

Report of 44 unrecorded bacterial species in Korea belonging to the class *Betaproteobacteria* and *Gammaproteobacteria* of the phylum *Pseudomonadota*, excavated during the survey in 2023

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The classes *Betaproteobacteria* and *Gammaproteobacteria* are two major classes within the phylum *Pseudomonadota*, encompassing a diverse range of Gram-negative, rod-shaped bacteria. Both classes are known for their metabolic versatility and ecological significance, inhabiting various environments. During a series of extensive surveys of indigenous prokaryotic species diversity in Korea, bacterial strains belonging to *Betaproteobacteria* and *Gammaproteobacteria* were isolated from various terrestrial environments. A total of 44 bacterial strains belonging to 30 genera in 17 families were identified as unrecorded species in Korea. The isolates assigned to *Betaproteobacteria* comprised 19 of the 44 unrecorded species, with *Burkholderiaceae* as the most abundant family. The most frequently isolated genus was *Burkholderia*. The isolates assigned to *Gammaproteobacteria* comprised 25 of the 44 unrecorded species, with *Lysobacteraceae* and *Pseudomonadaceae* as the most abundant families. The genera *Lysobacter* and *Pseudomonas* were the most frequently isolated genera. The detailed descriptions of each unrecorded species are provided.

Keywords: *Betaproteobacteria*, *Gammaproteobacteria*, *Pseudomonadota*, unrecorded species



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INTRODUCTION

The phylum *Pseudomonadota* is one of the most diverse and ubiquitous bacterial groups (Oren and Garrity, 2021). The classes *Betaproteobacteria* and *Gammaproteobacteria* are among the largest classes of the phylum. Currently, *Betaproteobacteria* encompasses four valid orders, namely

Burkholderiales, *Neisseriales*, *Rhodocyclales* and *Spirillales*, whereas *Gammaproteobacteria* encompasses 20 valid orders including *Pseudomonadales* and *Enterobacterales* (Parte *et al.*, 2020). *Pseudomonadota* includes largest number of Gram-negative, rod-shaped species with diverse metabolic capabilities. Examples of such capabilities are degradation of polymers and recalcitrants, bioremediation,

plant growth-promoting activities, and bioleaching (Oren and Garrity, 2021). They have been isolated from virtually everywhere in terrestrial and aquatic environments, and also in association with animals and plants.

In 2023, extensive surveys on prokaryotic diversity in Korea led to the isolation and taxonomic characterization of 44 novel strains within the classes *Betaproteobacteria* and *Gammaproteobacteria*, both belonging to the phylum *Pseudomonadota*. These strains were obtained from diverse environmental sources. As a result of this comprehensive analysis, 44 unrecorded species of *Pseudomonadota* in Korea were identified, and their detailed taxonomic properties are presented herein.

MATERIALS AND METHODS

A total of 44 bacterial strains were isolated from a variety of terrestrial and aquatic environmental sources, including agricultural soil, wetlands, sediments, sewage, tidal flat, seawater and various other soils (Table 1). The samples were put in sterile bottles or plastic bags, and transported to the labs under refrigeration. Each sample was processed individually, serially diluted, and the diluents spread onto various isolation media, including Luria-Bertani (LB) agar, marine agar (MA), peptone-tryptone-yeast extract-glucose (PTYG) agar, Reasoner's 2A (R2A), starch-casein agar (SCA) and tryptic soy agar (TSA). The inoculated plates were incubated at 25, 28 or 30°C for 2–7 days. Strain designations, isolation sources, growth media and growth conditions are summarized in Table 1 and also in the species descriptions. All isolates were purified through repeated subcultures to obtain single colonies. For long-term preservation, the strains were stored as suspensions in 20% (v/v) glycerol at –80°C and also as lyophilized ampoules. Colony morphology was observed on the same agar media used for cultivation. Cellular morphology and size dimensions were determined by either transmission electron microscopy (TEM) or scanning electron microscopy (SEM). Gram staining was performed according to standard protocols. Biochemical and physiological characteristics were determined using the API 20NE test kit (bioMérieux), following the instructions by the supplier.

The extraction of DNA, PCR amplification of the 16S rRNA gene, and sequencing were carried out as previously described (Joh *et al.*, 2023). The obtained sequences were compared with those of the related type strains using the EzBioCloud database (Kim *et al.*, 2012), and aligned together with related species using EzEditor2 (Jeon *et al.*, 2014). Phylogenetic trees were constructed based on the Jukes-Cantor distance model (Jukes and Cantor, 1969) and the neighbor-joining method (Saitou and Nei, 1987) using MEGA version 7.0 (Kumar *et al.*, 2016). The tree topologies were evaluated by bootstrap analyses with 1,000 re-

sampled datasets (Felsenstein, 1985).

RESULTS AND DISCUSSION

A total of 44 bacterial strains belonging to the classes *Betaproteobacteria* and *Gammaproteobacteria* within the phylum *Pseudomonadota* were isolated from various sources of terrestrial and aquatic environments in Korea. These strains represented 44 unrecorded species of Korea, which were distributed across 25 genera and 17 families within the two classes (Table 1). Among them, 19 species were assigned to *Betaproteobacteria* (Table 1A), and the remaining 25 to *Gammaproteobacteria* (Table 1B).

At order level, *Burkholderiales* of *Betaproteobacteria* was the largest in size, encompassing 18 species, whereas *Lysobacterales* (5 species), *Pseudomonadales* (5) and *Enterobacterales* (4) formed the major groups within *Gammaproteobacteria*.

The most abundant families were *Burkholderiaceae* (11 species), *Comamonadaceae* (3 species), *Alcaligenaceae* (2 species) and *Oxalobacteraceae* (2 species) of *Betaproteobacteria*, and *Lysobacteraceae* (7 species), *Pseudomonadaceae* (4 species), *Shewanellaceae*, *Chromatiaceae*, *Enterobacteriaceae* and *Vibrionaceae* (2 species each) of *Gammaproteobacteria*. Single species was recorded for *Zoogloeaceae* of *Betaproteobacteria*, and *Marinobacteraceae*, *Pectobacteriaceae*, *Yersiniaceae*, *Steroidobacteraceae*, *Alcanivoracaceae* and *Saccharospirillaceae*.

At genus level, *Burkholderia* (4 species) of *Betaproteobacteria*, and *Lysobacter* (4 species) and *Pseudomonas* (3 species) of *Gammaproteobacteria* were most abundant, while two species were recorded for *Pigmentiphaga*, *Pandora* and *Paraburkholderia* of *Betaproteobacteria*, and *Shewanella*, *Rheinheimera* and *Luteimonas* of *Gammaproteobacteria*. Single species were recorded for the remaining genera, *Cupriavidus*, *Limnobacter*, *Ralstonia*, *Comamonas*, *Ramlibacter*, *Rhodiferax*, *Herbaspirillum*, *Noviherbaspirillum* and *Azoarcus* of *Betaproteobacteria*, and *Marinobacter*, *Kluyvera*, *Siccibacter*, *Lonsdalea*, *Rahnella*, *Pseudoxanthomonas*, *Povalibacter*, *Alcanivorax*, *Salinibius*, *Azotobacter*, *Vibrio* and *Enterovibrio* of *Gammaproteobacteria*.

The detailed taxonomic affiliations of the obtained strains are listed in Table 1. These results would enhance our understanding on the bacterial diversity in Korea and also provide a basis for future studies in biotechnology and other applied sciences. Electron micrographs of the isolated strains are shown in Fig. 1, and phylogenetic relationships with closely related species are illustrated in Fig. 2 for *Betaproteobacteria* and Fig. 3 for *Gammaproteobacteria*. Detailed descriptions of each unrecorded species are provided below.

Table 1. List of unrecorded species belonging to the classes *Betaproteobacteria* and *Gammaproteobacteria*, and their taxonomic affiliations.**A. *Betaproteobacteria***

Affiliation	Strain code	NIBR ID ^a	Identification	Similarity (%)	Isolation source	Medium ^b	Culture conditions
<i>Burkholderiales</i>							
<i>Alcaligenaceae</i>	GDB4	NIBRBAC000510584	<i>Pigmentiphaga kullae</i>	99.93	Soil	R2A	25°C, 2 days
	AN070	NIBRBAC000510598	<i>Pigmentiphaga litoralis</i>	99.79	Wetland	R2A	28°C, 3 days
<i>Burkholderiaceae</i>	MAW7	NIBRBAC000510847	<i>Burkholderia australis</i>	99.31	Agricultural soil	R2A	28°C, 3 days
	M34	NIBRBAC000510732	<i>Burkholderia diffusa</i>	100	Soil	R2A	25°C, 3 days
	A6	NIBRBAC000510740	<i>Burkholderia pyrrocinia</i>	99.38	Soil	R2A	25°C, 3 days
	MMS23-Y8	NIBRBAC000510817	<i>Burkholderia thailandensis</i>	98.76	Soil	R2A	30°C, 3 days
	AN586	NIBRBAC000510608	<i>Cupriavidus neoaledonicus</i>	99.14	Wetland	R2A	28°C, 3 days
	WK11	NIBRBAC000510793	<i>Limnobacter litoralis</i>	99.45	Sewage	R2A	28°C, 3 days
	MMS23-hol29	NIBRBAC000510829	<i>Pandoraea fibrosis</i>	99.86	Soil	R2A	30°C, 3 days
	MMS23-hol49	NIBRBAC000510830	<i>Pandoraea iniqua</i>	100	Soil	R2A	30°C, 3 days
	B1W8	NIBRBAC000510802	<i>Paraburkholderia ribeironis</i>	98.76	Agricultural soil	R2A	28°C, 3 days
	MMS23-S7	NIBRBAC000510816	<i>Paraburkholderia solitisugae</i>	98.90	Soil	SCA	30°C, 7 days
	17N1M7	NIBRBAC000510543	<i>Ralstonia insidiosus</i>	99.72	Sediment	R2A	30°C, 2 days
<i>Comamonadaceae</i>	EM-0455	NIBRBAC000510791	<i>Comamonas aquaticum</i>	99.93	Agricultural soil	PTYG	28°C, 4 days
	AN668	NIBRBAC000510613	<i>Ramlibacter tataouinensis</i>	98.83	Wetland	R2A	28°C, 3 days
	BY2	NIBRBAC000510795	<i>Rhodoferrax sediminis</i>	100	Agricultural soil	R2A	28°C, 3 days
<i>Oxalobacteraceae</i>	AN613	NIBRBAC000510609	<i>Herbaspirillum denitrificans</i>	98.76	Wetland	R2A	28°C, 3 days
	AMW7	NIBRBAC000510842	<i>Noviherbaspirillum autotrophicum</i>	99.93	Agricultural soil	R2A	28°C, 3 days
<i>Rhodocyclales</i>							
<i>Zoogloeaceae</i>	GDB3	NIBRBAC000510561	<i>Azoarcus olearius</i>	99.03	Soil	R2A	30°C, 2 days

^aNational Institute of Biological Resources.^bMA, marine agar; R2A, Reasoner's 2A agar; PTYG, peptone-tryptone-yeast extract-glucose agar; TSA, tryptic soy agar; SCA, starch casein agar.

Table 1. Continued.

B. Gammaproteobacteria

Affiliation	Strain code	NIBR* ID	Identification	Similarity (%)	Isolation source	Medium ^b	Culture conditions
<i>Alteromonadales</i>							
<i>Marinobacteriaceae</i>	HPW14	NIBRBAC000510849	<i>Marinobacter zhejiangensis</i>	100	Tidal flat	MA	28°C, 3 days
<i>Shewanellaceae</i>	SBCC-1734	NIBRBAC000510514	<i>Shewanella jiangmenensis</i>	100	Seawater	MA	25°C, 3–5 days
	MBLB4244	NIBRBAC000510678	<i>Shewanella oncorhynchi</i>	98.87	Soil	R2A	30°C, 3 days
<i>Chromatiales</i>							
<i>Chromatiaceae</i>	gt1	NIBRBAC000510643	<i>Rheinheimera japonica</i>	99.65	Soil	MA	30°C, 3 days
	DE95	NIBRBAC000510644	<i>Rheinheimera mesophila</i>	99.03	Soil	R2A	30°C, 3 days
<i>Enterobacteriales</i>							
<i>Enterobacteriaceae</i>	MMS23-Ri17	NIBRBAC000510834	<i>Kluyvera georgiana</i>	99.24	Soil	LB	30°C, 3 days
	19H1E18	NIBRBAC000510551	<i>Sticcibacter collettis</i>	99.93	Sediment soil	R2A	30°C, 2 days
<i>Pectobacteriaceae</i>	19N1E17	NIBRBAC000510552	<i>Lonsdalea populi</i>	99.86	Sediment	R2A	30°C, 2 days
<i>Yersiniaceae</i>	16S1T7	NIBRBAC000510555	<i>Rahnella inusitata</i>	99.51	Sediment	R2A	30°C, 2 days
<i>Lysobacterales</i>							
<i>Lysobacteraceae</i>	MMS23-QF36	NIBRBAC000510828	<i>Lysobacter auxotrophicus</i>	100	Soil	R2A	30°C, 3 days
	CAU 1721	NIBRBAC000510778	<i>Lysobacter erysipheiresistens</i>	100	Soil	MA	30°C, 3 days
	BU5-26-2	NIBRBAC000510749	<i>Lysobacter prati</i>	99.73	Soil	R2A	25°C, 3 days
	FY17	NIBRBAC000510790	<i>Lysobacter tabacisoli</i>	99.73	Agricultural soil	PTYG	28°C, 4 days
	SBCC-2331	NIBRBAC000510522	<i>Luteimonas composti</i>	99.05	Seawater	MA	25°C, 7 days
	DG1-10	NIBRBAC000510731	<i>Luteimonas glva</i>	100.00	Soil	R2A	25°C, 3 days
	MBLB3122	NIBRBAC000510674	<i>Pseudoxanthomonas mexicana</i>	99.93	Soil	TSA	30°C, 3 days
<i>Nevskiales</i>							
<i>Steroidobacteraceae</i>	YT17	NIBRBAC000510797	<i>Povalibacter uvarum</i>	99.45	Agricultural soil	R2A	28°C, 3 days
<i>Oceanospirillales</i>							
<i>Alcanivoracaceae</i>	CAU 1719	NIBRBAC000510776	<i>Alcanivorax jadensis</i>	99.59	Seawater	MA	30°C, 3 days
<i>Saccharospirillaceae</i>	SBCC-2351	NIBRBAC000510518	<i>Salinibius halmophilus</i>	100	Tidal flat	MA	30°C, 5 days
<i>Pseudomonadales</i>							
<i>Pseudomonadaceae</i>	SBCC-2184	NIBRBAC000510520	<i>Pseudomonas lalucatii</i>	99.18	Tidal flat	MA	25°C, 5 days
	16S4M11	NIBRBAC000510542	<i>Pseudomonas allii</i>	100	Sediment	R2A	30°C, 2 days
	18S3F2	NIBRBAC000510553	<i>Pseudomonas guariconensis</i>	100	Sediment	R2A	30°C, 2 days
	MMS23-DY57	NIBRBAC000510836	<i>Azotobacter beijerinckii</i>	100	Soil	R2A	30°C, 3 days
<i>Vibrionales</i>							
<i>Vibrionaceae</i>	SBCC-2261	NIBRBAC000510509	<i>Vibrio echinoideorum</i>	99.93	Tidal flat	MA	25°C, 3 days
	SBCC-2194	NIBRBAC000510508	<i>Enterovibrio baiacu</i>	99.73	Seawater	MA	25°C, 3 days

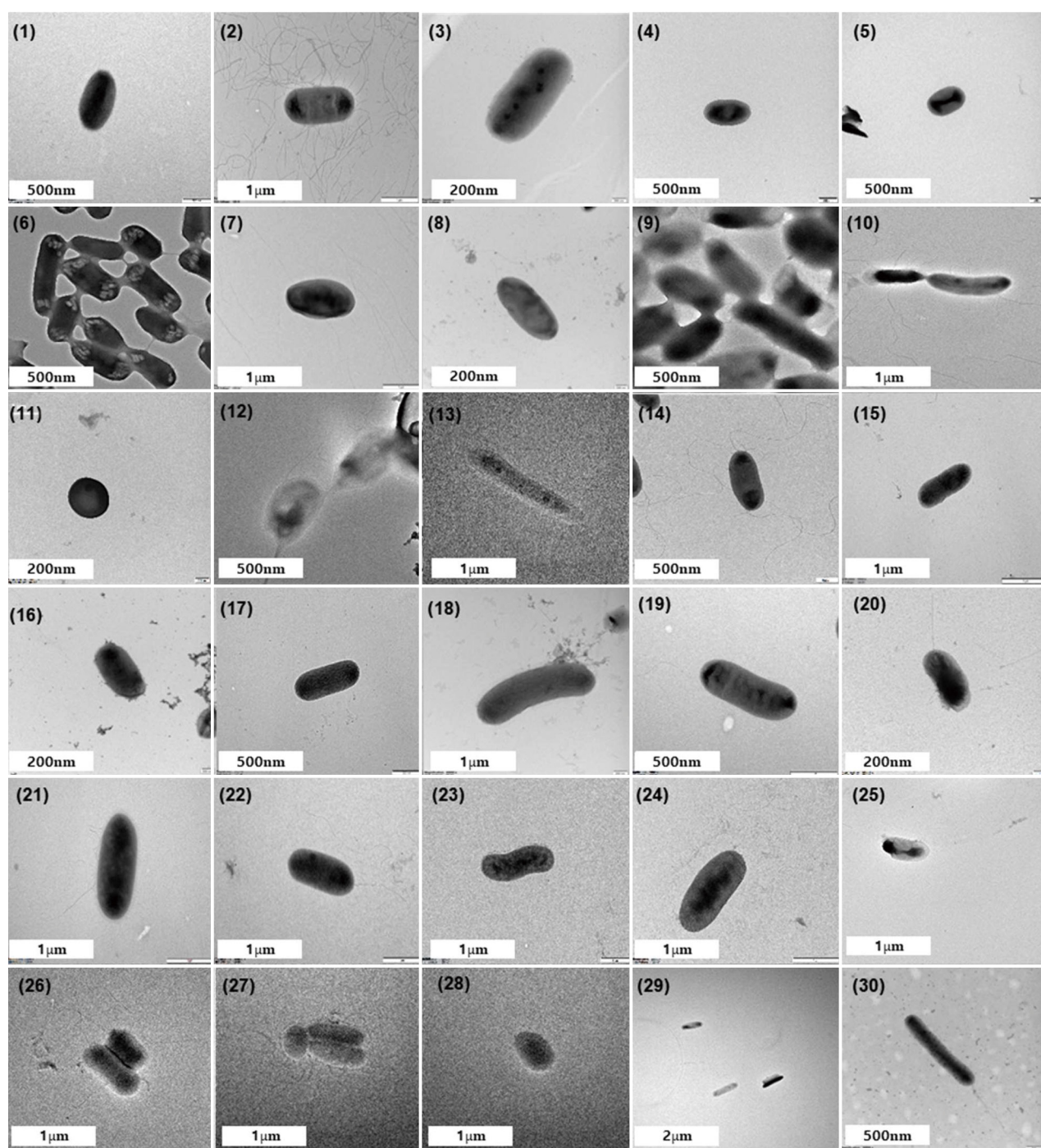


Fig. 1. Transmission electron or scanning electron micrographs of cells of the strains isolated in the study. Strains: 1, GDB4; 2, AN070; 3, MAW7; 4, M34; 5, A6; 6, MMS23-Y8; 7, AN586; 8, WK11; 9, MMS23-hol29; 10, MMS23-hol49; 11, B1W8; 12, MMS23-S7; 13, 17N1M7; 14, EM-0455; 15, AN668; 16, BY2; 17, AN613; 18, AMW7; 19, GDB3; 20, HPW14; 21, SBCC-1734; 22, MBLB4244; 23, gt1; 24, DE95; 25, MMS23-Ri17; 26, 19H1E18; 27, 19N1E17; 28, 16S1T7; 29, MMS23-QF36; 30, CAU 1721; 31, BU5-26-2; 32, FY17; 33, SBCC-2331; 34, DG1-10; 35, MBLB3122; 36, YT17; 37, CAU 1719; 38, SBCC-2351; 39, SBCC-2184; 40, 16S4M11; 41, 18S3F2; 42, MMS23-DY57; 43, SBCC-2261; 44, SBCC-2194.

Description of *Pigmentiphaga kullae* GDB4

Strain GDB4 (=NIBRBAC000510584), also isolated from soil in Oryu-dong, Seo-gu, Incheon, displays Gram-

stain-negative, rod-shaped cellular morphology. Colonies grown on R2A medium at 25°C for 2 days are circular and white. Physiologically, strain GDB4 is positive for esculin

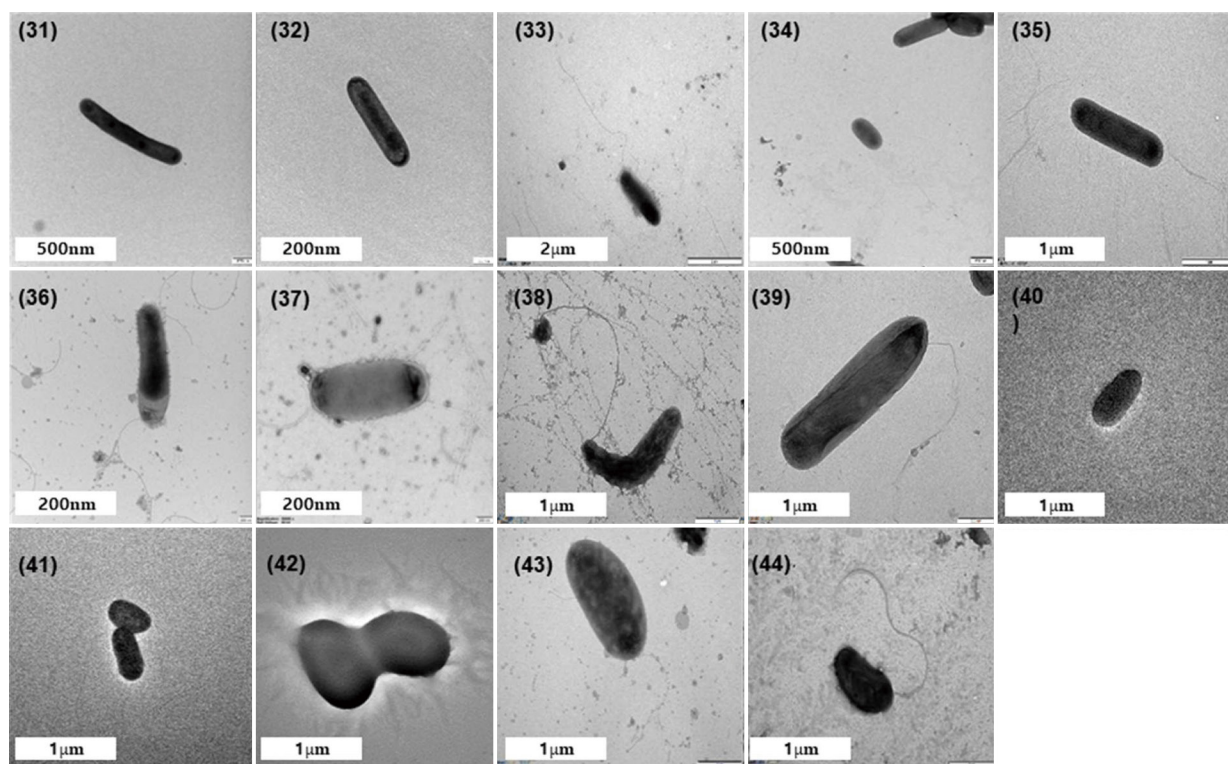


Fig. 1. Continued.

hydrolysis and cytochrome oxidase. It shows weakly positive results for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, gelatin hydrolysis, and β -galactosidase. It utilizes D-mannitol, potassium gluconate, malic acid, trisodium citrate, and phenylacetic acid, but does not D-glucose, L-arabinose, D-mannose, *N*-acetyl-glucosamine, D-maltose, capric acid, or adipic acid. The 16S rRNA gene sequence for strain GDB4 has been deposited in GenBank under accession number OR492368.

Description of *Pigmentiphaga litoralis* AN070

Strain AN070 (= NIBRBAC000510598), isolated from wetland sediment collected at Anseongcheon Stream, Anseong-si, Gyeonggi-do, Korea, is a Gram-stain-negative, rod-shaped bacterium. Colonies formed on R2A agar at 28°C after 3 days of incubation are circular with entire margins, flat, and yellow in color. The strain is negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease activity, esculin hydrolysis, gelatin hydrolysis, and β -galactosidase. It utilizes adipic acid, malic acid, and trisodium citrate as sole carbon sources, but not D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, or phenylacetic acid. The 16S rRNA gene sequence of strain AN070 has been deposited in GenBank under the accession number OR527133.

Description of *Burkholderia australis* MAW7

Strain MAW7 (= NIBRBAC000510847), isolated from agricultural soil sampled at Haksan-gil, Mureungdowon-myeon, Yeongwol-gun, Gangwon-do, Korea, is a Gram-stain-negative, rod-shaped bacterium. Colonies formed on R2A agar at 28°C after 3 days of incubation are circular, entire, convex, smooth, and white in color. The strain is positive for esculin hydrolysis and β -galactosidase, but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, and gelatin hydrolysis. It utilizes D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, potassium gluconate, and malic acid as sole carbon sources, but does not utilize D-maltose, capric acid, adipic acid, trisodium citrate, or phenylacetic acid. The 16S rRNA gene sequence for strain MAW7 has been deposited in GenBank under accession number OR759236.

Description of *Burkholderia diffusa* M34

Strain M34 (= NIBRBAC000510732), isolated from soil at Nowon-gu, Seoul, Korea, is a Gram-stain-negative, rod-shaped bacterium. Colonies formed on R2A agar at 25°C after 3 days of incubation are circular, slightly convex, glistening, and cream in color. The strain is positive for nitrate reduction, urease activity, esculin hydrolysis, and β -galactosidase, but negative for indole production, glucose fer-

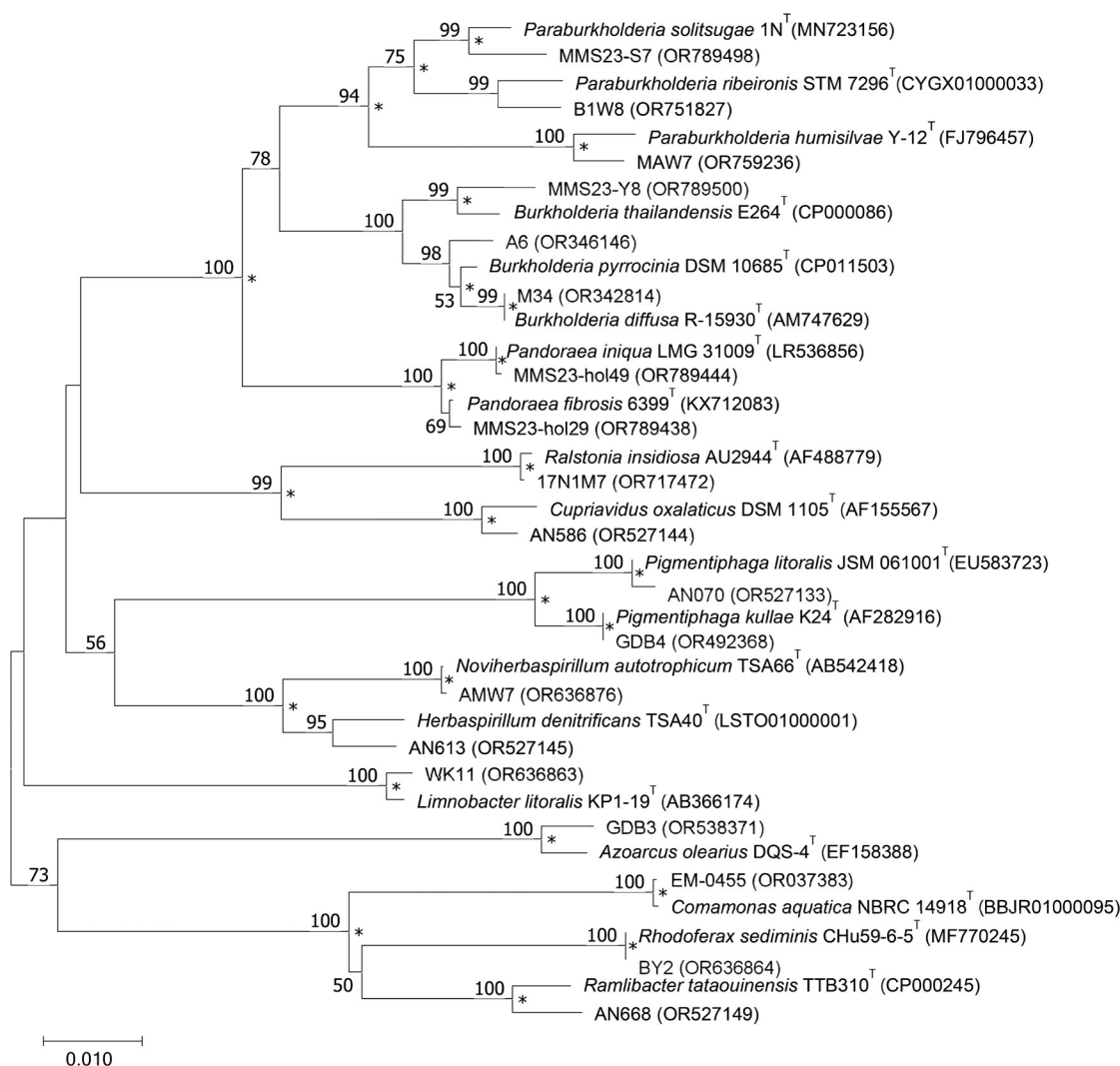


Fig. 2. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences showing the relationships between the strains isolated in this study and their relatives of the class *Betaproteobacteria* in the phylum *Pseudomonadota*. Bootstrap values (> 50%) are shown at branching points. Asterisks indicate the nodes also recovered in the maximum-likelihood and maximum-parsimony trees. Bar, 0.01 substitutions per nucleotide position.

mentation, arginine dihydrolase, and gelatin hydrolysis. It utilizes 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 as sole carbon sources. The 16S rRNA gene sequence for strain M34 has been deposited in Gen Bank under accession number OR342814.

Description of *Burkholderia pyrrocinia* A6

Strain A6 (= NIBRBAC000510740), isolated from soil sampled at Nowon-gu, Seoul, Korea, is a Gram-stain-negative, rod-shaped bacterium. Colonies formed on R2A agar at 25°C after 3 days of incubation are circular, slightly convex, glistening, and cream in color. The strain is positive

for nitrate reduction, urease activity, esculin hydrolysis, and β -galactosidase, but negative for indole production, glucose fermentation, arginine dihydrolase, and gelatin hydrolysis. It utilizes 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 as sole carbon sources. The 16S rRNA gene sequence for strain A6 has been deposited in GenBank under accession number OR346146.

Description of *Burkholderia thailandensis* MMS23-Y8

Strain MMS23-Y8 (= NIBRBAC000510817), isolated from soil collected at Singawon-dong, Seo-gu, Daejeon, Korea, is a Gram-stain-negative, rod-shaped bacterium.

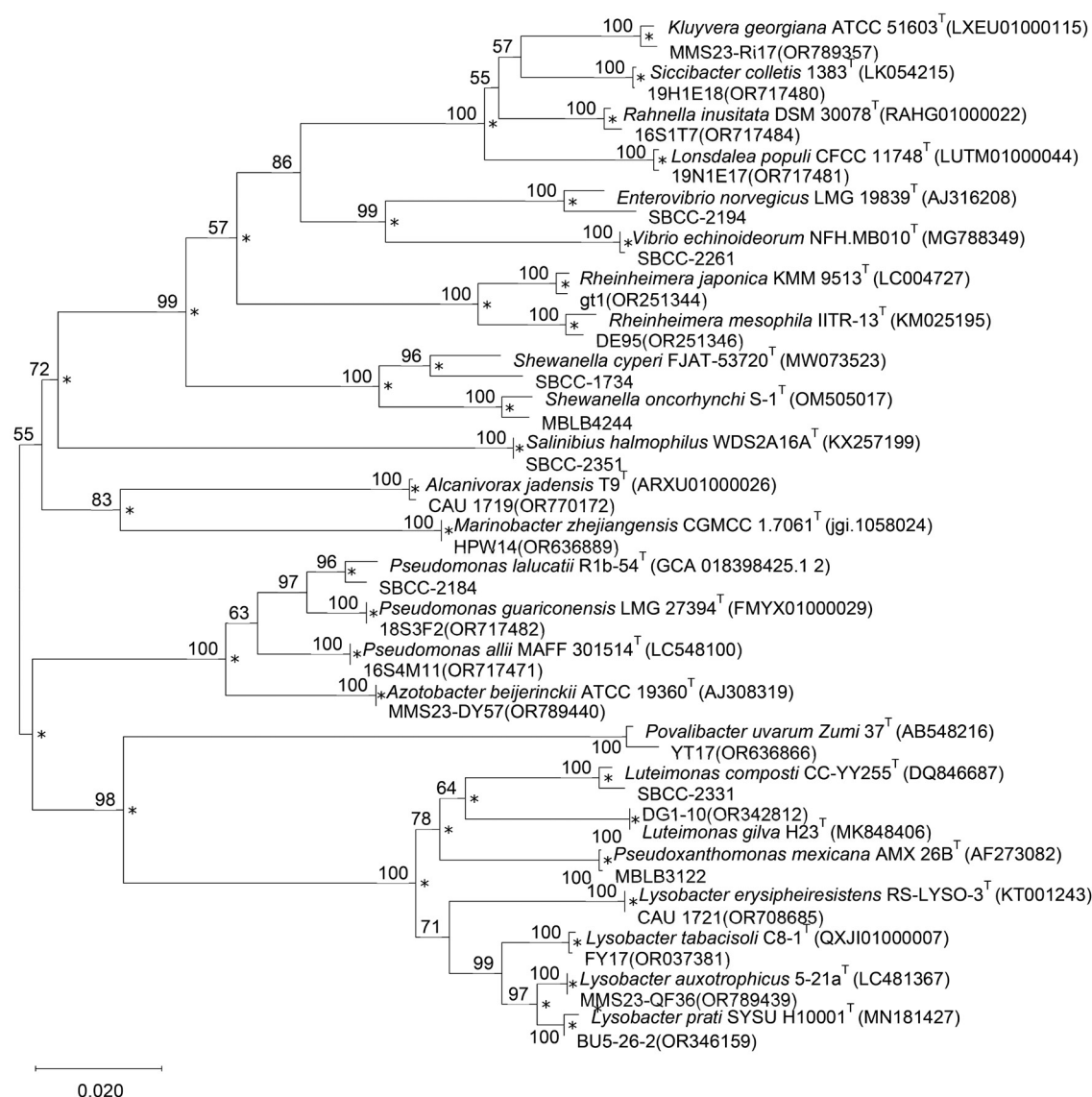


Fig. 3. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences showing the relationships between the strains isolated in this study and their relatives of the class *Gammaproteobacteria* in the phylum *Pseudomonadota*. Bootstrap values (> 50%) are shown at branching points. Asterisks indicate the nodes also recovered in the maximum-likelihood and maximum-parsimony trees. Bar, 0.02 substitutions per nucleotide position.

Colonies formed on R2A agar at 30°C after 7 days of incubation are circular, flat to slightly convex, smooth, glistening, and cream-colored. The strain is positive for nitrate reduction, glucose fermentation, arginine dihydrolase, urease activity, and gelatin hydrolysis, but negative for indole production, esculin hydrolysis, and β -galactosidase. It utilizes D-glucose, D-mannitol, *N*-acetyl-glucosamine, potassium gluconate, capric acid, malic acid, and trisodium citrate as sole carbon sources, but does not utilize L-arabinose, D-mannose, D-maltose, adipic acid, malic acid, or trisodium citrate. The 16S rRNA gene sequence of strain MMS23-Y8 has been deposited in GenBank under the accession number OR789500.

Description of *Cupriavidus neocaledonicus* AN586

Strain AN586 (= NIBRBAC000510608), isolated from wetland sediment collected at Anseongcheon Stream, Anseong-si, Gyeonggi-do, Korea, is a Gram-stain-negative, rod-shaped bacterium. Colonies grown on R2A agar at 28°C for 3 days are circular with entire margins, raised, and white in color. The strain is positive for glucose fermentation, arginine dihydrolase, and urease activity, but negative for nitrate reduction, indole production, esculin hydrolysis, gelatin hydrolysis, β -galactosidase, and cytochrome oxidase. It utilizes D-glucose, potassium gluconate, capric acid, adipic acid, and malic acid as sole carbon sources, but does not utilize L-arabinose, D-mannose, D-

mannitol, *N*-acetyl-glucosamine, D-maltose, trisodium citrate, or phenylacetic acid. The 16S rRNA gene sequence of strain AN586 has been deposited in GenBank under the accession number OR527144.

Description of *Limnobacter litoralis* WK11

Strain WK11 (=NIBRBAC000510793), isolated from sewage sampled at Sinun-ri, Buan-eup, Jeollabuk-do, Korea, is a Gram-stain-negative, rod-shaped bacterium. Colonies formed on R2A agar at 28°C after 3 days of incubation are circular, entire, convex, smooth, and white in color. The strain is positive for esculin hydrolysis, but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, gelatin hydrolysis, and β -galactosidase. It utilizes malic acid as a sole carbon source, but does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, trisodium citrate, or phenylacetic acid. The 16S rRNA gene sequence for strain WK11 has been deposited in GenBank under accession number OR636863.

Description of *Pandoraea fibrosis* MMS23-hol29

Strain MMS23-hol29 (=NIBRBAC000510829), isolated from soil collected at Hoenggye-ri, Daegwallyeong-myeon, Pyeongchang-gun, Gangwon State, Korea, is a Gram-stain-negative, rod-shaped bacterium. Colonies formed on R2A agar at 30°C after 3 days of incubation are circular, flat, and white in color. The strain is positive for arginine dihydrolase, urease activity, esculin hydrolysis, and β -galactosidase, but negative for nitrate reduction, indole production, glucose fermentation, and gelatin hydrolysis. It utilizes D-glucose, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, malic acid, trisodium citrate, and phenylacetic acid as sole carbon sources, but does not utilize L-arabinose, D-mannose, D-mannitol, capric acid, or adipic acid. The 16S rRNA gene sequence of strain MMS23-hol29 has been deposited in GenBank under the accession number OR789438.

Description of *Pandoraea iniqua* MMS23-hol49

Strain MMS23-hol49 (=NIBRBAC000510830), isolated from soil sampled at Okcheon-gun, Chungcheongbuk-do, Korea, is a Gram-stain-negative, rod-shaped bacterium. Colonies formed on R2A agar at 30°C after 3 days of incubation are circular, flat, and white in color. The strain is positive for arginine dihydrolase, urease activity, and esculin hydrolysis, but negative for nitrate reduction, indole production, glucose fermentation, gelatin hydrolysis, and β -galactosidase. It utilizes potassium gluconate, capric acid, malic acid, trisodium citrate, and phenylacetic acid as sole carbon sources, but does not utilize D-glucose, L-arabi-

nose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, or adipic acid. The 16S rRNA gene sequence for strain MMS23-hol49 has been deposited in GenBank under accession number OR789444.

Description of *Paraburkholderia ribeironis* B1W8

Strain B1W8 (=NIBRBAC000510802), isolated from agricultural soil sampled at 979-1 Geoje-dong, Yeonje-gu, Busan, Korea, is a Gram-stain-negative, coccus-shaped bacterium. Colonies formed on R2A agar at 28°C after 3 days of incubation are circular, entire, convex, smooth, and white in color. The strain is positive for esculin hydrolysis and β -galactosidase, but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, and gelatin hydrolysis. It does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, or phenylacetic acid as sole carbon sources. The 16S rRNA gene sequence for strain B1W8 has been deposited in GenBank under accession number OR75182.

Description of *Paraburkholderia solitsugae* MMS23-S7

Strain MMS23-S7 (=NIBRBAC000510816), isolated from soil collected at Songnisan Mountain, Boeun, North Chungcheong Province, Korea, is a Gram-stain-negative, rod-shaped bacterium. Colonies grown on starch-casein agar (SCA) at 30°C for 7 days are circular, flat to slightly convex, smooth, glistening, and cream-colored. The strain is positive for β -galactosidase activity, but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease activity, esculin hydrolysis, and gelatin hydrolysis. It utilizes *N*-acetyl-glucosamine as a sole carbon source, but does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, or phenylacetic acid. The 16S rRNA gene sequence of strain MMS23-S7 has been deposited in GenBank under the accession number OR789498.

Description of *Ralstonia insidiosa* 17N1M7

Strain 17N1M7 (=NIBRBAC000510543), isolated from sediment soil collected at Guman-ri, Gandong-myeon, Hwacheon-gun, Gangwon-do, Korea, is a Gram-stain-negative, rod-shaped bacterium. Colonies grown on R2A agar at 30°C for 2 days are circular with entire margins, glistening, and cream-colored. The strain is positive for urease activity, esculin hydrolysis, and gelatin hydrolysis, but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, β -galactosidase, and cytochrome oxidase. It utilizes D-glucose, *N*-acetyl-glucosa-

mine, potassium gluconate, capric acid, adipic acid, malic acid, and trisodium citrate as sole carbon sources, but does not utilize L-arabinose, D-mannose, D-mannitol, D-maltose, or phenylacetic acid. The 16S rRNA gene sequence of strain 17N1M7 has been deposited in GenBank under the accession number OR717472.

Description of *Comamonas aquaticum* EM-0455

Strain EM-0455 (= NIBRBAC000510791), isolated from agricultural soil sampled at 185 Okrim-ri, Ganghwa-eup, Ganghwa-gun, Incheon, Korea, is a Gram-stain-negative, rod-shaped bacterium. Colonies formed on PTYG agar at 28°C after 4 days of incubation are circular, entire, convex, smooth, and white in color. The strain is positive for nitrate reduction and esculin hydrolysis, but negative for indole production, glucose fermentation, arginine dihydrolase, urease, gelatin hydrolysis, β -galactosidase, and cytochrome oxidase. It utilizes capric acid, adipic acid, and malic acid as sole carbon sources, but does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, trisodium citrate, or phenylacetic acid. The 16S rRNA gene sequence for strain EM-0455 has been deposited in GenBank under accession number OR037383.

Description of *Ramlibacter tataouinensis* AN668

Strain AN668 (= NIBRBAC000510613), isolated from wetland sediment collected at Anseongcheon Stream, Anseong-si, Gyeonggi-do, Korea, is a Gram-stain-negative, rod-shaped bacterium. Colonies formed on R2A agar at 28°C after 3 days of incubation are circular with entire margins, flat, and white in color. The strain is negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease activity, esculin hydrolysis, gelatin hydrolysis, and β -galactosidase. It does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, or phenylacetic acid as sole carbon sources. The 16S rRNA gene sequence of strain AN668 has been deposited in GenBank under the accession number OR527149.

Description of *Rhodferax sediminis* BY2

Strain BY2 (= NIBRBAC000510795), isolated from agricultural soil sampled at 699-2 Heungup-ri, Heungup-myeon, Wonju-si, Gangwon-do, Korea, is a Gram-stain-negative, rod-shaped bacterium. Colonies formed on R2A agar at 28°C after 3 days of incubation are circular, entire, convex, smooth, and yellow in color. The strain is positive for nitrate reduction and esculin hydrolysis, but negative for indole production, glucose fermentation, arginine dihydrolase, urease, gelatin hydrolysis, β -galactosidase, and

cytochrome oxidase. It does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, or phenylacetic acid as sole carbon sources. The 16S rRNA gene sequence for strain BY2 has been deposited in GenBank under accession number OR636864.

Description of *Herbaspirillum denitrificans* AN613

Strain AN613 (= NIBRBAC000510609), isolated from wetland sediment collected at Anseongcheon Stream, Anseong-si, Gyeonggi-do, Korea, is a Gram-stain-negative, rod-shaped bacterium. Colonies formed on R2A agar at 28°C after 5 days of incubation are circular with entire margins, flat, and pale yellow in color. The strain is positive for nitrate reduction, but negative for indole production, glucose fermentation, arginine dihydrolase, urease activity, esculin hydrolysis, gelatin hydrolysis, and β -galactosidase. It utilizes D-glucose, D-mannose, D-mannitol, and adipic acid as sole carbon sources, but does not utilize L-arabinose, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, malic acid, trisodium citrate, or phenylacetic acid. The 16S rRNA gene sequence of strain AN613 has been deposited in GenBank under the accession number OR527145.

Description of *Noviherbaspirillum autotrophicum* AMW7

Strain AMW7 (= NIBRBAC000510842), isolated from agricultural soil sampled at 1260-18 Changgi-ri, Anmyeon-eup, Chungcheongnam-do, Korea, is a Gram-stain-negative, rod-shaped bacterium. Colonies formed on R2A agar at 28°C after 3 days of incubation are circular, entire, convex, smooth, and brown in color. The strain is positive for nitrate reduction and esculin hydrolysis, but negative for indole production, glucose fermentation, arginine dihydrolase, urease, gelatin hydrolysis, β -galactosidase, and cytochrome oxidase. It does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, or phenylacetic acid as sole carbon sources. The 16S rRNA gene sequence for strain AMW7 has been deposited in GenBank under accession number OR636876.

Description of *Azoarcus olearius* GDB3

Strain GDB3 (= NIBRBAC000510561), isolated from soil in Oryu-dong, Seo-gu, Incheon, exhibits Gram-stain-negative, rod-shaped cellular morphology. Colonies cultured on R2A medium at 30°C for 2 days are circular, convex, smooth, and yellowish. Physiologically, strain GDB3 is positive for esculin hydrolysis but negative for nitrate re-

duction, indole production, glucose fermentation, arginine dihydrolase, urease, gelatin hydrolysis, β -galactosidase, and cytochrome oxidase. It utilizes D-mannose, D-mannitol, D-maltose, potassium gluconate, adipic acid, and trisodium citrate as sole carbon sources, but does not D-glucose, L-arabinose, *N*-acetyl-glucosamine, capric acid, malic acid, or phenylacetic acid. The 16S rRNA gene sequence for strain GDB3 has been deposited in GenBank under accession number OR538371.

Description of *Marinobacter zhejiangensis* HPW14

Strain HPW14 (= NIBRBAC000510849), isolated from mudflat sampled at Samsan-myeon, Ganghwa-gun, Incheon, Korea, is a Gram-stain-negative, rod-shaped bacterium. Colonies formed on MA agar at 28°C after 3 days of incubation are circular, entire, convex, smooth, and white in color. The strain is positive for esculin hydrolysis, but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, gelatin hydrolysis, and β -galactosidase. It does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, or phenylacetic acid as sole carbon sources. The 16S rRNA gene sequence for strain HPW14 has been deposited in GenBank under accession number OR636889.

Description of *Shewanella jiangmenensis* SBCC-1734

Strain SBCC-1734 (= NIBRBAC000510514), isolated from seawater sampled at Seocheon-gun, Chungcheongnam-do, Korea, is a Gram-stain-negative, rod-shaped bacterium. Colonies formed on MA agar at 25°C after 3 days of incubation are circular, slightly convex, smooth, glistening, and light orange in color. The strain is positive for nitrate reduction, esculin hydrolysis, and gelatin hydrolysis, and weakly positive for β -galactosidase, but negative for indole production, glucose fermentation, arginine dihydrolase, and urease. It utilizes D-glucose, D-mannose, *N*-acetyl-glucosamine, D-maltose, and malic acid as sole carbon sources, but does not utilize L-arabinose, D-mannitol, potassium gluconate, capric acid, adipic acid, trisodium citrate, or phenylacetic acid.

Description of *Shewanella oncorhynchi* MBLB4244

Strain MBLB4244 (= NIBRBAC000510678), isolated from soil sampled at Jeodong, Gangneung-si, Gangwon State, Korea, is a Gram-stain-negative, rod-shaped bacterium. Colonies formed on R2A agar at 30°C after 3 days of incubation are round, umbonate, with entire margins, and cream in color. The strain is positive for nitrate reduction, urease activity, esculin hydrolysis, and gelatin hydrolysis, but negative for indole production, glucose fermentation,

arginine dihydrolase, and β -galactosidase. It utilizes *N*-acetyl-glucosamine, D-maltose, capric acid, and malic acid as sole carbon sources, but does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, potassium gluconate, adipic acid, trisodium citrate, or phenylacetic acid.

Description of *Rheinheimera japonica* gt1

Strain gt1 (= NIBRBAC000510643), isolated from soil sampled at Gaetgol Ecological Park in Janggok-dong, Siheung-si, Gyeonggi-do, Korea, is a Gram-stain-negative, rod-shaped bacterium. Colonies formed on MA agar at 30°C after 3 days of incubation are circular, convex, opaque, and yellow in color. The strain is positive for esculin hydrolysis and β -galactosidase, but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, gelatin hydrolysis, and β -galactosidase. It utilizes D-glucose, *N*-acetyl-glucosamine, and D-maltose as sole carbon sources, but does not utilize L-arabinose, D-mannose, D-mannitol, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, or phenylacetic acid. The 16S rRNA gene sequence for strain gt1 has been deposited in GenBank under accession number OR251344.

Description of *Rheinheimera mesophila* DE95

Strain DE95 (= NIBRBAC000510644), isolated from soil sampled at Dongguk University Biomedical Campus, Ilsan-dong-gu, Goyang-si, Gyeonggi-do, Korea, is a Gram-stain-negative, rod-shaped bacterium. Colonies formed on R2A agar at 30°C after 3 days of incubation are circular, convex, with brick-colored mycelium and yellow pigmentation. The strain is positive for esculin hydrolysis, gelatin hydrolysis, and β -galactosidase, but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, and urease. It utilizes *N*-acetyl-glucosamine and D-maltose as sole carbon sources, but does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, or phenylacetic acid. The 16S rRNA gene sequence for strain DE95 has been deposited in GenBank under accession number OR251346.

Description of *Kluyvera georgiana* MMS23-Ri17

Strain MMS23-Ri17 (= NIBRBAC000510834), isolated from soil sampled at Jang-dong, Daedeok-gu, Daejeon, Korea, is a Gram-stain-negative, rod-shaped bacterium. Colonies formed on LB agar at 30°C after 3 days of incubation are circular, smooth, glistening, and cream in color. The strain is positive for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis, and β -galactosidase, but negative for gelatin hydrolysis. It utilizes D-glucose, L-arabinose, D-

mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, malic acid, trisodium citrate, and phenylacetic acid as sole carbon sources, but does not utilize capric acid or adipic acid. The 16S rRNA gene sequence for strain MMS23-Ri17 has been deposited in GenBank under accession number OR789357.

Description of *Siccibacter colletis* 19H1E18

Strain 19H1E18 (=NIBRBAC000510551), isolated from sediment soil sampled at Wabu-eup, Namyangju-si, Gyeonggi-do, Korea, is a Gram-stain-negative, rod-shaped bacterium. Colonies formed on ISP2 agar at 30°C after 3 days of incubation are opaque, circular, and pale yellow in color. The strain is positive for nitrate reduction, glucose fermentation, esculin hydrolysis, and β -galactosidase, but negative for indole production, arginine dihydrolase, urease, gelatin hydrolysis, and cytochrome oxidase. It utilizes D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, malic acid, and trisodium citrate as sole carbon sources, but does not utilize capric acid, adipic acid, or phenylacetic acid. The 16S rRNA gene sequence for strain 19H1E18 has been deposited in GenBank under accession number OR717480.

Description of *Lonsdalea populi* 19N1E17

Strain 19N1E17 (=NIBRBAC000510552), isolated from sediment soil sampled at Okchun-gun, Guman-ri, Gandong-myeon, Hwacheon-gun, Gangwon-do, Korea, is a Gram-stain-negative, rod-shaped bacterium. Colonies formed on R2A agar at 30°C after 2 days of incubation are round, convex, and light cream in color. The strain is positive for glucose fermentation, arginine dihydrolase, urease, and esculin hydrolysis, but negative for nitrate reduction, indole production, gelatin hydrolysis, β -galactosidase, and cytochrome oxidase. It utilizes D-glucose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, and potassium gluconate as sole carbon sources, but does not utilize L-arabinose, D-maltose, capric acid, adipic acid, malic acid, trisodium citrate, or phenylacetic acid. The 16S rRNA gene sequence for strain 19N1E17 has been deposited in GenBank under accession number OR717481.

Description of *Rahnella inusitata* 16S1T7

Strain 16S1T7 (=NIBRBAC000510555), isolated from sediment soil sampled at Nampyeong-ri, Bukpyeong-myeon, Jeongseon-gun, Gangwon-do, Korea, is a Gram-stain-negative, rod-shaped bacterium. Colonies formed on R2A agar at 30°C after 2 days of incubation are round, convex, smooth with entire margins, and cream in color. The strain is positive for nitrate reduction, glucose fermentation, esculin hydrolysis, gelatin hydrolysis, and β -galactosidase, but negative for indole production, arginine dihydro-

lase, urease, and cytochrome oxidase. It utilizes D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, malic acid, and trisodium citrate as sole carbon sources, but does not utilize capric acid, adipic acid, or phenylacetic acid. The 16S rRNA gene sequence for strain 16S1T7 has been deposited in GenBank under accession number OR717484.

Description of *Lysobacter auxotrophicus* MMS23-QF36

Strain MMS23-QF36 (=NIBRBAC000510828), isolated from soil sampled at Heukseok-dong, Seo-gu, Daejeon, Korea, is a Gram-stain-negative, rod-shaped bacterium. Colonies formed on R2A agar at 30°C after 3 days of incubation are circular, flat, and pale yellow in color. The strain is positive for nitrate reduction, esculin hydrolysis, and gelatin hydrolysis, but negative for indole production, glucose fermentation, arginine dihydrolase, urease, and β -galactosidase. It utilizes *N*-acetyl-glucosamine and D-maltose as sole carbon sources, but does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, or phenylacetic acid. The 16S rRNA gene sequence for strain MMS23-QF36 has been deposited in GenBank under accession number OR789439.

Description of *Lysobacter erysipheiresistens* CAU 1721

Strain CAU 1721 (=NIBRBAC000510778), isolated from soil sampled at Cheongwon-gu, Cheongju-si, Chungcheongbuk-do, Korea, is a Gram-stain-negative, rod-shaped bacterium. Colonies formed on MA agar at 30°C after 3 days of incubation are circular, smooth, entire, convex, translucent, and yellow in color. The strain is positive for esculin hydrolysis, gelatin hydrolysis, and β -galactosidase, but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, and urease. It does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, or phenylacetic acid as sole carbon sources. The 16S rRNA gene sequence for strain CAU 1721 has been deposited in GenBank under accession number OR708685.

Description of *Lysobacter prati* BU5-26-2

Strain BU5-26-2 (=NIBRBAC000510749), isolated from soil sampled at Nowon-gu, Seoul, Korea, is a Gram-stain-negative, rod-shaped bacterium. Colonies formed on R2A agar at 25°C after 3 days of incubation are circular, slightly convex, glistening, and pale orange yellow in color. The strain is positive for nitrate reduction, arginine dihydrolase, esculin hydrolysis, gelatin hydrolysis, and β -galactosidase, but negative for indole production, glucose fermentation, and urease. It does not utilize D-glu-

cose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, or phenylacetic acid as sole carbon sources. The 16S rRNA gene sequence for strain BU5-26-2 has been deposited in GenBank under accession number OR346159.

Description of *Lysobacter tabacisoli* FY17

Strain FY17 (=NIBRBAC000510790), isolated from agricultural soil sampled at 644-3 Geumsan-ri, Seo-myeon, Chuncheon-si, Gangwon-do, Korea, is a Gram-stain-negative, rod-shaped bacterium. Colonies formed on PTYG agar at 28°C after 4 days of incubation are circular, undulate, convex, smooth, and yellow in color. The strain is positive for esculin hydrolysis, gelatin hydrolysis, and β -galactosidase, but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, and urease. It does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, or phenylacetic acid as sole carbon sources. The 16S rRNA gene sequence for strain FY17 has been deposited in GenBank under accession number OR037381.

Description of *Luteimonas composti* SBCC-2331

Strain SBCC-2331 (=NIBRBAC000510522), isolated from seawater sampled at Seogwipo-si, Jeju Island, Korea, is a Gram-stain-negative, rod-shaped bacterium. Colonies formed on MA agar at 7°C after 7 days of incubation are circular, convex, smooth, glistening, and yellow in color. The strain is positive for esculin hydrolysis, gelatin hydrolysis, and β -galactosidase, but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, and urease. It utilizes D-glucose, L-arabinose, *N*-acetyl-glucosamine, D-maltose, and adipic acid as sole carbon sources, but does not utilize D-mannose, D-mannitol, potassium gluconate, capric acid, malic acid, trisodium citrate, or phenylacetic acid.

Description of *Luteimonas gilva* DG1-10

Strain DG1-10 (=NIBRBAC000510731), isolated from soil sampled at Suseong-gu, Daegu, Korea, is a Gram-stain-negative, rod-shaped bacterium. Colonies formed on R2A agar at 25°C after 3 days of incubation are circular, slightly convex, glistening, and cream yellow in color. The strain is positive for esculin hydrolysis and gelatin hydrolysis, but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, and β -galactosidase. It does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, or phenylacetic acid as sole carbon sources. The 16S rRNA gene sequence for strain DG1-10 has

been deposited in GenBank under accession number OR342812.

Description of *Pseudoxanthomonas mexicana* MBLB3122

Strain MBLB3122 (=NIBRBAC000510674), isolated from soil sampled at Seo-gu, Incheon, Korea, is a Gram-stain-negative, rod-shaped bacterium. Colonies formed on ISP2 agar at 30°C after 3 days of incubation are circular, flat, translucent, and pale yellow in color. The strain is positive for esculin hydrolysis, gelatin hydrolysis, and β -galactosidase, but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, and urease. It utilizes D-glucose, D-mannose, *N*-acetyl-glucosamine, D-maltose, and malic acid as sole carbon sources, but does not utilize L-arabinose, D-mannitol, potassium gluconate, capric acid, adipic acid, trisodium citrate, or phenylacetic acid.

Description of *Poalibacter uvarum* YT17

Strain YT17 (=NIBRBAC000510797), isolated from agricultural soil sampled at 979-1 Geoje-dong, Yeonje-gu, Busan, Korea, is a Gram-stain-negative, rod-shaped bacterium. Colonies formed on PTYG agar at 28°C after 4 days of incubation are circular, entire, convex, smooth, and brown in color. The strain is positive for nitrate reduction, esculin hydrolysis, and β -galactosidase, but negative for indole production, glucose fermentation, arginine dihydrolase, urease, and gelatin hydrolysis. It does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, or phenylacetic acid as sole carbon sources. The 16S rRNA gene sequence for strain YT17 has been deposited in GenBank under accession number OR636866.

Description of *Alcanivorax jadensis* CAU 1719

Strain CAU 1719 (=NIBRBAC000510776), isolated from seawater sampled at Unchon Port, Haeundae-gu, Busan, Korea, is a Gram-stain-negative, rod-shaped bacterium. Colonies formed on MA agar at 30°C after 3 days of incubation are filamentous, raised, undulate, and white in color. The strain is negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis, gelatin hydrolysis, β -galactosidase, and cytochrome oxidase. It does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, or phenylacetic acid as sole carbon sources. The 16S rRNA gene sequence for strain CAU 1719 has been deposited in GenBank under accession number OR770172.

Description of *Salinibius halmophilus* SBCC-2351

Strain SBCC-2351 (=NIBRBAC000510518), isolated from tidal flat sampled at Taean-gun, Chungcheongnam-do, Korea, is a Gram-stain-negative, rod-shaped bacterium. Colonies formed on MA agar at 30°C after 5 days of incubation are circular, slightly convex, smooth, glistening, and light yellow in color. The strain is negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis, gelatin hydrolysis, and β -galactosidase. It does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, or phenylacetic acid as sole carbon sources.

Description of *Pseudomonas lalucatii* SBCC-2184

Strain SBCC-2184 (=NIBRBAC000510520), isolated from tidal flat sampled at Gunsan-si, Jeonbuk State, Korea, is a Gram-stain-negative, rod-shaped bacterium. Colonies formed on MA agar at 25°C after 5 days of incubation are filamentous, raised, undulate, and light yellow in color. The strain is positive for arginine dihydrolase and weakly positive for β -galactosidase, but negative for nitrate reduction, indole production, glucose fermentation, urease, esculin hydrolysis, and gelatin hydrolysis. It utilizes D-glucose, D-mannitol, D-maltose, potassium gluconate, capric acid, malic acid, and trisodium citrate as sole carbon sources, but does not utilize L-arabinose, D-mannose, *N*-acetyl-glucosamine, adipic acid, or phenylacetic acid.

Description of *Pseudomonas alii* 16S4M11

Strain 16S4M11 (=NIBRBAC000506170), isolated from sediment soil sampled at Gangsang-myeon, Yangpyeong-gun, Gyeonggi-do, Korea, is a Gram-stain-negative, rod-shaped bacterium. Colonies formed on R2A agar at 30°C after 2 days of incubation are opaque, round with entire margin, raised, smooth, glistening, and light cream in color. The strain is positive for nitrate reduction, arginine dihydrolase, esculin hydrolysis, and gelatin hydrolysis, but negative for indole production, glucose fermentation, urease, β -galactosidase, and cytochrome oxidase. It utilizes D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, malic acid, and trisodium citrate as sole carbon sources, but not adipic acid or phenylacetic acid. The 16S rRNA gene sequence for strain 16S4M11 has been deposited in GenBank under accession number OR717471.

Description of *Pseudomonas guariconensis* 18S3F2

Strain 18S3F2 (=NIBRBAC000510553), isolated from soil sampled at Okchun-gun, Chungcheongbuk-do, Korea,

is a Gram-stain-negative, rod-shaped bacterium. Colonies formed on R2A agar at 30°C after 2 days of incubation are circular, convex, translucent, and light cream in color. The strain is positive for arginine dihydrolase, urease, and esculin hydrolysis, but negative for nitrate reduction, indole production, glucose fermentation, gelatin hydrolysis, β -galactosidase, and cytochrome oxidase. It utilizes D-glucose, D-maltose, potassium gluconate, capric acid, malic acid, and trisodium citrate as sole carbon sources, but does not utilize L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, adipic acid, or phenylacetic acid. The 16S rRNA gene sequence for strain 18S3F2 has been deposited in GenBank under accession number OR717482.

Description of *Azotobacter beijerinckii* MMS23-DY57

Strain MMS23-DY57 (=NIBRBAC000510836), isolated from soil sampled at Okchun-gun, Chungcheongbuk-do, Korea, is a Gram-stain-negative, rod-shaped bacterium. Colonies formed on R2A agar at 30°C after 3 days of incubation are circular, smooth, glistening, and cream in color. The strain is positive for urease and esculin hydrolysis, but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, gelatin hydrolysis, and β -galactosidase. It does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, or phenylacetic acid as sole carbon sources. The 16S rRNA gene sequence for strain MMS23-DY57 has been deposited in GenBank under accession number OR789440.

Description of *Vibrio echinoideorum* SBCC-2261

Strain SBCC-2261 (=NIBRBAC000510509), isolated from tidal flat sampled at Taean-gun, Chungcheongnam-do, Korea, is a Gram-stain-negative, ovoid and rod-shaped bacterium. Colonies formed on MA agar at 25°C after 3 days of incubation are circular, flat to slightly convex, smooth, glistening, and cream in color. The strain is positive for nitrate reduction, glucose fermentation, and β -galactosidase, but negative for indole production, arginine dihydrolase, urease, esculin hydrolysis, and gelatin hydrolysis. It does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, or phenylacetic acid as sole carbon sources.

Description of *Enterovibrio baiacu* SBCC-2194

Strain SBCC-2194 (=NIBRBAC000510508), isolated from seawater sampled at Gampo in Gyeongju, Gyeong-sangbuk-do, Korea, is a Gram-stain-negative, rod-shaped bacterium. Colonies formed on MA agar at 25°C after

3 days of incubation are circular, flat to slightly convex, smooth, glistening, and cream in color. The strain is positive for nitrate reduction, glucose fermentation, and β -galactosidase, but negative for indole production, arginine dihydrolase, urease, esculin hydrolysis, and gelatin hydrolysis. It utilizes malic acid as a sole carbon source, but does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, N-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, trisodium citrate, or phenylacetic acid.

CONFLICTS OF INTEREST

The authors of this paper have no affiliation with any interests and are solely responsible for the paper.

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