, and flat. Oxidase activity is positive. In the API 20NE test, cells are positive for hydrolysis of aesculin and gelatin, but negative for nitrate reduction; indole production; glucose fermentation; activity of arginine dihydrolase, urease, and β-galactosidase; and assimilation of β-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 LPB0284 (= NIBRBAC000503340) was isolated from a soil sample collected from Seoul, Republic of Korea (37°22'56.8"N, 128°40'01.2"E).

**Description of Paenibacillus barengoltzii N17**

Gram-stain-positive, strictly aerobic, non-flagellated, long rod-shaped bacterium (0.3–0.6 μm wide, 3.1–3.3 μm long). Colonies grown on R2A are cream, circular, entire, and convex. Oxidase activity is positive. In the API 20NE test, cells are positive for nitrate reduction; aesculin hydrolysis; activity of urease and β-galactosidase; and assimilation of potassium gluconate, but negative for indole production; glucose fermentation; gelatin hydrolysis; arginine dihydrolase activity; and assimilation of d-glucose, l-arabinose, d-mannose, d-mannitol, N-acetyl-glucosamine, d-maltose, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain N17 (= NIBRBAC000503415) was isolated from a soil sample collected from Yeongju, Republic of Korea (36°53’51.5”N, 128°28’02.3”E).

**Description of Paenibacillus liaoningensis BT366**

Gram-stain-positive, aerobic, flagellated, rod-shaped bacterium (0.5–1.2 μm wide, 1.8–3.5 μm long). Colonies grown on R2A agar are white, circular, convex, and smooth. Oxidase activity is positive. In the API 20NE test, cells are positive for nitrate reduction; hydrolysis of aesculin and gelatin; β-galactosidase activity; and assimilation of d-glucose, l-arabinose, d-mannositol, d-maltose, and malic acid, but negative for indole production; glucose fermentation; activity of arginine dihydrolase and urease; and assimilation of d-mannose, N-acetyl-glucosamine, potassium gluconate, capric acid, adipic acid, trisodium citrate, and phenylacetic acid. Strain BT366 (= NIBRBAC000503003) was isolated from a soil sample collected from Seoul, Republic of Korea (37°37’48.8”N, 127°05’22.6”E).

**Description of Paenibacillus stellifer BT245**

Gram-stain-positive, aerobic, flagellated, rod-shaped bacterium (0.9–1.1 μm wide, 3.2–3.5 μm long). Colonies grown on R2A are white, circular, and smooth. Oxidase activity is positive. In the API 20NE test, cells are positive for glucose fermentation; aesculin hydrolysis; β-galactosidase activity, but negative for nitrate reduction; indole production; gelatin hydrolysis; activity of arginine dihydrolase and urease; and assimilation of 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 BT245 (= NIBRBAC000502995) was isolated from a soil sample collected from Uijeongbu, Republic of Korea (37°44’52.7”N, 127°06’20.8”E).

**Description of Paenibacillus zeae CAU 1600**

Gram-stain-positive, aerobic, flagellated, rod-shaped bacterium (0.6–0.7 μm wide, 2.0–2.2 μm long). Colonies grown on nutrient agar are cream, circular, convex, and smooth. Oxidase activity is negative. In the API 20NE test, cells are positive for aesculin hydrolysis; activity of urease and β-galactosidase, but negative for nitrate reduction; indole production; glucose fermentation; gelatin hydrolysis; arginine dihydrolase activity; and assimilation of 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 CAU 1600 (= NIBRBAC000503249) was isolated from a soil sample collected from Hampyeong, Republic of Korea (35°05’34.1”N, 126°32’20.8”E).
Description of *Chryseobacterium palamuruense* FS120

Gram-stain-positive, aerobic, non-flagellated, rod-shaped bacterium (0.6–0.8 µm wide, 1.3–1.5 µm long). Colonies grown on R2A are pale yellow, circular, convex, and smooth. Oxidase activity is negative. In the API 20NE test, cells are positive for nitrate reduction; indole production; glucose fermentation; hydrolysis of ascorbic acid and gelatin; activity of arginine dihydrolase, urease and β-galactosidase; and assimilation of 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 FS120 (= NIBRBAC000503293) was isolated from a soil sample collected from Suncheon, Republic of Korea (34°58'12.4"N, 127°28'53.0"E).

Description of *Lysinibacillus pakistanensis* CAU 1604

Gram-stain-positive, aerobic, non-flagellated, rod-shaped bacterium (1.1–1.2 µm wide, 3.1–4.3 µm long). Colonies grown on marine agar are cream, lobate, rough, and opaque. Oxidase activity is negative. In the API 20NE test, cells are positive for assimilation of D-glucose, potassium gluconate, adipic acid, and malic acid, but negative for nitrate reduction; indole production; glucose fermentation; hydrolysis of ascorbic acid and gelatin; activity of arginine dihydrolase, urease, and β-galactosidase; and assimilation of L-arabinose, D-mannose, D-mannitol, N-acetyl-glucosamine, D-maltose, capric acid, trisodium citrate, and phenylacetic acid. Strain CAU 1604 (= NIBRBAC000503251) was isolated from sediment of seashore collected from Incheon, Republic of Korea (37°32'41.0"N, 126°25'53.9"E).

Description of *Solibacillus cecembensis* BSSK_R2A22

Gram-stain-negative, aerobic, non-flagellated, long rod-shaped bacterium (0.7–0.8 µm wide, 3.2–4.9 µm long). Colonies grown on R2A agar are yellowish white, circular, convex, and glistening. Oxidase activity is negative. In the API 20NE test, cells are positive for nitrate reduction; hydrolysis of ascorbic acid and gelatin; β-galactosidase activity; and assimilation of D-glucose, L-arabinose, D-mannose, D-mannitol, N-acetyl-glucosamine, D-maltose, and potassium gluconate, but negative for indole production; glucose fermentation; activity of arginine dihydrolase and urease; and assimilation of capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain BSSK_R2A22 (= NIBRBAC00050330) was isolated from tidal flat collected from Boryeong, Republic of Korea (36°20'25.0"N, 126°38'7.0"E).

*Bacillus cecembensis* was reclassified as *Solibacillus cecembensis* (Gupta and Patel, 2019).

Description of *Staphylococcus cohnii subsp. urealyticus* DS-19

Gram-stain-positive, aerobic, non-flagellated, coc-cus-shaped bacterium (1.1–1.5 µm diameter). Colonies grown on R2A are light yellow, circular, entire, and convex. Oxidase activity is negative. In the API 20NE test, cells are positive for nitrate reduction; activity of urease and β-galactosidase; and assimilation of D-glucose, D-mannose, D-mannitol, D-maltose, and potassium gluconate, but negative for indole production; glucose fermentation; hydrolysis of ascorbic acid and gelatin; arginine dihydrolase activity; and assimilation of L-arabinose, N-acetyl-glucosamine, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain DS-19 (= NIBRBAC000503376) was isolated from a soil sample collected from Daejeon, Republic of Korea (36°22'35.4"N, 127°20’37.2"E).

*Clostridium celerecrescens* was reclassified as Lacrimispora celerecrescens (Haas and Blanchard, 2020).

Description of *Staphylococcus succinus subsp. succinus* NC2

Gram-stain-positive, aerobic, non-flagellated, coc-cus-shaped bacterium (0.9–1.0 µm wide, 1.0–1.2 µm long). Colonies grown on R2A agar are cream, convex, and smooth. Oxidase activity is negative. In the API 20NE test, cells are positive for nitrate reduction; glucose fermentation; ascorbic acid hydrolysis; activity of urease and β-galactosidase; and assimilation of D-glucose, L-arabinose, D-mannose, D-mannitol, N-acetyl-glucosamine, D-maltose, potassium gluconate, and malic acid, but negative for indole production; gelatin hydrolysis; arginine dihydrolase activity; and assimilation of capric acid, adipic acid, trisodium citrate, and phenylacetic acid. Strain NC2 (= NIBRBAC000503420) was isolated from a soil sample collected from Yeongju, Republic of Korea (36°53'51.5"N, 128°28'02.3"E).

Description of *Clostridium sardiniense* CAU 1563

Gram-stain-positive, anaerobic, flagellated, rod-shaped bacterium (1.0–1.2 µm wide, 2.5–3.2 µm long). Colonies grown on nutrient agar are cream, circular, convex, smooth, and shiny. Oxidase activity is negative. In the API 20NE test, cells are positive for glucose fermentation; hydrolysis of ascorbic acid and gelatin, but negative for nitrate reduction; indole production; activity of arginine dihydrolase, urease and β-galactosidase; and assimilation of 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 CAU 1563 (= NIBRBAC000503234) was isolated from a seashore sand sample collected from...
Incheon, Republic of Korea (37°31′50.8″N, 126°25′53.1″E).

Description of Lacrimispora celerecrescens CAU 1557

Gram-stain-positive, anaerobic, flagellated, rod-shaped bacterium (0.7–0.9 μm wide, 2.0–2.1 μm long). Colonies grown on nutrient agar are cream, circular, and shiny. Oxidase activity is negative. In the API 20NE test, cells are positive for indole production; glucose fermentation; aesculin hydrolysis; β-galactosidase activity, but negative for nitrate reduction; gelatin hydrolysis; activity of arginine dihydrolase and urease; and assimilation of 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 CAU 1557 ( = NIBRBAC000503243) was isolated from a sediment sample collected from Jeju, Republic of Korea (33°25′26.4″N, 126°55′41.0″E).

Description of Paenielostridium sordellii CAU 1572

Gram-stain-positive, anaerobic, flagellated, rod-shaped bacterium (0.1–0.2 μm wide, 0.6–0.7 μm long). Colonies grown on nutrient agar are cream, circular, convex, and shiny. Oxidase activity is negative. In the API 20NE test, cells are positive for gelatin hydrolysis; and assimilation of D-mannitol, N-acetyl-glucosamine, potassium gluconate, malic acid, and trisodium citrate, but negative for nitrate reduction; indole production; glucose fermentation; aesculin hydrolysis; activity of arginine dihydrolase, urease, and β-galactosidase; and assimilation of D-glucose, L-arabinose, D-mannose, D-maltose, capric acid, adipic acid, and phenylacetic acid. Strain CAU 1572 ( = NIBRBAC000503244) was isolated from a seashore soil sample collected from Yeosu, Republic of Korea (34°43′49.8″N, 127°43′58.2″E).

Description of Romboutsia hominis CAU 1562

Gram-stain-positive, anaerobic, flagellated, short rod-shaped bacterium (0.3–0.6 μm wide, 0.3–0.9 μm long). Colonies grown on nutrient agar are cream, circular, smooth, and shiny. Oxidase activity is negative. In the API 20NE test, cells are positive for indole production; glucose fermentation; hydorlysis of aesculin and gelatin; and assimilation of D-glucose, but negative for nitrate reduction; activity of arginine dihydrolase, urease, and β-galactosidase; and assimilation of 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 CAU 1562 ( = NIBRBAC000503233) was isolated from a soil sample collected from Incheon, Republic of Korea (37°31′56.3″N, 126°25′43.5″E).

Description of Catellicoccus marimammalium LPB0311

Gram-stain-positive, anaerobic, non-flagellated, cocccus-shaped bacterium (0.8–0.9 μm diameter). Colonies grown anaerobic basal agar are cream, circular, and shiny. Oxidase activity is negative. In the API 20A test, cells are positive for urease activity; and acidification of D-glucose, D-mannose, and D-trehalose, but negative for indole production; hydrolysis of aesculin and gelatin; and acidification of D-mannitol, D-lactose, sucrose, D-maltose, salicin, D-xylene, L-arabinose, glycerol, D-cellobiose, D-melezitose, D-raffinose, D-sorbitol, and D-rhamnose. Strain LPB0311 ( = NIBRBAC000503363) was isolated from a gull fecal sample collected from Taean, Republic of Korea (36°29′17.1″N, 126°20′02.3″E).

Description of Vagococcus lutrae LPB0214

Gram-stain-positive, anaerobic, non-flagellated, ovoid, rod-shaped bacterium (0.6–0.7 μm wide, 2.3–2.5 μm long). Colonies grown on anaerobic basal agar are cream, circular, entire, and convex. Oxidase activity is positive. In the API 20A test, cells are positive for urease activity; and acidification of D-glucose, D-mannitol, D-lactose, sucrose, D-maltose, salicin, glycerol, D-cellobiose, D-mannose, D-sorbitol, and D-trehalose, but negative for indole production; hydrolysis of aesculin and gelatin; and acidification of D-xylene, L-arabinose, D-melezitose, D-raffinose, and D-rhamnose. Strain LPB0214 ( = NIBRBAC000503358) was isolated from an animal intestine sample (mouse) collected from Daejeon, Republic of Korea (36°23′55.6″N, 127°23′42.5″E).

Description of Lactiplantibacillus plantarum YG19

Gram-stain-negative, aerobic, non-flagellated, ovoid, rod-shaped bacterium (0.5–0.7 μm wide, 1.1–1.2 μm long). Colonies grown on MRS agar are white, circular, convex, and glistening. Oxidase activity is negative. In the API 20NE test, cells are positive for nitrate reduction; aesculin hydrolysis; β-galactosidase activity, but negative for indole production; glucose fermentation; gelatin hydrolysis; activity of arginine dihydrolase and urease; and assimilation of 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 YG19 ( = NIBRBAC000503327) was isolated from a kimchi sample collected from Yeosu, Republic of Korea (34°44′26.0″N, 127°43′58.0″E).

Streptobacterium plantarum was reclassified as Lactiplantibacillus plantarum (Zheng et al., 2020).
Description of *Latilactobacillus sakei* subsp. *sakei* AM8

Gram-stain-negative, aerobic, non-flagellated, ovoid, rod-shaped bacterium (0.5–0.6 μm wide, 0.7–1.0 μm long). Colonies grown on MRS agar are white, circular, convex, and glistening. Oxidase activity is negative. In the API 20NE test, cells are positive for nitrate reduction; aesculin hydrolysis; β-galactosidase activity, but negative for indole production; glucose fermentation; gelatin hydrolysis; activity of arginine dihydrolase and urease; and assimilation of 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 AM8 (=NIBRBAC000503326) was isolated from a kimchi sample collected from Andong, Republic of Korea (36°33′54.0″N, 128°43′28.0″E).

*Lactobacillus sakei* subsp. *sakei* was reclassified as *Latilactobacillus sakei* subsp. *sakei* (Zheng et al., 2020).

Description of *Leuconostoc gelidum* subsp. *gascticomitatum* AM13

Gram-stain-positive, anaerobic, non-flagellated, coccoïd, ovoid-shaped bacterium (0.9–1.2 μm diameter). Colonies grown on MRS agar are white, circular, and convex. Oxidase activity is negative. In the API 20NE test, cells are negative for nitrate reduction; circular, and convex. Oxidase activity is negative. In the API 20NE test, cells are positive for aesculin hydrolysis; β-galactosidase activity, but negative for nitrate reduction; indole production; glucose fermentation; activity of arginine dihydrolase and urease; and assimilation of 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 AM13 (=NIBRBAC000503499) was isolated from a kimchi sample collected from Anseong, Republic of Korea (37°00′39.2″N, 127°15′50.8″E).

Description of *Streptococcus infantis* LPB0309

Gram-stain-positive, facultative anaerobic, non-flagellated, coccus-shaped bacterium (0.6–0.9 μm diameter). Colonies grown on chocolate agar are cream, circular, entire, and convex. Oxidase activity is negative. In the API 20NE test, cells are positive for hydrolysis of aesculin and gelatin; β-galactosidase activity, but negative for nitrate reduction; indole production; glucose fermentation; activity of arginine dihydrolase and urease; and assimilation of 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 LPB0309 (=NIBRBAC000503347) was isolated from a human respiratory tract sample collected from Seoul, Republic of Korea (37°34′47.5″N, 126°59′56.3″E).

Description of *Streptococcus rubneri* LPB0307

Gram-stain-positive, facultative anaerobic, non-flagellated, coccus-shaped bacterium (0.5–0.7 μm diameter). Colonies grown on brain heart infusion agar are cream, circular, entire, and convex. Oxidase activity is negative. In the API 20NE test, cells are positive for aesculin hydrolysis; β-galactosidase activity, but negative for nitrate reduction; indole production; glucose fermentation; gelatin hydrolysis; activity of arginine dihydrolase and urease; and assimilation of 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 LPB0307 (=NIBRBAC000503346) was isolated from a human respiratory tract sample collected from Seoul, Republic of Korea (37°34′48.0″N, 126°59′56.4″E).

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