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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 *Prolixibacteraceae* (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

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Introduction

The bacteria belonging to phyla *Bacteroidetes* and *Firmicutes* can be found from diverse natural habitats, as well as human and animal gastrointestinal tracts (Haakensen *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 Brain Heart Infusion (BHI) agars were 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 10−20% (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 (>1300 bp) 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 HMF 6964) were most closely related to following species (sequence similarity value), respectively: *Bacteroides fragilis* (99.6%), *Arachidicoccus rhizosphaerae* (98.9%), *Chitinophaga cymbidii* (98.9%), *Parasegetibacter luojiensis* (99.8%), *Dyadobacter jiangsuensis* (99.9%), *Aquaticitalea lipolytica* (100%), *Chryseobacterium luteum* (99.7%), *Chryseobacterium ureilyticum* (99.8%), *Empedobacter brevis* (100%), and *Mangrovibacterium marinum* (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 salacetis* (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%), *Brevibacillus halotolerans* (99.8%), *Paenibacillus barengoltzii* (98.7%), *Paenibacillus liaoningensis* (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%), *Lacrimispora celerecrescens* (99.6%), *Paeniclostridium sordellii* (99.7%), *Romboutsia hominis* (99.2%), *Caterllicoccus marimammalium* (99.9%), *Vagococcus lutrae* (99.9%), *Lactiplantibacillus plantarum* (100%), *Lactobacillus sakei* subsp. *sakei* (100%), *Leuconostoc gelidum* 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

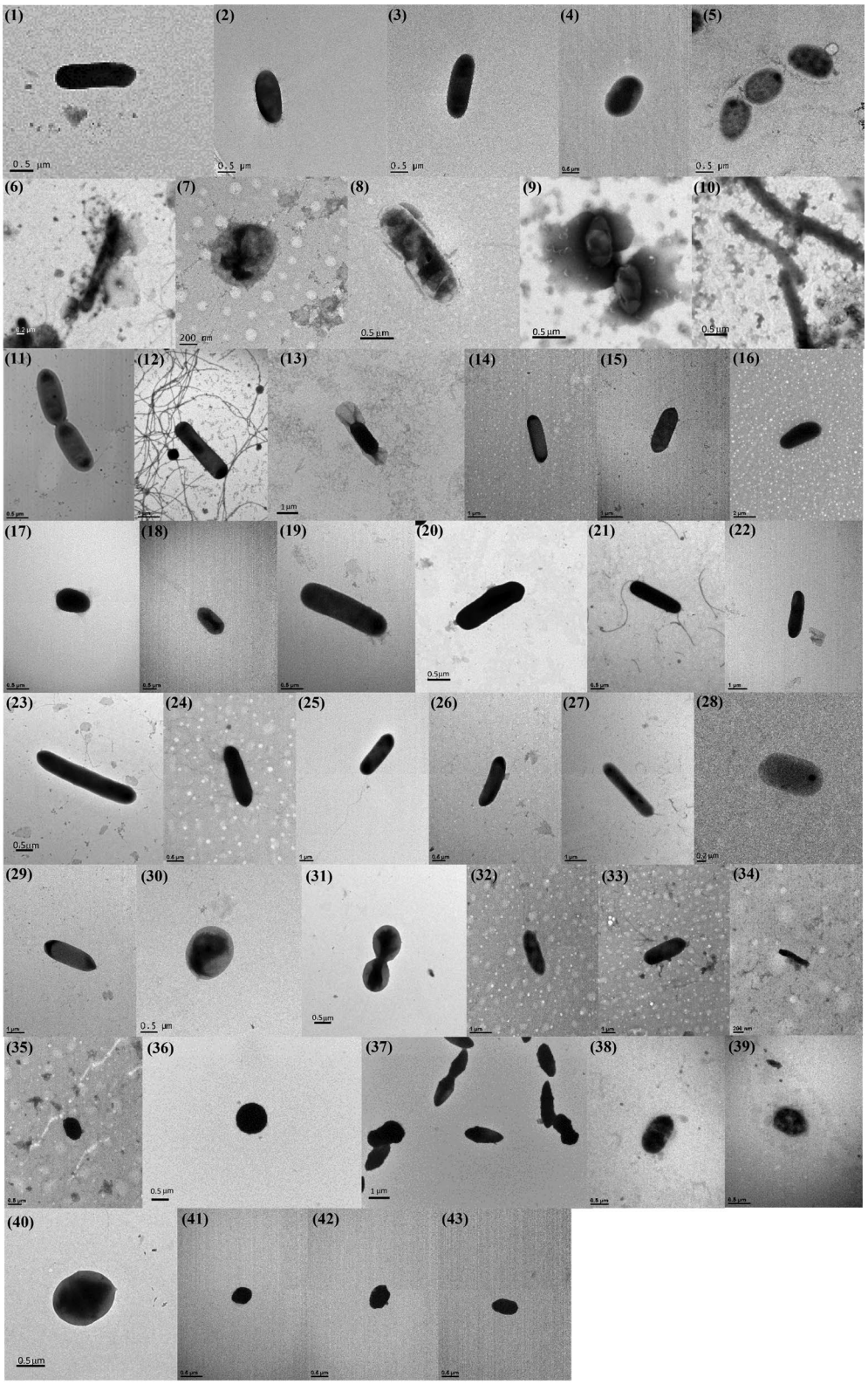

Fig. 1. Transmission electron micrographs of cells. Strains: 1, LPB0329; 2, SO92; 3, FS31; 4, BT243; 5, F-49; 6, HMF9403; 7, SS28; 8, HMF6110; 9, HMF6096; 10, HMF6964; 11, R20; 12, 19D1S38; 13, LPB0288; 14, CAU 1601; 15, LPB0313; 16, BT246; 17, JBTF-M5; 18, LPB0275; 19, 19D1F21; 20, DN10; 21, 19D1C9; 22, LPB0284; 23, N17; 24, BT366; 25, BT245; 26, CAU 1600; 27, BSSK_R2A22; 28, FS120; 29, CAU 1604; 30, DS-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.

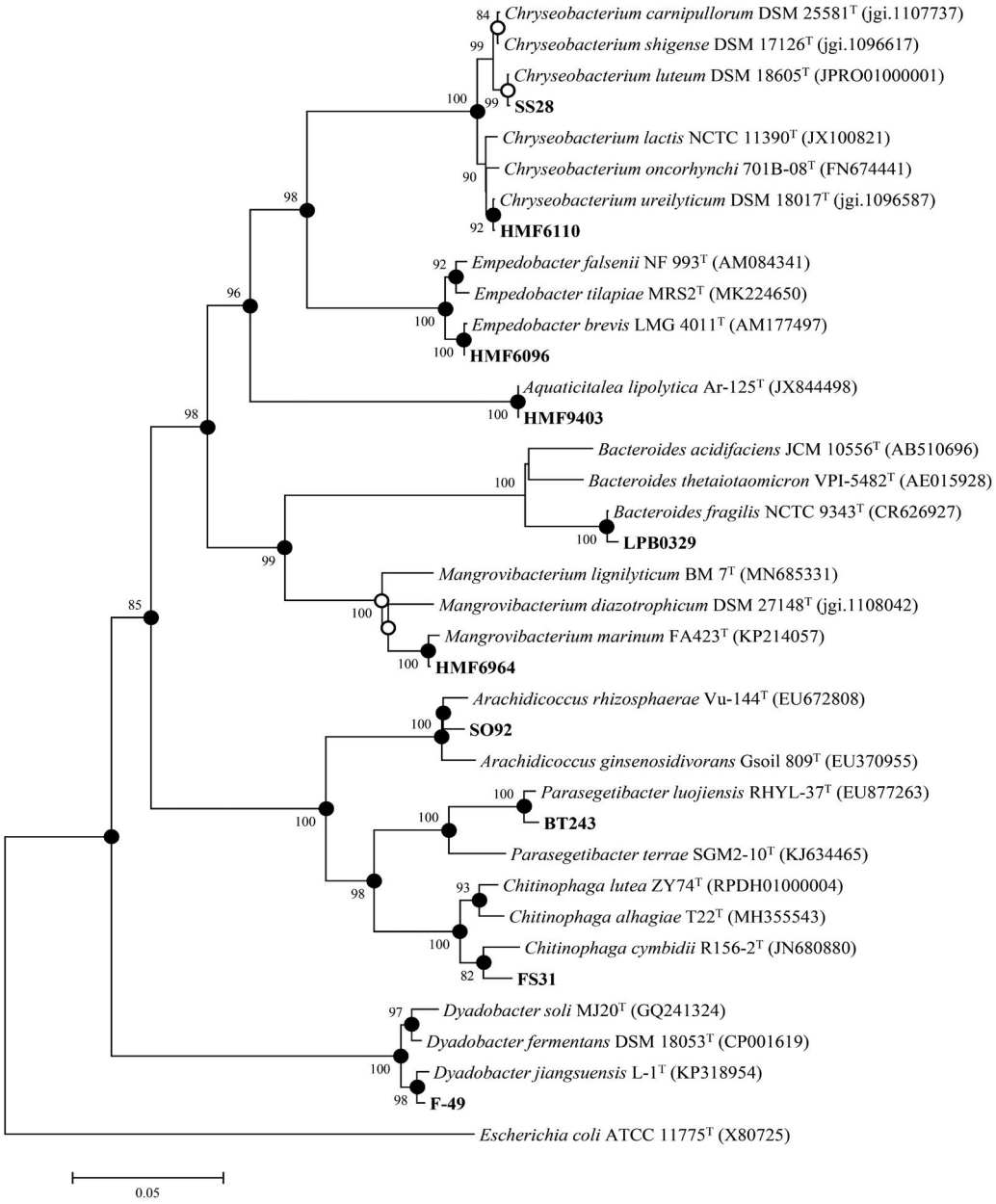

Fig. 2. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences, showing the relationship between the isolates and their relatives of the phylum *Bacteroidetes*. Bootstrap values (>70%) are shown. Filled circles indicate that both maximum-likelihood and maximum-parsimony trees obtained the same node arrangement, while empty circles indicate either only maximum-likelihood or maximum-parsimony obtained the same corresponding nodes. *Escherichia coli* ATCC 11775^T (X80725) was used as an outgroup. Bar, 0.05 substitutions per nucleotide position.

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,

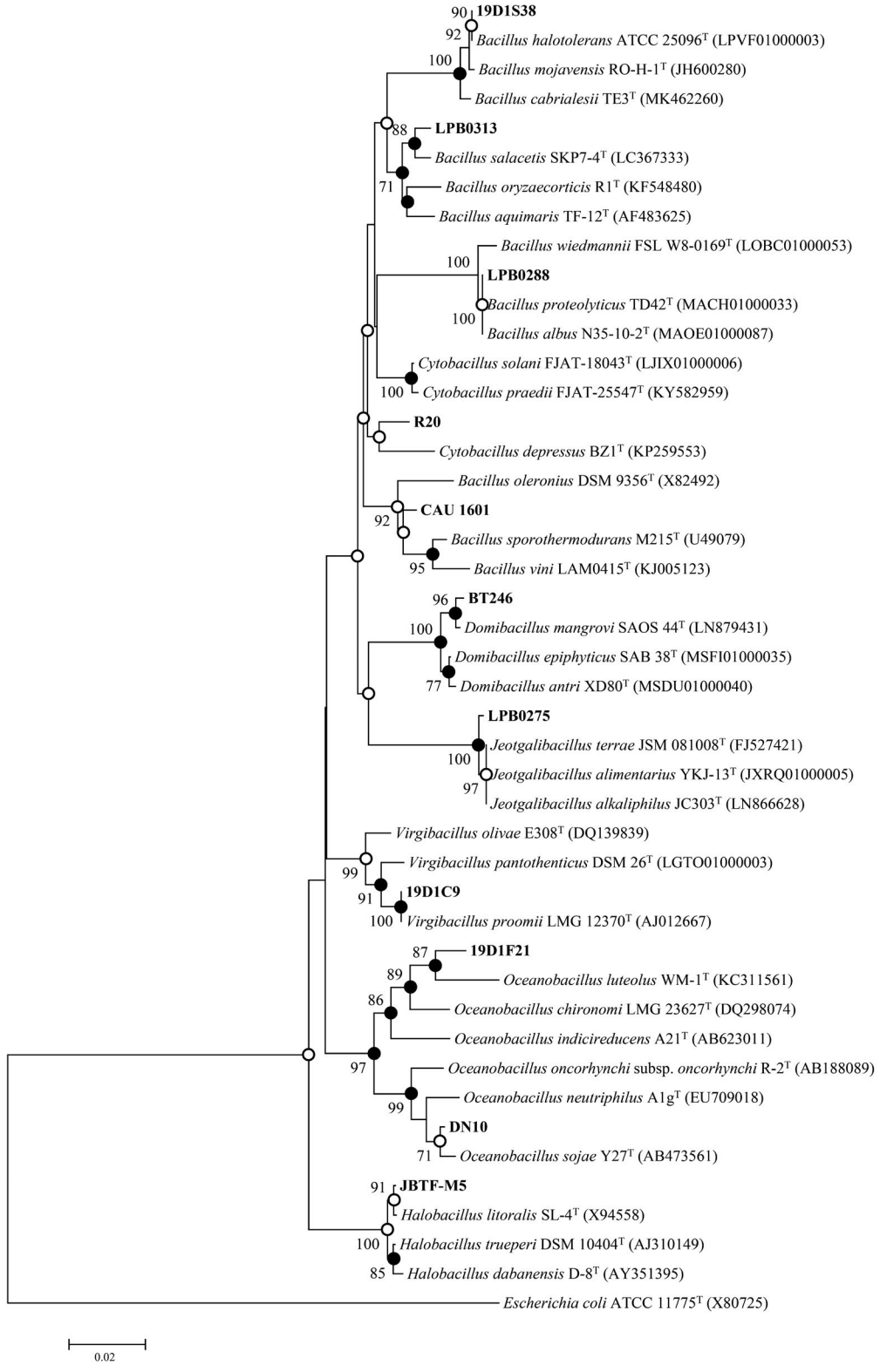

Fig. 3. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences, showing the relationship between the isolates and their relatives of the family *Bacillaceae*. Bootstrap values (>70%) are shown. Filled circles indicate that both maximum-likelihood and maximum-parsimony trees obtained the 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.

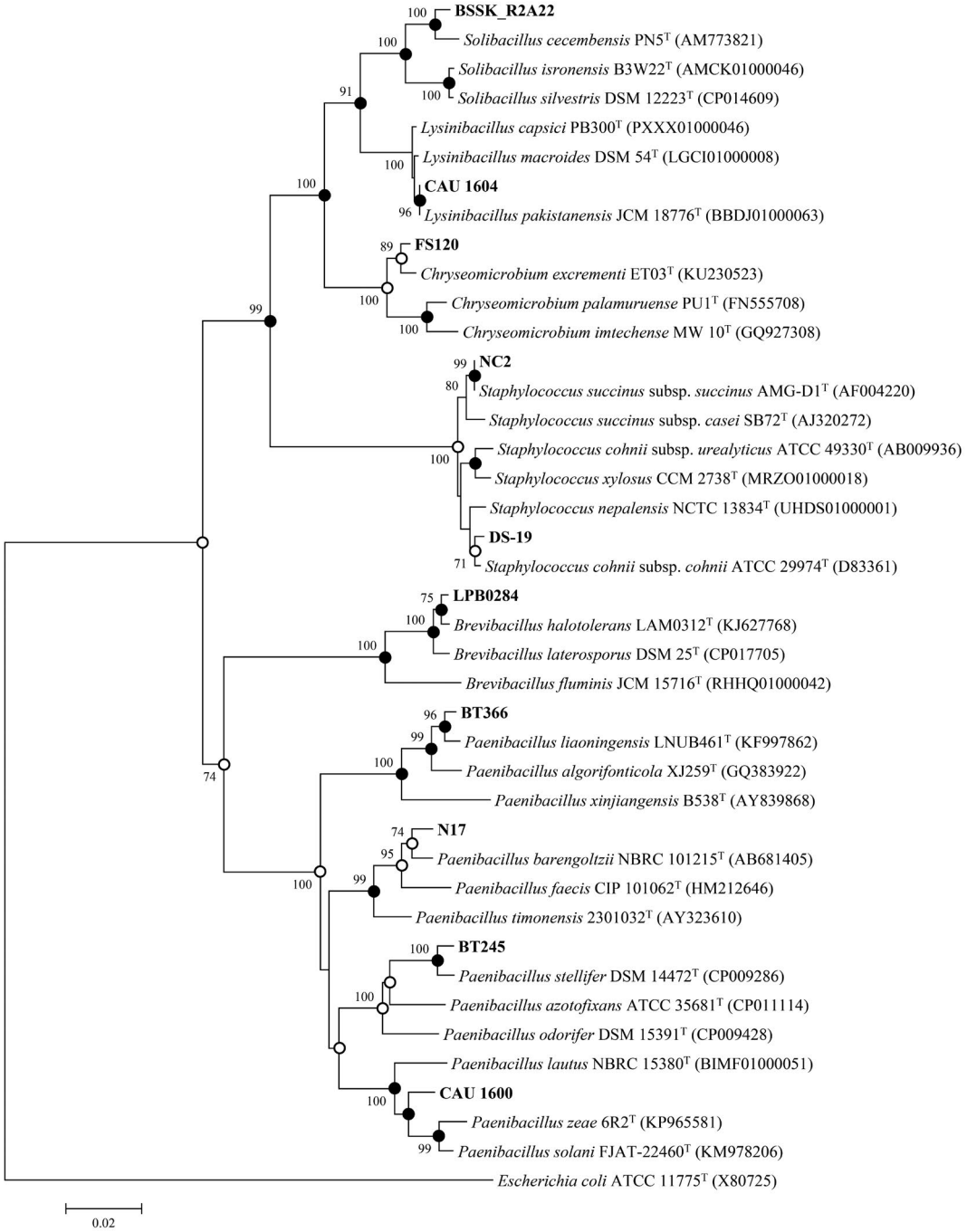

Fig. 4. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences, showing the relationship between the isolates and their relatives of the families *Paenibacillaceae*, *Planococcaceae* and *Staphylococcaceae*. Bootstrap values (>70%) are shown. Filled circles indicate that both maximum-likelihood 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 11775^T (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 (=NIBRBAC000503364) was isolated from an animal intestine sample (mouse) collected from Daejeon, Republic of Korea (36°23′56.5″N, 127°23′39.8″E).

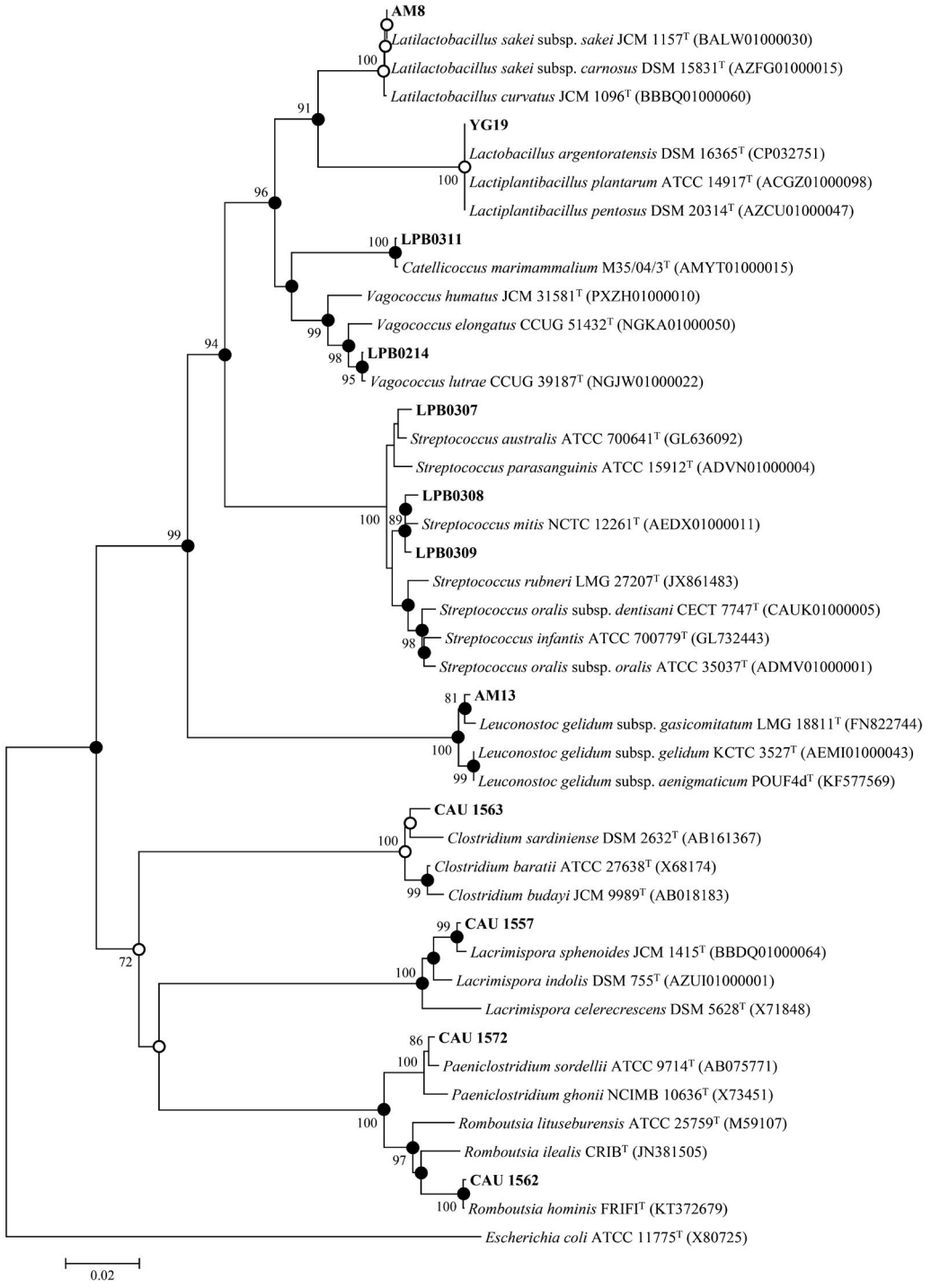

Fig. 5. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences, showing the relationship between the isolates and their relatives of the orders *Clostridiales* and *Lactobacillales*. Bootstrap values (>70%) are shown. Filled circles indicate that both maximum-likelihood and maximum-parsimony 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 11775^T (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-

Table 1. Taxonomic affiliation and isolation information of the isolates belonging to the phyla *Bacteroidetes* and *Firmicutes*.

Phylum	Order	Family	Strain ID	NIBR ID	Most closely related species	Similarity (%)	Isolation source	Medium	Incubation condition
Bacteroidetes	*Bacteroidales*	*Bacteroidaceae*	LPB0329	NIBRBAC000503364	*Bacteroides fragilis*	99.6%	Rat intestine	Anaerobe basal	30°C, 3d
	Chitinophagales	*Chitinophagaceae*	SO92	NIBRBAC000503296	*Arachidicoccus rhizosphaerae*	98.9%	Soil	R2A	25°C, 3d
			FS31	NIBRBAC000503298	*Chitinophaga cymbidii*	98.9%	Soil	R2A	25°C, 3d
			BT243	NIBRBAC000502993	*Parasegetibacter luojiensis*	99.9%	Soil	R2A	25°C, 3d
	Cytophagales	*Cytophagaceae*	F-49	NIBRBAC000503373	*Dyadobacter jiangsuensis*	99.9%	Soil	R2A	30°C, 3d
	Flavobacteriales	*Flavobacteriaceae*	HMF9403	NIBRBAC000503118	*Aquaticitalea lipolytica*	100%	Seawater	MA	30°C, 3d
			SS28	NIBRBAC000503391	*Chryseobacterium luteum*	99.7%	Soil	TSA	30°C, 3d
			HMF6110	NIBRBAC000503111	*Chryseobacterium ureilyticum*	99.8%	Seawater	R2A	30°C, 3d
			HMF6096	NIBRBAC000503110	*Empedobacter brevis*	100%	Seawater	R2A	30°C, 3d
	Marinilabiliales	*Prolixibacteraceae*	HMF6964	NIBRBAC000503117	*Mangrovibacterium marinum*	99.7%	Seashore sediment	MA	30°C, 3d
Firmicutes	*Bacillales*	*Bacillaceae*	19D1S38	NIBRBAC000503265	*Bacillus halotolerans*	99.9%	Soil	MH	30°C, 4d
			LPB0288	NIBRBAC000503338	*Bacillus proteolyticus*	100%	Sand	R2A	25°C, 3d
			CAU 1601	NIBRBAC000503250	*Bacillus sporothermodurans*	99.1%	Seashore sand	NA	30°C, 2–3d
			LPB0313	NIBRBAC000503350	*Bacillus salacetis*	98.9%	Seashore sand	MA	25°C, 3d
			R20	NIBRBAC000503217	*Cytobacillus depressus*	98.7%	Soil	R2A	6–40°C, 3d
			BT246	NIBRBAC000502996	*Domibacillus mangrovi*	99.4%	Soil	R2A	25°C, 3d
			JBTF-M5	NIBRBAC000503334	*Halobacillus litoralis*	99.7%	Tidal flat	MA	30°C, 3d
			LPB0275	NIBRBAC000503344	*Jeotgalibacillus terrae*	99.0%	Soil	MA	25°C, 3d
			19D1F21	NIBRBAC000503261	*Oceanobacillus luteolus*	99.8%	Soil	MH	30°C, 4d
			DN10	NIBRBAC000503400	*Oceanobacillus sojae*	99.9%	Pickled perilla leaves in soy sauce	R2A	25°C, 3d
			19D1C9	NIBRBAC000503257	*Virgibacillus proomii*	100%	Soil	MH	30°C, 4d
		Paenibacillaceae	LPB0284	NIBRBAC000503340	*Brevibacillus halotolerans*	99.8%	Soil	R2A	25°C, 3d
			N17	NIBRBAC000503415	*Paenibacillus barengoltzii*	98.7%	Soil	R2A	25°C, 3d
			BT366	NIBRBAC000503003	*Paenibacillus liaoningensis*	99.6%	Soil	R2A	25°C, 3d
			BT245	NIBRBAC000502995	*Paenibacillus stellifer*	99.5%	Soil	R2A	25°C, 3d
			CAU 1600	NIBRBAC000503249	*Paenibacillus zeae*	99.1%	Soil	NA	30°C, 2–3d
		Planococcaceae	FS120	NIBRBAC000503293	*Chryseomicrobium palamuruense*	99.8%	Soil	R2A	25°C, 5d
			CAU 1604	NIBRBAC000503251	*Lysinibacillus pakistanensis*	100%	Seashore sediment	MA	30°C, 2–3d
			BSSK_R2A22	NIBRBAC000503330	*Solibacillus cecembensis*	99.7%	Tidal flat	R2A	25°C, 2d
		Staphylococcaceae	DS-19	NIBRBAC000503376	*Staphylococcus cohnii* subsp. *urealyticus*	99.9%	Soil	R2A	30°C, 3d
			NC2	NIBRBAC000503420	*Staphylococcus succinus* subsp. *succinus*	100%	Soil	R2A	25°C, 3d
	Clostridiales	*Clostridiaceae*	CAU 1563	NIBRBAC000503234	*Clostridium sardiniense*	99.9%	Seashore sand	NA	37°C, 3d
		Lachnospiraceae	CAU 1557	NIBRBAC000503243	*Lacrimispora celerecrescens*	99.6%	Sediment	NA	37°C, 2d
		Peptostreptococcaceae	CAU 1572	NIBRBAC000503244	*Paeniclostridium sordellii*	99.7%	Soil	NA	37°C, 3d
		Peptostreptococcaceae	CAU 1562	NIBRBAC000503233	*Romboutsia hominis*	99.2%	Soil	NA	37°C, 3d
	Lactobacillales	*Enterococcaceae*	LPB0311	NIBRBAC000503363	*Caterllicoccus marimammalium*	99.9%	Seagull feces	Anaerobe basal	30°C, 3d
			LPB0214	NIBRBAC000503358	*Vagococcus lutrae*	99.9%	Rat intestine	Anaerobe basal	30°C, 3d
		Lactobacillaceae	YG19	NIBRBAC000503327	*Lactiplantibacillus plantarum*	100%	Kimchi	MRS	30°C, 5d
			AM8	NIBRBAC000503326	*Latilactobacillus sakei* subsp. *sakei*	100%	Kimchi	MRS	30°C, 3d
		Leuconostocaceae	AM13	NIBRBAC000503399	*Leuconostoc gelidum* subsp. *gasicomitatum*	100%	Kimchi	MRS	25°C, 3d
		Streptococcaceae	LPB0309	NIBRBAC000503348	*Streptococcus infantis*	99.2%	Human respiratory tract	Blood	37°C, 3d
			LPB0308	NIBRBAC000503347	*Streptococcus oralis* subsp. *dentisani*	99.3%	Human respiratory tract	Chocolate	37°C, 3d
			LPB0307	NIBRBAC000503346	*Streptococcus rubneri*	98.9%	Human respiratory tract	BHI	30°C, 3d

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 SO92 (=NIBRBAC000503296) was isolated from a soil sample collected from Yeongju, Republic of Korea (36°51′27.2″N, 128°27′28.6″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 D-mannitol, 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 (35°00′06.4″N, 127°30′28.5″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 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 Uijeongbu, Republic of Korea (37°44′34.9″N, 127°06′04.4″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 Daejeon, Republic of Korea (36°22′33.4″N, 127°20′33.8″E).

Description of *Aquaticitalea lipolytica* HMF9403

Gram-stain-negative, aerobic, flagellated, long rod-shaped bacterium (0.2–0.3 μm wide, 10.9–13.0 μm long). Colonies grown on marine agar are yellow, circular, convex, and smooth. 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 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 HMF9403 (=NIBRBAC000503118) was isolated from a seawater sample collected from Gangneung, Republic of Korea (37°49′54.0″N, 128°52′41.0″E).

Description of *Chryseobacterium luteum* SS28

Gram-stain-negative, aerobic, non-flagellated, coccus-shaped bacterium (0.7–0.9 μm diameter). Colonies grown on TSA are yellow, circular, convex, and entire. Oxidase activity is positive. In the API 20NE test, cells are positive for urease activity, hydrolysis of aesculin and gelatin, but negative for nitrate reduction; indole production; 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 SS28 (=NIBRBAC000503391) was isolated from a soil sample collected from Gurye, Republic of Korea (35°11′17.2″N, 127°32′46.9″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 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 β-galactosidase; 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 aesculin 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 aesculin 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 aesculin 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 aesculin 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-maltose, 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 aesculin 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 (=NIBRBAC000503350) was isolated from a seashore sand 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, flagellated, 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 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 R20 (=NIBRBAC000503217) 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-glucose 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, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain BT246 (=NIBRBAC000502996) 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 (=NIBRBAC000503334) 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, flagellated, 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 (=NIBRBAC000503344) 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 (=NIBRBAC000503261) was isolated from a soil sample collected from Jeongseon, Republic of Korea (37°22′56.8″N, 128°40′01.2″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, 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 proomii* 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, adipic 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 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 LPB0284 (=NIBRBAC000503340) was isolated from a soil sample collected from Seoul, Republic of Korea (37°35′06.1″N, 127°01′35.5″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-mannitol, 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 agar 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 *Chryseomicrobium 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 negative for nitrate reduction; indole production; glucose fermentation; hydrolysis of aesculin 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 aesculin 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 (=NIBR BAC000503251) 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 aesculin 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 (=NIBRBAC000503330) was isolated from tidal flat collected from Boryeong, Republic of Korea (36°20′25.0″N, 126°53′87.0″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, coccus-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 aesculin 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, coccoid or oval ovoid-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; aesculin 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 aesculin 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, convex, smooth, 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 *Paeniclostridium 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, smooth, 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, coccus-shaped bacterium (0.8−0.9 μm diameter). Colonies grown 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-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-xylose, 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 anaerobe 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-xylose, 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. *gasicomitatum* AM13

Gram-stain-positive, anaerobic, non-flagellated, coccoid, 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; indole production; glucose fermentation; hydrolysis of aesculin 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 AM13 (=NIBRBAC000503399) 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 (0.4−0.5 μm diameter). Colonies grown on blood 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 LPB0309 (=NIBRBAC000503348) was isolated from a human respiratory tract sample collected from Seoul, Republic of Korea (37°34′47.3″N, 126°59′56.6″E).

Description of *Streptococcus oralis* subsp. *dentisani* LPB0308

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 LPB0308 (=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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