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A report of 35 unrecorded bacterial species belonging to the classes *Alphaproteobacteria* and *Betaproteobacteria* in Korea

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During a comprehensive investigation of indigenous prokaryotic species in Korea, 25 and 10 bacterial strains assigned to the classes *Alphaproteobacteria* and *Betaproteobacteria*, respectively, were isolated from diverse environmental habitats, including soil, mud, tidal field, sea water, sand, rusted iron, and leaf. Based on their high 16S rRNA gene sequence similarities (>98.7%) and the formation of robust phylogenetic clades with type species, each strain was assigned to an independent and predefined bacterial species. Since there were no published or official reports regarding these 35 isolates in Korea, they - 25 species of 14 families in the 5 orders of *Alphaproteobacteria* and 10 species of 3 families in the two orders of *Betaproteobacteria* - have been reported as unrecorded species in Korea. In addition, Gram reaction, colony and cell morphology, basic biochemical characteristic, isolation source, and strain ID of each species are also described in the species description sections.

Keywords: *Alphaproteobacteria*, *Betaproteobacteria*, unrecorded species, bacterial diversity, 16S rRNA, taxonomy, indigenous prokaryotic species in Korea

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Introduction

The *Proteobacteria* is the largest bacterial phylum of Gram-negative bacteria, including the classes *Alphaproteobacteria*, *Betaproteobacteria*, *Gammaproteobacteria*, *Deltaproteobacteria*, *Epsilonproteobacteria*, *Zetaproteobacteria*, *Acidithiobacillia*, and *Oligoflexia* (Williams *et al*., 2013; Nakai *et al*., 2014). At the time of writing, the taxonomic classification based on 16S rRNA gene sequences showed that the class *Alphaproteobacteria* includes 16 orders: *Caulobacterales*, *Emcibacterales*, *Iodidimonadales*, *Kiloniellales*, *Kordiimonadales*, *Magnetococcales*, *Micropepsales*, *Minwuiales*, *Parvularculales*, *Pelagibacterales*, *Rhizobiales*, *Rhodobacterales*, *Rhodospirillales*, *Rickettsiales*, *Sneathiellales*, and *Sphingomonadales*. Among them, *Minwuiales* and *Micropepsales* were recently established (Harbison *et al*., 2017; Sun *et al*., 2018). The class *Betaproteobacteria* includes nine orders: *Burkholderiales*, *Ferritrophicales*, *Ferrovales*, *Gallionellales*, *Methylophilales*, *Neisseriales*, *Nitrosomonadales*, *Rhodocyclales*, and *Sulfuricellales*. In 2019, we collected large number of environmental samples from diverse habitats in Korea and isolated various novel and unrecorded bacterial species. In this study, we describe 25 and 10 bacterial species belonging to the *Alphaproteobacteria* and *Betaproteobacteria*, respectively that were previously not reported in Korea.

Materials and Methods

A total of 35 bacterial strains assigned to the class *Alphaproteobacteria* and *Betaproteobacteria* were isolated from various environmental habitats, including soil, mud, tidal field, sea water, sand, rusted iron, and leaf (Table 1). All environmental samples were processed independently, serially diluted, spread onto diverse culture agar media including Mueller-Hinton agar (MH; BD, USA), R2A agar (BD, USA), marine agar 2216 (MA; BD, USA), and tryptic soy agar (TSA; BD, USA) and incubated at 25–37°C for 2–5 days (Table 1). The designated strain identifications (IDs), isolation sources, culture media, and incubation conditions of the isolates are described in Table 1. All strains were isolated as pure cultures and stored as 10–20% glycerol suspension at −80°C and as lyophilized ampoules.

Colony morphology of the strains was observed by eye or a magnifying glass after the cells were cultivated to their stationary phase on their culture agar media. Cellular morphology and cell size were examined by using either transmission electron or scanning electron microscopy. Gram-staining tests were performed using a Gram-staining kit according to the standard procedures. Biochemical characteristics were evaluated by using the API 20NE kit (bioMérieux), according to the manufacturer's instruction.

Bacterial DNA extraction, PCR amplification, and 16S rRNA gene sequencing were performed using standard procedures as described elsewhere (Lee *et al*., 2014). The 16S rRNA gene sequences of the strains assigned to *Alphaproteobacteria* and *Betaproteobacteria* were compared with those of the type strains of validated bacterial species by using the nucleotide similarity search program in the EzBioCloud server (http://www.ezbiocloud.net/identify) (Yoon *et al*. 2017). For phylogenetic analyses, multiple alignments of the 16S rRNA gene sequences between the isolates and established bacterial species were carried out using the ClustalX program (Thompson *et al*., 1997). Evolutionary distances were calculated using the Kimura two-parameter model and the phylogenetic trees were constructed using the MEGA7 program (Kumar *et al*., 2016) based on the neighbor-joining algorithm with 1,000 replications.

Results and Discussion

Twenty-five strains of *Alphaproteobacteria* were distributed into five orders: one strain in *Caulobacterales*, 10 strains in *Rhizobiales*, five strains in *Rhodobacterales*, four strains in *Rhodospirillales*, and five strains in *Sphingomonadales* (Table 1). Ten strains of *Betaproteobacteria* were distributed into two orders: nine strains in *Burk-*

Table 1. Summary of strains isolated belonging to the *Alphaproteobacteria* and *Betaproteobacteia* and their taxonomic affiliations.

Class/phylum	Order	Family	Genus	Strain ID	NIBR ID	Most closely related species	Similarity (%)	Isolation source	Medium	Incubation conditions
Alphaproteobacteria	*Caulobacterales*	*Caulobacteraceae*	*Brevundimonas*	19D2A5	NIBRBAC000503268	*Brevundimonas faecalis*	99.4	soil	MH	30°C, 4d
	Rhizobiales	*Brucellaceae*	*Ochrobactrum*	19D1V26	NIBRBAC000503266	*Ochrobactrum thiophenivorans*	99.6	soil	MH	30°C, 4d
		Devosia_f	*Devosia*	BSSL-BR9	NIBRBAC000503333	*Devosia naphthalenivorans*	98.9	mud	R2A	25°C, 5d
		Methylobacteriaceae	*Microvirga*	MMS19-R33	NIBRBAC000503369	*Microvirga flocculans*	99.6	soil	R2A	30°C, 3d
		Nitrobacteraceae	*Bradyrhizobium*	MMS19-T29	NIBRBAC000503385	*Bradyrhizobium liaoningense*	100	soil	R2A	30°C, 3d
		Phyllobacteriaceae	*Mesorhizobium*	G187	NIBRBAC000503410	*Mesorhizobium plurifarium*	99.2	soil	R2A	25°C, 3d
			Phyllobacterium	BT55	NIBRBAC000502989	*Phyllobacterium zundukense*	100	soil	R2A	25°C, 3d
			Pseudaminobacter	19D1A35	NIBRBAC000503255	*Pseudaminobacter arsenicus*	99.2	soil	MH	30°C, 4d
		Rhizobiaceae	*Rhizobium*	HMF6710	NIBRBAC000503112	*Rhizobium straminoryzae*	98.9	tidal field	R2A	30°C, 3d
			Rhizobium	BT341	NIBRBAC000502997	*Rhizobium cauense*	99.2	soil	R2A	25°C, 3d
	Rhodobacterales	*Rhodobiaceae*	*Parvibaculum*	CAU 1597	NIBRBAC000503247	*Parvibaculum lavamentivorans*	99.6	sand	MA	30°C, 3–4d

Table 1. Continued.

Class/phylum	Order	Family	Genus	Strain ID	NIBR ID	Most closely related species	Similarity (%)	Isolation source	Medium	Incubation conditions
Alphaproteobacteria	*Rhodobacterales*	*Hyphomonadaceae*	*Euryhalocaulis*	CAU 1595	NIBRBAC000503245	*Euryhalocaulis caribicus*	99.3	sand	MA	30°C, 2–3d
		Rhodobacteraceae	*Nioella*	YSTF-M5	NIBRBAC000503332	*Nioella sediminis*	99.6	mud	MA	25°C, 3d
			Paracoccus	KYW1791	NIBRBAC000503285	*Paracoccus halotolerans*	99.5	sea water	MA	25°C, 3d
			Paracoccus	KYW1736	NIBRBAC000503286	*Paracoccus rhizosphaerae*	99.6	sea water	MA	25°C, 3d
			Salipiger	CAU 1521	NIBRBAC000503227	*Salipiger profundus*	99.7	sand	MA	30°C, 2d
	Rhodospirillales	*Acetobacteraceae*	*Roseomonas*	HMF5336	NIBRBAC000503107	*Roseomonas aquatica*	98.8	rusted iron	R2A	30°C, 3d
			Roseomonas	R36	NIBRBAC000503419	*Roseomonas wenyumeiae*	99.9	soil	R2A	25°C, 3d
			Roseomonas	19D1F4	NIBRBAC000503271	*Roseomonas mucosa*	100	soil	MH	30°C, 4d
		Rhodospirillaceae	*Indioceanicola*	KYW1819	NIBRBAC000503292	*Indioceanicola profundi*	99.8	sea water	MA	25°C, 5d
	Sphingomonadales	*Erythrobacteraceae*	*Erythrobacter*	KYW1376	NIBRBAC000503287	*Erythrobacter zhengii*	99.9	sea water	MA	25°C, 5d
		Sphingomonadaceae	*Sphingobium*	FS72	NIBRBAC000503299	*Sphingobium mellinum*	98.8	soil	R2A	25°C, 3d
			Sphingomonas	G119	NIBRBAC000503407	*Sphingomonas changbaiensis*	98.9	soil	R2A	25°C, 3d
			Sphingomonas	BT373	NIBRBAC000503006	*Sphingomonas mali*	99.6	soil	R2A	25°C, 3d
			Sphingomonas	HMF6093	NIBRBAC000503109	*Sphingomonas prati*	99	sea water	R2A	30°C, 3d
Betaproteobacteria	*Burkholderiales*	*Burkholderiaceae*	*Burkholderia*	BT358	NIBRBAC000502988	*Burkholderia contaminans*	99.8	soil	R2A	25°C, 3d
			Burkholderia	BT359	NIBRBAC000502999	*Burkholderia territorii*	99.9	soil	MA	37°C, 3d
			Caballeronia	BG9	NIBRBAC000503390	*Caballeronia glathei*	99.9	soil	TSA	30°C, 3d
			Paraburkholderia	HMF5328	NIBRBAC000503106	*Paraburkholderia caledonica*	99.9	soil	R2A	30°C, 3d
			Paraburkholderia	BT367	NIBRBAC000503004	*Paraburkholderia hiiakae*	99.3	soil	R2A	25°C, 3d
			Paraburkholderia	BT372	NIBRBAC000503005	*Paraburkholderia sabiae*	99.2	soil	R2A	25°C, 3d
		Comamonadaceae	*Azohydromonas*	BT39	NIBRBAC000502985	*Azohydromonas australica*	99.2	soil	R2A	25°C, 2d
			Pseudacidovorax	HMF4787	NIBRBAC000503105	*Pseudacidovorax intermedius*	99.8	leaf	R2A	30°C, 3d
			Ramlibacter	BT69	NIBRBAC000502987	*Ramlibacter henchirensis*	99.4	soil	R2A	25°C, 3d
	Rhodocyclales	*Zoogloeaceae*	*Thauera*	CAU 1556	NIBRBAC000503231	*Thauera chlorobenzoica*	99	sand	MA	30°C, 2d

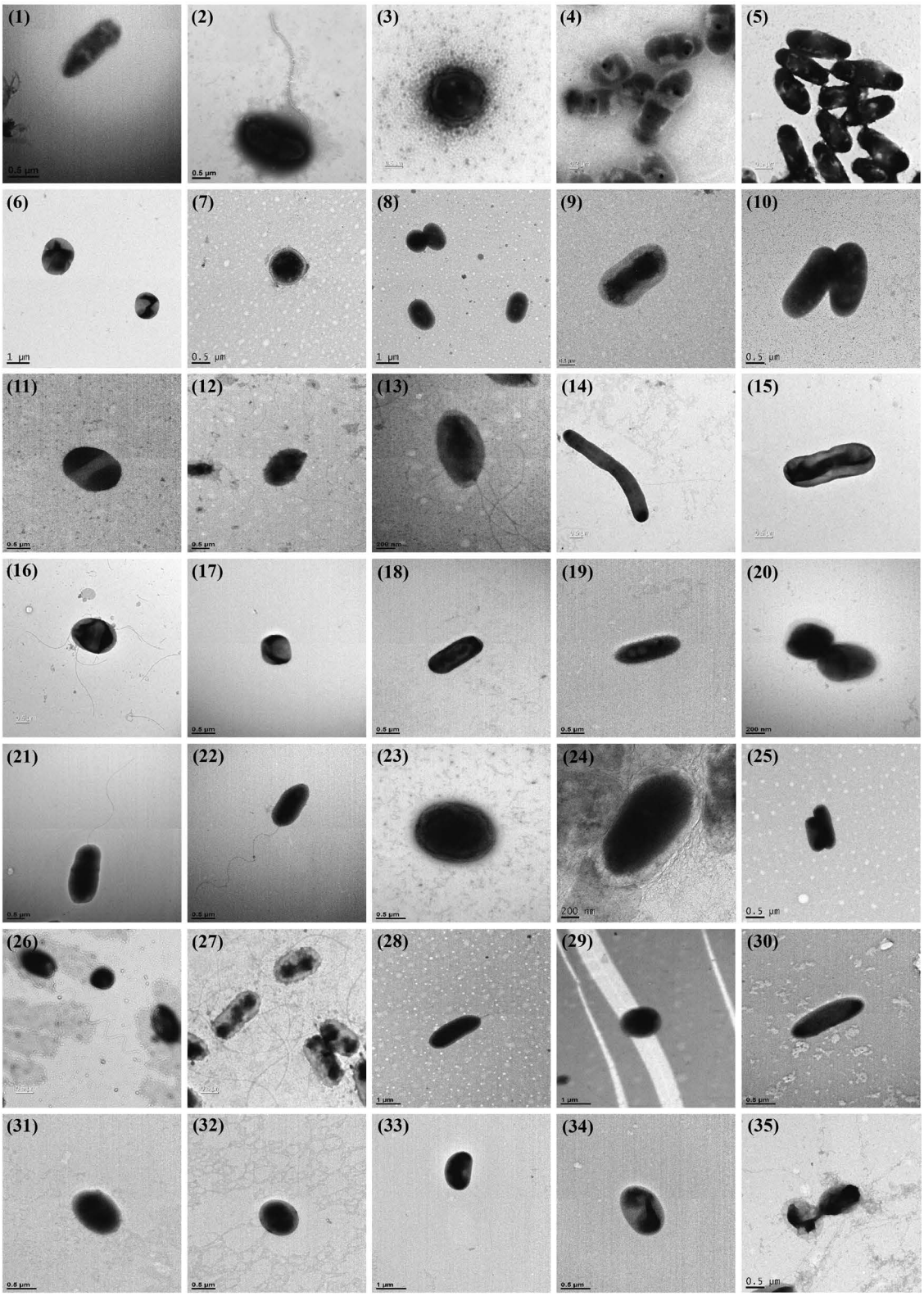

Fig. 1. Transmission electron micrographs or scanning electron micrographs showing the cell morphologies of the strains isolated in this study. The strains were cultured at their optimal growth conditions. Strains: 1, YSTF-M5; 2, BSSL-BR9; 3, HMF5336; 4, HMF6093; 5, HMF6710; 6, KYW1791; 7, KYW1736; 8, KYW1376; 9, KYW1819; 10, FS72; 11, CAU 1521; 12, CAU 1595; 13, CAU 1597; 14, G119; 15, G187; 16, R36; 17, BT55; 18, BT341; 19, BT373; 20, 19D1A35; 21, 19D1V26; 22, 19D2A5; 23, 19D1F4; 24, MMS19-R33; 25, MMS19-T29; 26, HMF4787; 27, HMF5328; 28, CAU 1556; 29, BT39; 30, BT69; 31, BT358; 32, BT359; 33, BT367; 34, BT372; 35, BG9.

holderiales and one strain in *Rhodocyclales*. All strains were Gram-staining-negative and chemoheterotrophic, and 27 strains were rod shaped and eight strains were cocci shaped (Fig. 1).

In the class of *Alphaproteobacteria*, one strain was assigned to the genus *Brevundimonas* of the family *Caulobacteraceae* in the order *Caulobacterales* and 10 strains in the order *Rhizobiales* belonged to seven different families: *Brucellaceae* (one strain), *Devosia_f* (one strain), *Methylobacteriaceae* (one strain), *Nitrobacteraceae* (one strain), *Phyllobacteriaceae* (three strains), *Rhizobiaceae* (two strains), and *Rhodobacteraceae* (one strain). Five strains in the order *Rhodobacterales* belonged to two separate families: *Hyphomonadaceae* (one strain) and *Rhodobacteraceae* (four strains), while four strains in the order *Rhodospirillales* were separated into two families: *Acetobacteraceae* (three strains) and *Rhodospirillaceae* (one strain), and five strains in the order *Sphingomonadales* were separated into two families: *Erythrobacteraceae* (one strain) and *Sphingomonadaceae* (four strains) (Fig. 2).

Ten strains were distributed into two orders, *Burkholderiales* and *Rhodocyclales* of the class *Betaproteobacteria*. Nine strains belonged to two families in the order of *Burkholderiales*: *Burkholderiaceae* (six strains) and *Comamonadaceae* (three strains). One strain belonged to the genus *Thauera* of the family *Zoogloeaceae* of the order *Rhodocyclales* (Fig. 3).

In conclusion, in this study we report 35 unrecorded bacterial species belonging to two proteobacterial classes, *Alphaproteobacteria* and *Betaproteobacteria*, which were isolated in Korea.

Description of *Nioella sediminis* YSTF-M5

Cells are Gram-staining-negative, flagellated and rod shaped. Colonies are circular, slightly convex, glistening, and yellowish gray colored after 3 days of incubation at 25°C on MA. Positive for nitrate reduction, esculin hydrolysis, and β-galactosidase activity. Negative for indole production, glucose fermentation, and arginine dihydrolase, urease activity, and gelatinase activities. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetylglucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain YSTF-M5 (=NIBRBAC000503332) was isolated from a mud sample, Incheon, Korea.

Description of *Devosia naphthalenivorans* BSSL-BR9

Cells are Gram-staining-negative, flagellated and rod shaped. Colonies are circular, convex, glistening, and yellowish white colored after 5 days of incubation at 25°C on R2A. Positive for nitrate reduction, esculin hydrolysis, and arginine dihydrolase, urease, and β-galactosidase activities. Negative for indole production, glucose fermentation, and gelatinase activity. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetylglucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain BSSL-BR9 (=NIBRBAC000503333) was isolated from a mud sample, Boryeong, Korea.

Description of *Roseomonas aquatica* HMF5336

Cells are Gram-staining-negative, non-flagellated and coccus shaped. Colonies are circular, convex, smooth, wet and pale red colored after 3 days of incubation at 30°C on R2A. Negative for nitrate reduction, indole production, glucose fermentation, esculin hydrolysis, and gelatinase, arginine dihydrolase, urease, and β-galactosidase activities. D-Mannitol, *N*-acetylglucosamine, and potassium gluconate are utilized. Does not utilize D-glucose, L-arabinose, D-mannose, D-maltose, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain HMF5336 (=NIBRBAC000503107) was isolated from a rusted iron sample, Yongin, Korea.

Description of *Sphingomonas prati* HMF6093

Cells are Gram-staining-negative, non-flagellated, and rod shaped. Colonies are circular, convex, smooth, and yellow colored after 3 days of incubation at 30°C on R2A. Positive for esculin hydrolysis and β-galactosidase activity. Negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, and gelatinase. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetylglucosamine, D-maltose and potassium gluconate are utilized. Does not utilize capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain HMF 6093 (=NIBRBAC000503109) was isolated from a sea water sample, Jeju, Korea.

Description of *Rhizobium straminoryzae* HMF6710

Cells are Gram-staining-negative, non-flagellated, and rod shaped. Colonies are circular, convex, smooth and cream colored after 3 days of incubation at 30°C on R2A or MA. Positive for esculin hydrolysis and urease and β-galactosidase activities. Negative for nitrate reduction, indole production, glucose fermentation, and arginine dihydrolase and gelatinase activities. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetylglucosamine, D-maltose, potassium gluconate and malic acid are utilized. Does not utilize capric acid, adipic acid, trisodium citrate and phenylacetic acid. Strain HMF6710 (=NIBRBAC000503112) was isolated from a tidal field sample, Wando, Korea.

Description of *Paracoccus halotolerans* KYW1791

Cells are Gram-staining-negative, non-flagellated, and coccus shaped. Colonies are circular, convex, smooth,

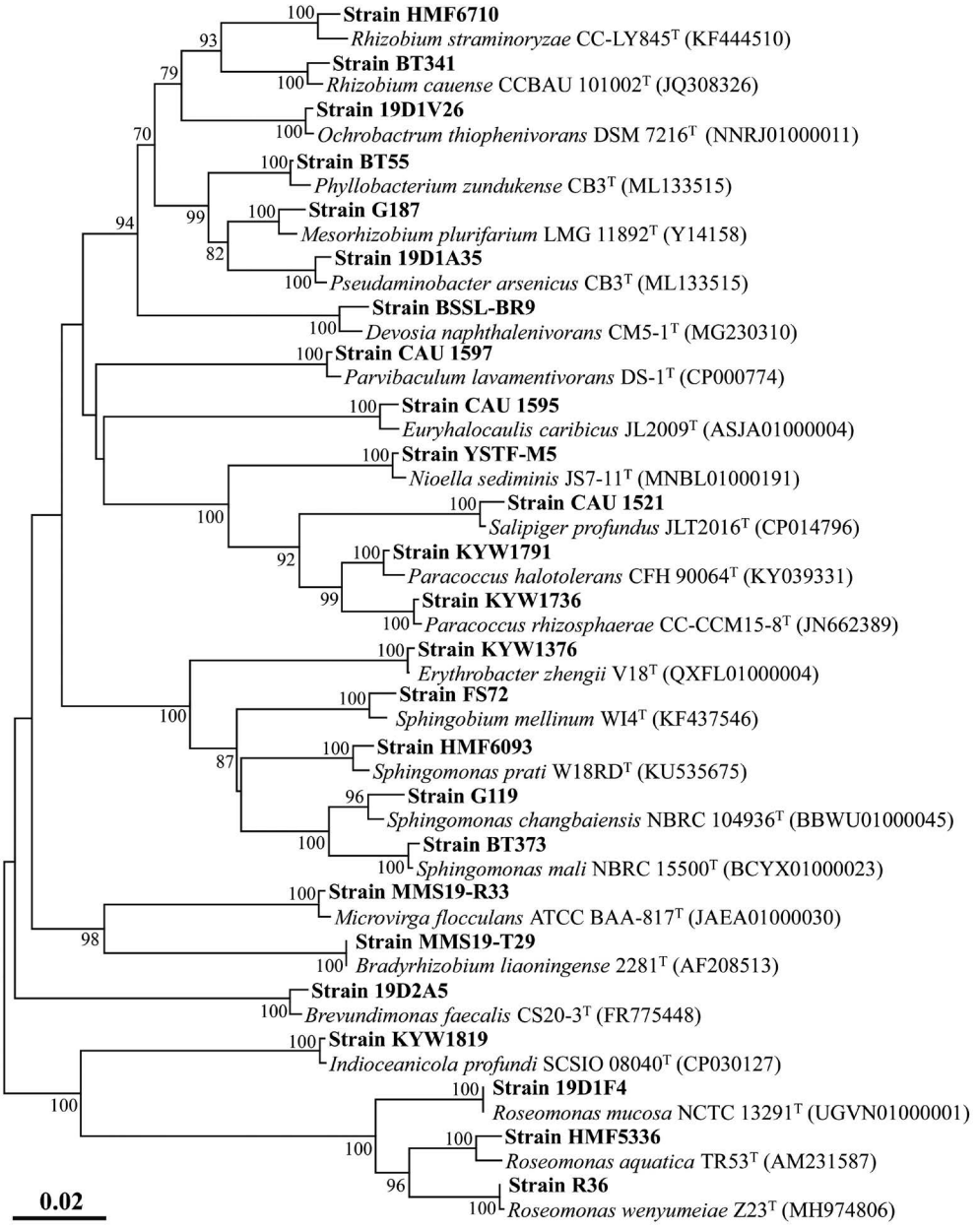

Fig. 2. A neighbor-joining phylogenetic tree, based on 16S rRNA gene sequences, showing the phylogenetic relationships between the strains isolated in this study and their relatives in the orders *Caulobacterales*, *Rhizobiales*, *Rhodobacterales*, *Rhodospirillales*, and *Sphingomonadales* of the class of *Alphaproteobacteria*. Bootstrap values (>70%) are shown above nodes. Scale bar: 0.02 changes per nucleotide.

opaque, and pale orange colored after 3 days of incubation at 25°C on MA. Positive for nitrate reduction, esculin hydrolysis, and β-galactosidase activity. Negative for indole production, glucose fermentation, arginine dihydrolase, and urease and gelatinase activities. D-Glucose, D-mannose, D-mannitol, D-maltose, potassium gluconate, malic acid, trisodium citrate are utilized. Does not utilize L-arabinose, *N*-acetylglucosamine, capric acid, adipic acid, and phenylacetic acid. Strain KYW1791 (=NIBRBAC000503285) was isolated from a sea water sample, Gwangyang, Korea.

Description of *Paracoccus rhizosphaerae* KYW1736

Cells are Gram-staining-negative, non-flagellated, and coccus shaped. Colonies are circular, smooth, convex, opaque, and pale orange colored after 3 days of incubation at 25°C on MA. Positive for nitrate reduction, esculin hydrolysis, and β-galactosidase activity. Negative for indole production, glucose fermentation, and arginine dihydrolase, urease, and gelatinase activities. D-Glucose, L-arabinose, D-mannitol, D-maltose, potassium gluconate and malic acid

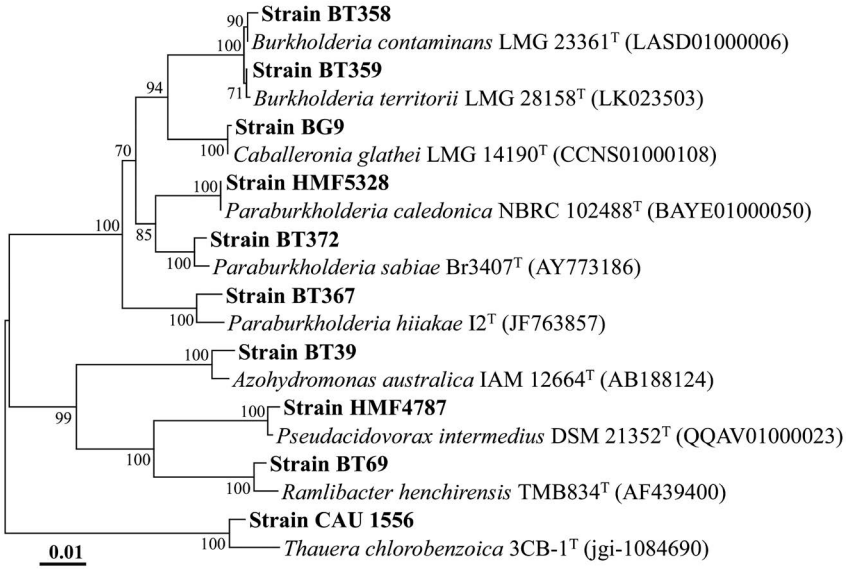

Fig. 3. A neighbor-joining phylogenetic tree, based on 16S rRNA gene sequences, showing the phylogenetic relationships between the strains isolated in this study and their relatives in the orders *Burkholderiales* and *Rhodocyclales* of the class of *Betaproteobacteria*. Bootstrap values (>70%) are shown above nodes. Scale bar: 0.01 changes per nucleotide.

are utilized. Does not utilize D-mannose, *N*-acetylglucosamine, capric acid, adipic acid, trisodium citrate, and phenylacetic acid. Strain KYW1736 (=NIBRBAC00050 3286) was isolated from a sea water sample, Gwangyang, Korea.

Description of *Erythrobacter zhengii* KYW1376

Cells are Gram-staining-negative, non-flagellated, and short rod or coccus shaped. Colonies are circular, smooth, convex, opaque, and orange-yellow colored after 5 days of incubation at 25°C on MA. Positive for indole production and esculin hydrolysis. Negative for nitrate reduction, glucose fermentation, and arginine dihydrolase, urease, gelatinase, and β-galactosidase activities. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetylglucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain KYW1376 (=NIBRBAC000503287) was isolated from a sea water sample, Gwangyang, Korea.

Description of *Indioceanicola profundi* KYW1819

Cells are Gram-staining-negative, non-flagellated, and rod shaped. Colonies are circular, smooth, convex, and pale pink colored after 5 days of incubation at 25°C on MA. Positive for indole production. Negative for nitrate reduction, glucose fermentation, esculin hydrolysis, and arginine dihydrolase, urease, gelatinase, and β-galactosidase activities. Malic acid is utilized. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetylglucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, trisodium citrate, and phenylacetic acid. Strain KYW1819 (=NIBRBAC000503292) was isolated from a sea water sample, Gwangyang, Korea.

Description of *Sphingobium mellinum* FS72

Cells are Gram-staining-negative, non-flagellated, and rod shaped. Colonies are circular, convex, smooth, and yellow colored after 3 days of incubation at 25°C on R2A. Positive for esculin hydrolysis. Negative for nitrate reduction, indole production, glucose fermentation, and arginine dihydrolase, urease, gelatinase, and β-galactosidase activities. D-Glucose is utilized. Does not utilize L-arabinose, D-mannose, D-mannitol, *N*-acetylglucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain FS72 (=NIBRBAC000503299) was isolated from a soil sample, Suncheon, Korea.

Description of *Salipiger profundus* CAU 1521

Cells are Gram-staining-negative, non-flagellated, and rod shaped. Colonies are circular, convex, mucoid, rough, opaque, and cream colored after 2 days of incubation at 30°C on MA. Positive for esculin hydrolysis and urease and β-galactosidase activities. Negative for nitrate reduction, indole production, glucose fermentation, and arginine dihydrolase and gelatinase activities. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetylglucosamine, D-maltose, potassium gluconate, capric acid,

adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain CAU 1521 (=NIBRBAC000503227) was isolated from a sand sample, Busan, Korea.

Description of *Euryhalocaulis caribicus* CAU 1595

Cells are Gram-staining-negative, flagellated, and short rod shaped. Colonies are circular, convex, shiny, opaque, and cream colored after 2−3 days of incubation at 30°C on MA. Positive for nitrate reduction, esculin hydrolysis, and gelatinase and urease activities. Negative for indole production, glucose fermentation, and arginine dihydrolase and β-galactosidase activities. D-Glucose and L-arabinose are utilized. Does not utilize D-mannose, D-mannitol, *N*-acetylglucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain CAU 1595 (=NIBRBAC000503245) was isolated from a sand sample, Incheon, Korea.

Description of *Parvibaculum lavamentivorans* CAU 1597

Cells are Gram-staining-negative, flagellated, and rod shaped. Colonies are circular, convex, smooth, opaque, and cream colored after 3−4 days of incubation at 30°C on MA. Positive for esculin hydrolysis and β-galactosidase activity. Negative for nitrate reduction, indole production, glucose fermentation, and arginine dihydrolase, urease, and gelatinase activities. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetylglucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain CAU 1597 (= NIBRBAC000503247) was isolated from a sand sample, Jeju, Korea.

Description of *Sphingomonas changbaiensis* G119

Cells are Gram-staining-negative, non-flagellated, and rod shaped. Colonies are circular, entire, and light-yellow colored after 3 days of incubation at 25°C on R2A. Negative for nitrate reduction, indole production, glucose fermentation, esculin hydrolysis, and arginine dihydrolase, urease, gelatinase, and β-galactosidase activities. D-Glucose, L-arabinose, D-mannose, D-maltose, and phenylacetic acid are utilized. Does not utilize D-mannitol, *N*-acetylglucosamine, potassium gluconate, capric acid, adipic acid, malic acid, and trisodium citrate. Strain G119 (=NIBRBAC000503407) was isolated from a soil sample, Yeongju, Korea.

Description of *Mesorhizobium plurifarium* G187

Cells are Gram-staining-negative, non-flagellated, and rod shaped. Colonies are circular, convex and cream colored after 3 days of incubation at 25°C on R2A. Positive for urease activity, esculin hydrolysis and β-galactosidase activities. Negative for nitrate reduction, indole production, glucose fermentation, and arginine dihydrolase and gelatinase activities. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetylglucosamine, and malic acid are utilized. Does not utilize D-maltose, potassium gluconate, capric acid, adipic acid, trisodium citrate, and phenylacetic acid. Strain G187 (=NIBRBAC000503410) was isolated from a soil sample, Yeongju, Korea.

Description of *Roseomonas wenyumeiae* R36

Cells are Gram-staining-negative, flagellated, and coccus or ovoid shaped. Colonies are circular, convex, smooth, and light orange colored after 3 days of incubation at 25°C on R2A. Positive for nitrate reduction, esculin hydrolysis, and gelatinase, arginine dihydrolase, and urease activities. Negative for indole production, glucose fermentation, and β-galactosidase activity. D-Glucose, D-mannose, D-mannitol, D-maltose, and trisodium citrate are utilized. Does not utilize L-arabinose, *N*-acetylglucosamine, potassium gluconate, capric acid, adipic acid, malic acid, and phenylacetic acid. Strain R36 (=NIBRBAC000503419) was isolated from a soil sample, Yeongju, Korea.

Description of *Phyllobacterium zundukense* BT55

Cells are Gram-staining-negative, non-flagellated, and short rod shaped. Colonies are circular, smooth, and white colored after 3 days of incubation at 25°C on R2A. Positive for nitrate reduction. Negative for indole production, glucose fermentation, esculin hydrolysis, and arginine dihydrolase, urease, gelatinase, and β-galactosidase activities. D-Glucose, D-maltose and malic acid are utilized. Does not utilize L-arabinose, D-mannose, D-mannitol, *N*-acetylglucosamine, potassium gluconate, capric acid, adipic acid, trisodium citrate, and phenylacetic acid. Strain BT55 (=NIBRBAC000502989) was isolated from a soil sample, Pyeongchang, Korea.

Description of *Rhizobium cauense* BT341

Cells are Gram-staining-negative, non-flagellated, and rod shaped. Colonies are circular, convex, smooth, and white colored after 3 days of incubation at 25°C on R2A. Positive for nitrate reduction, esculin hydrolysis, and urease and β-galactosidase activities. Negative for indole production, glucose fermentation, and arginine dihydrolase and gelatinase activities. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetylglucosamine, D-maltose, and malic acid are utilized. Does not utilize potassium gluconate, capric acid, adipic acid, trisodium citrate, and phenylacetic acid. Strain BT341 (=NIBRBAC000502997) was isolated from a soil sample, Jeju, Korea.

Description of *Sphingomonas mali* BT373

Cells are Gram-staining-negative, non-flagellated, and rod shaped. Colonies are circular, smooth, and yellow colored after 3 days of incubation at 25°C on R2A agar. Positive for esculin hydrolysis and β-galactosidase activity. Negative for nitrate reduction, indole production, glucose fermentation, and arginine dihydrolase, urease, and gelatinase activities. D-Glucose and D-maltose are utilized. Does not utilize L-arabinose, D-mannose, D-mannitol, *N*-acetylglucosamine, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain BT373 (=NIBRBAC000503006) was isolated from a soil sample, Cheongdo, Korea.

Description of *Pseudaminobacter arsenicus* 19D1A35

Cells are Gram-staining-negative, non-flagellated, and rod shaped. Colonies are circular, convex, glistening and brown colored after 4 days of incubation at 30°C on MH. Positive for esculin hydrolysis. Negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, and urease, gelatinase and β-galactosidase activities. D-Glucose, D-mannose, D-mannitol, *N*-acetylglucosamine, adipic acid, malic acid, trisodium citrate and phenylacetic acid are utilized. Does not utilize L-arabinose, D-maltose, potassium gluconate, and capric acid. Strain 19D1A35 (=NIBRBAC000503255) was isolated from a soil sample, Jeongseon, Korea.

Description of *Ochrobactrum thiophenivorans* 19D1V26

Cells are Gram-staining-negative, flagellated, and rod shaped. Colonies are circular, raised, umbonate, and cream colored after 4 days of incubation at 30°C on MH. Positive for nitrate reduction, esculin hydrolysis, and urease activity. Negative for indole production, glucose fermentation, arginine dihydrolase, gelatinase and β-galactosidase activities. D-Glucose, L-arabinose, D-mannose, *N*-acetylglucosamine and malic acid are utilized. Does not utilize D-mannitol, D-maltose, potassium gluconate, capric acid, adipic acid, trisodium citrate, and phenylacetic acid. Strain 19D1V26 (=NIBRBAC000503266) was isolated from a soil sample, Jeongseon, Korea.

Description of *Brevundimonas faecalis* 19D2A5

Cells are Gram-staining-negative, flagellated, and rod shaped. Colonies are circular, convex, glistening, and light yellow colored after 4 days of incubation at 30°C on MH. Positive for esculin hydrolysis. Negative for nitrate reduction, indole production, glucose fermentation, and arginine dihydrolase, urease, gelatinase, and β-galactosidase activities. Capric acid and malic acid are utilized. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetylglucosamine, D-maltose, potassium gluconate, adipic acid, trisodium citrate, and phenylacetic acid. Strain 19D2A5 (=NIBRBAC000503268) was isolated from a soil sample, Jeongseon, Korea.

Description of *Roseomonas mucosa* 19D1F4

Cells are Gram-staining-negative, non-flagellated, and coccus shaped. Colonies are circular, convex, glistening, and pink colored after 4 days of incubation at 30°C on MH. Positive for urease activity and esculin hydrolysis. Negative for nitrate reduction, indole production, glucose fermentation, and arginine dihydrolase, gelatinase, and β-galactosidase activities. D-Glucose, L-arabinose, D-mannitol, potassium gluconate, adipic acid, malic acid, trisodium citrate, and phenylacetic acid are utilized. Does not utilize D-mannose, *N*-acetylglucosamine, D-maltose, and capric acid. Strain 19D1F4 (=NIBRBAC000503271) was isolated from a soil sample, Jeongseon, Korea.

Description of *Microvirga flocculans* MMS19-R33

Cells are Gram-staining-negative, non-flagellated, and rod shaped. Colonies are circular, raised, entire, and pale-cream colored after 3 days of incubation at 30°C on R2A. Positive for nitrate reduction and esculin hydrolysis. Negative for indole production, glucose fermentation, and arginine dihydrolase, urease, gelatinase, and β-galactosidase activities. Does not utilize D-glucose, L-arabinose D-mannose, D-mannitol, *N*-acetylglucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain MMS19-R33 (=NIBRBAC000503369) was isolated from a soil sample, Gurye, Korea.

Description of *Bradyrhizobium liaoningense* MMS19-T29

Cells are Gram-staining-negative, non-flagellated, and rod shaped. Colonies are circular, convex, entire, and cream colored after 3 days of incubation at 30°C on R2A. Positive for nitrate reduction, esculin hydrolysis, and β-galactosidase activity. Negative for indole production, glucose fermentation, and arginine dihydrolase, urease, and gelatinase activities. Does not utilize D-glucose, L-arabinose D-mannose, D-mannitol, *N*-acetylglucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain MMS19-T29 (=NIBRBAC000503385) was isolated from a soil sample, Gurye, Korea.

Description of *Pseudacidovorax intermedius* HMF4787

Cells are Gram-staining-negative, non-flagellated, and short rod shaped. Colonies are circular, convex, smooth,

slimy, and light-yellow colored after 3 days of incubation at 30°C on R2A. Positive for urease activity. Negative for nitrate reduction, indole production, glucose fermentation, esculin hydrolysis, and arginine dihydrolase, gelatinase, and β-galactosidase activities. D-Glucose, potassium gluconate, and malic acid are utilized. Does not utilize L-arabinose, D-mannose, D-mannitol, *N*-acetylglucosamine, D-maltose, capric acid, adipic acid, trisodium citrate, and phenylacetic acid. Strain HMF4787 (=NIBRBAC00050 3105) was isolated from a leaf sample, Yongin, Korea.

Description of *Paraburkholderia caledonica* HMF5328

Cells are Gram-staining-negative, flagellated, and rod shaped. Colonies are circular, convex, smooth, and light-yellow colored after 3 days of incubation at 30°C on R2A. Positive for esculin hydrolysis and β-galactosidase activity. Negative for nitrate reduction, indole production, glucose fermentation, and arginine dihydrolase, urease, and gelatinase activities. D-Glucose, L-arabinose, D-mannitol, *N*-acetylglucosamine, and potassium gluconate are utilized. Does not utilize D-mannose, D-maltose, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain HMF5328 (=NIBRBAC000503106) was isolated from a soil sample, Gangneung, Korea.

Description of *Thauera chlorobenzoica* CAU 1556

Cells are Gram-staining-negative, flagellated, and rod shaped. Colonies are circular, convex, shiny, opaque, and cream colored after 2 days of incubation at 30°C on MA. Positive for nitrate reduction and esculin hydrolysis. Negative for indole production, glucose fermentation, and arginine dihydrolase, urease, gelatinase, and β-galactosidase activities. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetylglucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain CAU 1556 (=NIBRBAC000503231) was isolated from a sand sample, Jeju, Korea.

Description of *Azohydromonas australica* BT39

Cells are Gram-staining-negative, non-flagellated, and coccus shaped. Colonies are circular, smooth, and white colored after 3 days of incubation at 25°C on R2A. Positive for nitrate reduction. Negative for indole production, glucose fermentation, esculin hydrolysis, and arginine dihydrolase, urease, gelatinase, and β-galactosidase activities. D-Glucose is utilized. Does not utilize L-arabinose, D-mannose, D-mannitol, *N*-acetylglucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain BT39 (=NIBRBAC000502985) was isolated from a soil sample, Pyeongchang, Korea.

Description of *Ramlibacter henchirensis* BT69

Cells are Gram-staining-negative, non-flagellated, and rod shaped. Colonies are circular, smooth, and white colored after 3 days of incubation at 25°C on R2A. Positive for gelatinase activity. Negative for nitrate reduction, indole production, glucose fermentation, esculin hydrolysis, and arginine dihydrolase, urease, and β-galactosidase activities. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetylglucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain BT69 (=NIBRBAC000502987) was isolated from a soil sample, Pyeongchang, Korea.

Description of *Burkholderia contaminans* BT358

Cells are Gram-staining-negative, non-flagellated, and rod shaped. Colonies are circular, convex, smooth, and white colored after 3 days of incubation at 25°C on R2A. Positive for arginine dihydrolase, urease, and gelatinase activities. Negative for nitrate reduction, indole production, glucose fermentation, esculin hydrolysis, and β-galactosidase activity. D-Glucose, L-arabinose, potassium gluconate, malic acid, and trisodium citrate and are utilized. Does not utilize D-mannose, D-mannitol, *N*-acetylglucosamine, D-maltose, capric acid, adipic acid, and phenylacetic acid. Strain BT358 (=NIBRBAC000502988) was isolated from a soil sample, Jeju, Korea.

Description of *Burkholderia territorii* BT359

Cells are Gram-staining-negative, non-flagellated, and rod shaped. Colonies are circular, convex, smooth, and yellow colored after 3 days of incubation at 37°C on MA. Positive for esculin hydrolysis and arginine dihydrolase, urease, gelatinase, and β-galactosidase activities. Negative for nitrate reduction, indole production, and glucose fermentation. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetylglucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid are utilized. Strain BT359 (=NIBRBAC 000502999) was isolated from a soil sample, Jeju, Korea.

Description of *Paraburkholderia hiiakae* BT367

Cells are Gram-staining-negative, flagellated, and rod shaped. Colonies are circular, smooth, and white colored after 3 days of incubation at 25°C on R2A. Positive for arginine dihydrolase, urease, and β-galactosidase activities. Negative for nitrate reduction, indole production, glucose fermentation, esculin hydrolysis, and gelatinase activity. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetylglucosamine, potassium gluconate, capric acid, adipic

acid, malic acid, and phenylacetic acid are utilized. Does not utilize D-maltose and trisodium citrate. Strain BT367 (=NIBRBAC000503004) was isolated from a soil sample, Cheongdo, Korea.

Description of *Paraburkholderia sabiae* BT372

Cells are Gram-staining-negative, non-flagellated, and rod shaped. Colonies are circular, smooth, and white colored after 3 days of incubation at 25°C on R2A. Positive for nitrate reduction and β-galactosidase activity. Negative for indole production, glucose fermentation, esculin hydrolysis, and arginine dihydrolase, urease, and gelatinase activities. D-Glucose, D-mannose, D-mannitol, *N*-acetylglucosamine, potassium gluconate, capric acid, malic acid, and phenylacetic acid are utilized. Does not utilize L-arabinose, D-maltose, adipic acid, and trisodium citrate. Strain BT372 (=NIBRBAC000503005) was isolated from a soil sample, Cheongdo, Korea.

Description of *Caballeronia glathei* BG9

Cells are Gram-staining-negative, non-flagellated, and coccus shaped. Colonies are punctiform, convex, entire, and cream colored after 3 days of incubation at 30°C on TSA. Positive for glucose fermentation and arginine dihydrolase, urease, and β-galactosidase activities. Negative for nitrate reduction, indole production, esculin hydrolysis, and gelatinase activity. D-Glucose, L-arabinose, D-mannose, *N*-acetylglucosamine, potassium gluconate, capric acid, malic acid, trisodium citrate, and phenylacetic acid are utilized. Does not utilize D-mannitol, D-maltose, and adipic acid. Strain BG9 (=NIBRBAC000503390) was isolated from a soil sample, Gurye, Korea.

References

Harbison, A.B., L.E. Price, M.D. Flythe and S.L. Bräuer. 2017. *Micropepsis pineolensis* gen. nov., sp. nov., a mildly acidophilic *Alphaproteobacterium* isolated from a poor fen, and proposal of *Micropepsaceae* fam. nov. within *Micropepsales* ord. nov. International Journal of Systematic and Evolutionary Microbiology 67:839-844.

Kumar, S., G. Stecher and K. Tamura. 2016. MEGA7: molecular evolutionary genetics analysis version 7.0 for bigger datasets. Molecular Biology and Evolution 33:1870-1874.

Lee, H.J., S.E. Jeong, M.S. Cho, S.H. Kim, S.S. Lee, B.H. Lee and C.O. Jeon. 2014. *Flavihumibacter solisilvae* sp. nov., isolated from forest soil. International Journal of Systematic and Evolutionary Microbiology 64:2897-2901.

Nakai, R., M. Nishijima, N. Tazato, Y. Handa, F. Karray, S. Sayadi, H. Isoda and T. Naganuma. 2014. *Oligoflexus tunisiensis* gen. nov., sp. nov., a Gram-negative, aerobic, filamentous bacterium of a novel proteobacterial lineage, and description of *Oligoflexaceae* fam. nov., *Oligoflexales* ord. nov. and *Oligoflexia* classis nov. International Journal of Systematic and Evolutionary Microbiology 64:3353-3359.

Sun, C., L. Xu, X.Y. Yu, Z. Zhao, Y.H. Wu, A. Oren, C.S. Wang and X.W. Xu. 2018. *Minwuia thermotolerans* gen. nov., sp. nov., a marine bacterium forming a deep branch in the *Alphaproteobacteria*, and proposal of *Minwuiaceae* fam. nov. and *Minwuiales* ord. nov. International Journal of Systematic and Evolutionary Microbiology 68:3856-3862.

Thompson, J.D., T.J. Gibson, F. Plewniak, F. Jeanmougin and D.G. Higgins. 1997. The Clustal_X windows interface: flexible strategies for multiple sequence alignment aided by quality analysis tools. Nucleic Acids Research 25:4876-4882.

Williams, K.P. and D.P. Kelly. 2013. Proposal for a new class within the phylum *Proteobacteria*, *Acidithiobacillia* classis nov., with the type order *Acidithiobacillales*, and emended description of the class *Gammaproteobacteria*. International Journal of Systematic and Evolutionary Microbiology 63:2901-2906.

Yoon, S.H., S.M. Ha, S. Kwon, J. Lim, Y. Kim, H. Seo and J. Chun. 2017. Introducing EzBioCloud: A taxonomically united database of 16S rRNA and whole genome assemblies. International Journal of Systematic and Evolutionary Microbiology 67:1613-1617.

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