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A report of 156 unrecorded bacterial species of Republic of Korea belonging to the phyla *Acidobacteriota*, *Deinococcota*, *Actinomycetota*, *Bacillota*, *Bacteroidota*, and *Pseudomonadota* isolated in 2022

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As part of a comprehensive investigation of indigenous prokaryotic species in Republic of Korea in 2022, 156 bacterial strains were isolated from diverse environmental habitats. These strains were assigned to six phyla, namely *Acidobacteriota*, *Deinococcota*, *Actinomycetota*, *Bacillota*, *Bacteroidota*, and *Pseudomonadota*. Each strain was identified based on 16S rRNA gene sequence similarity (>98.7%) and the formation of robust phylogenetic clades with their closest reported species. Among isolates, there is one species belonging to the phylum *Acidobacteriota*, one species belonging to the phylum *Deinococcota*, 28 species belonging to the phylum *Actinomycetota*, 19 species belonging to the phylum *Bacillota*, 19 species belonging to the phylum *Bacteroidota*, and 88 species belonging to the phylum *Pseudomonadota* (comprising 34 species of the class *Alphaproteobacteria*, 20 species of the class *Betaproteobacteria*, and 34 species of the class *Gammaproteobacteria*). Based on 16S rRNA gene sequence analysis, each strain was assigned to independent and predefined bacterial species. Since there were no published or official reports regarding these 156 isolates in Republic of Korea, they are reported as unrecorded species in Republic of Korea. The Gram stain, colony and cell morphology, basic biochemical characteristic, isolation source, and strain ID of each species are described in the species descriptions.

Keywords: 16S rRNA, *Acidobacteriota*, *Actinomycetota*, *Bacillota*, *Bacteroidota*, *Deinococcota*, indigenous prokaryotic species in Republic of Korea, *Pseudomonadota*, taxonomy, unrecorded species

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INTRODUCTION

The *Acidobacteriota* is a bacterial phylum that underwent a renaming from "*Acidobacteria*" in 2021 (Oren and Garrity, 2021). The majority of *Acidobacteriota* species are Gram-negative bacteria and can be found in diverse environments. As of the time of this writing, the taxonomic classification based on 16S rRNA gene sequences divides the phylum *Acidobacteriota* into five classes: *Blastocatellia*, *Holophagae*, *Terriglobia*, *Thermoanaerobaculia*, and *Vicinamibacteria*.

Similarly, the *Actinomycetota* is another bacterial phylum that was renamed from "*Actinobacteria*" in 2021 (Oren and Garrity, 2021). Most species within the *Actinomycetota* phylum are Gram-positive bacteria and are also prevalent in various environments. The taxonomic classification based on 16S rRNA gene sequences currently includes six classes for the phylum *Actinomycetota*: *Acidimicrobiia*, *Actinomycetes*, *Coriobacteriia*, *Nitriliruptoria*, *Rubrobacteria*, and *Thermoleophilia*.

The phylum *Pseudomonadota* is the largest bacterial phylum and was renamed from "*Proteobacteria*" in 2021 (Oren and Garrity, 2021). The taxonomic classification based on 16S rRNA gene sequences includes six classes: *Acidithiobacillia*, *Alphaproteobacteria*, *Betaproteobacteria*, *Gammaproteobacteria*, *Hydrogenophilalia*, and *Zetaproteobacteria*. Most of the isolated *Pseudomonadota* species belong to the classes *Alphaproteobacteria*, *Betaproteobacteria*, and *Gammaproteobacteria*, and they are Gram-negative bacteria that thrive in diverse environments.

The *Bacteroidota* is another bacterial phylum that underwent a renaming from "*Bacteroidetes*" in 2021 (Oren and Garrity, 2021). Most *Bacteroidota* species are Gram-negative bacteria and are widely distributed in various environments, including soil, sediments, seawater, as well as the gut and skin of animals. According to the taxonomic classification based on 16S rRNA gene sequences, the phylum *Bacteroidota* is divided into six classes: *Bacteroidia*, *Chitinophagia*, *Cytophagia*, *Flavobacteriia*, *Saprospiria*, and *Sphingobacteriia*.

The *Deinococcus* is a bacterial genus within the phylum *Deinococcota*, which was renamed from "*Deinococcus-Thermus*" in 2021 (Oren and Garrity, 2021). The majority of *Deinococcota* species are found in diverse environments, ranging from extreme to common habitats. The taxonomic classification based on 16S rRNA gene sequences currently places the phylum *Deinococcota* into a single class, *Deinococci*.

Similarly, the *Bacillota* is a bacterial phylum that was renamed from "*Firmicutes*" in 2021 (Oren and Garrity, 2021; Vos *et al*., 2011). Most species within the phylum *Bacillota* are Gram-positive bacteria and can be found in diverse environments. The taxonomic classification based on 16S rRNA gene sequences includes seven classes for the phylum *Bacillota*: *Bacilli*, *Clostridia*, *Culicoidibacteria*, *Erysipelotrichia*, *Limnochordia*, *Negativicutes*, and *Thermolithobacteria*.

In our study conducted in 2022, we collected several environmental samples from diverse habitats in Republic of Korea and successfully isolated various novel and unrecorded bacterial species. As part of this study, we describe 156 bacterial species belonging to *Acidobacteriota*, *Actinomycetota*, *Pseudomonadota*, *Bacteroidota*, *Deinococcota*, and *Bacillota*, which have not been previously reported in Republic of Korea.

MATERIALS AND METHODS

A total of 156 bacterial strains were isolated from environmental samples including soil, agricultural soil, mud, tidal flat, solar saltern, seawater, marine algae, seaweed, marine sand, sediment, lake water, brackish water, breast milk, and healthy human urine (Table 1). Each sample was processed separately, spread onto several culture media including R2A agar (R2A), Glucose Yeast Extract agar (GYE), Marine agar 2216 (MA), ISP2 agar, ISP7 agar, Starch casein agar (SCA), Actinomycete isolation agar (AIA), De Man-Rogosa-Sharpe agar (MRS), or Trypticase soy agar (TSA), and incubated at 25 or 30°C for 2–10 days (Table 1). The designated strain ID, taxonomic information, isolation sources, culture media, and incubation conditions are summarized in Table 1. All strains were purified as single colonies after streaking and maintained at −80°C in a glycerol solution (20%, w/v) as well as lyophilized ampoules for long-term preservation.

Colony morphology of isolated strains was observed on agar plates after their cells were grown up to stationary phase. Cellular morphology and cell size were examined by light microscopy or transmission electron microscopy. Gram stain was performed using a Gram-stain kit (bioMérieux) or standard procedures. Phenotypic characteristics were tested by using API 20NE galleries (bioMérieux) according to the manufacturer's instructions.

DNA extraction, PCR amplificationof 16S rRNA gene, and Sanger sequencing of the 16S rRNA gene were performed using the standard procedures described elsewhere (Lee *et al*., 2023). The 16S rRNA gene sequences of the isolates were compared with those of other bacterial species with validly published names using the EzBioCloud database (Yoon *et al*., 2017). For phylogenetic analyses, alignment of sequences was carried out with CLUSTAL W software (Thompson *et al*., 1994). The phylogenetic tree was inferred by using the neighbour-joining algorithm (Saitou and Nei, 1987) implemented within the PHYLIP package (Felsenstein, 1993). Evolutionary distance matrices for the neighbour-joining method were calculated by using the algorithm of Jukes and Cantor (1969) with the program DNADIST. The stability of relationships was assessed by bootstrap analysis based on 1000 resamplings of the neighbour-joining dataset by using the programs SEQBOOT, DNADIST, NEIGHBOR, and CONSENSE of the PHYLIP package.

RESULTS AND DISCUSSION

Strains assigned to the phyla *Acidobacteriota* and *Deinococcota*

Based on 16S rRNA gene sequence comparisons and phylogenetic analyses, strains ST12-5 and CAU 1681 are assigned to the phyla *Acidobacteriota* and *Deinococcota*, respectively (Fig. 1). Strain ST12-5 belongs to the genus *Granulicella* in the family *Acidobacteriaceae* of the order *Acidobacteriales* (Table 1; Parte *et al*., 2020). Strain CAU 1681 belongs to the genus *Deinococcus* in the family *Deinococcaceae* of the order *Deinococcales* (Table 1; Parte *et al*., 2020). Phylogenetic analyses based on 16S rRNA gene sequences showed that strains ST12-5 and CAU 1681 were identified as members of *Granulicella pectinivorans* (Pankratov and Dedysh, 2010) and *Deinococcus radiodurans* (Brooks and Murray, 1981), respectively (Fig. 1, Table 1). Strains ST12-5 and CAU 1681 were isolated from soil and sea sand, respectively (Table 1). The two strains were Gram-stain-negative, chemoheterotrophic, and rod-shaped or coccoid bacteria. For morphological information, the transmission electron microscope images of the strains are presented in Fig. 2. Colony color, colony morphology, and other phenotypic characteristics are shown in the species descriptions.

Strains assigned to the phylum *Actinomycetota*

Based on 16S rRNA gene sequence comparisons and phylogenetic analyses, 28 strains are assigned to the phylum *Actinomycetota* and belong to 16 genera of nine families of nine orders (Fig. 3). Nine strains belong to the genus *Streptomyces* in the family *Streptomycetaceae* of the order *Streptomycetales* (Table 1). *Streptomyces* is currently the largest prokaryotic genus encompassing 713 validly described species (Parte *et al*., 2020). Two strains each belong to the genera *Modestobacter* of the family *Geodermatophilaceae*, *Micromonospora* of the family *Micromonosporaceae*, *Mycolicibacterium* of the family *Mycobacteriaceae*, and *Rhodococcus* of the family *Nocardiaceae* (Table 1). One strain is assigned to each genus as follows: *Brachybacterium*, *Agromyces*, *Chryseoglobus*, *Marisediminicola*, *Microbacterium*, *Arthrobacter*, *Paeniglutamicibacter*, *Psychromicrobium*, *Nocardia*, *Nocardioides*, and *Kitasatospora* (Table 1). The 28 strains were isolated from soil, seawater, wetland, root, moss, and tidal flat sediment (Table 1). For morphological information, the transmission or scanning electron microscope images of the strains are presented in Fig. 2. Colony color, colony morphology, and other phenotypic characteristics are shown in the species descriptions.

Strains assigned to the phylum *Bacillota*

Based on 16S rRNA gene sequence comparisons and phylogenetic analyses, 19 strains are assigned to the phylum *Bacillota* and belong to 12 genera of four families of two orders (Fig. 4). Eleven strains were assigned to the family *Bacillaceae*, six strains to the family *Paenibacillaceae*, one strain to the family *Planococcaceae*, and one strain to the family *Lactobacillaceae* (Table 1; Parte *et al*., 2020). Four strains belong to genus *Bacillus* of the family *Bacillaceae*, four strains belong to genus *Paenibacillus* of the family *Paenibacillaceae*, and two strains belong to genus *Virgibacillus* of the family *Bacillaceae* (Table 1; Parte *et al*., 2020). One strain is assigned to each genus as follows: *Alkalihalobacillus*, *Ectobacillus*, *Mesobacillus*, *Metabacillus*, *Niallia*, *Ammoniphilus*, *Aneurinibacillus*, *Lysinibacillus*, and *Lacticaseibacillus* (Table 1; Parte *et al*., 2020). The 19 strains were isolated from soil, seawater, solar saltern, tidal flat sediment, and breast milk, respectively (Table 1). For morphological information, the transmission electron microscope images of the strains are presented in Fig. 2. Colony color, colony morphology, and other phenotypic characteristics are shown in the species descriptions.

Strains assigned to the phylum *Bacteroidota*

On the basis of 16S rRNA gene sequence comparisons and phylogenetic analyses, 19 strains are assigned to the phylum *Bacteroidota* and belong to 15 genera of seven families of three orders (Fig. 5). Nine strains are assigned to the family *Flavobacteriaceae*, four strains to the family *Weeksellaceae*, two strains to the family *Spirosomaceae*, and one strain to each family as follows: *Hymenobacteraceae*, *Marivirgaceae*, *Reichenbachiellaceae*, and *Sphingobacteriaceae* (Table 1; Parte *et al*., 2020). Three strains belong to the genus *Chryseobacterium* in the family *Weeksellaceae*, two strains belong to the genus *Aquimarina* in the family *Flavobacteriaceae*, and two strains belong to the genus *Flavobacterium* in the family *Flavobacteriaceae* (Table 1; Parte *et al*., 2020). One strain is assigned to each genus as follows: *Pontibacter*, *Marivirga*, *Ekhidna*, *Aquirufa*, *Emticicia*, *Epilithonimonas*, *Flavicella*, *Formosa*, *Maribacter*, *Zhouia*, *Algoriella*, and *Pedobacter* (Table 1; Parte *et al*., 2020). The 19 strains were isolated from soil, seawater, wetland, seaweed, and tidal flat sediment (Table 1). For morphological information, the transmission electron microscope images of the strains are presented in Fig. 2. Colony color, colony morphology, and other phenotypic characteristics are shown in the species descriptions.

Strains assigned to the phylum *Pseudomonadota*

Based on 16S rRNA gene sequence comparisons and phylogenetic analyses, 88 strains are assigned to the phylum *Pseudomonadota*. Among them, 34, 20, and 34 strains belong to the class *Alphaproteobacteria*, *Betaproteobacteria*, and *Gammaproteobacteria*, respectively (Figs. 6–8). The 88 strains belong to 61 genera of 37 families of 21 orders (Figs. 6–8). A total of 10, 7, 5, 4, and 3 strains are assigned to the orders *Rhodobactera-*

les, *Rhizobiales*, *Sphingomonadales*, *Rhodospirillales*, and *Caulobacterales*, respectively, of *Alphaproteobacteria* (Table 1; Parte *et al*., 2020). Eighteen and two strains are assigned to the orders *Burkholderiales* and *Neisseriales*, respectively, of *Betaproteobacteria* (Table 1; Parte *et al*., 2020). A total of 14, 5, 4, 3, 3, and 2 strains are assigned to the orders *Pseudomonadales*, *Enterobacterales*, *Oceanospirillales*, *Alteromonadales*, *Vibrionales*, and *Moraxellales*, respectively, of *Gammaproteobacteria* (Table 1; Parte *et al*., 2020). Of strains assigned to the order *Rhodobacterales*, 10 strains are assigned to the family *Rhodobacteraceae* (Table 1; Parte *et al*., 2020). Of strains assigned to the order *Rhizobiales*, three strains are assigned to the family *Phyllobacteriaceae*, two strains to the family *Rhizobiaceae*, one strain to the family *Ahrensiaceae*, and one strain to the family *Nitrobacteraceae* (Table 1; Parte *et al*., 2020). Of strains assigned to the order *Sphingomonadales*, four strains are assigned to the family *Sphingomonadaceae*, and one strain to the family *Erythrobacteraceae* (Table 1; Parte *et al*., 2020). Of strains assigned to the order *Rhodospirillales*, two strains are assigned to the family *Rhodospirillaceae*, one strain to the family *Acetobacteraceae*, and 1 strain to the family *Rhodovibrionaceae* (Table 1; Parte *et al*., 2020). Of strains assigned to the order *Caulobacterales*, three strains are assigned to the family *Caulobacteraceae* (Table 1; Parte *et al*., 2020). Of strains assigned to the order *Burkholderiales*, 10 strains are assigned to the family *Oxalobacteraceae*, four strains to the family *Alcaligenaceae*, and four strains to the family *Comamonadaceae* (Table 1; Parte *et al*., 2020). Of strains assigned to the order *Neisseriales*, two strains are assigned to the families *Chromobacteriaceae* and *Neisseriaceae* (Table 1; Parte *et al*., 2020). Fourteen strains the order *Pseudomonadales* are assigned to the family *Pseudomonadaceae*, five strains of *Enterobacterales* to the families *Enterobacteriaceae* and *Erwiniaceae*, four strains of *Oceanospirillales* to the families *Alcanivoracaceae*, *Halomonadaceae*, *Oceanospirillaceae*, and *Saccharospirillaceae*, three strains of *Alteromonadales* to the families *Alteromonadaceae*, *Moritellaceae*, and *Pseudoalteromonadaceae*, three strains of *Vibrionales* to the family *Vibrionaceae*, and two strains of *Moraxellales* to the family *Moraxellaceae* (Table 1; Parte *et al*., 2020). The 88 strains were isolated from soil, seawater, wetland, marine algae, seaweed, solar saltern, sea sand, lakewater, and tidal flat sediment (Table 1). For morphological information, the transmission or scanning electron microscope images of the strains are presented in Fig. 2. Colony color, colony morphology, and other phenotypic characteristics are shown in the species descriptions.

In conclusion, there are no official reports that abovementioned 156 species have been isolated in Republic of Korea up to date; therefore, one species of the phylum *Acidobacteriota*, one species of the phylum *Deinococcota*, 28 species of the phylum *Actinomycetota*, 19 species of the phylum *Bacillota*, 19 species of the phylum *Bacteroidota*, and 88 species of the phylum *Pseudomonadota* are proposed as unrecorded prokaryotic species found in Republic of Korea.

Description of *Granulicella pectinivorans* ST12-5

Cells are Gram-stain-negative, non-flagellated, and rod shaped. Colonies are circular, slightly convex, glistening, and white colored after incubation for 3 days on R2A at 25°C. In the API 20NE system, positive for β-galactosidase activity and oxidase activity; but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease activity, esculin hydrolysis, and gelatin hydrolysis. L-Arabinose is utilized as a sole carbon source; while D-glucose, D-mannose, D-mannitol, *N*-acetylglucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid are not. Strain ST12-5 (=NIBRBAC000509715) was isolated from a soil sample at Hoengseong, Gangwon-do, Republic of Korea.

Description of *Deinococcus radiodurans* CAU 1681

Cells are Gram-stain-negative, non-flagellated, and coccoid. Colonies are circular, smooth, convex with entire margin, and light orange colored after incubation for 3 days on GYE at 30°C. In the API 20NE system, positive for esculin hydrolysis, gelatin hydrolysis, and oxidase activity; but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease activity, and β-galactosidase activity. D-Maltose, potassium gluconate, and adipic acid are utilized as sole carbon sources; while D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetylglucosamine, capric acid, malic acid, trisodium citrate, and phenylacetic acid are not. Strain CAU 1681 (=NIBRBAC000509668) was isolated from a sea sand sample at Incheon, Gyeonggi-do, Republic of Korea.

Description of *Brachybacterium faecium* 19_H4_S14

Cells are gram-stain-positive and coccoid rod shaped. Colonies are small, convex, smooth, and cream colored after incubation for 2 days on R2A at 30°C. In the API 20NE system, positive for nitrate reduction, esculin hydrolysis, and β-galactosidase; but negative for indole production, glucose fermentation, arginine dihydrolase, urease, gelatin hydrolysis, and cytochrome oxidase. Potassium gluconate and adipic acid are utilized as sole carbon sources; but D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, capric

Table 1. Summary of isolates belonging to the phyla *Acidobacteriota*, *Deinococcota*, *Actinomycetota*, *Bacillota*, *Bacteroidota*, *Pseudomonadota* and their taxonomic affiliations, isolations sources and culture conditions.

Order	Family	Genus	Strain no.	NIBR[a] ID	Closest species	16S rRNA gene sequence similarity (%)	Isolation Source	Medium for incubation	Condition for incubation
Phylum *Acidobacteriota*									
Acidobacteriales	*Acidobacteriaceae*	*Granulicella*	ST12-5	NIBRBAC000509715	*Granulicella pectinivorans*	98.94	Soil	R2A	25°C, 3d
Phylum *Deinococcota*									
Deinococcales	*Deinococcaceae*	*Deinococcus*	CAU 1681	NIBRBAC000509668	*Deinococcus radiodurans*	98.95	Sea sand	GYE	30°C, 3d
Phylum *Actinomycetota*									
Dermatophilales	*Dermabacteraceae*	*Brachybacterium*	19_H4_S14	NIBRBAC000509482	*Brachybacterium faecium*	99.86	Sediment soil	R2A	30°C, 2d
Geodermatophilales	*Geodermatophilaceae*	*Modestobacter*	BT830	NIBRBAC000509699	*Modestobacter caceresii*	99.84	Soil	R2A	25°C, 3d
			ST12-1	NIBRBAC000509713	*Modestobacter marinus*	99.86	Soil	R2A	25°C, 3d
Microbacteriales	*Microbacteriaceae*	*Agromyces*	BT825	NIBRBAC000509687	*Agromyces iriomotensis*	99.78	Soil	R2A	25°C, 3d
		Chryseoglobus	HMG3458	NIBRBAC000509562	*Chryseoglobus indicus*	99.85	Seawater	MA	25°C, 7d
		Marisediminicola	BT828	NIBRBAC000509697	*Marisediminicola antarctica*	99.58	Soil	R2A	25°C, 3d
		Microbacterium	HMG3454	NIBRBAC000509560	*Microbacterium algeriense*	99.93	Seawater	MA	25°C, 5d
Micrococcales	*Micrococcaceae*	*Arthrobacter*	LK01	NIBRBAC000509706	*Arthrobacter bussei*	99.86	Soil	R2A	25°C, 3d
		Paeniglutamicibacter	AS338	NIBRBAC000509510	*Paeniglutamicibacter antarcticus*	99.52	Wetland	R2A	28°C, 3d
		Psychromicrobium	16S1F15	NIBRBAC000509476	*Psychromicrobium lacuslunae*	99.31	Sediment soil	R2A	30°C, 2d
Micromonosporales	*Micromonosporaceae*	*Micromonospora*	CAU 1706	NIBRBAC000509685	*Micromonospora taraxaci*	99.72	Mud	ISP2	30°C, 10d
			MPA10	NIBRBAC000509581	*Micromonospora zingiberis*	99.93	Root of *Idesia polycarpa*	R2A	25°C, 4-5d
Mycobacteriales	*Mycobacteriaceae*	*Mycolicibacterium*	HMG3056	NIBRBAC000509536	*Mycolicibacterium arabiense*	99.86	Moss	R2A	25°C, 5d
			CAU 1693	NIBRBAC000509677	*Mycolicibacterium tokaiense*	99.86	Mud flat	MA	30°C, 3d
	Nocardiaceae	*Nocardia*	SJ125	NIBRBAC000509593	*Nocardia testacea*	99.93	Soil	R2A	30°C, 3d
		Rhodococcus	YR2-7	NIBRBAC000509650	*Rhodococcus aetherivorans*	99.85	Tidal flat	R2A	25°C, 3d
			YR2-2	NIBRBAC000509649	*Rhodococcus cercidiphylli*	100	Tidal flat	R2A	25°C, 3d
Propionibacteriales	*Nocardioidaceae*	*Nocardioides*	HMG3483	NIBRBAC000509563	*Nocardioides ginkgobilobae*	99.24	Seawater	MA	25°C, 5d
Streptomycetales	*Streptomycetaceae*	*Kitasatospora*	ST12-12	NIBRBAC000509714	*Kitasatospora viridis*	98.75	Soil	R2A	25°C, 3d
		Streptomyces	ST6-10	NIBRBAC000509708	*Streptomyces aldersoniae*	99.44	Soil	R2A	25°C, 3d
			MMS22-JCS7	NIBRBAC000509466	*Streptomyces atriruber*	98.66	Soil	SCA	30°C, 2d
			MMS22-HST12	NIBRBAC000509464	*Streptomyces cinerochromogenes*	100	Soil	TSA	30°C, 2d
			AS119	NIBRBAC000509499	*Streptomyces heliomycini*	99.86	Wetland	R2A	28°C, 3d
			LK45	NIBRBAC000509707	*Streptomyces jiujiangensis*	98.89	Soil	R2A	25°C, 3d
			WD-2	NIBRBAC000509592	*Streptomyces laurentii*	99.45	Soil	R2A	30°C, 2d
			MMS22-HSM7	NIBRBAC000509462	*Streptomyces levis*	99.65	Soil	MA	30°C, 2d

Table 1. Continued.

Order	Family	Genus	Strain no.	NIBR[a] ID	Closest species	16S rRNA gene sequence similarity (%)	Isolation Source	Medium for incubation	Condition for incubation
Streptomycetales	*Streptomycetaceae*	*Streptomyces*	CAU 1665	NIBRBAC000509663	*Streptomyces morookaense*	99.65	Soil	MA	30°C, 3d
			MMS22-HSR1	NIBRBAC000509463	*Streptomyces rameus*	100	Soil	R2A	30°C, 2d
Phylum *Bacillota*									
Bacillales	*Bacillaceae*	*Alkalihalobacillus*	CAU 1694	NIBRBAC000509678	*Alkalihalobacillus nanhaiisediminis*	99.60	Mud	MA	30°C, 3d
		Bacillus	HMG3331	NIBRBAC000509554	*Bacillus mesophilus*	99.70	Solar saltern	MA	25°C, 4d
			CAU 1705	NIBRBAC000509684	*Bacillus kexueae*	99.60	Mud	MA	30°C, 7d
			MMS22-S4-21	NIBRBAC000509455	*Bacillus fengqiuensis*	98.84	Soil	SCA	30°C, 7d
			ST10-2	NIBRBAC000509709	*Bacillus safensis* subsp. *safensis*	100	Soil	R2A	25°C, 3d
		Ectobacillus	MMS22-LL20	NIBRBAC000509457	*Ectobacillus antri*	99.38	Soil	SCA	30°C, 7d
		Mesobacillus	JPSW-M4	NIBRBAC000509644	*Mesobacillus boroniphilus*	99.66	Seawater	MA	25°C, 3d
		Metabacillus	MMS22-M6-3-14	NIBRBAC000509451	*Metabacillus crassostreae*	99.38	Soil	MA	30°C, 7d
		Niallia	JPSW-R6	NIBRBAC000509655	*Niallia oryzisoli*	98.85	Seawater	R2A	25°C, 3d
		Virgibacillus	MMS22-M6-3-15	NIBRBAC000509452	*Virgibacillus salarius*	100	Soil	MA	30°C, 7d
			MMS22-M6-3-16	NIBRBAC000509453	*Virgibacillus kapii*	99.39	Soil	MA	30°C, 7d
	Paenibacillaceae	*Ammoniphilus*	CAU 1689	NIBRBAC000509673	*Ammoniphilus resinae*	99.90	Mud flat	GYE	30°C, 7d
		Aneurinibacillus	Soil2	NIBRBAC000509569	*Aneurinibacillus migulanus*	99.70	Soil	R2A	25°C, 4-5d
		Paenibacillus	CAU 1690	NIBRBAC000509674	*Paenibacillus solani*	98.80	Mud flat	TSA	30°C, 3d
			CAU 1698	NIBRBAC000509681	*Paenibacillus segetis*	99.90	Mud flat	ISP2	30°C, 3d
			MMS22-AIC	NIBRBAC000509454	*Paenibacillus naphthalenovorans*	99.39	Soil	AIA	30°C, 7d
			LK11	NIBRBAC000509705	*Paenibacillus paridis*	99.38	Soil	R2A	25°C, 3d
	Planococcaceae	*Lysinibacillus*	CAU 1677	NIBRBAC000509664	*Lysinibacillus cavernae*	98.70	Mud	MA	30°C, 3d
Lactobacillales	*Lactobacillaceae*	*Lacticaseibacillus*	H15	NIBRBAC000509646	*Lacticaseibacillus rhamnosus*	100	Breast milk	MRS	30°C, 3d
Phylum *Bacteroidota*									
Cytophagales	*Hymenobacteraceae*	*Pontibacter*	MMS22-GI4	NIBRBAC000509460	*Pontibacter oryzae*	99.51	Soil	ISP2 agar	30°C, 2d
	Marivirgaceae	*Marivirga*	HMG3261	NIBRBAC000509548	*Marivirga tractuosa*	99.03	Seawater	MA	25°C, 3d
	Reichenbachiellaceae	*Ekhidna*	HMG3441	NIBRBAC000509557	*Ekhidna lutea*	99.42	Seawater	MA	25°C, 7d
	Spirosomaceae	*Aquirufa*	AS303	NIBRBAC000509515	*Aquirufa beregesia*	100	Wetland	R2A	28°C, 3d
		Emticicia	DJS-1-10	NIBRBAC000509573	*Emticicia oligotrophica*	99.44	Wetland	R2A	28°C, 3d
Flavobacteriales	*Flavobacteriaceae*	*Aquimarina*	HMG3252	NIBRBAC000509540	*Aquimarina celericrescens*	99.16	Seaweed	MA	25°C, 2d
			HMG3258	NIBRBAC000509545	*Aquimarina intermedia*	99.93	Seawater	MA	25°C, 2d
		Epilithonimonas	19_S1_T7	NIBRBAC000509483	*Epilithonimonas zeae*	99.44	Sediment soil	R2A	30°C, 2d
		Flavicella	HMG3255	NIBRBAC000509542	*Flavicella sediminum*	99.79	Seawater	MA	25°C, 2d
		Flavobacterium	AS316	NIBRBAC000509508	*Flavobacterium maotaiense*	99.93	Wetland	R2A	28°C, 3d
			LK23	NIBRBAC000509704	*Flavobacterium cupreum*	98.82	Soil	R2A	25°C, 3d
		Formosa	HMG3257	NIBRBAC000509544	*Formosa haliotis*	99.65	Seawater	MA	25°C, 2d
		Maribacter	DHSW-M12	NIBRBAC000509643	*Maribacter ulvicola*	99.86	Seawater	MA	25°C, 3d
		Zhouia	CAU 1682	NIBRBAC000509669	*Zhouia amylolytica*	100	Mud flat	MA	25°C, 3d

Table 1. Continued.

Order	Family	Genus	Strain no.	NIBR[a] ID	Closest species	16S rRNA gene sequence similarity (%)	Isolation Source	Medium for incubation	Condition for incubation
Flavobacteriales	*Weeksellaceae*	*Algoriella*	HMG3059	NIBRBAC000509539	*Algoriella xinjiangensis*	99.38	Soil	R2A	25°C, 3d
		Chryseobacterium	CAU 1697	NIBRBAC000509680	*Chryseobacterium candidae*	98.96	Mud	GYE	30°C, 3d
			16N2F1	NIBRBAC000509484	*Chryseobacterium balustinum*	99.28	Sediment soil	R2A	30°C, 2d
			18S2S17	NIBRBAC000509485	*Chryseobacterium endophyticum*	99.79	Sediment soil	R2A	30°C, 2d
Sphingobacteriales	*Sphingobacteriaceae*	*Pedobacter*	GF95	NIBRBAC000509603	*Pedobacter quisquiliarum*	99.93	Mud	R2A	30°C, 2d
Phylum *Pseudomonadota* (alpha)									
Caulobacterales	*Caulobacteraceae*	*Brevundimonas*	HMG3453	NIBRBAC000509559	*Brevundimonas abyssalis*	99.79	Seawater	MA	25°C, 5d
			16H4P11	NIBRBAC000509475	*Brevundimonas diminuta*	99.86	Sediment soil	R2A	30°C, 2d
			AS300	NIBRBAC000509507	*Brevundimonas denitrificans*	99.93	Wetland	R2A	28°C, 3d
Hyphomonadales	*Hyphomonadaceae*	*Hyphomonas*	HMG3436	NIBRBAC000509556	*Hyphomonas oceanitis*	100.00	Seawater	MA	25°C, 5d
Kordiimonadales	*Kordiimonadaceae*	*Kordiimonas*	CAU 1680	NIBRBAC000509667	*Kordiimonas lacus*	98.87	Seawater	MA	30°C, 3d
Maricaulales	*Robiginitomaculaceae*	*Algimonas*	HMG3263	NIBRBAC000509550	*Algimonas porphyrae*	99.25	Seawater	MA	25°C, 5d
Parvularculales	*Parvularculaceae*	*Marinicaulis*	D3-15	NIBRBAC000509598	*Marinicaulis aureus*	98.99	Marine algae	MA	20-30°C, 4d
Rhizobiales	*Ahrensiaceae*	*Ahrensia*	HMG3260	NIBRBAC000509547	*Ahrensia marina*	99.08	Seaweed	MA	25°C, 7d
	Nitrobacteraceae	*Bradyrhizobium*	ST10-3	NIBRBAC000509712	*Bradyrhizobium guangxiense*	99.84	Soil	R2A	25°C, 3d
	Phyllobacteriaceae	*Mesorhizobium*	BT829	NIBRBAC000509698	*Mesorhizobium erdmanii*	99.93	Soil	R2A	25°C, 3d
			ST14-1	NIBRBAC000509710	*Mesorhizobium carmichaelinearum*	99.77	Soil	R2A	25°C, 3d
		Phyllobacterium	BT831	NIBRBAC000509700	*Phyllobacterium loti*	99.54	Soil	R2A	25°C, 3d
	Rhizobiaceae	*Neorhizobium*	MMS22-HSS5	NIBRBAC000509468	*Neorhizobium huautlense*	99.79	Soil	SCA	30°C, 2d
		Rhizobium	TS35	NIBRBAC000509497	*Rhizobium endophyticum*	99.10	Wetland	R2A	28°C, 3d
Rhodobacterales	*Rhodobacteraceae*	*Albibacillus*	CAU 1678	NIBRBAC000509665	*Albibacillus kandeliae*	99.93	Sea sand	MA	30°C, 3d
		Cypionkella	AS330	NIBRBAC000509509	*Cypionkella collinsensis*	99.71	Wetland	R2A	28°C, 3d
		Defluviimonas	CAU 1704	NIBRBAC000509683	*Defluviimonas denitrificans*	99.93	Seawater	MA	30°C, 3d
		Luteovulum	YMSW-R8	NIBRBAC000509642	*Luteovulum johrii*	99.64	Seawater	R2A	25°C, 5d
		Pararhodobacter	KJ81-7	NIBRBAC000509605	*Pararhodobacter zhoushanensis*	99.49	Marine algae	MA	20-35°C, 2d
		Roseovarius	HMG3309	NIBRBAC000509552	*Roseovarius nitratireducens*	100.00	Solar saltern	MA	25°C, 5d
		Ruegeria	CAU 1702	NIBRBAC000509682	*Ruegeria mediterranea*	98.98	Seawater	MA	30°C, 3d
		Seohaeicola	CAU 1679	NIBRBAC000509666	*Seohaeicola zhoushanensis*	99.20	Mud flat	MA	30°C, 3d
		Sulfitobacter	YMSW-M15	NIBRBAC000509645	*Sulfitobacter guttiformis*	99.42	Seawater	MA	25°C, 3d
		Tateyamaria	HMG3499	NIBRBAC000509565	*Tateyamaria pelophila*	98.97	Seawater	MA	25°C, 7d
Rhodospirillales	*Acetobacteraceae*	*Acetobacter*	HMG3057	NIBRBAC000509537	*Acetobacter indonesiensis*	99.71	Soil	R2A	25°C, 5d

Table 1. Continued.

Order	Family	Genus	Strain no.	NIBR[a] ID	Closest species	16S rRNA gene sequence similarity (%)	Isolation Source	Medium for incubation	Condition for incubation
Rhodospirillales	*Rhodospirillaceae*	*Novispirillum*	MMS22-HSWR3	NIBRBAC000509467	*Novispirillum itersonii* subsp. *Nipponicum*	100.00	Soil	R2A	30°C, 2d
		Tistrella	HMG3457	NIBRBAC000509561	*Tistrella bauzanensis*	99.65	Seawater	MA	25°C, 5d
	Rhodovibrionaceae	*Tistlia*	HMG3317	NIBRBAC000509553	*Tistlia consotensis*	98.79	Solar saltern	MA	25°C, 7d
Sneathiellales	*Sneathiellaceae*	*Oceanibacterium*	HMG3443	NIBRBAC000509558	*Oceanibacterium hippocampi*	100.00	Seawater	MA	25°C, 7d
Sphingomonadales	*Erythrobacteraceae*	*Erythrobacter*	CAU 1691	NIBRBAC000509675	*Erythrobacter mangrovi*	99.57	Mud flat	MA	30°C, 3d
	Sphingomonadaceae	*Parasphingopyxis*	HMG3435	NIBRBAC000509555	*Parasphingopyxis lamellibrachiae*	99.00	Seawater	MA	25°C, 3d
		Sphingobium	MMS22-PI21	NIBRBAC000509469	*Sphingobium xenophagum*	99.04	Soil	ISP7	30°C, 7d
			AS227	NIBRBAC000509504	*Sphingobium fuliginis*	98.72	Wetland	R2A	28°C, 3d
		Sphingomonas	BT835	NIBRBAC000509703	*Sphingomonas molluscorum*	99.85	Soil	R2A	25°C, 3d
Phylum *Pseudomonadota* (beta)									
Burkholderiales	*Alcaligenaceae*	*Achromobacter*	18S3T11	NIBRBAC000509486	*Achromobacter aegrifaciens*	99.58	Sediment soil	R2A	30°C, 2d
		Alcaligenes	17H7M7	NIBRBAC000509479	*Alcaligenes aquatilis*	100	Sediment soil	R2A	30°C, 2d
			16H6L6	NIBRBAC000509474	*Alcaligenes faecalis* subsp. *phenolicus*	99.44	Sediment soil	R2A	30°C, 2d
		Bordetella	18N1V4	NIBRBAC000509480	*Bordetella tumulicola*	100	Sediment soil	R2A	30°C, 2d
	Comamonadaceae	*Aquincola*	MMS22-GI39	NIBRBAC000509471	*Aquincola tertiaricarbonis*	98.66	Soil	ISP7	30°C, 7d
		Hydrogenophaga	AS624	NIBRBAC000509513	*Hydrogenophaga aromaticivorans*	99.14	Wetland	R2A	30°C, 3d
		Polaromonas	AS644	NIBRBAC000509514	*Polaromonas cryoconiti*	99.18	Wetland	R2A	30°C, 3d
		Rubrivivax	CAU 1695	NIBRBAC000509679	*Rubrivivax albus*	99.38	Mud	MA	30°C, 3d
	Oxalobacteraceae	*Collimonas*	BT826	NIBRBAC000509695	*Collimonas silvisoli*	99.24	Soil	R2A	25°C, 3d
		Duganella	CM27	NIBRBAC000509498	*Duganella vulcania*	99.45	Wetland	R2A	28°C, 3d
		Empedobacter	MMS22-GI34	NIBRBAC000509470	*Empedobacter haloabium*	99.70	Soil	ISP7	30°C, 7d
		Herbaspirillum	AS214	NIBRBAC000509503	*Herbaspirillum frisingense*	99.11	Wetland	R2A	28°C, 3d
			MMS22-36	NIBRBAC000509456	*Herbaspirillum huttiense* subsp. *huttiense*	100	Soil	SCA	30°C, 7d
			MMS22-18	NIBRBAC000509459	*Herbaspirillum huttiense* subsp. *putei*	99.86	Soil	SCA	30°C, 7d
		Janthinobacterium	BT827	NIBRBAC000509696	*Janthinobacterium rivuli*	99.86	Soil	R2A	30°C, 3d
		Massilia	MMS22-GR6	NIBRBAC000509461	*Massilia consociata*	99.02	Soil	R2A	30°C, 2d
			MMS22-MBR12	NIBRBAC000509465	*Massilia flava*	99.79	Soil	R2A	30°C, 2d
			AS504	NIBRBAC000509511	*Massilia frigida*	99.66	Wetland	R2A	28°C, 3d
Neisseriales	*Chromobacteriaceae*	*Chromobacterium*	MMS22-SS45	NIBRBAC000509458	*Chromobacterium piscinae*	99.16	Soil	SCA	30°C, 7d
	Neisseriaceae	*Chitinibacter*	UHG6	NIBRBAC000509594	*Chitinibacter fontanus*	99.79	Lake water	R2A	28°C, 5d

Table 1. Continued.

Order	Family	Genus	Strain no.	NIBR[a] ID	Closest species	16S rRNA gene sequence similarity (%)	Isolation Source	Medium for incubation	Condition for incubation
Phylum *Pseudomonadota* (gamma)									
Aeromonadales	*Aeromonadaceae*	*Oceanisphaera*	GPSW-R9	NIBRBAC000509652	*Oceanisphaera psychrotolerans*	99.29	Soil	R2A	25°C, 3d
Alteromonadales	*Alteromonadaceae*	*Alteromonas*	HMG3253	NIBRBAC000509541	*Alteromonas stellipolaris*	99.86	Tidal flat	MA	25°C, 2d
	Moritellaceae	*Motilimonas*	HMG3259	NIBRBAC000509546	*Motilimonas cestriensis*	99.18	Tidal flat	MA	25°C, 2d
	Pseudoalteromonadaceae	*Pseudoalteromonas*	GPSW-M14	NIBRBAC000509651	*Pseudoalteromonas luteoviolacea*	98.97	Seawater	MA	25°C, 3d
Cellvibrionales	*Halieaceae*	*Haliea*	HMG3484	NIBRBAC000509564	*Haliea salexigens*	99.31	Seawater	MA	25°C, 7d
Enterobacterales	*Enterobacteriaceae*	*Enterobacter*	16S3A9	NIBRBAC000509477	*Enterobacter quasiroggenkampii*	99.39	Sediment soil	R2A	30°C, 2d
			16SBF1	NIBRBAC000509478	*Enterobacter chengduensis*	99.72	Sediment soil	R2A	30°C, 2d
			CASP060_16_ECC	NIBRBAC000509491	*Enterobacter wuhouensis*	99.59	Agricultural soil	R2A	30°C, 2d
		Escherichia	16H2E9	NIBRBAC000509488	*Escherichia ruysiae*	99.38	Sediment soil	R2A	30°C, 2d
	Erwiniaceae	*Erwinia*	19S3E3	NIBRBAC000509481	*Erwinia endophytica*	99.86	Sediment soil	R2A	30°C, 2d
Lysobacterales	*Rhodanobacteraceae*	*Rhodanobacter*	BT834	NIBRBAC000509702	*Rhodanobacter panaciterrae*	99.31	Soil	R2A	25°C, 3d
Moraxellales	*Moraxellaceae*	*Acinetobacter*	HMG3058	NIBRBAC000509538	*Acinetobacter albensis*	99.30	Soil	R2A	25°C, 3d
			DB12	NIBRBAC000509584	*Acinetobacter rudis*	99.30	Lake water	R2A	30°C, 2d
Oceanospirillales	*Alcanivoracaceae*	*Alcanivorax*	CAU 1685	NIBRBAC000509672	*Alcanivorax borkumensis*	99.52	Sea sand	MA	30°C, 3d
	Halomonadaceae	*Halomonas*	BIM5	NIBRBAC000509648	*Halomonas venusta*	99.93	Tidal flat	MA	25°C, 3d
	Oceanospirillaceae	*Marinomonas*	HMG3262	NIBRBAC000509549	*Marinomonas primoryensis*	99.08	Seawater	MA	25°C, 2d
	Saccharospirillaceae	*Saccharospirillum*	HMG3308	NIBRBAC000509551	*Saccharospirillum alexandrii*	99.93	Solar saltern	MA	25°C, 3d
Pseudomonadales	*Pseudomonadaceae*	*Pseudomonas*	CAU 1683	NIBRBAC000509670	*Pseudomonas linyingensis*	99.86	Mud flat	MA	30°C, 3d
			CAU 1692	NIBRBAC000509676	*Pseudomonas oryzae*	99.52	Mud flat	MA	30°C, 3d
			LSCA30_12_PSE	NIBRBAC000509492	*Pseudomonas asiatica*	100	Agricultural soil	R2A	30°C, 2d
			16H1M10	NIBRBAC000509487	*Pseudomonas juntendi*	99.86	Sediment soil	R2A	30°C, 2d
			16H3F9	NIBRBAC000509489	*Pseudomonas orientalis*	99.65	Sediment soil	R2A	30°C, 2d
			16H6M3	NIBRBAC000509490	*Pseudomonas helleri*	99.59	Sediment soil	R2A	30°C, 2d
			AS204	NIBRBAC000509500	*Pseudomonas glycinae*	100.00	Wetland	R2A	28°C, 3d
			AS212	NIBRBAC000509501	*Pseudomonas chlororaphis*	99.66	Wetland	R2A	28°C, 3d
			AS213	NIBRBAC000509502	*Pseudomonas atagonensis*	99.73	Wetland	R2A	28°C, 3d
			AS247	NIBRBAC000509505	*Pseudomonas cedrina*	99.73	Wetland	R2A	28°C, 3d
			AS279	NIBRBAC000509506	*Pseudomonas qingdaonensis*	99.93	Wetland	R2A	28°C, 3d
			AS568	NIBRBAC000509512	*Pseudomonas capeferrum*	98.7	Wetland	R2A	28°C, 3d
			BT833	NIBRBAC000509701	*Pseudomonas paraversuta*	100	Soil	R2A	25°C, 3d
			ST11-10	NIBRBAC000509711	*Pseudomonas edaphica*	99.86	Soil	R2A	25°C, 3d
Vibrionales	*Vibrionaceae*	*Vibrio*	BIM3	NIBRBAC000509647	*Vibrio kanaloae*	99.93	Tidal flat	MA	25°C, 3d
			HMG3256	NIBRBAC000509543	*Vibrio pacinii*	99.93	Seawater	MA	25°C, 2d
			CAU 1684	NIBRBAC000509671	*Vibrio fluvialis*	99.80	Sea sand	MA	30°C, 3d

[a]National Institute of Biological Resources.

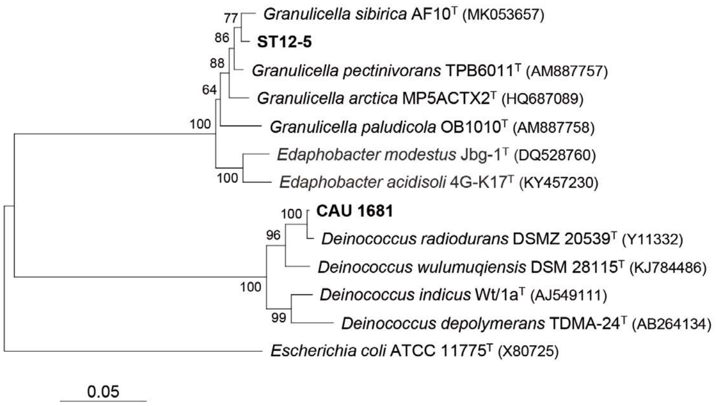

Fig. 1. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences showing the relationships of strains ST12-5 and CAU 1681 isolated in this study and their relatives in the phyla *Acidobacteriota* and *Deinococcota*. Only bootstrap values greater than 50% are shown at branching points. *Bacillus subtilis* IAM 12118^T (GenBank accession no. AB042061) was used as an outgroup. Bar, 0.05 substitutions per nucleotide position.

acid, malic acid, trisodium citrate, and phenylacetic acid are not. Strain 19_H4_S14 (=NIBRBAC000509482) was isolated from a sediment soil sample at Seoul, Republic of Korea.

Description of *Modestobacter caceresii* BT830

Cells are gram-stain-positive and short rod shaped. Colonies are circular, slightly convex, glistening, and brown colored after incubation for 3 days on R2A at 25°C. In the API 20NE system, positive for nitrate reduction and cytochrome oxidase, but negative for indole production, glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis, gelatin hydrolysis, and β-galactosidase. 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 are not utilized as sole carbon sources. Strain BT830 (=NIBRBAC000509699) was isolated from soil at Hoengseong-gun, Gangwon-do, Republic of Korea.

Description of *Modestobacter marinus* ST12-1

Cells are gram-stain-positive and rod shaped. Colonies are circular, slightly convex, and orange colored after incubation for 3 days on R2A at 25°C. In the API 20NE system, negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis, gelatin hydrolysis, β-galactosidase, and cytochrome oxidase. 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 are not utilized as sole carbon sources. Strain ST12-1 (=NIBRBAC000509713) was isolated from soil sample at Ulju-gun, Ulsan, Republic of Korea.

Description of *Agromyces iriomotensis* BT825

Cells are gram-stain-positive and rod shaped. Colonies are circular, convex, glistening, and yellow colored after incubation for 3 days on R2A at 25°C. In the API 20NE system, positive for esculin hydrolysis and cytochrome oxidase; weakly positive for nitrate reduction; but negative for indole production, glucose fermentation, arginine dihydrolase, urease, gelatin hydrolysis, and β-galactosidase. D-Glucose, D-mannitol, D-maltose, and malic acid are utilized as sole carbon sources; while L-arabinose, D-mannose, *N*-acetyl-glucosamine, potassium gluconate, capric acid, adipic acid, trisodium citrate, and phenylacetic acid are not. Strain BT825 (=NIBRBAC000509687) was isolated from a soil smple at Hoengseong-gun, Gangwon-do, Republic of Korea.

Description of *Chryseoglobus indicus* HMG3458

Cells are gram-stain-positive and rod shaped. Colonies are circular, convex, smooth, and light-yellow colored after incubation for 7 days on MA at 25°C. In the API 20NE system, positive for esculin hydrolysis and β-galactosidase; but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, gelatin hydrolysis, and cytochrome oxidase. 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 are not utilized as sole carbon sources. Strain HMG3458 (=NIBRBAC000509562) was isolated from a seawater sample at Pohang, Gyeongsangbuk-do, Republic of Korea.

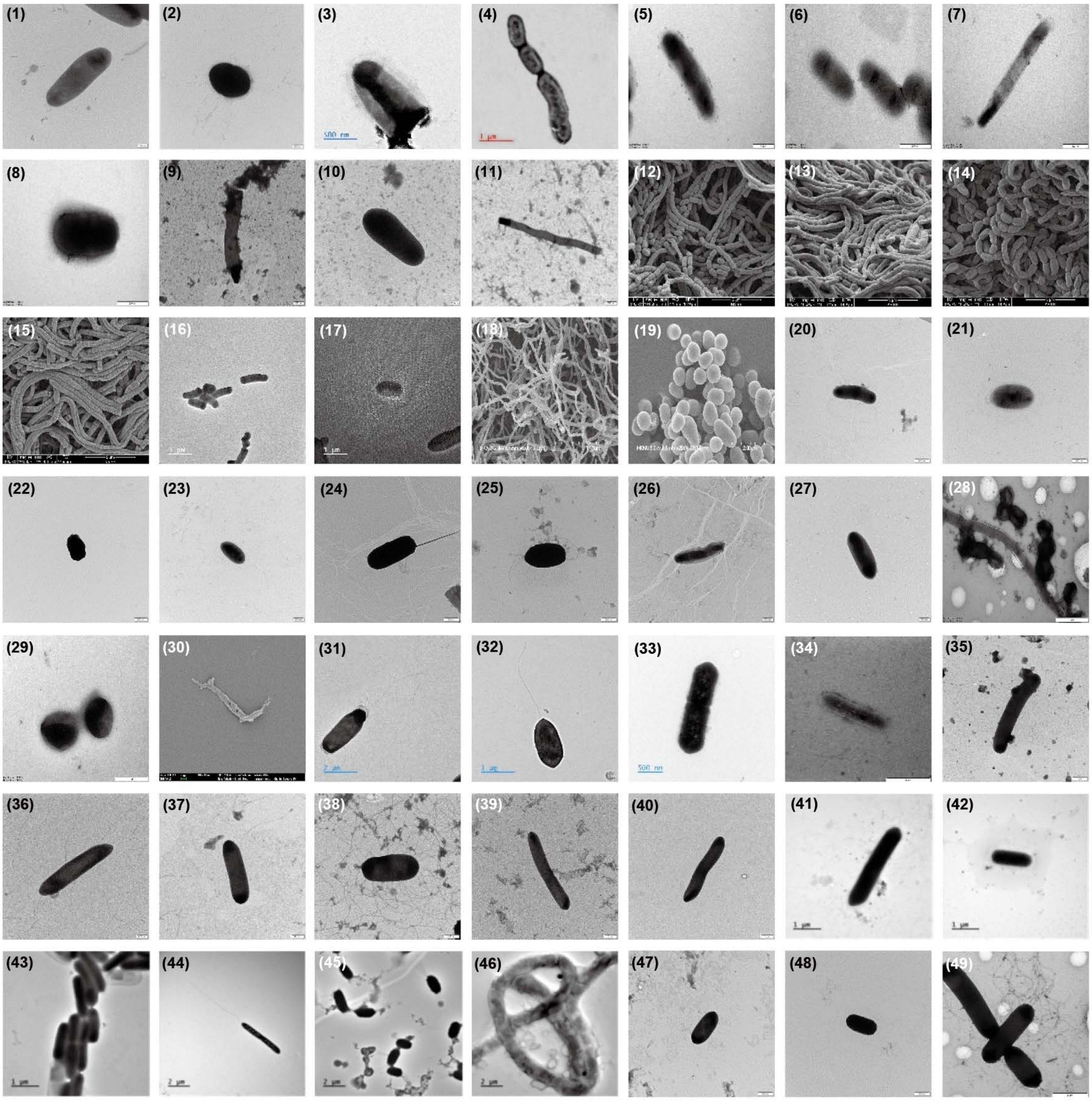

Fig. 2. Transmission electron or scanning electron micrographs of cells of the strains isolated in this study. Strains: 1, ST12-5; 2, CAU 1681; 3, YR2-2; 4, YR2-7; 5, HMG3056; 6, HMG3454; 7, HMG3458; 8, HMG3483; 9, CAU 1665; 10, CAU 1693; 11, CAU 1706; 12, MMS22-HSM7; 13, MMS22-HSR1; 14, MMS22-HST12; 15, MMS22-JCS7; 16, 16S1F15; 17, 19_H4_S14; 18, AS119; 19, AS338; 20, BT825; 21, BT828; 22, BT830; 23, LK01; 24, LK45; 25, ST6-10; 26, ST12-1; 27, ST12-12; 28, SJ125; 29, MPA10; 30, WD-2; 31, JPSW-R6; 32, JPSW-M4; 33, H15; 34, HMG3331; 35, CAU 1677; 36, CAU 1689; 37, CAU 1690; 38, CAU 1694; 39, CAU 1698; 40, CAU 1705; 41, MMS22-M6-3-14; 42, MMS22-M6-3-15; 43, MMS22-M6-3-16; 44, MMS22-AIC; 45, MMS22-S4-21; 46, MMS22-LL20; 47, LK11; 48, ST10-2; 49, Soil2; 50, DHSW-M12; 51, GF95; 52, HMG3059; 53, HMG3252; 54, HMG3255; 55, HMG3257; 56, HMG3258; 57, HMG3261; 58, HMG3441; 59, CAU 1682; 60, CAU 1697; 61, MMS22-GI4; 62, 19_S1_T7; 63, 16N2F1; 64, 18S2S17; 65, AS303; 66, AS316; 67, LK23; 68, DJS-1-10; 69, HMG3453; 70, 16H4P11; 71, AS300; 72, HMG3436; 73, CAU 1680; 74, HMG3263; 75, D3-15; 76, HMG3260; 77, MMS22-HSS5; 78, TS35; 79, BT829; 80, BT831; 81, ST14-1; 82, ST10-3; 83, YMSW-R8; 84, YMSW-M15; 85, KJ81-7; 86, HMG3309; 87, HMG3499; 88, CAU 1678; 89, CAU 1679; 90, CAU 1702; 91, CAU 1704; 92, AS330; 93, HMG3057; 94, HMG3317; 95, HMG3457; 96, MMS22-HSWR3; 97, HMG3443; 98, CAU 1691; 99, HMG3435; 100, MMS22-PI21; 101, AS227; 102, BT835; 103, 18S3T11; 104, 17H7M7; 105, 16H6L6; 106, MMS22-GI39; 107, 18N1V4; 108, UHG6; 109, MMS22-SS45; 110, BT826; 111, MMS22-GI34; 112, AS214; 113, MMS22-36; 114, MMS22-18; 115, AS624; 116, BT827; 117, MMS22-GR6; 118, MMS22-MBR12; 119, AS504; 120, AS644; 121, CAU 1695; 122, CM27; 123, GPSW-R9; 124, HMG3253; 125, HMG3259; 126, GPSW-M14; 127, HMG3484; 128, 16S3A9; 129, 16SBF1; 130, CASP060_16_ECC; 131, 16H2E9; 132, 19S3E3; 133, BT834; 134, HMG3058; 135, DB12; 136, CAU 1685; 137, BIM5; 138, HMG3262; 139, HMG3308; 140, CAU 1683; 141, CAU 1692; 142, LSCA30_12_PSE; 143, 16H1M10; 144, 16H3F9; 145, 16H6M3; 146, AS204; 147, AS212; 148, AS213; 149, AS247; 150, AS279; 151, AS568; 152, BT833; 153, ST11-10; 154, BIM3; 155, HMG3256; 156, CAU 1684.

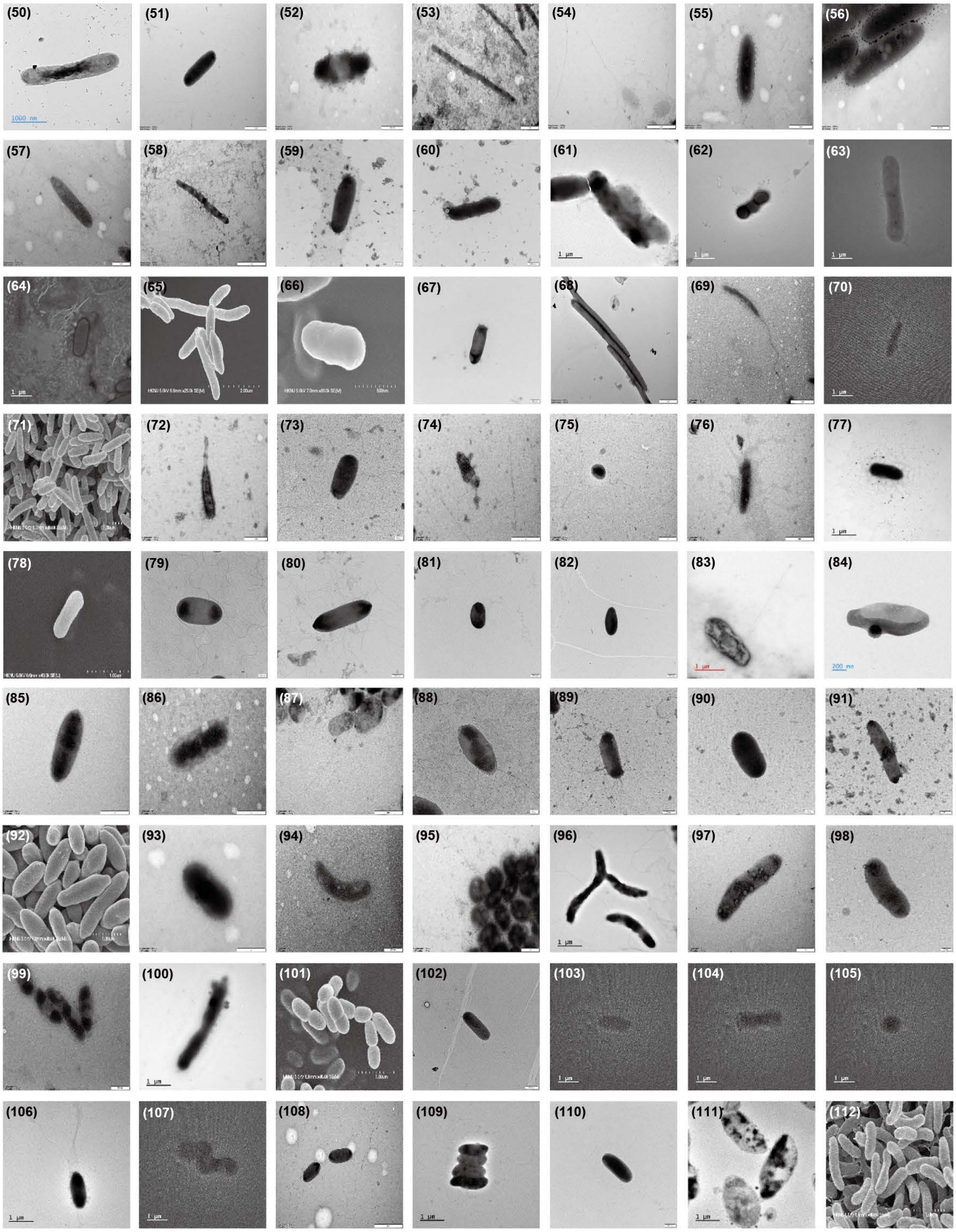

Fig. 2. Continued.

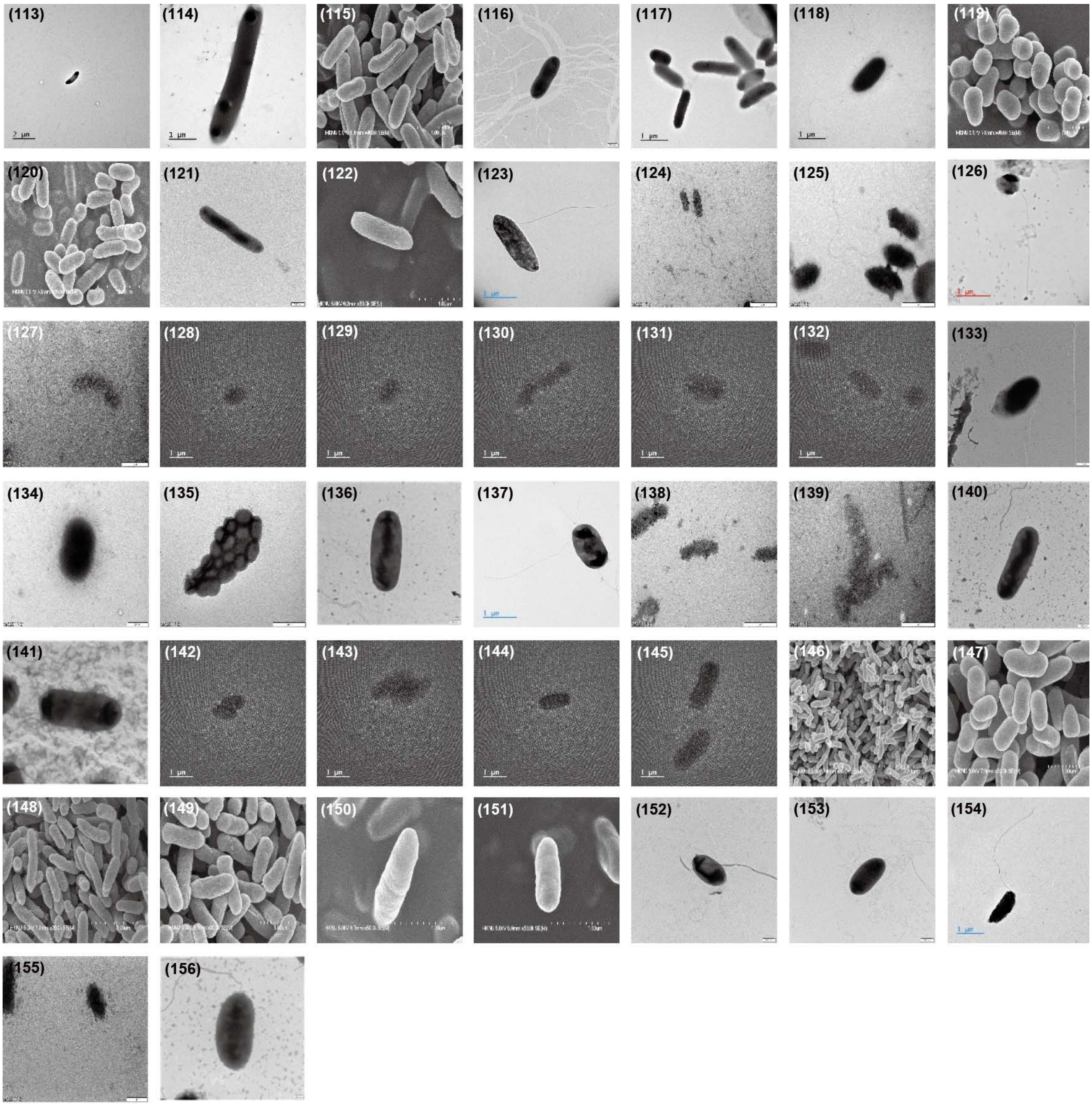

Fig. 2. Continued.

Description of *Marisediminicola antarctica* BT828

Cells are gram-stain-positive and rod shaped. Colonies are circular, slightly convex, glistening, and yellow colored after incubation for 3 days on R2A at 25°C. In the API 20NE system, positive for β-galactosidase; but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis, gelatin hydrolysis, and cytochrome oxidase. 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 are not utilized as sole carbon sources. Strain BT828 (=NIBRBAC000509697) was isolated from a soil sample at Hoengseong-gun, Gangwon-do, Republic of Korea.

Description of *Microbacterium algeriense* HMG3454

Cells are gram-stain-positive and rod shaped. Colonies are circular, convex, smooth, and light-yellow colored after incubation for 5 days on MA at 25°C. In the API

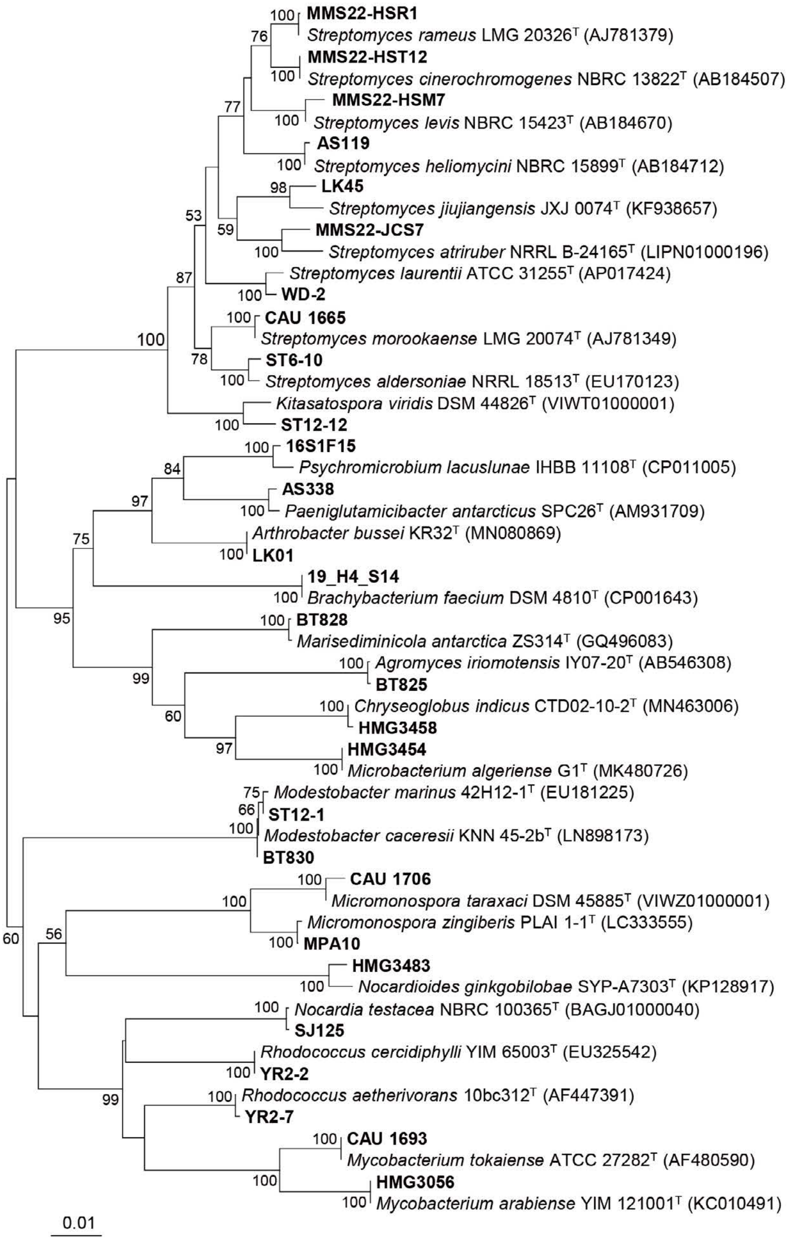

Fig. 3. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences showing the relationships between 28 strains isolated in this study and their relatives in the phylum *Actinomycetota*. *Bacillus subtilis* IAM 12118^T (GenBank accession no. NR_112116.2) was used as an outgroup. Only bootstrap values greater than 50% are shown at branching points. Bar, 0.01 substitutions per nucleotide position.

20NE system, positive for esculin hydrolysis, gelatin hydrolysis, and β-galactosidase; but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, and cytochrome oxidase. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, and potassium gluconate are utilized as sole carbon sources, while capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid are not. Strain HMG3454 (=NIBRBAC000509560) was isolated from a seawater sample at Pohang, Gyeongsangbuk-do, Republic of Korea.

Description of *Arthrobacter bussei* LK01

Cells are gram-stain-positive and short rod shaped. Colonies are circular, slightly convex, glistening, and pink colored after incubation for 3 days on R2A at 25°C. In the API 20NE system, positive for β-galactosidase and cytochrome oxidase; but negative for nitrate reduction, indole production, glucose fermentation, arginine

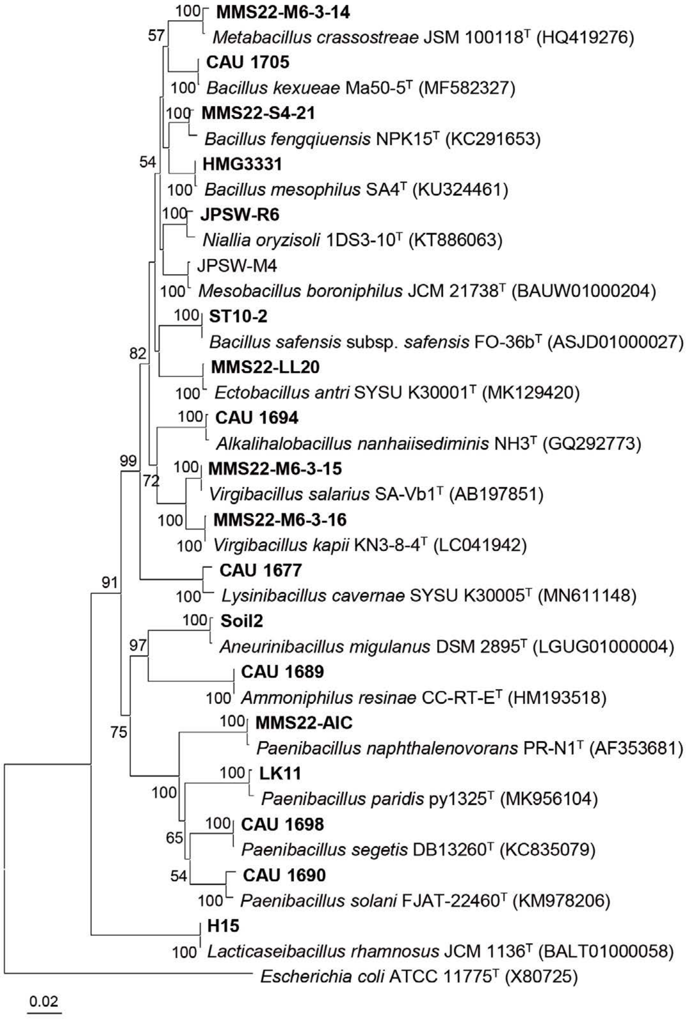

Fig. 4. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences showing the relationships of 19 strains isolated in this study and their relatives in the phylum *Bacillota*. Only bootstrap values greater than 50% are shown at branching points. *Escherichia coli* ATCC 11775^T (GenBank accession no. X80725) was used as an outgroup. Bar, 0.02 substitutions per nucleotide position.

dihydrolase, urease, esculin hydrolysis, and gelatin hydrolysis. 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 are not utilized as sole carbon sources. Strain LK01 (=NIBRBAC000509706) was isolated from a soil sample at Hoengseong-gun, Gangwon-do, Republic of Korea.

Description of *Paeniglutamicibacter antarcticus* AS338

Cells are gram-stain-positive and oval or coccoid shaped. Colonies are round, entire, raised, and pale-yellow colored after incubation for 3 days on R2A at 28°C. In the API 20NE system, negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis, gelatin hydrolysis, *β*-galactosidase, and cytochrome oxidase. D-Glucose, D-mannose, D-maltose, potassium gluconate, malic acid, trisodium citrate, and phenylacetic acid are utilized as sole carbon sources; while L-arabinose, D-mannitol, *N*-acetyl-glucosamine, capric acid, and adipic acid are not. Strain AS338 (=NIBRBAC000509510) was isolated from a wetland sample at Anseong, Gyeonggi-do, Republic of Korea.

Description of *Psychromicrobium lacuslunae* 16S1F15

Cells are gram-stain-positive and rod shaped. Colonies are smooth, opaque, convex, and cream colored after incubation for 2 days on R2A at 30°C. In the API 20NE system, positive for nitrate reduction, glucose fermentation, and esculin hydrolysis; but negative for indole pro-

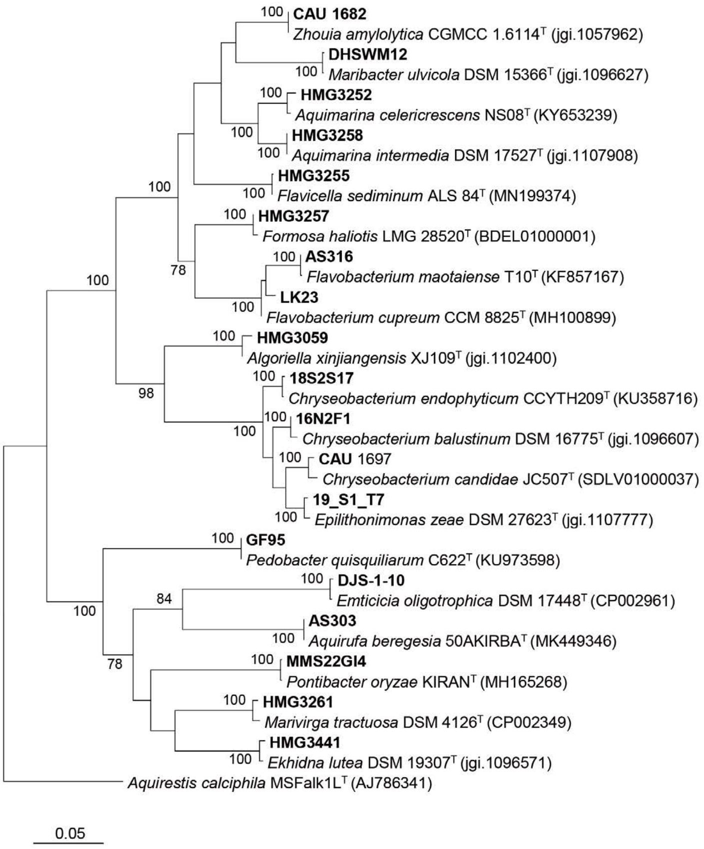

Fig. 5. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences showing the relationships of 19 strains isolated in this study and their relatives in the phylum *Bacteroidota*. Only bootstrap values greater than 50% are shown at branching points. *Aquirestis calciphila* MSFalk1L^T (GenBank accession no. AJ786341) was used as an outgroup. Bar, 0.05 substitutions per nucleotide position.

duction, arginine dihydrolase, urease, gelatin hydrolysis, *β*-galactosidase, and cytochrome oxidase. L-Arabinose, malic acid, trisodium citrate, and phenylacetic acid are utilized as sole carbon sources; while D-glucose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, and adipic acid are not. Strain 16S1F15 (=NIBRBAC000509476) was isolated from a sediment soil sample at Jeongseon-gun, Gangwon-do, Republic of Korea.

Description of *Micromonospora taraxaci* CAU 1706

Cells are gram-stain-positive and filamentous. Colonies are circular, rough, entire margin, pulvinate, opaques, and brown-black colored after incubation for 10 days on ISP2 at 30°C. In the API 20NE system, positive for esculin hydrolysis, gelatin hydrolysis, *β*-galactosidase, and cytochrome oxidase; but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, and urease. L-Arabinose, D-mannose, D-mannitol, and D-maltose are utilized as sole carbon sources; while D-Glucose, *N*-acetyl-glucosamine, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid are not. Strain CAU 1706 (=NIBRBAC000509685) was isolated from a mud sample at Ansan, Gyeonggi-do, Republic of Korea.

Description of *Micromonospora zingiberis* MPA10

Cells are gram-stain-positive and rod shaped. Colonies are circular, convex, and pale orange or strong orange colored after incubation for 4–5 days on R2A at 25°C. In the API 20NE system, positive for esculin hydrolysis; but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, gelatin hydrolysis, *β*-galactosidase, and cytochrome oxidase. 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 are not utilized as sole carbon sources. Strain MPA10 (=NIBRBAC000509581) was isolated from root of *Idesia polycarpa* at Goyang, Gyeonggi-do, Republic of Korea.

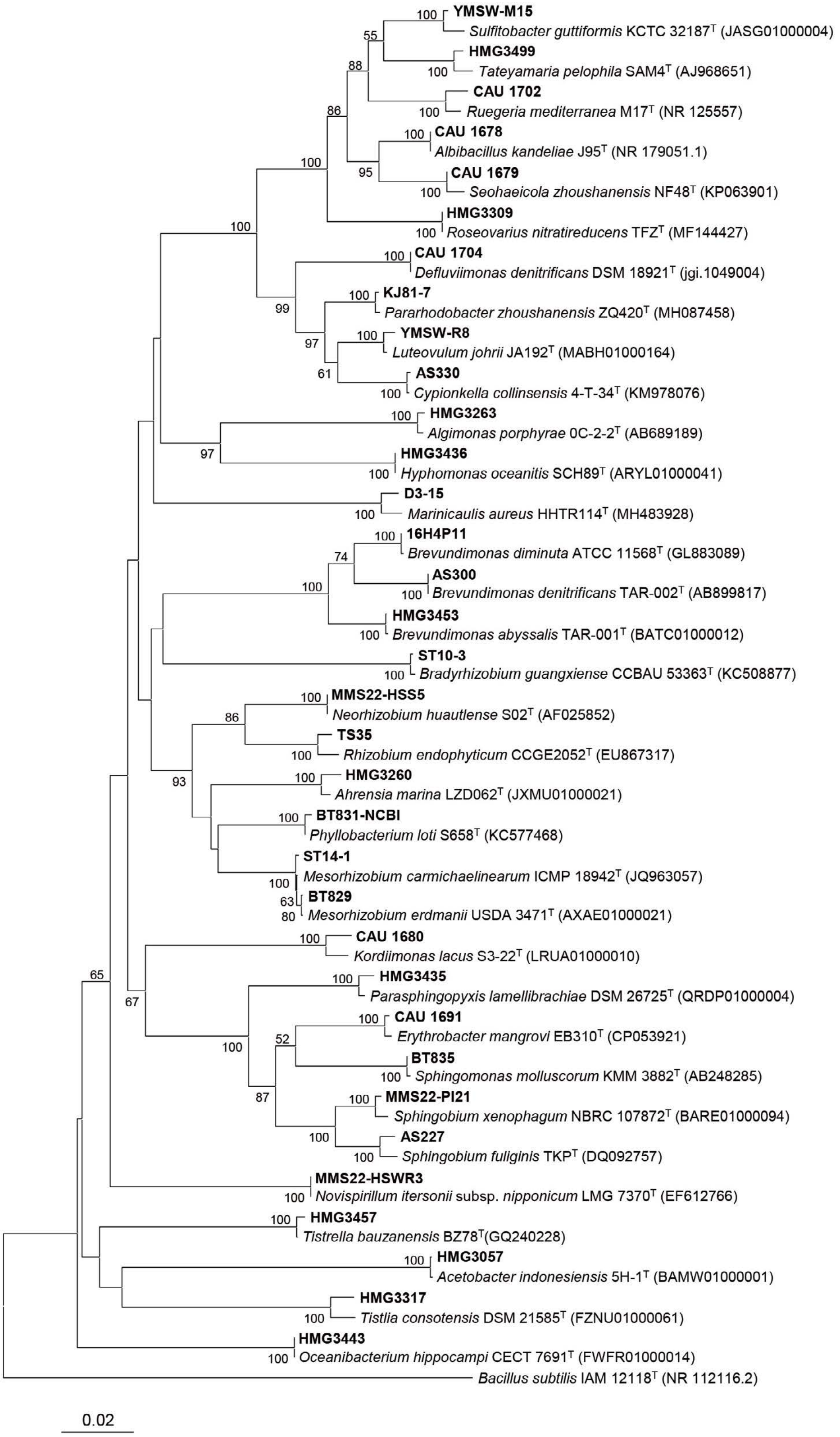

Fig. 6. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences showing the relationships of 34 strains isolated in this study and their relatives in the class *Alphaproteobacteria* of the phylum *Pseudomonadota*. Only bootstrap values greater than 50% are shown at branching points. *Bacillus subtilis* IAM 12118^T (GenBank accession no. NR_112116.2) was used as an outgroup. Bar, 0.02 substitutions per nucleotide position.

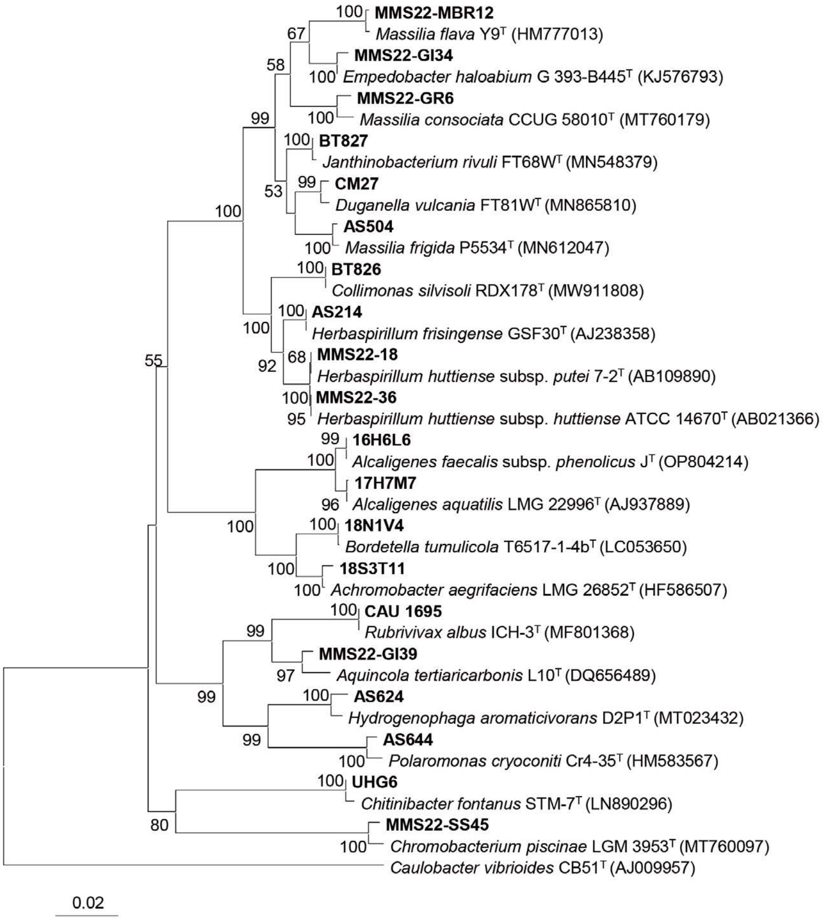

Fig. 7. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences showing the relationships of 20 strains isolated in this study and their relatives in the class *Betaproteobacteria* of the phylum *Pseudomonadota*. Only bootstrap values greater than 50% are shown at branching points. *Caulobacter vibrioides* CB51^T (GenBank accession no. AJ009957) was used as an outgroup. Bar, 0.02 substitutions per nucleotide position.

Description of *Mycolicibacterium arabiense* HMG3056

Cells are gram-stain-positive and rod shaped. Colonies are circular, convex, smooth, and orange-pink colored after incubation for 5 days on R2A at 25°C. In the API 20NE system, positive for urease; but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, esculin hydrolysis, gelatin hydrolysis, β-galactosidase, and cytochrome oxidase. L-Arabinose, D-mannitol, potassium gluconate, and malic acid are utilized as sole carbon sources; while D-glucose, D-mannose, *N*-acetyl-glucosamine, D-maltose, capric acid, adipic acid, trisodium citrate, and phenylacetic acid are not. Strain HMG3056 (=NIBRBAC000509536) was isolated from a moss sample at Yongin, Gyeonggi-do, Republic of Korea.

Description of *Mycolicibacterium tokaiense* CAU 1693

Cells are gram-stain-positive and rod shaped. Colonies are circular, smooth, entire margin, convex, opaque, and yellow colored after incubation for 3 days on MA at 30°C. In the API 20NE system, positive for urease and esculin hydrolysis; but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, gelatin hydrolysis, β-galactosidase, and cytochrome oxidase. D-Glucose, L-arabinose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, and malic acid are utilized as sole carbon source; while D-mannose, capric acid, adipic acid, trisodium citrate, and phenylacetic acid are not. Strain CAU 1693 (=NIBRBAC000509677) was isolated from a mud flat sample at Ansan, Gyeonggi-do, Republic of Korea.

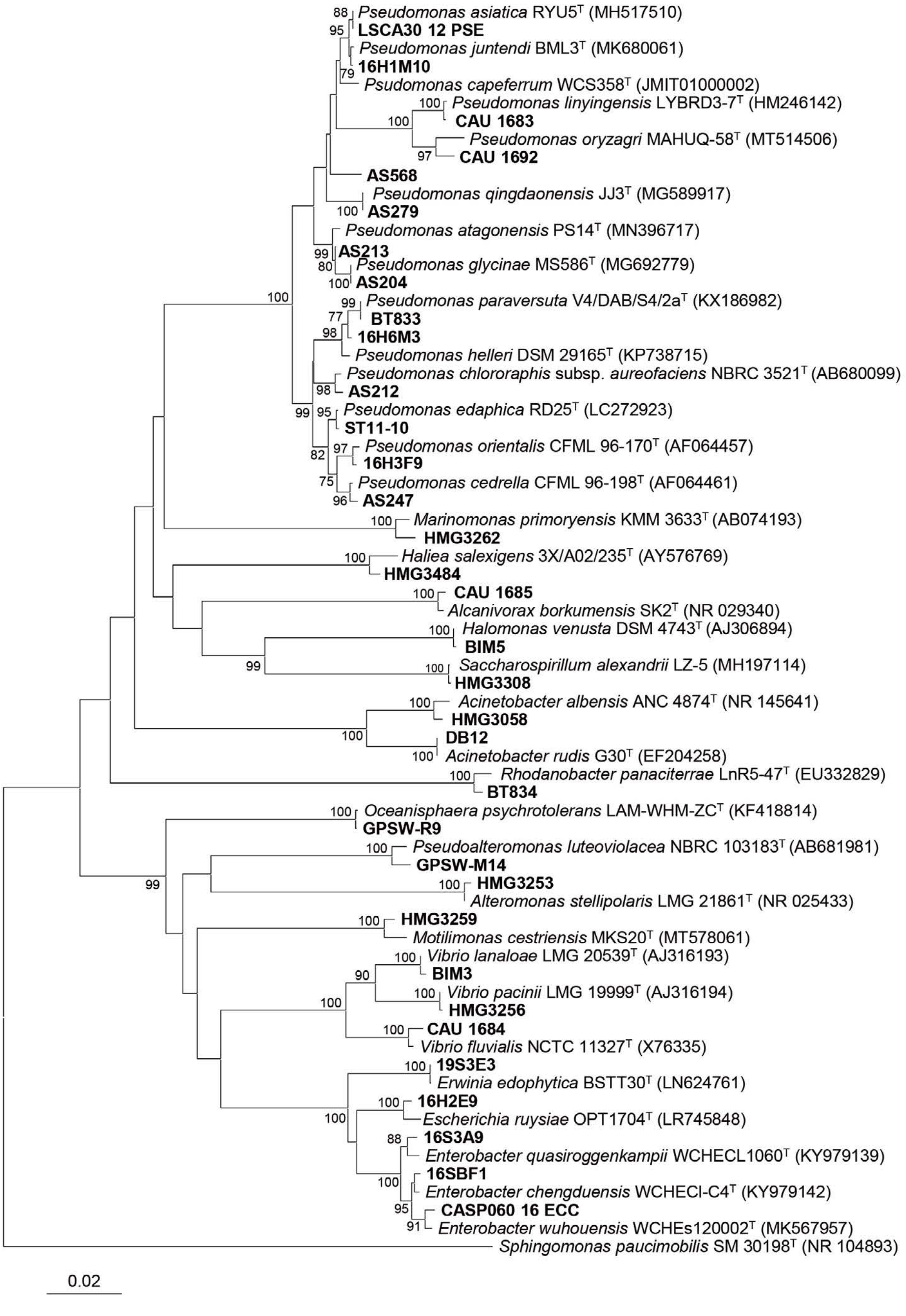

Fig. 8. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences showing the relationships of 34 strains isolated in this study and their relatives in the class *Gammaproteobacteria* of the phylum *Pseudomonadota*. Only bootstrap values greater than 50% are shown at branching points. *Sphingomonas paucimobilis* SM 30198^{T} (GenBank accession no. NR 104893) was used as an outgroup. Bar, 0.02 substitutions per nucleotide position.

Description of *Nocardia testacea* SJ125

Cells are gram-stain-positive and rod shaped. Colonies are circular, convex, brick colored mycelium, and orange to brick colored after incubation for 3 days on R2A at 30°C. In the API 20NE system, positive for nitrate reduction and gelatin hydrolysis; but negative for indole production, glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis, *β*-galactosidase, and cytochrome oxidase. D-Glucose, L-arabinose, D-mannitol, D-maltose, and phenylacetic acid are utilized as sole carbon sources; while D-mannose, *N*-acetyl-glucosamine, potassium gluconate, capric acid, adipic acid, malic acid, and trisodium citrate are not. Strain SJ125 (=NIBRBAC000509593) was isolated from a soil sample at Seoul, Republic of Korea.

Description of *Rhodococcus aetherivorans* YR2-7

Cells are gram-stain-positive and rod shaped. Colonies are circular, convex, glistening, and light-yellow colored after incubation for 3 days on R2A at 25°C. In the API 20NE system, positive for urease, esculin hydrolysis, and β-galactosidase; but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, gelatin hydrolysis, and cytochrome oxidase. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, potassium gluconate, malic acid, trisodium citrate, and phenylacetic acid are utilized as sole carbon sources; but D-maltose, capric acid, and adipic acid are not. Strain YR2-7 (=NIBRBAC000509650) was isolated from a tidal flat sample at Gunsan, Jeollabuk-do, Republic of Korea.

Description of *Rhodococcus cercidiphylli* YR2-2

Cells are gram-stain-positive and rod shaped. Colonies are circular, convex, glistening, and light-yellow colored after incubation for 3 days on R2A at 25°C. In the API 20NE system, positive for nitrate reduction, esculin hydrolysis, and β-galactosidase; but negative for indole production, glucose fermentation, arginine dihydrolase, urease, gelatin hydrolysis, and cytochrome oxidase. D-Glucose, D-mannose, D-mannitol, and malic acid are utilized as sole carbon sources; while L-arabinose *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, trisodium citrate, and phenylacetic acid are not. Strain YR2-2 (=NIBRBAC000509649) was isolated from a tidal flat sample at Gunsan, Jeollabuk-do, Republic of Korea.

Description of *Nocardioides ginkgobilobae* HMG3483

Cells are gram-stain-positive and rod shaped. Colonies are circular, convex, smooth, and light-yellow colored after incubation for 5 days on MA at 25°C. In the API 20NE system, positive for esculin hydrolysis, gelatin hydrolysis, and β-galactosidase; but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, and cytochrome oxidase. D-Maltose and potassium gluconate are utilized as sole carbon sources; while D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid are not. Strain HMG3483 (=NIBRBAC000509563) was isolated from a seawater sample at Sinan-gun, Jeollanam-do, Republic of Korea.

Description of *Kitasatospora viridis* ST12-12

Cells are gram-stain-positive and short rod shaped. Colonies are circular, flat, glistening, and white colored after incubation for 3 days on R2A at 25°C. In the API 20NE system, positive for esculin hydrolysis, gelatin hydrolysis, and cytochrome oxidase; but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, and β-galactosidase. *N*-Acetyl-glucosamine, potassium gluconate, and capric acid are utilized as sole carbon sources; while D-glucose, L-arabinose, D-mannose, D-mannitol, D-maltose, adipic acid, malic acid, trisodium citrate, and phenylacetic acid are not. Strain ST12-12 (=NIBRBAC000509714) was isolated from a soil sample at Ulju-gun, Ulsan, Republic of Korea.

Description of *Streptomyces aldersoniae* ST6-10

Cells are gram-stain-positive and short rod shaped. Colonies are circular, flat, dry, and white colored after incubation for 3 days on R2A at 25°C. In the API 20NE system, positive for β-galactosidase and cytochrome oxidase; but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis, and gelatin hydrolysis. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, potassium gluconate, and malic acid are utilized as sole carbon sources; while D-maltose, capric acid, adipic acid, trisodium citrate, and phenylacetic acid are not. Strain ST6-10 (=NIBRBAC000509708) was isolated from a soil sample at Hoengseong-gun, Gangwon-do, Republic of Korea.

Description of *Streptomyces atriruber* MMS22-JCS7

Cells are gram-stain-positive and filamentous. Colonies are filamentous, raised, undulate, and yellow colored after incubation for 2 days on SCA at 30°C. In the API 20NE system, positive for nitrate reduction, glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis, gelatin hydrolysis, β-galactosidase, and cytochrome oxidase; but negative for indole production. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, malic acid, trisodium citrate, and phenylacetic acid are utilized as sole carbon sources; while capric acid and adipic acid are not. Strain MMS22-JCS7 (=NIBRBAC000509466) was isolated from a soil sample at Sejong, Republic of Korea.

Description of *Streptomyces cinerochromogenes* MMS22-HST12

Cells are gram-stain-positive and filamentous. Colonies are filamentous, raised, undulate, and brown colored after incubation for 2 days on TSA at 30°C. In the API 20NE system, positive for glucose fermentation, urease, esculin hydrolysis, gelatin hydrolysis, β-galactosidase, and cytochrome oxidase; but negative for nitrate reduction, indole production, and arginine dihydrolase. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, adipic acid, malic acid, trisodium citrate, and phenylacetic acid are utilized as sole carbon sources; while capric acid is not. Strain MMS22-HST12 (=NIBRBAC000509464) was isolated from a soil sample at Sejong, Republic of Korea.

Description of *Streptomyces heliomycini* AS119

Cells are gram-stain-positive and filamentous. Colonies are filamentous, unbonate, and white to brown colored after incubation for 3 days on R2A at 28°C. In the API 20NE system, positive for esculin hydrolysis, and β-galactosidase; but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, gelatin hydrolysis, cytochrome oxidase. D-Glucose, L-arabinose, *N*-acetyl-glucosamine, potassium gluconate, and malic acid are utilized as sole carbon sources; while D-mannose, D-mannitol, D-maltose, capric acid, adipic acid, trisodium citrate, and phenylacetic acid are not. Strain AS119 (=NIBRBAC000509499) was isolated from a wetland sample at Anseong, Gyeonggi-do, Republic of Korea.

Description of *Streptomyces jiujiangensis* LK45

Cells are gram-stain-positive and rod shaped. Colonies are circular, flat, dry, and brown colored after incubation for 3 days on R2A at 25°C. In the API 20NE system, positive for nitrate reduction, esculin hydrolysis, gelatin hydrolysis, and cytochrome oxidase; weakly positive for urease; but negative for indole production, glucose fermentation, arginine dihydrolase, and β-galactosidase. Capric acid and adipic acid are utilized as sole carbon sources; while D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, malic acid, trisodium citrate, and phenylacetic acid are not. Strain LK45 (=NIBRBAC000509707) was isolated from a soil sample at Hoengseong-gun, Gangwon-do, Republic of Korea.

Description of *Streptomyces laurentii* WD-2

Cells are gram-stain-positive and forming mycelia. Colonies are round and light brown colored after incubation for 2 days on R2A at 30°C. In the API 20NE system, positive for nitrate reduction, esculin hydrolysis, gelatin hydrolysis, β-galactosidase, and cytochrome oxidase; but negative for indole production, glucose fermentation, arginine dihydrolase, and urease. D-Glucose, L-arabinose, D-mannose, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, and malic acid are utilized as sole carbon sources; while D-mannitol, capric acid, adipic acid, trisodium citrate, and phenylacetic acid are not. Strain WD-2 (=NIBRBAC000509592) was isolated from a soil sample at Goyang, Gyeonggi-do, Republic of Korea.

Description of *Streptomyces levis* MMS22-HSM7

Cells are gram-stain-positive and filamentous. Colonies are filamentous, raised, undulate, and brown colored after incubation for 2 days on MA at 30°C. In the API 20NE system, positive for glucose fermentation, esculin hydrolysis, gelatin hydrolysis, β-galactosidase, and cytochrome oxidase; but negative for nitrate reduction, indole production, arginine dihydrolase, and urease. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, adipic acid, malic acid, trisodium citrate, and phenylacetic acid are utilized as sole carbon sources; while capric acid is not. Strain MMS22-HSM7 (=NIBRBAC000509462) was isolated from a soil sample at Sejong, Republic of Korea.

Description of *Streptomyces morookaense* CAU 1665

Cells are gram-stain-positive and filamentous. Colonies are circular, smooth, entire margin, convex, opaques, and cream colored after incubation for 3 days on MA at 30°C. In the API 20NE system, positive for esculin hydrolysis and β-galactosidase; but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, gelatin hydrolysis, and cytochrome oxidase. D-Glucose, *N*-acetyl-glucosamine, potassium gluconate, and adipic acid are utilized as sole carbon sources; while L-arabinose, D-mannose, D-mannitol, D-maltose, capric acid, malic acid, trisodium citrate, and phenylacetic acid are not. Strain CAU 1665 (=NIBRBAC000509663) was isolated from a soil sample at Incheon, Republic of Korea.

Description of *Streptomyces rameus* MMS22-HSR1

Cells are gram-stain-positive and filamentous. Colonies are filamentous, raised, undulate, and white colored after incubation for 2 days on R2A at 30°C. In the API 20NE system, positive for urease, esculin hydrolysis, gelatin hydrolysis, β-galactosidase, and cytochrome oxidase; but negative for nitrate reduction, indole production, glucose fermentation, and arginine dihydrolase. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, adipic acid, malic acid, trisodium citrate, and phenylacetic acid are utilized as sole carbon sources; while capric acid is not. Strain MMS22-HSR1 (=NIBRBAC000509463) was isolated from a soil sample at Sejong, Republic of Korea.

Description of *Alkalihalobacillus nanhaiisediminis* CAU 1694

Cells are Gram-stain-positive, motile with flagella, and rod-shaped. Colonies are creamy white-colored, circular, smooth, entire margin, flat, and opaque after incubation for 3 days on MA plates at 30°C. In the API 20NE system, positive for esculin hydrolysis; but negative for nitrate reaction, indole production, glucose fermentation, arginine dihydrolase, urease, gelatin hydrolysis, and β-galactosidase. Malic acid is utilized as a sole carbon source; while D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-β-glucosamine, D-maltose, potassium glutamate, capric acid, adipic acid, trisodium citrate, and phenylacetic acid are not. Strain CAU 1694 (=NIBRBAC000509678) was isolated from a mud sample at Ansan, Gyeonggi-do, Republic of Korea.

Description of *Bacillus mesophilus* HMG3331

Cells are Gram-stain-positive, motile with flagella, and rod shaped. Colonies are light pink colored, circular, convex, and smooth after incubation for 4 days on MA plates at 25°C. In the API 20NE system, positive for esculin hydrolysis and β-galactosidase activity; but negative for nitrate reaction, indole production, glucose fermentation, arginine dihydrolase, urease, and gelatin hydrolysis. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-β-glucosamine, D-maltose, potassium glutamate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid are not utilized as sole carbon sources. Strain HMG3331 (=NIBRBAC000509554) was isolated from a solar saltern sample at Sinan-gun, Jeollanam-do, Republic of Korea.

Description of *Bacillus kexueae* CAU 1705

Cells are Gram-stain-positive, non-flagellated, and rod shaped. Colonies are white colored, circular, smooth, entire, margin, convex, and translucent after incubation for 7 days on MA plates at 30°C. In the API 20NE system, positive for nitrate reaction, esculin hydrolysis, and β-galactosidase; but negative for indole production, glucose fermentation, arginine dihydrolase, urease, and gelatin hydrolysis. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-β-glucosamine, D-maltose, and potassium glutamate are utilized as sole carbon sources; while capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid are not. Strain CAU 1705 (=NIBRBAC000509684) was isolated from a mud sample at Ansan, Gyeonggi-do, Republic of Korea.

Description of *Bacillus fengqiuensis* MMS22-S4-21

Cells are Gram-stain-positive, aerobic, non-flagellated, and rod shaped. Colonies are yellowish, punctiform, convex, and entire after incubation for 7 days on SCA plates at 30°C. In the API 20NE system, positive for esculin hydrolysis and β-galactosidase; but negative for nitrate reaction, indole production, glucose fermentation, arginine dihydrolase, urease, and gelatin hydrolysis. *N*-Acetyl-β-glucosamine, D-maltose, potassium glutamate, and phenylacetic acid are utilized as sole carbon sources; while D-glucose, L-arabinose, D-mannose, D-mannitol, capric acid, adipic acid, malic acid, and trisodium citrate are not. Strain MMS22-S4-21 (=NIBRBAC000509455) was isolated from a soil sample at Pohang, Gyeongsangbuk-do, Republic of Korea.

Description of *Bacillus safensis* subsp. *safensi* ST10-2

Cells are Gram-stain-positive, aerobic, non-flagellated, and rod shaped. Colonies are white, circular, slightly convex, and glistening after incubation for 3 days on R2A plates at 25°C. In the API 20NE system, positive for β-galactosidase; but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis, and gelatin hydrolysis. D-Glucose, L-arabinose, D-mannose, D-mannitol, and *N*-acetyl-β-glucosamine are utilized as sole carbon sources; while D-maltose, potassium glutamate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid are not. Strain ST10-2 (=NIBRBAC000509709) was isolated from a soil sample at Hoengseong-gun, Gangwon-do, Republic of Korea.

Description of *Ectobacillus antri* MMS22-LL20

Cells are Gram-stain-positive, aerobic, non-flagellated, and rod shaped. Colonies are pale yellow, punctiform, convex, and entire when incubated for 7 days on SCA plates at 30°C. In the API 20NE system, positive for esculin hydrolysis, gelatin hydrolysis, and β-galactosidase; but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, and urease. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-β-glucosamine, D-maltose, potassium glutamate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid are not utilized as sole carbon sources. Strain MMS22-LL20 (=NIBRBAC000509457) was isolated from a soil sample at Gapyeong, Gyeonggi-do, Republic of Korea.

Description of *Mesobacillus boroniphilus* JPSW-M4

Cells are Gram-stain-positive, motile with flagella, and rod-shaped. Colonies are light orange-colored, circular, convex, and glistening when incubated for 3 days on marine agar plates at 25°C. In the API 20NE system, positive for nitrate reaction, esculin hydrolysis, and gelatin hydrolysis; but negative for indole production, glucose fermentation, arginine dihydrolase, urease, and β-galactosidase. D-Glucose, potassium glutamate, and malic acid are utilized as sole carbon sources; while L-arabinose, D-mannose, D-mannitol, *N*-acetyl-β-glucosamine, D-maltose, capric acid, adipic acid, trisodium citrate, and phenylacetic acid are not. Strain JPSW-M4 (=NIBRBAC000509644) was isolated from a seawater sample at Buan-gun, Jeollabuk-do, Republic of Korea.

Description of *Metabacillus crassostreae* MMS22-M6-3-14

Cells are Gram-stain-positive, motile with flagella, and rod shaped. Colonies are yellowish colored, punctiform, flat, and entire when incubated for 7 days on MA plates at 30°C. In the API 20NE system, positive for urease, esculin hydrolysis, gelatin hydrolysis, *β*-galactosidase, and utilization of D-mannose, D-mannitol, D-maltose, and potassium glutamate; but negative for nitrate reduction, indole production, glucose fermentation, and arginine dihydrolase. D-Glucose, L-arabinose, *N*-acetyl-*β*-glucosamine, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid are not utilized as sole carbon sources. Strain MMS22-M6-3-14 (=NIBRBAC000509451) was isolated from a soil sample at Gangneung, Gangwon-do, Republic of Korea.

Description of *Niallia oryzisoli* JPSW-R6

Cells are Gram-stain-positive, motile with flagella, and rod shaped. Colonies are white colored, circular, slightly convex, and glistening when incubated for 3 days on R2A agar plates at 25°C. In the API 20NE system, positive for nitrate reaction and urease; but negative for indole production, glucose fermentation, arginine dihydrolase, esculin hydrolysis, gelatin hydrolysis, and *β*-galactosidase. D-Glucose, D-mannitol, D-maltose, and phenylacetic acid are utilized as sole carbon sources; while L-arabinose, D-mannose, *N*-acetyl-*β*-glucosamine, potassium glutamate, capric acid, adipic acid, malic acid, and trisodium citrate are not. Strain JPSW-R6 (=NIBRBAC000509655) was isolated from a seawater sample at Buan-gun, Jeollabuk-do, Republic of Korea.

Description of *Virgibacillus salarius* MMS22-M6-3-15

Cells are Gram-stain-positive, non-flagellated, and rod shaped. Colonies are light purple colored, circular, convex, and filamentous when incubated for 7 days on MA plates at 30°C. In the API 20NE system, positive for nitrate reduction, urease, esculin hydrolysis, gelatin hydrolysis, and *β*-galactosidase; but negative for indole production, glucose fermentation, and arginine dihydrolase. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-*β*-glucosamine, D-maltose, potassium glutamate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid are not utilized as sole carbon sources. Strain MMS22-M6-3-15 (=NIBRBAC000509452) was isolated from a soil sample at Gangneung, Gangwon-do, Republic of Korea.

Description of *Virgibacillus kapii* MMS22-M6-3-16

Cells are Gram-stain-positive, non-flagellated, aerobic, and rod shaped. Colonies are yellow, circular, raised, and undulate when incubated for 7 days on MA plates at 25°C. In the API 20NE system, positive for esculin hydrolysis, gelatin hydrolysis, and *β*-galactosidase; but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, and urease. Potassium gluconate is utilized as a sole carbon source; while D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-*β*-glucosamine, D-maltose, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid are not. Strain MMS22-M6-3-16 (=NIBRBAC000509453) was isolated from a soil sample at Gangneung, Gangwon-do, Republic of Korea.

Description of *Ammoniphilus resinae* CAU 1689

Cells are Gram-stain-variable, motile with flagella, and rod shaped. Colonies are cream colored, circular, smooth, entire margin, convex, and opaque when incubated for 7 days on GYE plates at 30°C. In the API 20NE system, positive for urease and esculin hydrolysis; but negative for nitrate reaction, indole production, glucose fermentation, arginine dihydrolase, gelatin hydrolysis, and *β*-galactosidase. D-Mannitol, potassium glutamate, and malic acid are utilized as sole carbon sources; while D-glucose, L-arabinose, D-mannose, *N*-acetyl-*β*-glucosamine, D-maltose, capric acid, adipic acid, trisodium citrate, and phenylacetic acid are not. Strain CAU 1689 (=NIBRBAC000509673) was isolated from a mud flat sample at Incheon, Republic of Korea.

Description of *Aneurinibacillus migulanus* Soil2

Cells are Gram-stain-positive, aerobic, motile with flagella, and rod shaped. Colonies are light yellow, circular, and flat when incubated for 4–5 days on R2A plates at 25°C. In the API 20NE system, positive for nitrate reduction; but negative for indole production, glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis, gelatin hydrolysis, and *β*-galactosidase. Potassium glutamate, malic acid, and phenylacetic acid are utilized as sole carbon sources; while D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-*β*-glucosamine, D-maltose, capric acid, adipic acid, trisodium citrate, and phenylacetic acid are not. Strain Soil2 (=NIBRBAC000509569) was isolated from a soil sample at Goyang, Gyeonggi-do, Republic of Korea.

Description of *Paenibacillus solani* CAU 1690

Cells are Gram-stain-positive, motile with flagella, and rod shaped. Colonies are cream colored, irregular, rough, undulate, margin, flat, and opaque when incubated for 3 days on TSA plates at 30°C. In the API 20NE system, positive for urease, esculin hydrolysis, and β-galactosidase; but negative for nitrate reaction, indole production, glucose fermentation, arginine dihydrolase, and gelatin hydrolysis. D-Glucose, D-mannose, D-mannitol, *N*-acetyl-β-glucosamine, D-maltose, and potassium glutamate are utilized as sole carbon sources; while L-arabinose, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid are not. Strain CAU 1690 (=NIBRBAC000509674) was isolated from a mud flat sample at Ansan, Gyeonggi-do, Republic of Korea.

Description of *Paenibacillus segetis* CAU 1698

Cells are Gram-stain-positive, non-flagellated, and rod shaped. Colonies are cream colored, circular, smooth, entire, margin, flat, and translucent when incubated for 3 days on ISP2 plates at 30°C. In the API 20NE system, positive for esculin hydrolysis and β-galactosidase; but negative for nitrate reaction, indole production, glucose fermentation, arginine dihydrolase, urease, and gelatin hydrolysis. L-Arabinose is utilized as a sole carbon source; while D-glucose, D-mannose, D-mannitol, *N*-acetyl-β-glucosamine, D-maltose, potassium glutamate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid are not. Strain CAU 1698 (=NIBRBAC000509681) was isolated from a mud flat sample at Ansan, Gyeonggi-do, Republic of Korea.

Description of *Paenibacillus naphthalenovorans* MMS22-AIC

Cells are aerobic, motile with flagella, and rod shaped. Colonies are white, irregular, pulvinate, and entire when incubated for 7 days on Actinomycete Isolation agar plates at 30°C. In the API 20NE system, positive for nitrate reaction, urease, esculin hydrolysis, and β-galactosidase; but negative for indole production, glucose fermentation, arginine dihydrolase, and gelatin hydrolysis. D-Glucose, D-mannose, D-mannitol, D-maltose, and malic acid are utilized as sole carbon sources; while L-arabinose, *N*-acetyl-β-glucosamine, potassium glutamate, capric acid, adipic acid, trisodium citrate, and phenylacetic acid are not. Strain MMS22-AIC (=NIBRBAC000509454) was isolated from a soil sample at Pohang, Gyeongsangbuk-do, Republic of Korea.

Description of *Paenibacillus paridis* LK11

Cells are Gram-stain-positive, aerobic, non-flagellated, and rod shaped. Colonies are white, circular, slightly convex, and glistening when incubated for 3 days on R2A plates at 25°C. In the API 20NE system, positive for esculin hydrolysis and β-galactosidase; but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, and gelatin hydrolysis. L-Arabinose, D-mannitol, and D-maltose are utilized as sole carbon sources; while D-glucose, D-mannose, *N*-acetyl-β-glucosamine, potassium glutamate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid are not. Strain LK11 (=NIBRBAC000509705) was isolated from a soil sample at Namyangju, Gyeonggi-do, Republic of Korea.

Description of *Lysinibacillus cavernae* CAU 1677

Cells are Gram-stain-positive, motile with flagella, and rod shaped. Colonies are cream colored, circular, smooth, entire margin, convex, and opaque when incubated for 3 days on MA plates at 30°C. In the API 20NE system, positive for esculin hydrolysis; but negative for nitrate reaction, indole production, glucose fermentation, arginine dihydrolase, urease, gelatin hydrolysis, and β-galactosidase. Malic acid is utilized as a sole carbon source; while D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-β-glucosamine, D-maltose, potassium glutamate, capric acid, adipic acid, trisodium citrate, and phenylacetic acid are not. Strain CAU 1677 (=NIBRBAC000509664) was isolated from a mud sample at Gijang-gun, Busan, Republic of Korea.

Description of *Lacticaseibacillus rhamnosus* H15

Cells are Gram-stain-positive, non-flagellated, and rod shaped. Colonies are yellowish or white colored, circular, convex, and glistening when incubated for 3 days on MRS agar plates at 30°C. In the API 20NE system, positive results for esculin hydrolysis and β-galactosidase; but negative for nitrate reaction, indole production, D-glucose fermentation, arginine dihydrolase, urease, and gelatin hydrolysis. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-β-glucosamine, D-maltose, potassium glutamate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid are not utilized as sole carbon sources. Strain H15 (=NIBRBAC000509646) was isolated from a breast milk sample at Ansan, Gyeonggi-do, Republic of Korea.

Description of *Pontibacter oryzae* MMS22-GI4

Cells are Gram-stain-negative, non-flagellated, and rod shaped. Colonies are circular, convex, entire, and red pink after incubation for 2 days on ISP2 at 30°C. In the API 20NE system, positive for esculin hydrolysis, gelatin hydrolysis and cytochrome oxidase; but negative for nitrate reduction, indole production, glucose acidification, arginine dihydrolase, urease, and β-galactosidase. *N*-Acetyl-D-glucosamine and D-maltose are utilized as sole carbon sources; while D-glucose, L-arabinose, D-mannose, D-mannitol, gluconate, capric acid, adipic acid, malic acid, citrate, and phenyl-acetate are not. Strain MMS22-GI4 (=NIBRBAC000509460) was isolated from a soil sample at Gangneung, Gangwon-do, Republic of Korea.

Description of *Marivirga tractuosa* HMG3261

Cells are Gram-stain-negative, non-flagellated, and rod shaped. Colonies are circular, convex, smooth, and orange after incubation for 3 days on MA at 25°C. In the API 20NE system, positive for esculin hydrolysis, gelatin hydrolysis, β-galactosidase, and cytochrome oxidase; but negative for nitrate reduction, indole production, glucose acidification, arginine dihydrolase, and urease. D-Maltose is utilized as a sole carbon source; while but D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, gluconate, capric acid, adipic acid, malic acid, citrate, and phenyl-acetate are not. Strain HMG3261 (=NIBRBAC000509548) was isolated from a seawater sample at Hwaseong, Gyeonggi-do, Republic of Korea.

Description of *Ekhidna lutea* HMG3441

Cells are Gram-stain-negative, non-flagellated, and rod shaped. Colonies are circular, convex, smooth, and yellow after incubation for 7 days on MA at 25°C. In the API 20NE system, positive for cytochrome oxidase; but negative for nitrate reduction, indole production, glucose acidification, arginine dihydrolase, urease, esculin hydrolysis, gelatin hydrolysis, and β-galactosidase. Adipic acid is utilized as a sole carbon source; while D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, gluconate, capric acid, malic acid, citrate, and phenyl-acetate are not. Strain HMG3441 (=NIBRBAC000509557) was isolated from a seawater sample at Gangneung, Gangwon-do, Republic of Korea.

Description of *Aquirufa beregesia* AS303

Cells are Gram-stain-negative, non-flagellated, and rod shaped. Colonies are round, entire, convex, and orange after incubation for 3 days on R2A at 28°C. In the API 20NE system, positive for β-galactosidase; but negative for nitrate reduction, indole production, glucose acidification, arginine dihydrolase, urease, esculin hydrolysis, gelatin hydrolysis, and cytochrome oxidase. D-Mannose, D-mannitol, D-maltose, and citrate are utilized as sole carbon sources; while D-glucose, L-arabinose, *N*-acetyl-D-glucosamine, gluconate, capric acid, adipic acid, malic acid, and phenyl-acetate are not. Strain AS303 (=NIBRBAC000509515) was isolated from wetland sample at Anseong, Gyeonggi-do, Republic of Korea.

Description of *Emticicia oligotrophica* DJS-1-10

Cells are Gram-stain-negative, non-flagellated, and rod shaped. Colonies are circular, raised, and white and red dot after incubation for 3 days on R2A at 28°C. In the API 20NE system, positive for glucose acidification, arginine dihydrolase, urease, gelatin hydrolysis, and β-galactosidase; but negative for nitrate reduction, indole production, esculin hydrolysis, and cytochrome oxidase. D-Mannitol and *N*-acetyl-D-glucosamine are utilized as sole carbon sources; while D-glucose, L-arabinose, D-mannose, D-maltose, gluconate, capric acid, adipic acid, malic acid, citrate, and phenyl-acetate are not. Strain DJS-1-10 (=NIBRBAC000509573) was isolated from a wetland sample at Goyang, Gyeonggi-do, Republic of Korea.

Description of *Aquimarina celericrescens* HMG3252

Cells are Gram-stain-negative, non-flagellated, and rod shaped. Colonies are circular, convex, smooth, and orange after incubation for 2 days on MA at 25°C. In the API 20NE system, positive for esculin hydrolysis, β-galactosidase, and cytochrome oxidase; but negative for nitrate reduction, indole production, glucose acidification, arginine dihydrolase, urease, and gelatin hydrolysis. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, gluconate, capric acid, adipic acid, malic acid, citrate, and phenyl-acetate are not utilized as sole carbon sources. Strain HMG3252 (=NIBRBAC000509540) was isolated from a seaweed sample at Hwaseong, Gyeonggi-do, Republic of Korea.

Description of *Aquimarina intermedia* HMG3258

Cells are Gram-stain-negative, non-flagellated, and rod shaped. Colonies are circular, convex, smooth, and orange after incubation for 2 days on MA at 25°C. In the API 20NE system, positive for esculin hydrolysis, gelatin hydrolysis, and cytochrome oxidase; but negative for nitrate reduction, indole production, glucose acidification, arginine dihydrolase, urease, and β-galactosidase. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, gluconate, capric acid, adipic acid, malic acid, citrate, and phenyl-acetate are not utilized as sole carbon sources. Strain HMG3258 (=NIBRBAC000509545) was isolated from a seawater sample at Hwaseong, Gyeonggi-do, Republic of Korea.

Description of *Epilithonimonas zeae* 19_S1_T7

Cells are Gram-stain-negative, non-flagellated, and rod shaped. Colonies are smooth, convex, and yellow after incubation for 2 days on R2A at 30°C. In the API 20NE system, positive for esculin hydrolysis and gelatin hydrolysis; but negative for nitrate reduction, indole production, glucose acidification, arginine dihydrolase, urease, β-galactosidase, and cytochrome oxidase. D-Glucose, L-arabinose, D-mannose, D-maltose, adipic acid, malic acid, and citrate are utilized as sole carbon sources; while D-mannitol, *N*-acetyl-D-glucosamine, gluconate, capric acid, and phenyl-acetate are not. Strain 19_S1_T7 (= NIBRBAC000509483) was isolated from a sediment soil sample at Jeongseon-gun, Gangwon-do, Republic of Korea.

Description of *Flavicella sediminum* HMG3255

Cells are Gram-stain-negative, flagellated, and rod shaped. Colonies are circular, convex, smooth, and light yellow after incubation for 2 days on MA at 25°C. In the API 20NE system, positive for esculin hydrolysis, β-galactosidase, and cytochrome oxidase; but negative for nitrate reduction, indole production, glucose acidification, arginine dihydrolase, urease, and gelatin hydrolysis. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, gluconate, capric acid, adipic acid, malic acid, citrate, and phenyl-acetate are not utilized as sole carbon sources. Strain HMG3255 (= NIBRBAC000509542) was isolated from a seawater sample at Hwaseong, Gyeonggi-do, Republic of Korea.

Description of *Flavobacterium maotaiense* AS316

Cells are Gram-stain-negative, non-flagellated, and rod shaped. Colonies are round, entire, raised, and yellow after incubation for 3 days on R2A at 28°C. In the API 20NE system, positive for cytochrome oxidase; but negative for nitrate reduction, indole production, glucose acidification, arginine dihydrolase, urease, esculin hydrolysis, gelatin hydrolysis, and β-galactosidase. D-Mannose and D-maltose are utilized as sole carbon sources; while D-glucose, L-arabinose, D-mannitol, *N*-acetyl-D-glucosamine, gluconate, capric acid, adipic acid, malic acid, citrate, and phenyl-acetate are not. Strain AS316 (= NIBRBAC000509508) was isolated from a wetland sample at Anseong, Gyeonggi-do, Republic of Korea.

Description of *Flavobacterium cupreum* LK23

Cells are Gram-stain-negative, non-flagellated, and rod shaped. Colonies are circular, flat, glistening, and yellow after incubation for 3 days on R2A at 25°C. In the API 20NE system, positive for β-galactosidase, and cytochrome oxidase; but negative for nitrate reduction, indole production, glucose acidification, arginine dihydrolase, urease, esculin hydrolysis, and gelatin hydrolysis. D-Glucose, L-arabinose, D-mannitol, and D-maltose are utilized as sole carbon sources; while D-mannose, *N*-acetyl-D-glucosamine, gluconate, capric acid, adipic acid, malic acid, citrate, and phenyl-acetate are not. Strain LK23 (= NIBRBAC000509704) was isolated from a soil sample at Hoengseong-gun, Gangwon-do, Republic of Korea.

Description of *Formosa haliotis* HMG3257

Cells are Gram-stain-negative, non-flagellated, and rod shaped. Colonies are circular, convex, smooth, and cream after incubation for 2 days on MA at 25°C. In the API 20NE system, positive for esculin hydrolysis, β-galactosidase, and cytochrome oxidase; but negative for nitrate reduction, indole production, glucose acidification, arginine dihydrolase, urease, and gelatin hydrolysis. L-Arabinose, D-mannose, and D-maltose are utilized as sole carbon sources; while D-glucose, D-mannitol, *N*-acetyl-D-glucosamine, gluconate, capric acid, adipic acid, malic acid, citrate, and phenyl-acetate are not. Strain HMG3257 (= NIBRBAC000509544) was isolated from a seawater sample at Hwaseong, Gyeonggi-do, Republic of Korea.

Description of *Maribacter ulvicola* DHSW-M12

Cells are Gram-stain-negative, non-flagellated, and rod shaped. Colonies are circular, convex, glistening, and vivid yellow after incubation for 3 days on MA at 25°C. In the API 20NE system, positive for esculin hydrolysis and β-galactosidase; but negative for nitrate reduction, indole production, glucose acidification, arginine dihydrolase, urease, gelatin hydrolysis, and cytochrome oxidase. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, gluconate, capric acid, adipic acid, malic acid, citrate, and phenyl-acetate are not utilized as sole carbon sources. Strain DHSW-M12 (= NIBRBAC000509643) was isolated from a seawater sample at Goseong-gun, Gangwon-do, Republic of Korea.

Description of *Zhouia amylolytica* CAU 1682

Cells are Gram-stain-negative, non-flagellated, and rod shaped. Colonies are circular, smooth, entire margin, convex, translucent, and yellow after incubation for 3 days on MA at 30°C. In the API 20NE system, positive for esculin hydrolysis and β-galactosidase; but negative for nitrate reduction, indole production, glucose acidification, arginine dihydrolase, urease, gelatin hydrolysis, and cytochrome oxidase. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, gluconate, capric acid, adipic acid, malic acid, citrate, and phenyl-acetate are not utilized as sole carbon sources. Strain CAU 1682 (= NIBRBAC000509669) was isolated from a mud sample at Incheon, Republic of Korea.

Description of *Algoriella xinjiangensis* HMG3059

Cells are Gram-stain-negative, non-flagellated, and rod shaped. Colonies are circular, convex, smooth, and yellow after incubation for 3 days on R2A at 25°C. In the API 20NE system, positive for esculin hydrolysis, gelatin hydrolysis, and cytochrome oxidase; but negative for nitrate reduction, indole production, glucose acidification, arginine dihydrolase, urease, and β-galactosidase. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, gluconate, capric acid, adipic acid, malic acid, citrate, and phenyl-acetate are not utilized as sole carbon sources. Strain HMG3059 (=NIBRBAC000509539) was isolated from a soil sample at Yongin, Gyeonggi-do, Republic of Korea.

Description of *Chryseobacterium candidae* CAU 1697

Cells are Gram-stain-negative, non-flagellated, and rod shaped. Colonies are circular, smooth, entire margin, convex, translucent, and orange after incubation for 3 days on GYE at 30°C. In the API 20NE system, positive for esculin hydrolysis, gelatin hydrolysis, and cytochrome oxidase; but negative for nitrate reduction, indole production, glucose acidification, arginine dihydrolase, urease, and β-galactosidase. D-Glucose, D-mannose, D-maltose, gluconate, citrate, and phenyl-acetate are utilized as sole carbon sources; while L-arabinose, D-mannitol, *N*-acetyl-D-glucosamine, capric acid, adipic acid, and malic acid are not. Strain CAU 1697 (=NIBRBAC000509680) was isolated from a mud sample at Incheon, Republic of Korea.

Description of *Chryseobacterium balustinum* 16N2F1

Cells are Gram-stain-negative, non-flagellated, and rod shaped. Colonies are smooth, convex, and yellow after incubation for 2 days on R2A at 30°C. In the API 20NE system, positive for nitrate reduction, esculin hydrolysis and gelatin hydrolysis; but negative for indole production, glucose acidification, arginine dihydrolase, urease, β-galactosidase, and cytochrome oxidase. D-Mannose, gluconate, capric acid, adipic acid, malic acid, citrate, and phenyl-acetate are utilized as sole carbon sources; while D-glucose, L-arabinose, D-mannitol, *N*-acetyl-D-glucosamine, and D-maltose are not. Strain 16N2F1 (=NIBRBAC000509484) was isolated from a sediment soil sample at Chuncheon, Gangwon-do, Republic of Korea.

Description of *Chryseobacterium endophyticum* 18S2S17

Cells are Gram-stain-negative, non-flagellated, and rod shaped. Colonies are smooth, convex, and yellow after incubation for 2 days on R2A at 30°C. In the API 20NE system, positive for esculin hydrolysis and gelatin hydrolysis; but negative for nitrate reduction, indole production, glucose acidification, arginine dihydrolase, urease, β-galactosidase, and cytochrome oxidase. D-Glucose, L-arabinose, D-mannose, D-maltose, adipic acid, malic acid, and citrate are utilized as sole carbon sources; while D-mannitol, *N*-acetyl-D-glucosamine, gluconate, capric acid, and phenyl-acetate are not. Strain 18S2S17 (=NIBRBAC000509485) was isolated from a sediment soil sample at Chungju, Chungcheongbuk-do, Republic of Korea.

Description of *Pedobacter quisquiliarum* GF95

Cells are Gram-stain-negative, non-flagellated, and rod shaped. Colonies are circular and yellow after incubation for 2 days on R2A at 30°C. In the API 20NE system, positive for esculin hydrolysis, gelatin hydrolysis, β-galactosidase, and cytochrome oxidase; but negative for nitrate reduction, indole production, glucose acidification, arginine dihydrolase, and urease. D-Glucose, D-mannose, *N*-acetyl-D-glucosamine, D-maltose, malic acid, and citrate are utilized as sole carbon sources; while L-arabinose, D-mannitol, gluconate, capric acid, adipic acid, and phenyl-acetate are not. Strain GF95 (=NIBRBAC000509603) was isolated from a mud sample at Wando-gun, Jeollanam-do, Republic of Korea.

Description of *Brevundimonas abyssalis* HMG3453

Cells are Gram-stain-negative, non-flagellated, and rod shaped. Colonies are circular, convex, smooth, and light yellow after incubation for 5 days on MA at 25°C. In the API 20NE system, positive for cytochrome oxidase, esculin hydrolysis and β-galactosidase; but negative for urease, arginine dihydrolase, nitrate reduction, glucose fermentation, gelatin hydrolysis, and indole production. Malic acid is utilized as a sole carbon source; while arabinose, glucose, mannose, mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, adipic acid, capric acid, trisodium citrate, and phenylacetic acid are not. Strain HMG3453 (=NIBRBAC000509559) was isolated from a seawater sample at Pohang, Gyeongsangbuk-do, Republic of Korea.

Description of *Brevundimonas diminuta* 16H4P11

Cells are Gram-stain-negative, non-flagellated, and rod shaped. Colonies are round, smooth, convex, and cream after incubation for 2 days on R2A at 30°C. In the API 20NE system, positive for esculin hydrolysis; but negative for cytochrome oxidase, indole production, β-galactosidase, gelatin hydrolysis, glucose fermentation, nitrate reduction, arginine dihydrolase, and urease. Capric acid, trisodium citrate, and phenylacetic acid are utilized as sole carbon sources; while glucose, mannitol, adipic acid, acid malic acid, D-maltose, mannose, arabinose, *N*-acetyl-glucosamine, and potassium gluconate are not. Strain 16H4P11 (=NIBRBAC000509475) was isolated from a sediment soil sample at Goyang, Gyeonggi-do, Republic of Korea.

Description of *Brevundimonas denitrificans* AS300

Cells are Gram-stain-negative, non-flagellated, and rod shaped. Colonies are round, entire, raised, and white after incubation for 3 days on R2A at 28°C. In the API 20NE system, positive for arginine dihydrolase and urease; but negative for cytochrome oxidase, esculin hydrolysis, indole production, gelatin hydrolysis, glucose fermentation, nitrate reduction, and β-galactosidase. Mannitol, mannose, arabinose, and *N*-acetyl-glucosamine are utilized as sole carbon sources; while glucose, D-maltose, capric acid, malic acid, adipic acid, trisodium citrate, phenylacetic acid, and potassium gluconate are not. Strain AS300 (=NIBRBAC000509507) was isolated from a wetland sample at Anseong, Gyeonggi-do, Republic of Korea.

Description of *Hyphomonas oceanitis* HMG3436

Cells are Gram-stain-negative, non-flagellated, and round to oval shaped. Colonies are circular, convex, smooth, and cream after incubation for 5 days on MA at 25°C. In the API 20NE system, positive for cytochrome oxidase, esculin hydrolysis, and β-galactosidase; but negative for nitrate reduction, urease, glucose fermentation, gelatin hydrolysis, indole production, and arginine dihydrolase. Glucose and adipic acid are utilized as sole carbon sources; while arabinose, mannose, mannitol, *N*-acetyl-glucosamine, D-maltose, malic acid, potassium gluconate, capric acid, trisodium citrate, and phenylacetic acid are not. Strain HMG3436 (=NIBRBAC000509556) was isolated from a seawater sample at Gangneung, Gangwon-do, Republic of Korea.

Description of *Kordiimonas lacus* CAU 1680

Cells are Gram-stain-negative, non-flagellated, and rod shaped. Colonies are circular, convex, smooth, entire margin, translucent, and cream after incubation for 3 days on MA at 30°C. In the API 20NE system, positive for cytochrome oxidase and esculin hydrolysis; but negative for indole production, gelatin hydrolysis, urease, β-galactosidase, nitrate reduction, arginine dihydrolase, and glucose fermentation. Mannose, glucose, *N*-acetyl-glucosamine, arabinose, adipic acid, malic acid, capric acid, D-maltose, potassium gluconate, mannitol, trisodium citrate, and phenylacetic acid are not utilized as sole carbon sources. Strain CAU 1680 (=NIBRBAC000509667) was isolated from a seawater sample at Goseong-gun, Gangwon-do, Republic of Korea.

Description of *Algimonas porphyrae* HMG3263

Cells are Gram-stain-negative, non-flagellated, and rod shaped. Colonies are circular, convex, smooth, and orange red after incubation for 5 days on MA at 25°C. In the API 20NE system, positive for cytochrome oxidase, gelatin hydrolysis, esculin hydrolysis, and β-galactosidase; but negative for nitrate reduction, glucose fermentation, indole production, urease, and arginine dihydrolase. Glucose, arabinose, mannose, mannitol, D-maltose, potassium gluconate, *N*-acetyl-glucosamine, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid are not utilized as sole carbon sources. Strain HMG3263 (=NIBRBAC000509550) was isolated from a seawater sample at Hwaseong, Gyeonggi-do, Republic of Korea.

Description of *Maeinicaulis aureus* D3-15

Cells are Gram-stain-negative, non-flagellated, and rod shaped. Colonies are circular and yellow after incubation for 4 days on MA at 20–30°C. In the API 20NE system, positive for cytochrome oxidase, esculin hydrolysis, urease, and arginine dihydrolase; but negative for nitrate reduction, glucose fermentation, gelatin hydrolysis, β-galactosidase, and indole production. Mannose, glucose, *N*-acetyl-glucosamine, D-maltose, malic acid, trisodium citrate, and phenylacetic acid are utilized as sole carbon sources; while arabinose, potassium gluconate, adipic acid, mannitol, and capric acid are not. Strain D3-15 (=NIBRBAC000509598) was isolated from a marine algae sample at Daejin-ri, Gangwon-do, Republic of Korea.

Description of *Ahrensia marina* HMG3260

Cells are Gram-stain-negative, non-flagellated, and rod shaped. Colonies are circular, convex, smooth, and light pink after incubation for 7 days on MA at 25°C. In the API 20NE system, positive for cytochrome oxidase, esculin hydrolysis, and β-galactosidase; but negative for nitrate reduction, glucose fermentation, indole production, urease, arginine dihydrolase, and gelatin hydrolysis. Glucose, arabinose, mannose, mannitol, D-maltose, potassium gluconate, *N*-acetyl-glucosamine, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid are not utilized as sole carbon sources. Strain HMG3260 (=NIBRBAC000509547) was isolated from a seaweed sample at Hwaseong, Gyeonggi-do, Republic of Korea.

Description of *Bradyrhizobium guangxiense* ST10-3

Cells are Gram-stain-positive, non-flagellated, and short rod shaped. Colonies are circular, slightly, convex, glistening, and cream after incubation for 3 days on R2A at 25°C. In the API 20NE system, positive for nitrate reduction and indole production; but negative for cytochrome oxidase, arginine dihydrolase, β-galactosidase, urease, gelatin hydrolysis esculin hydrolysis, and glucose fermentation. Mannitol, glucose, capric acid, mannose, arabinose, D-maltose, adipic acid, trisodium citrate, potassium gluconate, malic acid, *N*-acetyl-glucosamine, and phenylacetic acid are not utilized as sole carbon sources. Strain ST10-3 (=NIBRBAC000509712) was isolated from a soil sample at Nanyangju, Gyeonggi-do, Republic of Korea.

Description of *Mesorhizobium erdmanii* BT829

Cells are Gram-stain-negative, non-flagellated, and rod shaped. Colonies are circular, slightly, convex, glistening, and white after incubation for 3 days on R2A at 25°C. In the API 20NE system, negative for cytochrome oxidase, esculin hydrolysis, indole production, glucose fermentation, nitrate reduction, arginine dihydrolase, urease, gelatin hydrolysis, and β-galactosidase. Glucose, mannitol, mannose, arabinose, *N*-acetyl-glucosamine, D-maltose, capric acid, malic acid, adipic acid, trisodium citrate, phenylacetic acid, and potassium gluconate are not utilized as sole carbon sources. Strain BT829 (=NIBRBAC000509698) was isolated from a soil sample at Hoengseong-gun, Gangwon-do, Republic of Korea.

Description of *Mesorhizobium carmichaelinearum* ST14-1

Cells are Gram-stain-negative, non-flagellated, and rod shaped. Colonies are circular, slightly, convex, glistening, and cream after incubation for 3 days on R2A at 25°C. In the API 20NE system, positive for nitrate reduction; but negative for cytochrome oxidase, arginine dihydrolase, β-galactosidase, urease, gelatin hydrolysis esculin hydrolysis, indole production, and glucose fermentation. Mannitol, glucose, capric acid, mannose, arabinose, D-maltose, adipic acid, trisodium citrate, potassium gluconate, malic acid, *N*-acetyl-glucosamine, and phenylacetic acid are not utilized as sole carbon sources. Strain ST14-1 (=NIBRBAC000509710) was isolated from a soil sample at Hoengseong-gun, Gangwon-do, Republic of Korea.

Description of *Phyllobacterium loti* BT831

Cells are Gram-stain-negative, non-flagellated, and rod shaped. Colonies are circular, slightly, convex, glistening, and white after incubation for 3 days on R2A at 25°C. In the API 20NE system, positive for cytochrome oxidase, urease, gelatin hydrolysis, glucose fermentation; but negative for β-galactosidase, arginine dihydrolase, esculin hydrolysis, indole production, and nitrate reduction. Potassium gluconate, malic acid, and *N*-acetyl-glucosamine are utilized as sole carbon sources; while mannitol, capric acid, glucose, mannose, arabinose, D-maltose, adipic acid, trisodium citrate, and phenylacetic acid are not. Strain BT831 (=NIBRBAC000509700) was isolated from a soil sample at Hoengseong-gun, Gangwon-do, Republic of Korea.

Description of *Neorhizobium huautlense* MMS22-HSS5

Cells are Gram-stain-negative, non-flagellated, and rod shaped. Colonies are circular, convex, entire, and white after incubation for 2 days on SCA at 30°C. In the API 20NE system, positive for cytochrome oxidase, esculin hydrolysis, nitrate reduction, arginine dihydrolase, urease, and β-galactosidase; but negative for indole production, gelatin hydrolysis, and glucose fermentation. Mannose, arabinose, *N*-acetyl-glucosamine, glucose, mannitol, D-maltose, and malic acid are utilized as sole carbon sources; while capric acid, adipic acid, potassium gluconate, trisodium citrate, and phenylacetic acid. Are not Strain MMS22-HSS5 (=NIBRBAC000509468) was isolated from a soil sample at Sejong, Republic of Korea.

Description of *Rhizobium endophyticum* TS35

Cells are Gram-stain-negative, non-flagellated, and rod shaped. Colonies are round, entire, convex, and cream after incubation for 3 days on R2A at 28°C. In the API 20NE system, positive for cytochrome oxidase, glucose fermentation, esculin hydrolysis, urease, and β-galactosidase; but negative for indole production, gelatin hydrolysis, nitrate reduction, and arginine dihydrolase. Glucose, mannitol, mannose, arabinose, *N*-acetyl-glucosamine, D-maltose, capric acid, and malic acid are utilized as sole carbon sources; while adipic acid, trisodium citrate, phenylacetic acid, and potassium gluconate are not. Strain TS35 (=NIBRBAC000509497) was isolated from a wetland sample at Seoul, Republic of Korea.

Description of *Albibacillus kandeliae* CAU 1678

Cells are Gram-stain-negative, non-flagellated, and rod shaped. Colonies are circular, convex, smooth, entire margin, translucent, and cream after incubation for 3 days on MA at 30°C. In the API 20NE system, positive for cytochrome oxidase, gelatin hydrolysis, urease, and esculin hydrolysis; but negative for indole production, β-galactosidase, nitrate reduction, arginine dihydrolase, and glucose fermentation. Mannitol, malic acid, and phenylacetic acid are utilized as sole carbon sources; while mannose, arabinose, glucose, capric acid, adipic acid, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, and trisodium citrate are not. Strain CAU 1678 (=NIBRBAC000509665) was isolated from a sea sand sample at Geoje, Gyeongsangnam-do, Republic of Korea.

Description of *Cypionkella collinsensis* AS330

Cells are Gram-stain-negative, non-flagellated, and rod shaped. Colonies are round, entire, raised, and white after incubation for 3 days on R2A at 28°C. In the API 20NE system, positive for cytochrome oxidase and β-galactosidase; but negative for arginine dihydrolase, esculin hydrolysis, urease, indole production, gelatin hydrolysis, glucose fermentation, and nitrate reduction. Glucose, mannose, arabinose, D-maltose, adipic acid, and *N*-acetyl-glucosamine are utilized as sole carbon sources; while mannitol, capric acid, malic acid, trisodium citrate, phenylacetic acid, and potassium gluconate are not. Strain AS330 (=NIBRBAC000509509) was isolated from a wetland sample at Anseong, Gyeonggi-do, Republic of Korea.

Description of *Defluviimonas denitrificans* CAU 1704

Cells are Gram-stain-negative, non-flagellated, and rod shaped. Colonies are circular, convex, smooth, entire margin, opaque, and cream after incubation for 3 days on MA at 30°C. In the API 20NE system, positive for cytochrome oxidase and esculin hydrolysis; but negative for indole production, nitrate reduction, β-galactosidase, gelatin hydrolysis, urease, arginine dihydrolase, and glucose fermentation. Mannose, *N*-acetyl-glucosamine, arabinose, malic acid, capric acid, glucose, D-maltose, adipic acid, potassium gluconate, mannitol, trisodium citrate, and phenylacetic acid are not utilized as sole carbon sources. Strain CAU 1704 (=NIBRBAC000509683) was isolated from seawater at Busan, Republic of Korea.

Description of *Luteovulum johrii* YMSW-R8

Cells are Gram-stain-negative, non-flagellated, and rod shaped. Colonies are circular, convex, glistening, and grayish yellowish pink after incubation for 5 days on R2A at 25°C. In the API 20NE system, positive for nitrate reduction, urease, and esculin hydrolysis; but negative for cytochrome oxidase, arginine dihydrolase, gelatin hydrolysis, β-galactosidase, indole production, and glucose fermentation. Arabinose, potassium gluconate, adipic acid, trisodium citrate, glucose, mannose, mannitol, *N*-acetyl-glucosamine, D-maltose, capric acid, malic acid, and phenylacetic acid are not utilized as sole carbon sources. Strain YMSW-R8 (=NIBRBAC000509642) was isolated from aseawater sample at Gunsan, Jeollabuk-do, Republic of Korea.

Description of *Pararhodobacter zhoushanensis* KJ81-7

Cells are Gram-stain-negative, non-flagellated, and rod shaped. Colonies are circular and light yellow after incubation for 2 days on MA at 20–35°C. In the API 20NE system, positive for cytochrome oxidase, nitrate reduction, esculin hydrolysis, urease, and arginine dihydrolase; but negative for glucose fermentation, gelatin hydrolysis, β-galactosidase, and indole production. Arabinose, glucose, mannitol, malic acid, adipic acid, trisodium citrate, and phenylacetic acid are utilized as sole carbon sources; while mannose, D-maltose, potassium gluconate, *N*-acetyl-glucosamine, and capric acid are not. Strain KJ81-7 (=NIBRBAC000509605) was isolated from a marine algae sample at Gwangjin-ri, Gangwon-do, Republic of Korea.

Description of *Roseovarius nitratireducens* HMG3309

Cells are Gram-stain-negative, non-flagellated, and ovoid to rod shaped. Colonies are circular, convex, smooth, and cream after incubation for 5 days on MA at 25°C. In the API 20NE system, positive for cytochrome oxidase and nitrate reduction; but negative for glucose fermentation, gelatin hydrolysis, esculin hydrolysis, β-galactosidase, indole production, urease, and arginine dihydrolase. Malic acid is utilized as a sole carbon source; while glucose, arabinose, mannose, mannitol, D-maltose, potassium gluconate, *N*-acetyl-glucosamine, capric acid, adipic acid, trisodium citrate, and phenylacetic acid are not. Strain HMG3309 (=NIBRBAC000509552) was isolated from a solar saltern sample at Sinan-gun, Jeollanam-do, Republic of Korea.

Description of *Ruegeria mediterranea* CAU 1702

Cells are Gram-stain-negative, non-flagellated, and rod shaped. Colonies are circular, convex, smooth, entire margin, opaque, and cream after incubation for 3 days on MA at 30°C. In the API 20NE system, positive for cytochrome oxidase, nitrate reduction, esculin hydrolysis, β-galactosidase, and gelatin hydrolysis; but negative for indole production, urease, arginine dihydrolase, and glucose fermentation. Mannose, *N*-acetyl-glucosamine, arabinose, malic acid, capric acid, glucose, D-maltose, adipic acid, potassium gluconate, mannitol, trisodium citrate, and phenylacetic acid are not utilized as sole carbon sources. Strain CAU 1702 (=NIBRBAC000509682) was isolated from a seawater sample at Busan, Republic of Korea.

Description of *Seohaeicola zhoushanensis* CAU 1679

Cells are Gram-stain-negative, non-flagellated, and rod shaped. Colonies are circular, convex, smooth, entire margin, opaque, and cream after incubation for 3 days on MA at 30°C. In the API 20NE system, positive for cytochrome oxidase; but negative for indole production, gelatin hydrolysis, urease, esculin hydrolysis, β-galactosidase, nitrate reduction, arginine dihydrolase, and glucose fermentation. Glucose, *N*-acetyl-glucosamine, arabinose, adipic acid, malic acid, and phenylacetic acid are utilized as sole carbon sources; while mannose, capric acid, D-maltose, potassium gluconate, mannitol, and trisodium citrate are not. Strain CAU 1679 (=NIBRBAC000509666) was isolated from a mud flat sample at Ganghwa-gun, Incheon, Republic of Korea.

Description of *Sulfitobacter guttiformis* YMSW-M15

Cells are Gram-stain-negative, non-flagellated, and rod shaped. Colonies are circular, convex, glistening, and grayish yellow after incubation for 3 days on MA at 25°C. In the API 20NE system, positive for esculin hydrolysis; but negative for cytochrome oxidase, nitrate reduction, urease, arginine dihydrolase, gelatin hydrolysis, β-galactosidase, indole production, and glucose fermentation. Arabinose, potassium gluconate, adipic acid, trisodium citrate, glucose, mannose, mannitol, *N*-acetyl-glucosamine, D-maltose, capric acid, malic acid, and phenylacetic acid are not utilized as sole carbon sources. Strain YMSW-M15 (=NIBRBAC000509645) was isolated from a seawater sample at Gunsan, Jeollabuk-do, Republic of Korea.

Description of *Tateyamaria pelophila* HMG3499

Cells are Gram-stain-negative, non-flagellated, and rod shaped. Colonies are circular, convex, smooth, and cream after incubation for 7 days on MA at 25°C. In the API 20NE system, positive for cytochrome oxidase, esculin hydrolysis, β-galactosidase, and nitrate reduction; but negative for indole production, urease, arginine dihydrolase, glucose fermentation, and gelatin hydrolysis. Mannose, mannitol, malic acid, arabinose, glucose, capric acid, adipic acid, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, trisodium citrate, and phenylacetic acid are not utilized as sole carbon sources. Strain HMG3499 (=NIBRBAC000509565) was isolated from a seawater sample at Gangneung, Gangwon-do, Republic of Korea.

Description of *Acetobacter indonesiensis* HMG3057

Cells are Gram-stain-negative, non-flagellated, and rod shaped. Colonies are circular, convex, smooth, and cream after incubation for 5 days on R2A at 25°C. In the API 20NE system, positive for nitrate reduction, glucose fermentation, esculin hydrolysis, indole production, urease, arginine dihydrolase, and gelatin hydrolysis; but negative for cytochrome oxidase, and β-galactosidase. Glucose, arabinose, mannose, mannitol, D-maltose, potassium gluconate, *N*-acetyl-glucosamine, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid are not utilized as sole carbon sources. Strain HMG3057 (=NIBRBAC000509537) was isolated from soil at Yongin, Gyeonggi-do, Republic of Korea.

Description of *Novispirillum itersonii* subsp. *nipponicum* MMS22-HSWR3

Cells are Gram-stain-negative, non-flagellated, and rod shaped. Colonies are circular, convex, entire, and white after incubation for 2 days on R2A at 30°C. In the API 20NE system, positive for cytochrome oxidase, esculin hydrolysis, nitrate reduction, arginine dihydrolase, and urease; but negative for indole production, gelatin hydrolysis, β-galactosidase, and glucose fermentation. Glucose, capric acid, mannitol (weak), malic acid, trisodium citrate, and phenylacetic acid are utilized as sole carbon sources; while adipic acid, mannose, arabinose, *N*-acetyl-glucosamine, D-maltose, and potassium gluconate are not. Strain MMS22-HSWR3 (=NIBRBAC000509467) was isolated from a soil sample at Sejong, Republic of Korea.

Description of *Tistrella bauzanenesis* HMG3457

Cells are Gram-stain-negative, non-flagellated, and rod shaped. Colonies are circular, convex, smooth, and cream after incubation for 5 days on MA at 25°C. In the API 20NE system, positive for cytochrome oxidase, indole production, and nitrate reduction; but negative for urease, esculin hydrolysis, β-galactosidase, arginine dihydrolase, glucose fermentation, and gelatin hydrolysis. Malic acid, arabinose, glucose, capric acid, and adipic acid are utilized as sole carbon sources; while mannose, mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, trisodium citrate, and phenylacetic acid are not. Strain HMG3457 (=NIBRBAC000509561) was isolated from a seawater sample at Pohang, Gyeongsangbuk-do, Republic of Korea.

Description of *Tistlia consotensis* HMG3317

Cells are Gram-stain-negative, non-flagellated, and rod shaped. Colonies are circular, convex, smooth, and cream after incubation for 7 days on MA at 25°C. In the API 20NE system, positive for cytochrome oxidase, nitrate reduction, and urease; but negative for glucose fermentation, gelatin hydrolysis, esculin hydrolysis, β-galactosidase, indole production, and arginine dihydrolase. Arabinose, mannose, mannitol, *N*-acetyl-glucosamine, D-maltose, adipic acid, malic acid, glucose, and potassium gluconate are utilized as sole carbon sources; while capric acid, trisodium citrate, and phenylacetic acid are not. Strain HMG3317 (=NIBRBAC000509553) was isolated from a solar saltern sample at Sinan-gun, Jeollanam-do, Republic of Korea.

Description of *Oceanibacterium hippocampi* HMG3443

Cells are Gram-stain-negative, non-flagellated, and rod shaped. Colonies are circular, convex, smooth, and cream after incubation for 7 days on MA at 25°C. In the API 20NE system, positive for cytochrome oxidase, arginine dihydrolase, and nitrate reduction; but negative for esculin hydrolysis, β-galactosidase, urease, glucose fermentation, gelatin hydrolysis, and indole production. Adipic acid is utilized as a sole carbon source; while arabinose, glucose, mannose, mannitol, *N*-acetyl-glucosamine, D-maltose, malic acid, potassium gluconate, capric acid, trisodium citrate, and phenylacetic acid are not. Strain HMG3443 (=NIBRBAC000509558) was isolated from a seawater sample at Gangneung, Gangwon-do, Republic of Korea.

Description of *Erythrobacter mangrovi* CAU 1691

Cells are Gram-stain-negative, non-flagellated, and rod shaped. Colonies are circular, convex, smooth, entire margin, translucent, and yellow after incubation for 3 days on MA at 30°C. In the API 20NE system, positive for cytochrome oxidase, nitrate reduction, and esculin hydrolysis; but negative for indole production, gelatin hydrolysis, urease, β-galactosidase, arginine dihydrolase, and glucose fermentation. Glucose, D-maltose, and adipic acid are utilized as sole carbon sources; while *N*-acetyl-glucosamine, arabinose, malic acid, capric acid, potassium gluconate, mannitol, trisodium citrate, and phenylacetic acid are not. Strain CAU 1691 (=NIBRBAC000509675) was isolated from a mud flat sample at Ansan, Gyeonggi-do, Republic of Korea.

Description of *Parasphingopyxis lamellibrachiae* HMG3435

Cells are Gram-stain-negative, non-flagellated, and rod shaped. Colonies are circular, convex, smooth, and yellow after incubation for 3 days on MA at 25°C. In the API 20NE system, positive for cytochrome oxidase; but negative for nitrate reduction, urease, glucose fermentation, gelatin hydrolysis, esculin hydrolysis, β-galactosidase, indole production, and arginine dihydrolase. Adipic acid is utilized as a sole carbon source; while arabinose, mannose, mannitol, *N*-acetyl-glucosamine, D-maltose, malic acid, glucose, potassium gluconate, capric acid, trisodium citrate, and phenylacetic acid are not. Strain HMG3435 (=NIBRBAC000509555) was isolated from a seawater sample at Gangneung, Gangwon-do, Republic of Korea.

Description of *Sphingobium xenophagum* MMS22-PI21

Cells are Gram-stain-negative, non-flagellated, and rod shaped. Colonies are punctiform, convex, entire, and yellow after incubation for 7 days on ISP7 at 30°C. In the API 20NE system, positive for cytochrome oxidase, β-galactosidase, and esculin hydrolysis; but negative for indole production, gelatin hydrolysis, glucose fermentation, nitrate reduction, arginine dihydrolase, and urease. Malic acid (weak) and D-maltose are utilized as sole carbon sources; while glucose, capric acid, mannitol, adipic acid, mannose, arabinose, *N*-acetyl-glucosamine, trisodium citrate, phenylacetic acid, and potassium gluconate are not. Strain MMS22-PI21 (=NIBRBAC000509469) was isolated from a soil sample at Pohang, Gyeongsangbuk-do, Republic of Korea.

Description of *Sphingobium fuliginis* AS227

Cells are Gram-stain-negative, non-flagellated, and oval shaped. Colonies are round, entire, raised, and yellow after incubation for 3 days on R2A at 28°C. In the API 20NE system, positive for cytochrome oxidase, gelatin hydrolysis, urease, and β-galactosidase; but negative for esculin hydrolysis, indole production, glucose fermentation, nitrate reduction, and arginine dihydrolase. Glucose, mannitol, mannose, arabinose, *N*-acetyl-glucosamine, D-maltose, capric acid, malic acid, adipic acid, trisodium citrate, phenylacetic acid, and potassium gluconate are not utilized as sole carbon sources. Strain AS227 (=NIBRBAC000509504) was isolated from a wetland sample at Anseong, Gyeonggi-do, Republic of Korea.

Description of *Sphingomonas molluscorum* BT835

Cells are Gram-stain-negative, non-flagellated, and rod shaped. Colonies are circular, slightly, convex, glistening, and yellow after incubation for 3 days on R2A at 25°C. In the API 20NE system, positive for β-galactosidase, urease, and gelatin hydrolysis; but negative for cytochrome oxidase, arginine dihydrolase, esculin hydrolysis, indole production, nitrate reduction, and glucose fermentation. Glucose is utilized as a sole carbon source; while mannitol, capric acid, mannose, arabinose, D-maltose, adipic acid, trisodium citrate, potassium gluconate, malic acid, *N*-acetyl-glucosamine, and phenylacetic acid are not. Strain BT835 (=NIBRBAC000509703) was isolated from a soil sample at Hoengseong-gun, Gangwon-do, Republic of Korea.

Description of *Achromobacter aegrifaciens* 18S3T11

Cells are Gram-stain-negative, flagellated, and rod shaped. Colonies are circular, convex, opaque, and cream-colored after incubation for 2 days on R2A at 30°C. In API 20NE system, positive for nitrate reduction and esculin hydrolysis; but negative for indole production, glucose fermentation, arginine dihydrolase, urease, gelatinase, and β-galactosidase. L-Arabinose, D-mannose, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid are utilized as sole carbon sources; while D-glucose and D-mannitol are not. Strain 18S3T11 (=NIBRBAC000509486) was isolated from a sediment soil sample at Yeoju, Gyeonggi-do, Republic of Korea.

Description of *Alcaligenes aquatilis* 17H7M7

Cells are Gram-stain-negative, flagellated, and coccobacilli shaped. Colonies are circular, convex, smooth, and cream colored after incubation for 2 days on R2A at 30°C. In API 20NE system, positive reactions are obtained for esculin hydrolysis; but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, gelatinase, and β-galactosidase. Capric acid, malic acid, trisodium citrate, and phenylacetic acid are utilized as sole carbon sources; while D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, and adipic acid are not. Strain 17H7M7 (=NIBRBAC000509479) was isolated from a sediment soil sample at Goyang, Gyeonggi-do, Republic of Korea.

Description of *Alcaligenes faecalis* subsp. *phenolicus* 16H6L6

Cells are Gram-stain-negative, flagellated, and coccobacilli shaped. Colonies are circular, convex, smooth, and cream colored after incubation for 2 days on R2A at 30°C. In API 20NE system, positive reactions are obtained for esculin hydrolysis; but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, gelatinase, and β-galactosidase. Capric acid, malic acid, trisodium citrate, and phenylacetic acid are utilized as sole carbon sources; while D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, and adipic acid are not. Strain 16H6L6 (=NIBRBAC000509474) was isolated from a sediment soil sample at Goyang, Gyeonggi-do, Republic of Korea.

Description of *Aquincola tertiaricarbonis* MMS22-GI39

Cells are Gram-stain-negative, flagellated, and rod shaped. Colonies are with entire margin, punctiform, convex, and white colored after incubation for 7 days on ISP7 at 30°C. In API 20NE system, positive reactions are obtained for arginine dihydrolase, urease, gelatinase, and cytochrome oxidase; but negative for nitrate reduction, indole production, glucose fermentation, esculin hydrolysis, and β-galactosidase. D-Glucose, D-mannitol, and potassium gluconate are utilized as sole carbon sources; while L-arabinose, D-mannose, *N*-acetyl-glucosamine, capric acid, adipic acid, trisodium citrate, and phenylacetic acid are not. D-maltose and malic acid are weakly utilized. Strain MMS22-GI39 (=NIBRBAC000509471) was isolated from a soil sample at Gapyeong, Gyeonggi-do, Republic of Korea.

Description of *Bordetella tumulicola* 18N1V4

Cells are Gram-stain-negative, non-flagellated, and coccobacilli shaped. Colonies are convex, smooth, opaque, and pale yellow colored after incubation for 2 days on R2A at 30°C. In API 20NE system, positive reactions are obtained for nitrate reduction and esculin hydrolysis; but negative for indole production, glucose fermentation, arginine dihydrolase, urease, gelatinase, and β-galactosidase. L-Arabinose, adipic acid, trisodium citrate, and phenylacetic acid are utilized as sole carbon sources; while D-glucose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, and malic acid are not. Strain 18N1V4 (=NIBRBAC000509480) was isolated from a sediment soil sample at Hwacheon, Gangwon-do, Republic of Korea.

Description of *Chitinibacter fontanus* UHG6

Cells are Gram-stain-negative, flagellated, and rod shaped. Colonies are circular, convex, transparent, and milky white colored after incubation for 5 days on R2A at 28°C. In API 20NE system, positive reactions are obtained for nitrate reduction and cytochrome oxidase; but negative for indole production, glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis, gelatinase, and β-galactosidase. D-Glucose, D-mannose, *N*-acetyl-glucosamine, and potassium gluconate are utilized as sole carbon sources; while L-arabinose, D-mannitol, D-maltose, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid are not. Strain UHG6 (=NIBRBAC000509594) was isolated from a lake water sample at Paju, Gyeonggi-do, Republic of Korea.

Description of *Chromobacterium piscinae* MMS22-SS45

Cells are Gram-stain-negative, flagellated, and rod shaped. Colonies are punctiform, convex, entire, and pale yellow colored after incubation for 7 days on SCA at 30°C. In API 20NE system, positive reactions are obtained for nitrate reduction, glucose fermentation, arginine dihydrolase, gelatinase, and cytochrome oxidase; but negative for indole production, urease, and β-galactosidase. Weakly positive reaction is obtained for esculin hydrolysis. D-Glucose, *N*-acetyl-glucosamine, potassium gluconate, capric acid, and malic acid are utilized as sole carbon sources; while L-arabinose, D-mannose, D-mannitol, D-maltose, adipic acid, trisodium citrate, and phenylacetic acid are not. Strain MMS22-SS45 (=NIBRBAC000509458) was isolated from a soil sample at Gapyeong, Gyeonggi-do, Republic of Korea.

Description of *Collimonas silvisoli* BT826

Cells are Gram-stain-negative, flagellated, and rod shaped. Colonies are circular, slightly convex, glistening, and white colored after incubation for 3 days on R2A at 25°C. In API 20NE system, positive reactions are obtained for nitrate reduction, arginine dihydrolase, urease, esculin hydrolysis, gelatinase, and β-galactosidase; but negative for glucose fermentation, and cytochrome oxidase. Weakly positive reaction is obtained for indole production. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, potassium gluconate, malic acid, and trisodium citrate are utilized as sole carbon sources; while D-maltose, capric acid, adipic acid, and phenylacetic acid are not. Strain BT826 (＝NIBRBAC000509695) was isolated from a soil sample at Hoengseong, Gangwon-do, Republic of Korea.

Description of *Duganella vulcania* CM27

Cells are Gram-stain-negative, flagellated, and rod shaped. Colonies are round, entire, convex, and white to purple colored after incubation for 3 days on R2A at 28°C. In API 20NE system, positive reactions are obtained for esculin hydrolysis, β-galactosidase, and cytochrome oxidase; but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, and gelatinase. L-Arabinose, D-mannose, D-maltose, potassium gluconate, and phenylacetic acid are utilized as sole carbon sources; while D-mannitol, *N*-acetyl-glucosamine, capric acid, adipic acid, and malic acid are not. D-Glucose and trisodium citrate are weakly utilized. Strain CM27 (＝NIBRBAC000509498) was isolated from a wetland sample at Seoul, Republic of Korea.

Description of *Empedobacter haloabium* MMS22-GI34

Cells are Gram-stain-negative, non-flagellated, and rod shaped. Colonies are punctiform, convex, entire, and yellow colored after incubation for 7 days on ISP7 at 30°C. In API 20NE system, positive reactions are obtained for esculin hydrolysis and gelatinase; but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, β-galactosidase, and cytochrome oxidase. 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 are not utilized as sole carbon sources. Strain MMS22-GI34 (＝NIBRBAC000509470) was isolated from a soil sample at Gapyeong, Gyeonggi-do, Republic of Korea.

Description of *Herbaspirillum frisingense* AS214

Cells are Gram-stain-negative, flagellated, and rod shaped. Colonies are round, entire, raised, and cream colored after incubation for 3 days on R2A at 28°C. In API 20NE system, positive reactions are obtained for glucose fermentation, β-galactosidase, and cytochrome oxidase; but negative for nitrate reduction, indole production, arginine dihydrolase, urease, esculin hydrolysis, and gelatinase. D-Glucose, L-arabinose, D-mannitol, potassium gluconate, capric acid, malic acid, trisodium citrate, and phenylacetic acid are utilized as sole carbon sources; while D-mannose, *N*-acetyl-glucosamine, D-maltose, and adipic acid are not. Strain AS214 (＝NIBRBAC000509503) was isolated from a wetland sample at Anseong, Gyeonggi-do, Republic of Korea.

Description of *Herbaspirillum huttiense* subsp. *huttiense* MMS22-36

Cells are Gram-stain-negative, flagellated, and rod shaped. Colonies are punctiform, raised, entire, and yellow colored after incubation for 7 days on SCA at 30°C. In API 20NE system, positive reactions are obtained for glucose fermentation, urease, β-galactosidase, and cytochrome oxidase; but negative for nitrate reduction, indole production, arginine dihydrolase, and gelatinase. Weakly positive reaction is obtained for esculin hydrolysis. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid are utilized as sole carbon sources; while D-maltose is not. Strain MMS22-36 (＝NIBRBAC000509456) was isolated from a soil sample at Gapyeong, Gyeonggi-do, Republic of Korea.

Description of *Herbaspirillum huttiense* subsp. *putei* MMS22-18

Cells are Gram-stain-negative, flagellated, and rod shaped. Colonies are irregular, raised, undulate, and yellow colored after incubation for 7 days on SCA at 30°C. In API 20NE system, positive reactions are obtained for arginine dihydrolase, urease, gelatinase, and cytochrome oxidase; but negative for nitrate reduction, indole production, glucose fermentation, and β-galactosidase. Weakly positive reaction is obtained for esculin hydrolysis. *N*-Acetyl-glucosamine, capric acid, malic acid, and trisodium citrate are utilized as sole carbon sources; while D-glucose, L-arabinose, D-mannose, D-mannitol, D-maltose, potassium gluconate, adipic acid, and phenylacetic acid are not. Strain MMS22-18 (＝NIBRBAC000509459) was isolated from a soil sample at Gapyeong, Gyeonggi-do, Republic of Korea.

Description of *Hydrogenophaga aromaticivorans* AS624

Cells are Gram-stain-negative, non-flagellated, and rod shaped. Colonies are round, entire, convex, and cream colored after incubation for 3 days on R2A at 30°C. In API 20NE system, positive reactions are obtained for nitrate reduction and cytochrome oxidase; but negative for indole production, glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis, gelatinase, and β-galactosidase. D-Glucose, L-arabinose, D-mannose, D-mannitol, and D-maltose are utilized as sole carbon sources; while *N*-acetyl-glucosamine, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid are not. Strain AS624 (=NIBRBAC000509513) was isolated from a wetland sample at Anseong, Republic of Korea.

Description of *Janthinobacterium rivuli* BT827

Cells are Gram-stain-negative, flagellated, and rod shaped. Colonies are circular, slightly convex, glistening, violet, and white colored after incubation for 3 days on R2A at 25°C. In API 20NE system, positive reactions are obtained for nitrate reduction, glucose fermentation, arginine dihydrolase, esculin hydrolysis, and cytochrome oxidase; but negative for indole production, urease, gelatinase, and β-galactosidase. D-Glucose, L-arabinose, D-mannitol, *N*-acetyl-glucosamine, and D-maltose are utilized as sole carbon sources; while D-mannose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid are not. Strain BT827 (=NIBRBAC000509696) was isolated from a soil sample at Hoengseong, Republic of Korea.

Description of *Massilia consociata* MMS22-GR6

Cells are Gram-stain-negative, flagellated, and rod shaped. Colonies are circular, convex, entire, and beige colored after incubation for 2 days on R2A at 30°C. In API 20NE system, positive reactions are obtained for nitrate reduction, arginine dihydrolase, urease, esculin hydrolysis, gelatinase, β-galactosidase, and cytochrome oxidase; but negative for indole production and glucose fermentation. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, adipic acid, malic acid, trisodium citrate, and phenylacetic acid are utilized as sole carbon sources; while capric acid is not. Strain MMS22-GR6 (=NIBRBAC0000509461) was isolated from a soil sample at Gangneung, Republic of Korea.

Description of *Massilia flava* MMS22-MBR12

Cells are Gram-stain-negative, flagellated, and rod shaped. Colonies are circular, convex, entire, and brown colored after incubation for 2 days on R2A at 30°C. In API 20NE system, positive reactions are obtained for nitrate reduction, arginine dihydrolase, urease, esculin hydrolysis, gelatinase, β-galactosidase, and cytochrome oxidase; but negative for indole production and glucose fermentation. D-Glucose, L-arabinose, D-mannose, D-maltose, potassium gluconate, malic acid, trisodium citrate, and phenylacetic acid are utilized as sole carbon sources; while capric acid is not. D-Mannitol, *N*-acetyl-glucosamine, and adipic acid are weakly utilized. Strain MMS22-MBR12 (=NIBRBAC000509465) was isolated from a soil sample at Sejong, Republic of Korea.

Description of *Massilia frigida* AS504

Cells are Gram-stain-negative, flagellated, and oval shaped. Colonies are irregular, entire, convex, and ivory colored after incubation for 3 days on R2A at 28°C. In API 20NE system, positive reactions are obtained for glucose fermentation and gelatinase; but negative for nitrate reduction, indole production, arginine dihydrolase, urease, esculin hydrolysis, β-galactosidase, and cytochrome oxidase. 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 are not utilized as sole carbon sources. Strain AS504 (=NIBRBAC000509511) was isolated from a wetland sample at Anseong, Republic of Korea.

Description of *Polaromonas cryoconiti* AS644

Cells are Gram-stain-negative, non-flagellated, and rod shaped. Colonies are round, entire, raised, and white colored after incubation for 3 days on R2A at 30°C. In API 20NE system, positive reactions are obtained for nitrate reduction and cytochrome oxidase; but negative for indole production, glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis, gelatinase, and β-galactosidase. Potassium gluconate, adipic acid, and malic acid are utilized as sole carbon sources; while D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, capric acid, trisodium citrate, and phenylacetic acid are not. Strain AS644 (=NIBRBAC000509514) was isolated from a wetland sample at Anseong, Republic of Korea.

Description of *Rubrivivax albus* CAU 1695

Cells are Gram-stain-negative, non-flagellated, and rod shaped. Colonies are with entire margin, circular, convex, smooth, opaque, and white colored after incubation for 3 days on MA at 30°C. In API 20NE system, positive reactions are obtained for esculin hydrolysis, gelatinase, and cytochrome oxidase; but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, and β-galactosidase. D-Mannitol, D-maltose, potassium gluconate, adipic acid, malic acid, and trisodium citrate are utilized as sole carbon sources; while D-glucose, L-arabinose, D-mannose, *N*-acetyl-glucosamine, capric acid, and phenylacetic acid are not. Strain CAU 1695 (=NIBRBAC000509679) was isolated from a mud sample at Ansan, Republic of Korea.

Description of *Oceanisphaera psychrotolerans* GPSW-R9

Cells are Gram-stain-negative, non-flagellated, and rod shaped. Colonies are yellowish white colored after incubation for 3 days on R2A at 25°C. In the API 20NE system, positive for nitrate reduction and arginine dihydrolase; but negative for indole production, glucose fermentation, urease, esculin hydrolysis, gelatin hydrolysis, *β*-galactosidase, and cytochrome oxidase. D-Mannose is utilized as a sole carbon source; while D-glucose, L-arabinose, D-mannose, *N*-acetyl-D-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid are not. Strain GPSW-R9 (=NIBRBAC000509652) was isolated from a soil sample at Gyeongju, Gyeongsangbuk-do, Republic of Korea.

Description of *Alteromonas stellipolaris* HMG3253

Cells are Gram-stain-negative, non-flagellated, and rod shaped. Colonies are cream colored after incubation for 2 days on MA at 25°C. In the API 20NE system, positive for esculin hydrolysis, gelatin hydrolysis, *β*-galactosidase, and cytochrome oxidase; but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, and urease. D-Glucose and potassium gluconate are utilized as sole carbon sources; while L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid are not. Strain HMG3253 (=NIBRBAC000509541) was isolated from a soil sample at Hwaseong, Gyeonggi-do, Republic of Korea.

Description of *Motilimonas cestriensis* HMG3259

Cells are Gram-stain-negative, non-flagellated, and rod shaped. Colonies are cream colored after incubation for 2 days on MA at 25°C. In the API 20NE system, positive for nitrate reduction, glucose fermentation, and gelatin hydrolysis; but negative for indole production, arginine dihydrolase, urease, esculin hydrolysis, *β*-galactosidase, and cytochrome oxidase. D-Glucose, D-mannose, and malic acid are utilized as sole carbon sources; while L-arabinose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, trisodium citrate, and phenylacetic acid are not. Strain HMG3259 (=NIBRBAC000509546) was isolated from a soil sample at Hwaseong, Gyeonggi-do, Republic of Korea.

Description of *Pseudoalteromonas luteoviolacea* GPSW-M14

Cells are Gram-stain-negative, non-flagellated, and rod shaped. Colonies are brownish gray colored after incubation for 3 days on MA at 25°C. In the API 20NE system, positive for esculin hydrolysis and gelatin hydrolysis; but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, *β*-galactosidase, and cytochrome oxidase. D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid are not utilized as sole carbon sources. Strain GPSW-M14 (=NIBRBAC000509651) was isolated from a soil sample at Gyeongju, Gyeongsangbuk-do, Republic of Korea.

Description of *Haliea salexigens* HMG3484

Cells are Gram-stain-negative, non-flagellated, and rod shaped. Colonies are cream colored after incubation for 7 days on MA at 25°C. In the API 20NE system, positive for cytochrome oxidase; but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis, gelatin hydrolysis, and *β*-galactosidase. Adipic acid and malic acid are utilized as sole carbon sources; while D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, potassium gluconate, capric acid, trisodium citrate, and phenylacetic acid are not. Strain HMG3484 (=NIBRBAC000509564) was isolated from a soil sample at Sinan-gun, Jeollanam-do, Republic of Korea.

Description of *Enterobacter quasiroggenkampii* 16S3A9

Cells are Gram-stain-negative, non-flagellated, and rod shaped. Colonies are white colored after incubation for 2 days on R2A at 30°C. In the API 20NE system, positive for nitrate reduction, glucose fermentation, arginine dihydrolase, esculin hydrolysis, and *β*-galactosidase; but negative for indole production, urease, gelatin hydrolysis, and cytochrome oxidase. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, potassium gluconate, malic acid, trisodium citrate, and phenylacetic acid are utilized as sole carbon sources; while capric acid and adipic acid are not. Strain 16S3A9 (=NIBRBAC000509477) was isolated from a soil sample at Yeoju, Gyeonggi-do, Republic of Korea.

Description of *Enterobacter chengduensis* 16SBF1

Cells are Gram-stain-negative, non-flagellated, and rod shaped. Colonies are white colored after incubation for 2 days on R2A at 30°C. In the API 20NE system, positive nitrate reduction, glucose fermentation, arginine dihydrolase, esculin hydrolysis, and β-galactosidase; but negative for indole production, urease, gelatin hydrolysis, and cytochrome oxidase. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, potassium gluconate, malic acid, trisodium citrate, and phenylacetic acid are utilized as sole carbon sources; while capric acid and adipic acid are not. Strain 16SBF1 (=NIBRBAC000509478) was isolated from a soil sample at Yeoju, Gyeonggi-do, Republic of Korea.

Description of *Enterobacter wuhouensis* CASP060_16_ECC

Cells are Gram-stain-negative, non-flagellate, and rod shaped. Colonies are white colored after incubation for 2 days on R2A at 30°C. In the API 20NE system, positive for nitrate reduction, glucose fermentation, arginine dihydrolase, esculin hydrolysis, and β-galactosidase; but negative for indole production, urease, gelatin hydrolysis, and cytochrome oxidase. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, potassium gluconate, malic acid, trisodium citrate, and phenylacetic acid are utilized as sole carbon sources; while capric acid and adipic acid are not. Strain CASP060_16_ECC (=NIBRBAC000509491) was isolated from a soil sample at Wanju-gun, Jeollabuk-do, Republic of Korea.

Description of *Escherichia ruysiae* 16H2E9

Cells are Gram-stain-negative, non-flagellate, and rod shaped. Colonies are grey white colored after incubation for 2 days on R2A at 30°C. In the API 20NE system, positive for nitrate reduction, glucose fermentation, arginine dihydrolase, esculin hydrolysis, and β-galactosidase; but negative for indole production, urease, gelatin hydrolysis, and cytochrome oxidase. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, potassium gluconate, malic acid, and phenylacetic acid are utilized as sole carbon sources; while capric acid, adipic acid, and trisodium citrate are not. Strain 16H2E9 (=NIBRBAC000509488) was isolated from a soil sample at Guri, Gyeonggi-do, Republic of Korea.

Description of *Erwinia endophytica* 19S3E3

Cells are Gram-stain-negative, non-flagellated, and rod shaped. Colonies are beige colored after incubation for 2 days on R2A at 30°C. In API 20NE system, positive for glucose fermentation, esculin hydrolysis, and β-galactosidase; but negative for nitrate reduction, indole production, arginine dihydrolase, urease, gelatin hydrolysis, and cytochrome oxidase. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, potassium gluconate, malic acid, and trisodium citrate are utilized as sole carbon sources; while capric acid, adipic acid and phenylacetic acid are not. Strain 19S3E3 (=NIBRBAC000509481) was isolated from a soil sample at Yeoju, Gyeonggi-do, Republic of Korea.

Description of *Rhodanobacter panaciterrae* BT834

Cells are Gram-stain-negative, non-flagellated, and rod shaped. Colonies are yellow colored after incubation for 3 days on R2A at 25°C. In the API 20NE system, positive for β-galactosidase and cytochrome oxidase; but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis, and gelatin hydrolysis. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid are not utilized as sole carbon sources. Strain BT834 (=NIBRBAC000509702) was isolated from a soil sample at Hoengseong, Gangwon-do, Republic of Korea.

Description of *Acinetobacter albensis* HMG3058

Cells are Gram-stain-negative, non-flagellated, and coccobacilli shaped. Colonies are cream colored after incubation for 3 days on R2A at 25°C. In the API 20NE system, positive for urease; but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, esculin hydrolysis, gelatin hydrolysis, β-galactosidase, and cytochrome oxidase. D-Glucose, L-arabinose, potassium gluconate, capric acid, malic acid, and trisodium citrate are utilized as sole carbon sources; while D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, adipic acid, and phenylacetic acid are not. Strain HMG3058 (=NIBRBAC000509538) was isolated from a soil sample at Yongin, Gyeonggi-do, Republic of Korea.

Description of *Acinetobacter rudis* DB12

Cells are Gram-stain-negative, non-flagellated, and coccobacilli shaped. Colonies are ivory white colored after incubation for 2 days on R2A at 30°C. In the API 20NE system, positive for esculin hydrolysis; but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, gelatin hydrolysis, β-galactosidase, and cytochrome oxidase. Capric acid, malic acid, trisodium citrate, and phenylacetic acid are utilized as sole carbon sources; while D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, potassium gluconate, and adipic acid are not. Strain DB12 (= NIBRBAC000509584) was isolated from a soil sample at Goyang, Gyeonggi-do, Republic of Korea.

Description of *Alcanivorax borkumensis* CAU 1685

Cells are Gram-stain-negative, non-flagellated, and rod shaped. Colonies are white colored after incubation for 3 days on MA at 30°C. In the API 20NE system, positive for esculin hydrolysis and cytochrome oxidase; but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, gelatin hydrolysis, and β-galactosidase. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid are not utilized as sole carbon sources. Strain CAU 1685 (= NIBRBAC000509672) was isolated from a soil sample at Incheon, Republic of Korea.

Description of *Halomonas venusta* BIM5

Cells are Gram-stain-negative, non-flagellated and rod shaped. Colonies are yellowish-white colored after incubation for 3 days on MA at 25°C. In the API 20NE system, positive for nitrate reduction, glucose fermentation, and esculin hydrolysis; but negative for indole production, arginine dihydrolase, urease, gelatin hydrolysis, β-galactosidase, and cytochrome oxidase. D-Glucose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, potassium gluconate, adipic acid, malic acid, trisodium citrate, and phenylacetic acid are utilized as sole carbon sources; while L-arabinose and capric acid. Strain BIM5 (= NIBRBAC000509648) was isolated from a soil sample at Seocheon-gun, Chungcheongnam-do, Republic of Korea.

Description of *Marinomonas primoryensis* HMG3262

Cells are Gram-stain-negative, non-flagellate, and rod shaped. Colonies are light yellow colored after incubation for 2 days on MA at 25°C. In the API 20NE system, positive for esculin hydrolysis and β-galactosidase; but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, gelatin hydrolysis, and cytochrome oxidase. D-Glucose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, potassium gluconate, malic acid, and trisodium citrate are utilized as sole carbon sources; while L-arabinose, capric acid, adipic acid, and phenylacetic acid are not. Strain HMG3262 (= NIBRBAC000509549) was isolated from a soil sample at Hwaseong, Gyeonggi-do, Republic of Korea.

Description of *Saccharospirillum alexandrii* HMG3308

Cells are Gram-stain-negative, non-flagellate, and rod shaped. Colonies are cream colored after incubation for 3 days on MA at 25°C. In the API 20NE system, positive for esculin hydrolysis, β-galactosidase, and cytochrome oxidase; but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, and gelatin hydrolysis. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, malic acid, and trisodium citrate are utilized as sole carbon sources; while potassium gluconate, capric acid, adipic acid, and phenylacetic acid are not. Strain HMG3308 (= NIBRBAC000509551) was isolated from a soil sample at Inan-gun, Jeollanam-do, Republic of Korea.

Description of *Pseudomonas linyingensis* CAU 1683

Cells are Gram-stain-negative, non-flagellate, and rod shaped. Colonies are white colored after incubation for 3 days on MA at 30°C. In the API 20NE system, positive for esculin hydrolysis and cytochrome oxidase; but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, and gelatin hydrolysis. Capric acid, malic acid, and phenylacetic acid are utilized as sole carbon sources; while potassium gluconate, adipic acid, β-galactosidase, D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, and trisodium citrate are not. Strain CAU 1683 (= NIBRBAC000509670) was isolated from a soil sample at Ganghwa-gun, Incheon, Republic of Korea.

Description of *Pseudomonas oryzae* CAU 1692

Cells are Gram-stain-negative, non-flagellate, and rod shaped. Colonies are white colored after incubation for 3 days on MA at 30°C. In the API 20NE system, positive for urease, esculin hydrolysis, and cytochrome oxidase; but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, gelatin hydrolysis, and β-galactosidase. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, potassium gluconate, capric acid, malic acid, and trisodium citrate are utilized as sole carbon sources; while adipic acid and phenylacetic acid are not. Strain CAU 1692 (= NIBRBAC000509676) was isolated from a soil sample at Ansan, Gyeonggi-do, Republic of Korea.

Description of *Pseudomonas asiatica* LSCA30_12_PSE

Cells are Gram-stain-negative, non-flagellate, and rod shaped. Colonies are cream colored after incubation for 2 days on R2A at 30°C. In the API 20NE system, positive for arginine dihydrolase and esculin hydrolysis; but negative for nitrate reduction, indole production, glucose fermentation, urease, gelatin hydrolysis, β-galactosidase, and cytochrome oxidase. D-Glucose, L-arabinose, potassium gluconate, capric acid, malic acid, trisodium citrate, and phenylacetic acid are utilized as sole carbon sources; while adipic acid, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, and D-maltose are not. Strain LSCA30_12_PSE (=NIBRBAC000509492) was isolated from a soil sample from Wanju-gun, Jeollabuk-do, Republic of Korea.

Description of *Pseudomonas juntendi* 16H1M10

Cells are Gram-stain-negative, non-flagellate, and rod shaped. Colonies are cream colored after incubation for 2 days on R2A at 30°C. In the API 20NE system, positive for glucose fermentation, arginine dihydrolase, urease, and esculin hydrolysis; but negative for nitrate reduction, indole production, gelatin hydrolysis, β-galactosidase, and cytochrome oxidase. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid are utilized as sole carbon sources. Strain 16H1M10 (=NIBRBAC000509487) was isolated from a soil sample at Hanam, Gyeonggi-do, Republic of Korea.

Description of *Pseudomonas orientalis* 16H3F9

Cells are Gram-stain-negative, non-flagellate, and rod shaped. Colonies are white grey colored after incubation for 2 days on R2A at 30°C. In the API 20NE system, positive for arginine dihydrolase, esculin hydrolysis, and gelatin hydrolysis; but negative for nitrate reduction, indole production, glucose fermentation, urease, β-galactosidase, and cytochrome oxidase. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, potassium gluconate, capric acid, malic acid, and trisodium citrate are utilized as sole carbon sources; while D-maltose, adipic acid and phenylacetic acid are not. Strain 16H3F9 (=NIBRBAC000509489) was isolated from a soil sample at Seoul, Republic of Korea.

Description of *Pseudomonas helleri* 16H6M3

Cells are Gram-stain-negative, non-flagellate, and rod shaped. Colonies are white colored after incubation for 2 days on R2A at 30°C. In the API 20NE system, positive for arginine dihydrolase, urease, and esculin hydrolysis; but negative for nitrate reduction, indole production, glucose fermentation, gelatin hydrolysis, β-galactosidase, and cytochrome oxidase. Potassium gluconate, capric acid, malic acid, and trisodium citrate are utilized as sole carbon sources; while D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, adipic acid, and phenylacetic acid are not. Strain 16H6M3 (=NIBRBAC000509490) was isolated from a soil sample at Seoul, Republic of Korea.

Description of *Pseudomonas glycinae* AS204

Cells are Gram-stain-negative, non-flagellate, and rod shaped. Colonies are cream colored after incubation for 3 days on R2A at 28°C. In the API 20NE system, positive for arginine dihydrolase and cytochrome oxidase; but negative for nitrate reduction, indole production, glucose fermentation, urease, esculin hydrolysis, gelatin hydrolysis, and β-galactosidase. D-Glucose, L-arabinose, D-mannose, D-mannitol, potassium gluconate, capric acid, malic acid, and trisodium citrate are utilized as sole carbon sources; while *N*-acetyl-D-glucosamine, D-maltose, adipic acid, and phenylacetic acid are not Strain AS204 (=NIBRBAC000509500) was isolated from a soil sample at Anseong, Gyeonggi-do, Republic of Korea.

Description of *Pseudomonas chlororaphis* subsp. *aureofaciens* AS212

Cells are Gram-stain-negative, non-flagellated, and rod shaped. Colonies are ivory colored after incubation for 3 days on R2A at 28°C. In the API 20NE system, positive for glucose fermentation, arginine dihydrolase, urease, gelatin hydrolysis, and cytochrome oxidase; but negative for nitrate reduction, indole production, esculin hydrolysis, and β-galactosidase. D-Glucose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, potassium gluconate, capric acid, malic acid, trisodium citrate, and phenylacetic acid are utilized as sole carbon sources; while L-arabinose, D-maltose, and adipic acid are not. Strain AS212 (=NIBRBAC000509501) was isolated from a soil sample at Anseong, Gyeonggi-do, Republic of Korea.

Description of *Pseudomonas atagonensis* AS213

Cells are Gram-stain-negative, non-flagellated, and rod shaped. Colonies are cream colored after incubation for 3 days on R2A at 28°C. In the API 20NE system, positive for arginine dihydrolase, gelatin hydrolysis, and cytochrome oxidase; but negative for nitrate reduction, indole production, glucose fermentation, urease, esculin hydrolysis, and β-galactosidase. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, potassium gluconate, and capric acid are utilized as sole carbon sources; while D-maltose, adipic acid, and phenylacetic acid are not. Strain AS213 (=NIBRBAC000509502) was isolated from a soil sample at Anseong, Gyeonggi-do, Republic of Korea.

Description of *Pseudomonas cedrina* subsp. *cedrina* AS247

Cells are Gram-stain-negative, non-flagellated, and rod shaped. Colonies are cream colored after incubation for 3 days on R2A at 28°C. In the API 20NE system, positive for arginine dihydrolase, urease, gelatin hydrolysis, and cytochrome oxidase; but negative for nitrate reduction, indole production, glucose fermentation, esculin hydrolysis, and β-galactosidase. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, potassium gluconate, capric acid, malic acid, and trisodium citrate are utilized as sole carbon sources; while D-maltose, adipic acid, and phenylacetic acid are not. Strain AS247 (=NIBRBAC000509505) was isolated from a soil sample at Anseong, Gyeonggi-do, Republic of Korea.

Description of *Pseudomonas qingdaonensis* AS279

Cells are Gram-stain-negative, non-flagellated, and rod shaped. Colonies are pale brown colored after incubation for 3 days ion on R2A at 28°C. In the API 20NE system, positive for glucose fermentation, arginine dihydrolase, urease, and cytochrome oxidase; but negative for nitrate reduction, indole production, esculin hydrolysis, gelatin hydrolysis, and β-galactosidase. D-Glucose, potassium gluconate, capric acid, malic acid, trisodium citrate, and phenylacetic acid are utilized as sole carbon sources; while L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, and adipic acid are not. Strain AS279 (=NIBRBAC000509506) was isolated from a soil at Anseong-si, Gyeonggi-do, Republic of Korea.

Description of *Pseudomonas capeferrum* AS568

Cells are Gram-stain-negative, non-flagellated, and rod shaped. Colonies are cream colored after incubation for 3 days on R2A at 28°C. In the API 20NE system, positive for nitrate reduction, arginine dihydrolase, esculin hydrolysis, and cytochrome oxidase; but negative for indole production, glucose fermentation, urease, gelatin hydrolysis, and β-galactosidase. Capric acid and malic acid are utilized as sole carbon sources; while D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, adipic acid, trisodium citrate, and phenylacetic acid are not. Strain AS568 (=NIBRBAC000509512) was isolated from a soil sample at Anseong, Gyeonggi-do, Republic of Korea.

Description of *Pseudomonas paraversuta* BT833

Cells are Gram-stain-negative, non-flagellated, and short rod shaped. Colonies are white colored after incubation for 3 days on R2A at 25°C. In the API 20NE system, positive for nitrate reduction, indole production, arginine dihydrolase, esculin hydrolysis, gelatin hydrolysis, and cytochrome oxidase; but negative for glucose fermentation, urease, and β-galactosidase. D-Glucose, L-arabinose, D-mannose, potassium gluconate, malic acid, trisodium citrate, and phenylacetic acid are utilized as sole carbon sources; while D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, capric acid, and adipic acid are not. Strain BT833 (=NIBRBAC000509701) was isolated from a soil sample at Hoengseong-gun, Gangwon-do, Republic of Korea.

Description of *Pseudomonas edaphica* ST11-10

Cells are Gram-stain-negative, non-flagellated, and short rod shaped. Colonies are cream colored after incubation for 3 days on R2A at 25°C. In the API 20NE system, positive for arginine dihydrolase, urease, and gelatin hydrolysis; but negative for nitrate reduction, indole production, glucose fermentation, esculin hydrolysis, and β-galactosidase. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, potassium gluconate, capric acid, malic acid, and trisodium citrate are utilized as sole carbon sources; while D-maltose, adipic acid, and phenylacetic acid are not. Strain ST11-10 (=NIBRBAC000509711) was isolated from a soil sample at Hoengseong-gun, Gangwon-do, Republic of Korea.

Description of *Vibrio kanaloae* BIM3

Cells are Gram-stain-negative, non-flagellated, and rod shaped. Colonies are yellowish white colored after incubation for 3 days on MA at 25°C. In the API 20NE system, positive for nitrate reduction, glucose fermentation, esculin hydrolysis, and gelatin hydrolysis; but negative for indole production, arginine dihydrolase, urease, β-galactosidase, and cytochrome oxidase. Potassium gluconate is utilized as a sole carbon source; while D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid are not. Strain BIM3 (=NIBRBAC000509647) was isolated from a soil sample at Seocheon-gun, Chungcheongnam-do, Republic of Korea.

Description of *Vibrio pacinii* HMG3256

Cells are Gram-stain-negative, non-flagellated, and rod shaped. Colonies are cream colored after incubation for 2 days on MA at 25°C. In the API 20NE system, positive for nitrate reduction, glucose fermentation, arginine dihydrolase, esculin hydrolysis, gelatin hydrolysis, β-galactosidase, and cytochrome oxidase; but negative for indole production and urease. D-Glucose, L-arabinose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, potassium gluconate, malic acid, trisodium citrate are utilized as sole carbon sources; while D-mannose, capric acid, adipic acid, and phenylacetic acid are not. Strain HMG3256 (=NIBRBAC000509543) was isolated from a soil sample at Hwaseong, Gyeonggi-do, Republic of Korea.

Description of *Vibrio fluvialis* CAU 1684

Cells are Gram-stain-negative, non-flagellated, and rod shaped. Colonies are cream colored after incubation for 3 days on MA at 30°C. In the API 20NE system, positive for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, esculin hydrolysis, gelatin hydrolysis, β-galactosidase, and cytochrome oxidase; but negative for urease. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, potassium gluconate, capric acid, malic acid, and trisodium citrate are utilized as sole carbon sources; while adipic acid and phenylacetic acid are not. Strain CAU 1684 (=NIBRBAC000509671) was isolated from a soil sample at Incheon, Republic of Korea.

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