

A report of 46 unrecorded bacterial species in Korea belonging to the classes *Alphaproteobacteria*, *Betaproteobacteria*, *Deltaproteobacteria* and *Epsilonproteobacteria*

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During a comprehensive investigation of indigenous prokaryotic species in Korea, a total of 46 bacterial strains assigned to the classes *Alphaproteobacteria*, *Betaproteobacteria*, *Deltaproteobacteria*, and *Epsilonproteobacteria* were isolated from a diversity of habitats including freshwater, seawater, brackish water, ginseng soil, plant roots, natural caves, and tidal flats. Based on their high 16S rRNA gene sequence similarities (>98.7%) and formation of strongly-supported phylogenetic clades with the closest type species, each strain was assigned to an independent, predefined bacterial species. Since there were no published or official reports regarding the isolation of these 46 species in Korea, here we report them as new species to Korea: 34 species in 14 families in the five orders of *Alphaproteobacteria*, 10 species in five families in the three orders of *Betaproteobacteria*, one species of *Deltaproteobacteria* and one species of *Epsilonproteobacteria*. Gram reaction, colony and cell morphology, basic biochemical characteristics, isolation source, and strain IDs are described in the species description section.

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

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INTRODUCTION

Proteobacteria is the largest bacteria phylum of gram-negative bacteria including the classes *Alphaproteobacteria*, *Betaproteobacteria*, *Gammaproteobacteria*, *Deltaproteobacteria*, *Epsilonproteobacteria*, *Acidithiobacillia*

and *Oligoflexia* (Williams *et al.*, 2013; Nakai *et al.*, 2014). At the time of writing, the taxonomic classification based on 16S rRNA sequences shows the class *Alphaproteobacteria* includes 15 orders: *Caulobacteriales*, *Emcibacteriales*, *Iodidimonadales*, *Kiloniellales*, *Kordiimonadales*, *Magnetococcales*, *Micropepsales*, *Parvularculales*, *Pe-*

lagibacterales, *Rhizobiales*, *Rhodobacterales*, *Rhodospirillales*, *Rickettsiales*, *Sneathiellales*, and *Sphingomonadales*. Among them, *Emcibacterales*, *Iodidimonadales*, and *Micropepsales* were established within the last three years (Iino *et al.*, 2016; Harbison *et al.*, 2017). The class *Betaproteobacteria* includes eight orders: *Burkholderiales*, *Ferritrophicales*, *Gallionellales*, *Methylophilales*, *Neisseriales*, *Nitrosomonadales*, *Rhodocyclales*, and *Sulfuricellales*. The order *Sulfuricellales* was established in 2015 (Watanabe *et al.*, 2015). The class *Deltaproteobacteria* includes nine orders: *Bradymonadales*, *Desulfarcu-lales*, *Desulfobacterales*, *Desulfovibrionales*, *Desulfurellales*, *Desulfuromonadales*, *Myxococcales*, *Nitrospinales*, and *Syntrophobacterales*, and the class *Gammaproteobacteria* consists of 20 orders: *Acidiferrobacterales*, *Aeromonadales*, *Alteromonadales*, *Arenicellales*, *Cardiobacteriales*, *Cellvibrionales*, *Chromatiales*, *Enterobacterales*, *Immundisolibacterales*, *Legionellales*, *Methylococcales*, *Nevskiales*, *Oceanospirillales*, *Orbales*, *Pasteurellales*, *Pseudomonadales*, *Salinisphaerales*, *Thiotrichales*, *Vibrionales*, and *Xanthomonadales*.

In 2017, we collected environmental samples from a diversity of habitats in Korea and isolated many novel and unrecorded bacterial species. This study describes 46 previously unrecorded bacterial species to Korea belonging to the classes *Alphaproteobacteria*, *Betaproteobacteria*, *Deltaproteobacteria*, and *Epsilonproteobacteria*.

MATERIALS AND METHODS

A total of 46 bacterial strains are assigned to the classes *Alphaproteobacteria*, *Betaproteobacteria*, *Deltaproteobacteria*, and *Epsilonproteobacteria* were isolated from a variety of habitats, including marine algae, mud, red algae, salt plant, salt pond, sand, butterfly (*Hippoarchia autonoe*), seawater, soil, tidal flat, tree, and wetland (Table 1). All environmental samples were independently processed, serially diluted, spread onto diverse culture agar media including ISP 2 agar (BD, USA), marine agar 2216 (MA; BD, USA), R2A agar (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 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 API 20NE galler-

ies (bioMérieux), according to the manufacturer's instructions.

Bacterial DNA extraction, PCR amplification, and 16S rRNA sequencing were performed using standard procedures as described elsewhere (Lee *et al.*, 2014). The 16S rRNA sequences of the strains assigned to the classes *Alphaproteobacteria*, *Betaproteobacteria*, *Deltaproteobacteria*, and *Epsilonproteobacteria* were compared with those of valid type strains using the EzTaxon-e server (Kim *et al.*, 2012). For phylogenetic analyses, multiple alignments of the 16S rRNA sequences between the isolates and established bacterial species were carried out using Clustal X (Thompson *et al.*, 1997). Evolutionary distances were calculated using the Kimura two-parameter model and the phylogenetic trees were constructed using a neighbor-joining algorithm with bootstrap values based on 1000 replications (Felsenstein, 2002).

RESULTS AND DISCUSSION

Thirty-four strains of *Alphaproteobacteria* were distributed into five orders: one strain in the *Parvularculales*, 16 strains in *Rhizobiales*, 10 strains in *Rhodobacterales*, three strains in *Rhodospirillales*, and four strains in *Sphingomonadales* (Table 1). Ten strains of *Betaproteobacteria* were distributed into three orders: seven strains in *Burkholderiales*, two strains in *Neisseriales*, and one strain in *Rhodocyclales*. One strain belonged to the order *Desulfovibrionales* of *Deltaproteobacteria* and one strain to the order *Campylobacterales* of *Epsilonproteobacteria*. All strains were gram-staining-negative and chemoheterotrophic, while in terms of shape, 38 strains were rod-shaped, three strains were cocci-shaped, and five strains were ovoid-shaped (Fig. 1).

In the class of *Alphaproteobacteria*, one strain was assigned to the genus *Parvularcula* of the family *Parvularculaceae* in the order *Parvularculales* and 16 strains in the order *Rhizobiales* belonged to seven different families (Fig. 2): *Brucellaceae* (one strain), *Hyphomicrobiaceae* (five strains), *Aurantimonadaceae* (one strain), *Parvibaculum* (one strain), *Phyllobacteriaceae* (two strains), *Rhizobiaceae* (three strains), and *Stappia* (two strains). Ten strains in the order *Rhodobacterales* belonged to two families: *Hyphomonadaceae* (one strain) and *Rhodobacteraceae* (nine strains). Three strains in the order *Rhodospirillales* were separated into two families: *Acetobacteraceae* (one strain) and *Rhodospirillaceae* (two strains). Lastly, four strains in the order *Sphingomonadales* were separated into two families: *Erythrobacteraceae* (two strains) and *Sphingomonadaceae* (two strains) (Fig. 3).

Ten strains were distributed into three orders, *Burkholderiales*, *Neisseriales*, and *Rhodocyclales*, of the class *Betaproteobacteria*. Seven strains belonged to three fam-

Table 1. Summary of strains isolated belonging to the classes *Alphaproteobacteria*, *Betaproteobacteria*, *Deltaproteobacteria*, and *Epsilonproteobacteria* and their taxonomic affiliations.

Class/phylum	Order	Family	Genus	Strain ID	NIBR ID	Most closely related species	Similarity (%)	Isolation source	Medium	Incubation conditions
<i>Alphaproteobacteria</i>	<i>Parvularculales</i>	<i>Parvularculaceae</i>	<i>Parvularcula</i>	HMF8467	VYWGBC000000193	<i>Parvularcula oceanus</i>	100	Salt pond	MA	30°C, 3d
				Ibu_S_3	VYWGBC000000108	<i>Pseudochrobactrum saccharolyticum</i>	99.9	Soil	R2A	30°C, 3d
<i>Rhizobiales</i>	<i>Hyphomicrobiales</i>	<i>Hyphomicrobiaceae</i>	<i>Devosia</i>	17J27-16	VYWGBC000000397	<i>Devosia submarina</i>	99.3	Soil	R2A	25°C, 4d
				IMCC34164	VYWGBC000000116	<i>Devosia pacifica</i>	99.8	Tidal flat	R2A agar (seawater)	25°C, 3d
				Gsoil 1028	VYWGBC000000011	<i>Devosia insulanae</i>	99.1	Soil	R2A	30°C, 2d
				Gsoil 824	VYWGBC000000008	<i>Devosia neptuniae</i>	99.7	Soil	R2A	30°C, 2d
				HMF7868	VYWGBC000000186	<i>Devosia psychrophila</i>	98.9	Tree	R2A	30°C, 3d
				GH2-6	VYWGBC000000066	<i>Marteletella radialis</i>	99.1	Salt plant	MA	30°C, 5d
				LPB0211	VYWGBC000000044	<i>Parvibaculum hydrocarboniclasticum</i>	99.9	Seawater	MA	25°C, 3d
				IMCC34184	VYWGBC000000113	<i>Ahrensia kielenis</i>	99.4	Tidal flat	R2A agar (seawater)	25°C, 5d
				Gsoil 1111	VYWGBC000000012	<i>Mesorhizobium qingshengii</i>	100	Soil	R2A	30°C, 2d
				17J44-22	VYWGBC000000379	<i>Rhizobium herbae</i>	98.8	Soil	R2A	25°C, 4d
<i>Stappia</i>	<i>Stappia</i>	<i>Stappia</i>	MMS17-SY214	VYWGBC000000226	<i>Ensifer meliloti</i>	99.9	Soil	MA	30°C, 3d	
			Gsoil318-1	VYWGBC000000023	<i>Mesorhizobium tamadayeense</i>	98.7	Soil	R2A	30°C, 2d	
			HMF8046	VYWGBC000000191	<i>Stappia indica</i>	99.1	Salt pond	MA	30°C, 3d	
			LPB0183	VYWGBC000000035	<i>Pseudovibrio ascidiacetola</i>	100	Seawater	MA	25°C, 3d	
			GH4-12	VYWGBC000000059	<i>Stappia stellulata</i>	99.6	Tidal flat	MA	30°C, 5d	
			IMCC34185	VYWGBC000000119	<i>Litorionas cladophorae</i>	98.8	Tidal flat	R2A agar (seawater)	25°C, 3d	
			HMF8042	VYWGBC000000189	<i>Nesiobacter exalbescens</i>	100	Salt pond	MA	30°C, 3d	
			KYW1385	VYWGBC000000159	<i>Paracoccus tibetensis</i>	99.0	Seawater	MA	25°C, 3d	
			BMW10	VYWGBC000000160	<i>Roseobacter littoralis</i>	99.4	Seawater	MA	25°C, 5d	
			IMCC34207	VYWGBC000000118	<i>Gemmobacter lanyuensis</i>	99.9	Sand	R2A agar (seawater)	25°C, 3d	
<i>Rhodobacteriales</i>	<i>Rhodobacteraceae</i>	<i>Rhodobacteraceae</i>	<i>Rhodobacter</i>	GH1-7	VYWGBC000000064	<i>Thioclava atlantica</i>	98.8	Tidal flat	MA	30°C, 5d
				HMF8205	VYWGBC000000192	<i>Roseobacterium beibuensis</i>	99.8	Salt pond	MA	30°C, 3d
				HMF8483	VYWGBC000000194	<i>Palleronia abyssalis</i>	99.6	Salt pond	MA	30°C, 3d
				HMF8486	VYWGBC000000195	<i>Palleronia marisminoris</i>	99.1	Salt pond	MA	30°C, 3d
				F-nm3	VYWGBC000000346	<i>Anylibacter lutimaris</i>	100	Tidal flat	MA	30°C, 2d
				HMF7612	VYWGBC000000183	<i>Roseomonas vinacea</i>	100	Tree	R2A	30°C, 3d
				IMCC34233	VYWGBC000000125	<i>Thalassospira lucentensis</i>	99.5	Sand	R2A agar (seawater)	25°C, 3d
				MMS17-GJ036	VYWGBC000000228	<i>Inquilinus limosus</i>	99.0	Soil	ISP 2 agar	30°C, 3d
				GH1-10	VYWGBC000000065	<i>Erythrobacter longus</i>	98.8	Tidal flat	MA	30°C, 5d
				SIC2	VYWGBC000000350	<i>Altererythrobacter ishigakiensis</i>	99.1	Red algae	MA	30°C, 3d
<i>Sphingomonadales</i>	<i>Sphingomonadaceae</i>	<i>Sphingomonadaceae</i>	<i>Novosphingobium Marinobacter</i>	HMF7644	VYWGBC000000184	<i>Novosphingobium guangzhouense</i>	99.2	Tree	R2A	30°C, 3d
				S-1	VYWGBC000000345	<i>Marinobacter saluginis</i>	100	Marine algae	MA	30°C, 3d

Table 1. Continued.

Class/phyllum	Order	Family	Genus	Strain ID	NIBR ID	Most closely related species	Similarity (%)	Isolation source	Medium	Incubation conditions
Betaproteobacteria	Burkholderiales	Burkholderiaceae	<i>Burkholderia</i>	WD42	VYWGBAC000000148	<i>Burkholderia daboshanensis</i>	99.0	Soil	R2A	25°C, 2d
				kw. 8	VYWGBAC000000094	<i>Paraburkholderia tropica</i>	98.8	Mud	R2A	30°C, 4d
				MMS17-GJ039	VYWGBAC000000242	<i>Paraburkholderia hospita</i>	99.8	Soil	ISP 2 agar	30°C, 3d
				Gsoil 096	VYWGBAC000000002	<i>Paraburkholderia sartisoli</i>	99.8	Soil	R2A	30°C, 2d
Oxalobacteraceae			<i>Burkholderia</i>	HMF7693	VYWGBAC000000185	<i>Burkholderia peredens</i>	98.8	Tree	R2A	30°C, 3d
				JMn9	VYWGBAC000000143	<i>Massilia timonae</i>	99.2	Tidal flat	R2A	25°C, 3d
Ralstoniaceae			<i>Ralstonia</i>	BR3409	VYWGBAC000000172	<i>Ralstonia pickettii</i>	99.7	Sangultuk Nabi	R2A	37°C
				HMF7346	VYWGBAC000000182	<i>Neisseria perflava</i>	99.8	Soil	R2A	30°C, 4d
Neisseriales		Neisseriaceae	<i>Neisseria</i>	HMF7887	VYWGBAC000000188	<i>Amantichitinum ursilacus</i>	99.9	Tree	R2A	30°C, 3d
				HMF4721	VYWGBAC000000180	<i>Uliginosibacterium paludis</i>	99.6	Wetland	R2A	30°C, 3d
Deltaproteobacteria	Desulfovibrionales	Desulfovibrionaceae	<i>Halodesulfivibrio</i>	LPB0172	VYWGBAC000000030	<i>Halodesulfivibrio marinesedimentis</i>	99.1	Seawater	MA	30°C, 3d
				LPB0305	VYWGBAC000000046	<i>Arcobacter bivalviorum</i>	99.6	Seawater	MA	25°C, 3d
Epsilonproteobacteria	Campylobacteriales	Campylobacteraceae	<i>Arcobacter</i>							

ilies in the order of *Burkholderiales*: *Burkholderiaceae* (five strains), *Oxalobacteraceae* (one strain) and *Ralstoniaceae* (one strain) (Fig. 4). Two strains belonged to the genera *Neisseria* and *Amantichitinum* of the family *Neisseriaceae* of the order *Neisseriales*, respectively and one strain belonged to the genus *Uliginosibacterium* of the family of *Rhodocyclaceae* in the order *Rhodocyclales* (Fig. 4). One strain was assigned to the genus *Halodesulfivibrio* of the family *Desulfovibrionaceae* in the order *Desulfovibrionales* and one strain was assigned to the genus *Arcobacter* of the family *Campylobacteraceae* in the order *Campylobacteriales* (Figs. 5 and 6).

In conclusion, we report 46 previously unrecorded bacterial species to Korea belonging to four proteobacterial classes *Alphaproteobacteria*, *Betaproteobacteria*, *Deltaproteobacteria*, and *Epsilonproteobacteria*.

Description of *Pseudovibrio ascidiaceicola* LPB0183

Cells are gram-staining-negative, flagellated, and rod-shaped. Colonies are circular, convex, smooth, mucoid, and cream-colored after three days of incubation at 25°C on MA. Positive for nitrate reduction, indole production, glucose fermentation, and gelatinase and β -galactosidase activity. Negative for arginine dihydrolase and urease activity and esculin hydrolysis. 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, and phenylacetic acid. Strain LPB0183 (= VYWGBAC000000035) was isolated from a seawater sample, Jeju, Korea.

Description of *Parvibaculum hydrocarboniasticum* LPB0211

Cells are gram-staining-negative, flagellated, and rod-shaped. Colonies are circular, convex, smooth, and cream-colored after three days of incubation at 25°C on MA. Negative for nitrate reduction, indole production, glucose fermentation, esculin hydrolysis, and arginine dihydrolase, urease, gelatinase, and β -galactosidase activity. 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, and phenylacetic acid. Strain LPB0211 (= VYWGBAC000000044) was isolated from a seawater sample, Incheon, Korea.

Description of *Rhizobium herbae* 17J44-22

Cells are gram-staining-negative, flagellated, and rod-shaped. Colonies are circular, convex, smooth, and cream-colored after four days of incubation at 25°C on R2A agar. Positive for esculin hydrolysis and arginine dihydrolase, urease, gelatinase, and β -galactosidase activity. Neg-

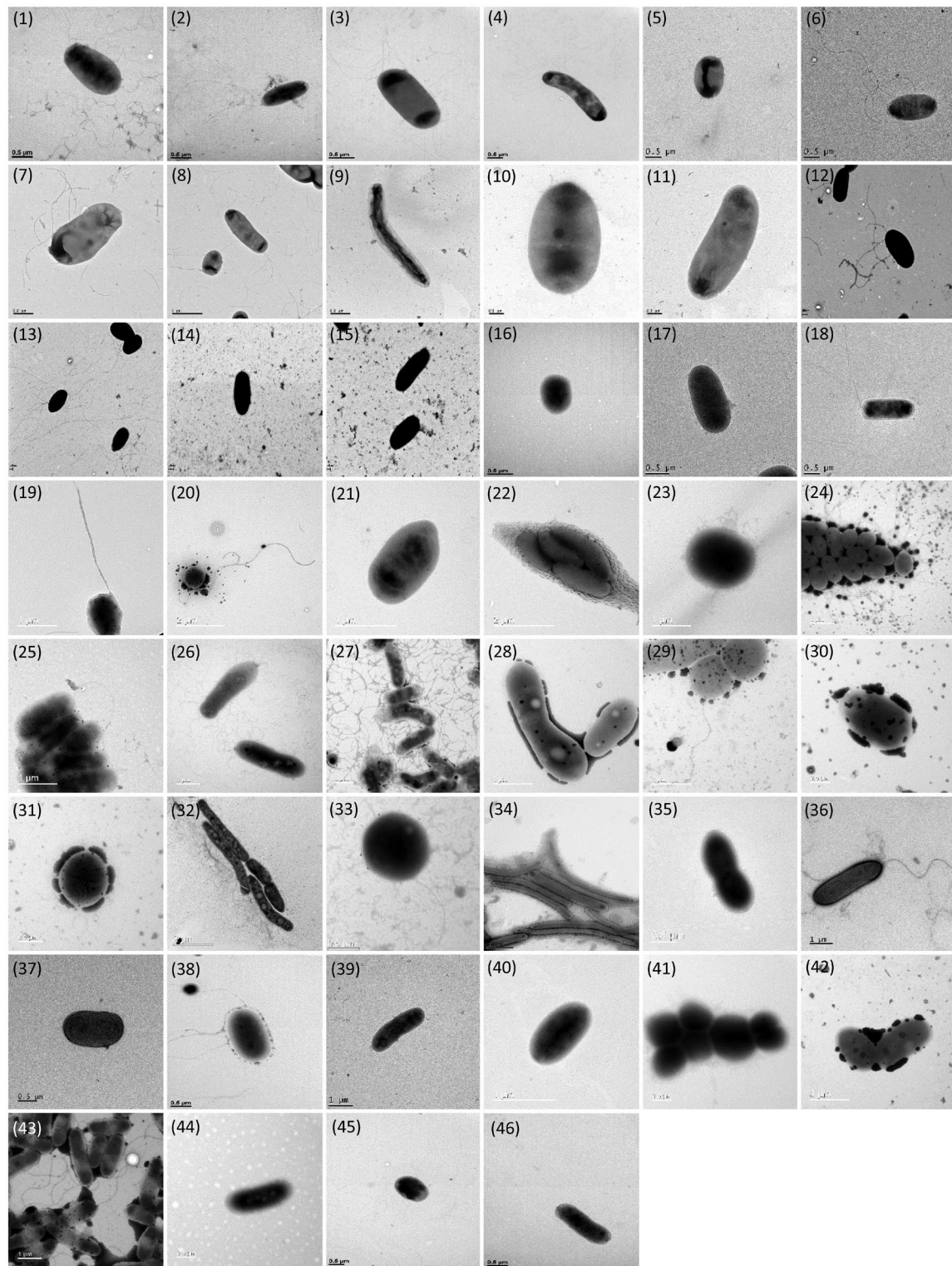


Fig. 1. Transmission electron micrographs or scanning electron micrographs of cells of the strains isolated in this study. The cells were cultured at their optimal growth conditions. Strains: 1, LPB0183; 2, LPB0211; 3, 17J44-22; 4, 17J27-16; 5, KYW1385; 6, BMW10; 7, IMCC34164; 8, IMCC34184; 9, IMCC34185; 10, IMCC34207; 11, IMCC34233; 12, GH4-12; 13, GH1-7; 14, GH1-10; 15, GH2-6; 16, Ibu_S_3; 17, MMS17-GJ036; 18, MMS17-SY214; 19, Gsoil 1028; 20, Gsoil 1111; 21, Gsoil318-1; 22, Gsoil 824; 23, HMF7612; 24, HMF7644; 25, HMF7868; 26, HMF8042; 27, HMF8046; 28, HMF8205; 29, HMF8467; 30, HMF8483; 31, HMF8486; 32, S-1; 33, F-mm3; 34, StC2; 35, BR3409; 36, JMn9; 37, WD42; 38, kw_8; 39, MMS17-GJ039; 40, Gsoil 096; 41, HMF7346; 42, HMF7693; 43, HMF7887; 44, HMF4721; 45, LPB0172; 46, LPB0305.

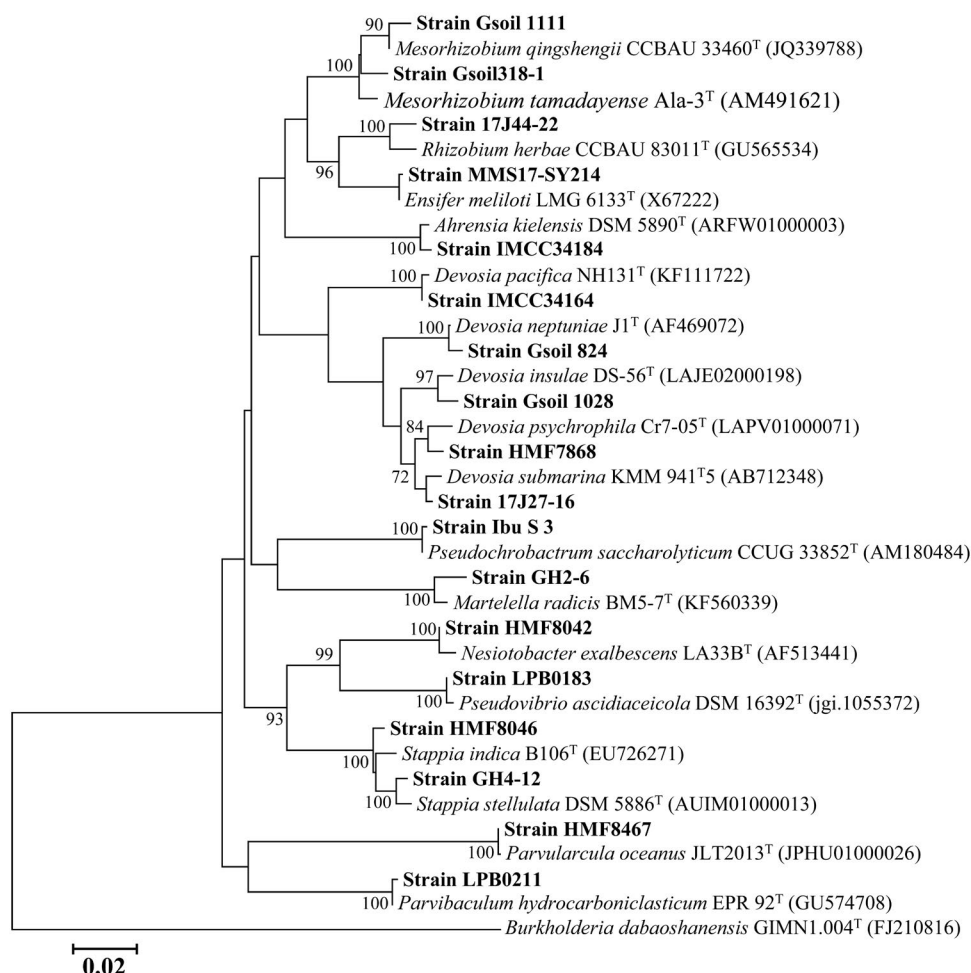


Fig. 2. Neighbor-joining phylogenetic tree, based on 16S rRNA sequences, showing the phylogenetic relationship between strains isolated in this study and their relatives in the orders *Parvularculales* and *Rhizobiales* in the class *Alphaproteobacteria*. *Burkholderia dabaoshanensis* GIMN1.004^T (FJ210816) was used as an outgroup. Bootstrap values (>70%) are shown above nodes. Scale bar: 0.02 changes per nucleotide.

ative for nitrate reduction, indole production, and glucose fermentation. Utilizes D-glucose, D-mannose, D-maltose, potassium gluconate and malic acid. Does not utilize L-arabinose, D-mannitol, N-acetyl-glucosamine, capric acid, adipic acid, trisodium citrate and phenylacetic acid. Strain 17J44-22 (= VYWGBAC000000379) was isolated from a soil sample, Jeju, Korea.

Description of *Devosia submarina* 17J27-16

Cells are gram-staining-negative, non-flagellated, and rod-shaped. Colonies are circular, convex, smooth, and cream-colored after four days of incubation at 25°C on R2A agar. Positive for nitrate reduction, esculin hydrolysis, and arginine dihydrolase, urease, and β -galactosidase activity. Negative for indole production, glucose fermentation, and gelatinase activity. Utilizes D-Glucose, L-arabinose, D-mannose, D-mannitol, N-acetyl-glucosamine, D-maltose, and potassium gluconate. Does not

utilize capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain 17J27-16 (= VYWG-BAC000000397) was isolated from a soil sample, Jeju, Korea.

Description of *Paracoccus tibetensis* KYW1385

Cells are gram-staining-negative, non-flagellated, and short rod-shaped. Colonies are circular, convex, smooth, entire, and pale yellow-colored after three days of incubation at 25°C on MA. Positive for esculin hydrolysis. Negative for nitrate reduction, indole production, glucose fermentation, and arginine dihydrolase, urease, gelatinase, and β -galactosidase activity. 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, and phenylacetic acid. Strain KYW1385 (= VYWGBAC000000159) was isolated from a seawater sample, Gwangyang, Korea.

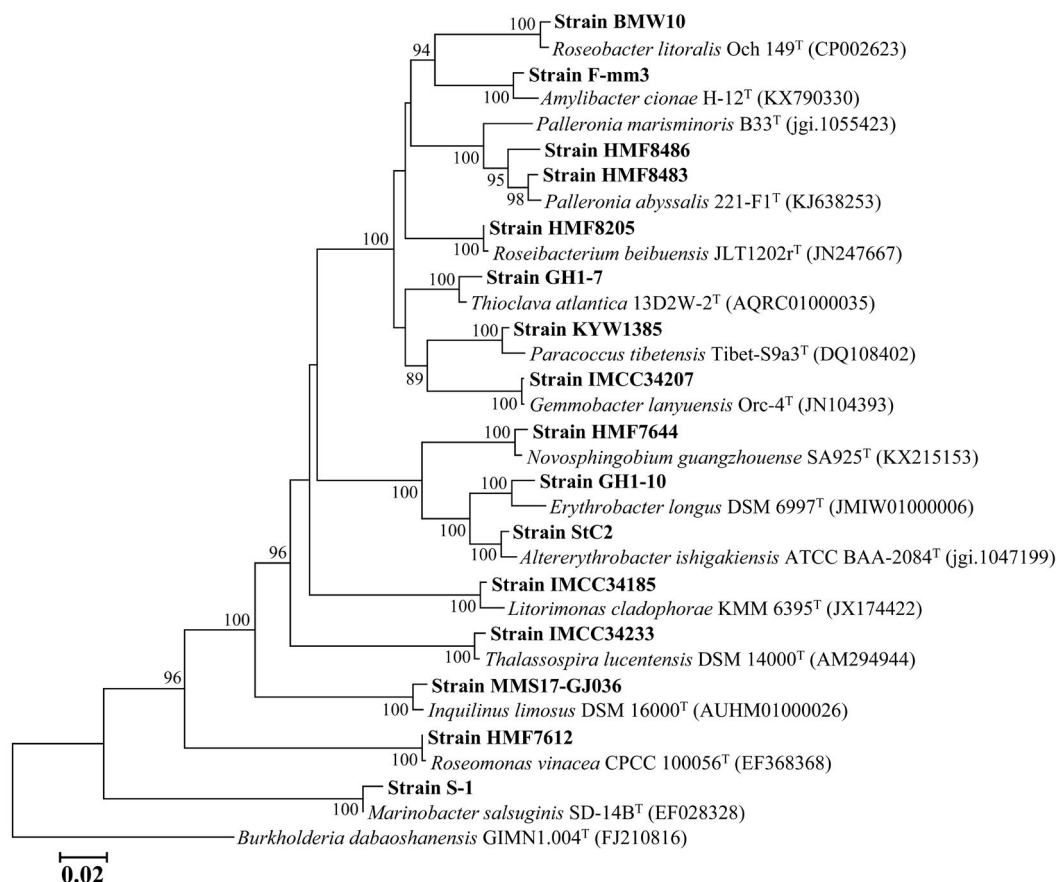


Fig. 3. Neighbor-joining phylogenetic tree, based on 16S rRNA sequences, showing the phylogenetic relationship between strains isolated in this study and their relatives in the orders *Rhodobacterales*, *Rhodospirillales*, and *Sphingomonadales* in the class *Alphaproteobacteria*. *Burkholderia dabaoshanensis* GIMN1.004^T (FJ210816) was used as an outgroup. Bootstrap values (>70%) are shown above nodes. Scale bar: 0.02 changes per nucleotide.

Description of *Roseobacter littoralis* BMW10

Cells are gram-staining-negative, flagellated, and ovoid-shaped. Colonies are circular, convex, smooth, opaque, and pale pink red-colored after five days of incubation at 25°C on MA. Positive for esculin hydrolysis. Negative for nitrate reduction, indole production, glucose fermentation, and arginine dihydrolase, urease, gelatinase, and β -galactosidase activity. 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, and phenylacetic acid. Strain BMW10 (= VYWGBAC000000160) was isolated from a seawater sample, Boseong, Korea.

Description of *Devosia pacifica* IMCC34164

Cells are gram-staining-negative, flagellated, and rod-shaped. Colonies are circular, entire, convex, and pale white-colored after three days of incubation at 25°C on R2A agar using seawater. Positive for esculin hydrolysis

and urease and β -galactosidase activity. Negative for nitrate reduction, indole production, glucose fermentation, and arginine dihydrolase and gelatinase activity. 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 and phenylacetic acid. Strain IMCC34164 (= VYWGBAC000000116) was isolated from a tidal flat sample, Incheon, Korea.

Description of *Ahrensia kielensis* IMCC34184

Cells are gram-staining-negative, flagellated, and rod-shaped. Colonies are circular, entire, convex, and pale white-colored after five days of incubation at 25°C on R2A agar using seawater. Positive for esculin hydrolysis and urease and β -galactosidase activity. Negative for nitrate reduction, indole production, glucose fermentation, and arginine dihydrolase and gelatinase activity. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol,

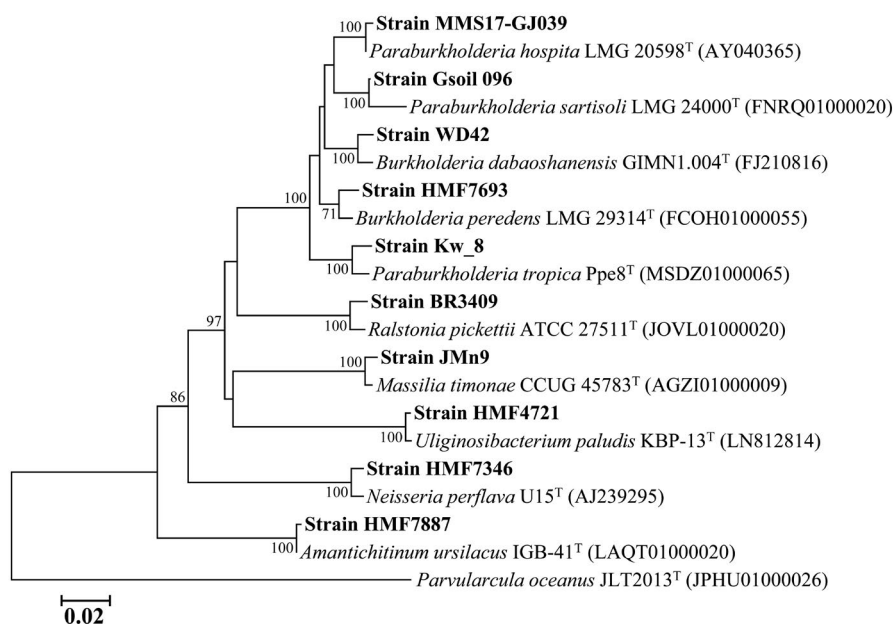


Fig. 4. Neighbor-joining phylogenetic tree, based on 16S rRNA sequences, showing the phylogenetic relationship between strains isolated in this study and their relatives in the orders *Burkholderiales*, *Neisseriales*, and *Rhodocyclales* in the class *Betaproteobacteria*. *Parvularcula oceanus* JLT2013^T (JPHU01000026) was used as an outgroup. Bootstrap values (>70%) are shown above nodes. Scale bar: 0.02 changes per nucleotide.

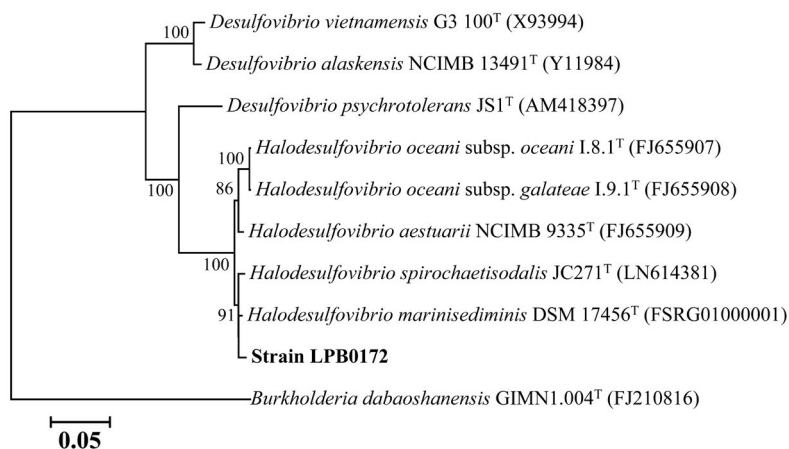


Fig. 5. Neighbor-joining phylogenetic tree, based on 16S rRNA sequences, showing the phylogenetic relationship between strain LPB0172 isolated in this study and its relatives in the order *Desulfovibrionales* in the class *Deltaproteobacteria*. *Burkholderia dabaoshanensis* GIMN1.004^T (FJ210816) was used as an outgroup. Bootstrap values (>70%) are shown above nodes. Scale bar: 0.05 changes per nucleotide.

N-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain IMCC34184 (= VYWG-BAC00000113) was isolated from a tidal flat sample, Incheon, Korea.

Description of *Litorimonas cladophorae* IMCC34185

Cells are gram-staining-negative, non-flagellated, and

rod-shaped. Colonies are circular, entire, raised, and red orange-colored after three days of incubation at 25°C on R2A agar using seawater. Positive for esculin hydrolysis and β -galactosidase activity. Negative for nitrate reduction, indole production, glucose fermentation, and arginine dihydrolase, urease, and gelatinase activity. 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,

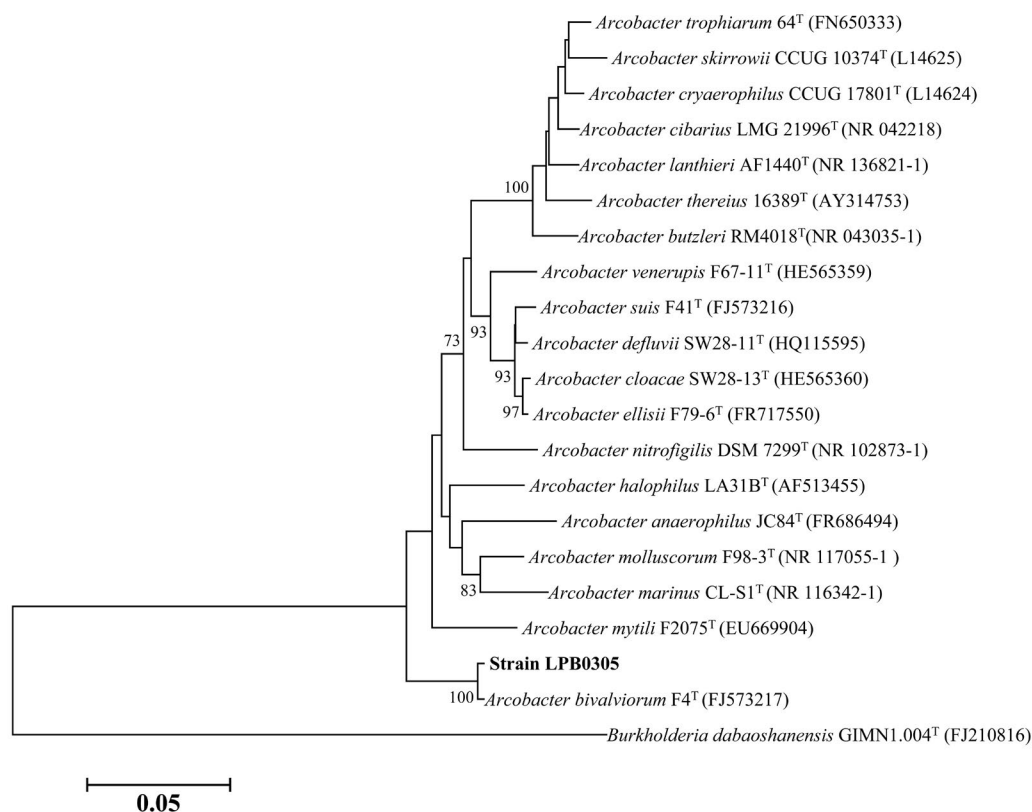


Fig. 6. Neighbor-joining phylogenetic tree, based on 16S rRNA sequences, showing the phylogenetic relationship between strain LPB0305 isolated in this study and its relatives in the order *Campylobacterales* in the class *Epsilonproteobacteria*. *Burkholderia dabaoshanensis* GIMN1.004^T (FJ210816) was used as an outgroup. Bootstrap values (>70%) are shown above nodes. Scale bar: 0.02 changes per nucleotide.

and phenylacetic acid. Strain IMCC34185 (= VYWG-BAC000000119) was isolated from a tidal flat sample, Incheon, Korea.

Description of *Gemmobacter lanyuensis* IMCC34207

Cells are gram-staining-negative, non-flagellated, and rod-shaped. Colonies are circular, entire, convex, and cream-colored after three days of incubation at 25°C on R2A agar using seawater. Positive for nitrate reduction, esculin hydrolysis, and arginine dihydrolase, urease, and β -galactosidase activity. Negative for indole production, glucose fermentation, and gelatinase activity. Utilizes D-mannitol, D-maltose, malic acid, and phenylacetic acid. Does not utilize D-glucose, L-arabinose, D-mannose, N-acetyl-glucosamine, potassium gluconate, capric acid, adipic acid, and trisodium citrate. Strain IMCC34207 (= VYWGBAC000000118) was isolated from a sand sample, Wando, Korea.

Description of *Thalassospira lucentensis* IMCC34233

Cells are gram-staining-negative, non-flagellated, and rod-shaped. Colonies are circular, entire, convex, and

cream beige-colored after three days of incubation at 25°C on R2A agar using seawater. Positive for esculin hydrolysis. Negative for nitrate reduction, indole production, glucose fermentation, and arginine dihydrolase, urease, gelatinase, and β -galactosidase activity. Utilizes D-Glucose, L-arabinose, D-mannose, D-mannitol, N-acetyl-glucosamine, and potassium gluconate. Does not utilize D-maltose, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain IMCC34233 (= VYWGBAC000000125) was isolated from a sand sample, Wando, Korea.

Description of *Stappia stellulata* GH4-12

Cells are gram-staining-negative, flagellated, and rod-shaped. Colonies are circular, entire, convex, and cream-colored after five days of incubation at 30°C on MA. Negative for nitrate reduction, indole production, glucose fermentation, esculin hydrolysis, and arginine dihydrolase, urease, gelatinase, and β -galactosidase activity. 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, and phenylacetic acid. Strain GH4-12 (= VYWG-

BAC00000059) was isolated from a tidal flat sample, Incheon, Korea.

Description of *Thioclava atlantica* GH1-7

Cells are gram-staining-negative, flagellated, and rod-shaped. Colonies are circular, entire, convex, and cream-colored after five days of incubation at 30°C on MA. Negative for nitrate reduction, indole production, glucose fermentation, esculin hydrolysis, and arginine dihydro-lase, urease, gelatinase, and β -galactosidase activity. Utilizes D-Mannitol. Does not utilize D-glucose, L-arabinose, D-mannose, N-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain GH1-7 (= VYWG-BAC000000064) was isolated from a tidal flat sample, Incheon, Korea.

Description of *Erythrobacter longus* GH1-10

Cells are gram-staining-negative, non-flagellated, and rod-shaped. Colonies are circular, entire, convex, and orange-colored after five days of incubation at 30°C on MA. Positive for esculin hydrolysis. Negative for nitrate reduction, indole production, glucose fermentation, and arginine dihydro-lase, urease, gelatinase, and β -galactosidase activity. 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, and phenylacetic acid. Strain GH1-10 (= VYWGBAC000000065) was isolated from a tidal flat sample, Incheon, Korea.

Description of *Martellella radialis* GH2-6

Cells are gram-staining-negative, non-flagellated, and rod-shaped. Colonies are irregular, entire, convex, and cream-colored after five 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 dihydro-lase, urease, and gelatinase activity. 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, and phenylacetic acid. Strain GH2-6 (= VYWGBAC000000066) was isolated from a salt plant sample, Incheon, Korea.

Description of *Pseudochrobactrum saccharolyticum* Ibu_S_3

Cells are gram-staining-negative, non-flagellated, and rod-shaped. Colonies are circular, and cream-colored after three days of incubation at 30°C on R2A agar. Positive for nitrate reduction, esculin hydrolysis, and gelatinase and

β -galactosidase activity. Negative for indole production, glucose fermentation, and arginine dihydro-lase and urease activity. Utilizes D-Glucose, D-mannose, N-acetyl-glucosamine, malic acid, and trisodium citrate. Does not utilize L-arabinose, D-mannitol, D-maltose, potassium gluconate, capric acid, adipic acid, and phenylacetic acid. Strain Ibu_S_3 (= VYWGBAC000000108) was isolated from a soil sample, Anseong, Korea.

Description of *Inquilinus limosus* MMS17-GJ036

Cells are gram-staining-negative, non-flagellated, and rod-shaped. Colonies are Irregular, convex, glistening, watery, and translucent beige-colored after three days of incubation at 30°C on ISP 2 agar. Positive for esculin hydrolysis and β -galactosidase activity. Negative for nitrate reduction, indole production, glucose fermentation and arginine dihydro-lase, urease, and gelatinase activity. Utilizes D-Glucose, L-arabinose, D-mannose, D-mannitol, N-acetyl-glucosamine, D-maltose, potassium gluconate, malic acid, and trisodium citrate. Does not utilize capric acid, adipic acid, and phenylacetic acid. Strain MMS17-GJ036 (= VYWGBAC000000228) was isolated from a soil sample, Daejeon, Korea.

Description of *Ensifer meliloti* MMS17-SY214

Cells are gram-staining-negative, flagellated, and rod-shaped. Colonies are circular, convex, entire, glistening, and beige-colored after three days of incubation at 30°C on MA. Positive for esculin hydrolysis and urease, gelatinase, and β -galactosidase activity. Negative for nitrate reduction, indole production, glucose fermentation, and arginine dihydro-lase activity. Utilizes D-Glucose, L-arabinose, D-mannose, D-mannitol, N-acetyl-glucosamine, D-maltose and malic acid. Does not utilize potassium gluconate, capric acid, adipic acid, trisodium citrate, and phenylacetic acid. Strain MMS17-SY214 (= VYWGBAC000000226) was isolated from a soil sample, Gusan, Korea.

Description of *Devosia insulae* Gsoil 1028

Cells are gram-staining-negative, flagellated, and ovoid-shaped. Colonies are circular, raised, and white-colored after two days of incubation at 30°C on R2A agar. Positive for esculin hydrolysis and gelatinase activity. Negative for nitrate reduction, indole production, glucose fermentation, and arginine dihydro-lase, urease, and β -galactosidase activity. 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, and phenylacetic acid. Strain Gsoil 1028 (= VYWGBAC000000011) was isolated from a soil sample, Pocheon, Korea.

Description of *Mesorhizobium qingshengii* Gsoil 1111

Cells are gram-staining-negative, flagellated, and ovoid-shaped. Colonies are circular, convex, smooth, glistening, and white-colored after two days of incubation at 30°C on R2A agar. Positive for esculin hydrolysis. Negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, and urease, gelatinase, and β -galactosidase activity. Utilizes D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, potassium gluconate, adipic acid, malic acid, and phenylacetic acid. Does not utilize D-maltose, capric acid, and trisodium citrate. Strain Gsoil 1111 (= VYWGBAC000000012) was isolated from a soil sample, Pocheon, Korea.

Description of *Mesorhizobium tamadayense* Gsoil318-1

Cells are gram-staining-negative, non-flagellated, and ovoid-shaped. Colonies are circular, raised, and white-colored after two days of incubation at 30°C on R2A agar. Positive for esculin hydrolysis. Negative for nitrate reduction, indole production, glucose fermentation, and arginine dihydrolase, urease, gelatinase and β -galactosidase activity. Utilizes D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, and D-maltose. Does not utilize potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain Gsoil318-1 (= VYWGBAC000000023) was isolated from a soil sample, Pocheon, Korea.

Description of *Devosia neptuniae* Gsoil 824

Cells are gram-staining-negative, non-flagellated, and rod-shaped. Colonies are circular, convex, smooth, glistening, and cream-colored after two days of incubation at 30°C on R2A agar. Positive for urease activity. Negative for nitrate reduction, indole production, glucose fermentation, esculin hydrolysis, and arginine dihydrolase, gelatinase, and β -galactosidase activity. Utilizes *N*-Acetyl-glucosamine and D-maltose. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain Gsoil 824 (= VYWGBAC000000008) was isolated from a soil sample, Pocheon, Korea.

Description of *Roseomonas vinacea* HMF7612

Cells are gram-staining-negative, non-flagellated, and coccobacillus-shaped. Colonies are circular, convex, smooth, and red-colored after three days of incubation at 30°C on R2A agar. Negative for nitrate reduction, indole production, glucose fermentation, esculin hydrolysis, and arginine dihydrolase, urease, gelatinase, and β -galactosidase activity. Utilizes adipic acid and malic acid. Does

not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, trisodium citrate, and phenylacetic acid. Strain HMF7612 (= VYWGBAC000000183) was isolated from a tree sample, Yongin, Korea.

Description of *Novosphingobium guangzhouense* HMF7644

Cells are gram-staining-negative, non-flagellated, and rod-shaped. Colonies are circular, convex, smooth, and pale yellow-colored after three days of incubation at 30°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 activity. Utilizes D-Glucose, L-arabinose, D-mannose, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, malic acid and trisodium citrate. Does not utilize D-mannitol, capric acid, adipic acid, and phenylacetic acid. Strain HMF7644 (= VYWGBAC000000184) was isolated from a tree sample, Seoul, Korea.

Description of *Devosia psychrophila* HMF7868

Cells are gram-staining-negative, flagellated, and rod-shaped. Colonies are circular, convex, smooth, and white-colored after three days of incubation at 30°C on R2A agar. Positive for esculin hydrolysis and urease and β -galactosidase activity. Negative for nitrate reduction, indole production, glucose fermentation, and arginine dihydrolase and gelatinase activity. D-Glucose, L-arabinose, D-mannose, D-mannitol, and D-maltose are utilized. Does not utilize *N*-acetyl-glucosamine, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain HMF7868 (= VYWGBAC000000186) was isolated from a tree sample, Yongin, Korea.

Description of *Nesiotobacter exalbescens* HMF8042

Cells are gram-staining-negative, flagellated, and rod-shaped. Colonies are circular, convex, smooth, and white-colored after three days of incubation at 30°C on MA. Positive for indole production, glucose fermentation, and urease activity. Negative for nitrate reduction, esculin hydrolysis, and arginine dihydrolase, gelatinase, and β -galactosidase activity. Utilizes D-Glucose, D-mannose, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, and phenylacetic acid. Does not utilize L-arabinose, D-mannitol, capric acid, adipic acid, malic acid, and trisodium citrate. Strain HMF8042 (= VYWGBAC000000189) was isolated from a water sample from a salt pond, Shinan, Korea.

Description of *Stappia indica* HMF8046

Cells are gram-staining-negative, non-flagellated, and rod-shaped. Colonies are circular, convex, smooth, and pale orange-colored after three days of incubation at 30°C on MA. Negative for nitrate reduction, indole production, glucose fermentation, esculin hydrolysis, and arginine dihydrolase, urease, gelatinase, and β -galactosidase activity. Utilizes D-Glucose, L-arabinose, D-mannose, D-mannitol, N-acetyl-glucosamine, D-maltose, potassium gluconate, adipic acid, malic acid, trisodium citrate and phenylacetic acid. Does not utilize capric acid. Strain HMF8046 (= VYWGBAC000000191) was isolated from a water sample from a salt pond, Shinan, Korea.

Description of *Roseibacterium beibuensis* HMF8205

Cells are gram-staining-negative, non-flagellated, and short-ovoid to rod-shaped. Colonies are circular, convex, smooth, and pale red-colored after three days of incubation at 30°C on MA. Positive for urease activity and esculin hydrolysis. Negative for nitrate reduction, indole production, glucose fermentation, and arginine dihydrolase, gelatinase, and β -galactosidase activity. 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 and phenylacetic acid. Strain HMF8205 (= VYWGBAC000000192) was isolated from a water sample from a salt pond, Shinan, Korea.

Description of *Parvularcula oceanus* HMF8467

Cells are gram-staining-negative, flagellated, and short rod-shaped. Colonies are circular, convex, smooth, and orange-colored after three 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 activity. 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, and phenylacetic acid. Strain HMF8467 (= VYWGBAC000000193) was isolated from a water samples from a salt pond, Shinan, Korea.

Description of *Palleronia abyssalis* HMF8483

Cells are gram-staining-negative, non-flagellated, and short rod-shaped. Colonies are circular, convex, smooth, and pale red-colored after three 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 activity. Utilizes D-Glucose, L-arabinose, D-mannose, D-mannitol, N-acetyl-glucos-

amine, potassium gluconate, adipic acid, and malic acid. Does not utilize D-maltose, capric acid, trisodium citrate, and phenylacetic acid. Strain HMF8483 (= VYWGBAC000000194) was isolated from a water sample from a salt pond, Shinan, Korea.

Description of *Palleronia marisminoris* HMF8486

Cells are gram-staining-negative, non-flagellated, and short rod-shaped. Colonies are circular, convex, smooth, and ivory-colored after three days of incubation at 30°C on MA. Positive for esculin hydrolysis and urease and β -galactosidase activity. Negative for nitrate reduction, indole production, glucose fermentation, and arginine dihydrolase and gelatinase activity. Utilizes D-Glucose, L-arabinose, D-mannitol, D-maltose, and malic acid. Does not utilize D-mannose, N-acetyl-glucosamine, potassium gluconate, capric acid, adipic acid, trisodium citrate, and phenylacetic acid. Strain HMF8486 (= VYWGBAC000000195) was isolated from a water sample from a salt pond, Shinan, Korea.

Description of *Marinobacter salsuginis* S-1

Cells are gram-staining-negative, non-flagellated, and rod-shaped. Colonies are round, smooth, and white-colored after three days of incubation at 30°C on MA. Positive for nitrate reduction and gelatinase activity. Negative for indole production, glucose fermentation, esculin hydrolysis, and arginine dihydrolase, urease, and β -galactosidase activity. Utilizes L-Arabinose, D-mannose, and capric acid. Does not utilize D-glucose, D-mannitol, N-acetyl-glucosamine, D-maltose, potassium gluconate, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain S-1 (= VYWGBAC000000345) was isolated from a marine algae sample, Gangjin, Korea.

Description of *Amylibacter lutimaris* F-mm3

Cells are gram-staining-negative, flagellated, and rod-shaped. Colonies are round, convex, smooth, and light yellow-colored after two days of incubation at 30°C on MA. Positive for nitrate reduction, esculin hydrolysis, and urease and gelatinase activity. Negative for indole production, glucose fermentation, and arginine dihydrolase and β -galactosidase activity. Utilizes D-Glucose, D-mannose, D-mannitol, D-maltose, potassium gluconate, and malic acid. Does not utilize L-arabinose, N-acetyl-glucosamine, capric acid, adipic acid, trisodium citrate, and phenylacetic acid. Strain F-mm3 (= VYWGBAC000000346) was isolated from a tidal flat sample, Asan, Korea.

Description of *Altererythrobacter ishigakiensis* StC2

Cells are gram-staining-negative, non-flagellated, and rod-shaped. Colonies are round, smooth, and orange-col-

ored after three days of incubation at 30°C on MA. Positive for esculin hydrolysis. Negative for nitrate reduction, indole production, glucose fermentation, and arginine dihydrolase, urease, gelatinase, and β -galactosidase activity. Utilizes adipic acid and trisodium citrate. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, N-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, malic acid, and phenylacetic acid. Strain StC2 (= VYWGBAC000000350) was isolated from a red algae sample, Yeosu, Korea.

Description of *Ralstonia pickettii* BR3409

Cells are gram-staining-negative, non-flagellated, and ovoid rod-shaped. Colonies are circular, convex, hard, and yellow-colored incubation at 37°C on R2A. Positive for esculin hydrolysis and urease and gelatinase activity. Negative for nitrate reduction, indole production, glucose fermentation, and arginine dihydrolase and β -galactosidase activity. 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. Strain BR3409 (= VYWG-BAC000000172) was isolated from a butterfly (*Hipparchia autonoe*) sample, Jeju, Korea.

Description of *Massilia timonae* JMn9

Cells are gram-staining-negative, flagellated, and rod-shaped. Colonies are circular, smooth, flat, entire, and pale yellow-colored after three days of incubation at 25°C on R2A. Positive for esculin hydrolysis and urease, gelatinase, and β -galactosidase activity. Negative for nitrate reduction, indole production, glucose fermentation, and arginine dihydrolase activity. Utilizes L-Arabinose, D-mannose, D-maltose, malic acid, and trisodium citrate. Does not utilize D-glucose, D-mannitol, N-acetyl-glucosamine, potassium gluconate, capric acid, adipic acid, and phenylacetic acid. Strain JMn9 (= VYWGBAC000000143) was isolated from a tidal flat sample, Suncheon, Korea.

Description of *Burkholderia dabaoshanensis* WD42

Cells are gram-staining-negative, non-flagellated, and rod-shaped. Colonies are circular, smooth, convex, opaque, and ivory-colored after two days of incubation at 25°C on R2A. Positive for nitrate reduction, glucose fermentation, esculin hydrolysis, and β -galactosidase activity. Negative for indole production and arginine dihydrolase, urease, and gelatinase activity. Utilizes D-Glucose, D-mannose, D-mannitol, N-acetyl-glucosamine, and malic acid. Does not utilize L-arabinose, D-maltose, potassium gluconate, capric acid, adipic acid, trisodium citrate, and phenylacetic acid. Strain WD42 (= VYWGBAC000000148) was isolated from a soil sample, Wando, Korea.

Description of *Paraburkholderia tropica* Kw_8

Cells are gram-staining-negative, flagellated, and rod-shaped. Colonies are circular, convex, and cream/pale yellow-colored after four days of incubation at 30°C on R2A. Positive for glucose fermentation, esculin hydrolysis, and gelatinase and β -galactosidase activity. Negative for nitrate reduction, indole production, and arginine dihydrolase and urease activity. Utilizes D-Glucose, L-arabinose, D-mannose, D-mannitol, N-acetyl-glucosamine, potassium gluconate, capric acid, malic acid, trisodium citrate, and phenylacetic acid. Does not utilize D-maltose and adipic acid. Strain Kw_8 (= VYWGBAC000000094) was isolated from a mud sample, Hwacheon, Korea.

Description of *Paraburkholderia hospita* MMS17-GJ039

Cells are gram-staining-negative, non-flagellated, and rod-shaped. Colonies are circular, convex, entire, smooth, and pale yellow-colored after three days of incubation at 30°C on ISP 2 agar. Positive for esculin hydrolysis and β -galactosidase activity. Negative for nitrate reduction, indole production, glucose fermentation, and arginine dihydrolase, urease, and gelatinase activity. Utilizes D-Glucose, L-arabinose, D-mannose, D-mannitol, N-acetyl-glucosamine, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic. Does not utilize D-maltose. Strain MMS17-GJ039 (= VYWG-BAC000000242) was isolated from a soil sample, Daejeon, Korea.

Description of *Paraburkholderia sartisoli* Gsoil 096

Cells are gram-staining-negative, non-flagellated, and rod-shaped. Colonies are circular, convex, entire, and cream-colored after two days of incubation at 30°C on R2A. Positive for nitrate reduction. Negative for indole production, glucose fermentation, esculin hydrolysis and arginine dihydrolase, urease, and gelatinase β -galactosidase activity. Utilizes D-Glucose, L-arabinose, D-mannose, D-mannitol, N-acetyl-glucosamine, potassium gluconate, capric acid, malic acid, trisodium citrate, and phenylacetic acid. Does not utilize D-maltose and adipic acid. Strain Gsoil 096 (= VYWGBAC000000002) was isolated from a soil sample, Pocheon, Korea.

Description of *Neisseria perflava* HMF7346

Cells are gram-staining-negative, non-flagellated, and cocci chain-shaped. Colonies are circular, convex, smooth, and pale yellow-colored after four days of incubation at 30°C on R2A. Positive for glucose fermentation. Negative for nitrate reduction, indole production, esculin hydrolysis, and arginine dihydrolase, urease, gelati-

nase, and β -galactosidase activity. Utilizes D-Glucose, and D-maltose. Does not utilize L-arabinose, D-mannose, D-mannitol, N-acetyl-glucosamine, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain HMF7346 (= VYWG-BAC000000182) was isolated from a soil sample, Yongin, Korea

Description of *Burkholderia peredens* HMF7693

Cells are gram-staining-negative, non-flagellated, and rod-shaped. Colonies are circular, convex, smooth, and white-colored after three days of incubation at 30°C on R2A. Positive for arginine dihydrolase and urease activity. Negative for nitrate reduction, indole production, glucose fermentation, esculin hydrolysis, and gelatinase and β -galactosidase activity. Utilizes D-Glucose, L-arabinose, D-mannose, D-mannitol, N-acetyl-glucosamine, potassium gluconate, capric acid, malic acid, trisodium citrate, and phenylacetic acid. Does not utilize D-maltose and adipic acid. Strain HMF7693 (= VYWGBAC000000185) was isolated from a tree sample, Yongin, Korea

Description of *Amantichitinum ursilacus* HMF7887

Cells are gram-staining-negative, flagellated, and rod-shaped. Colonies are wrinkled, hilly, wavy, and white-colored after three days of incubation at 30°C on R2A. Positive for nitrate reduction, glucose fermentation, esculin hydrolysis, and β -galactosidase activity. Negative for indole production and arginine dihydrolase, urease and gelatinase activity. Utilizes D-Glucose, L-arabinose, D-mannose, D-mannitol, N-acetyl-glucosamine, D-maltose, and potassium gluconate. Does not utilize capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain HMF7887 (= VYWGBAC000000188) was isolated from a tree sample, Boseong, Korea

Description of *Amantichitinum ursilacus* HMF7887

Cells are gram-staining-negative, flagellated, and rod-shaped. Colonies are wrinkled, hilly, wavy, and white-colored after three days of incubation at 30°C on R2A. Positive for nitrate reduction, glucose fermentation, esculin hydrolysis, and β -galactosidase activity. Negative for indole production and arginine dihydrolase, urease, and gelatinase activity. Utilizes D-Glucose, L-arabinose, D-mannose, D-mannitol, N-acetyl-glucosamine, D-maltose, and potassium gluconate. Does not utilize capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain HMF7887 (= VYWGBAC000000188) was isolated from a tree sample, Boseong, Korea

Description of *Uliginosibacterium paludis* HMF4721

Cells are gram-staining-negative, non-flagellated, and

rod-shaped. Colonies are circular, convex, smooth, and pale yellow-colored after three days of incubation at 30°C on R2A. Positive for nitrate reduction and urease activity. Negative for indole production, glucose fermentation, esculin hydrolysis, and arginine dihydrolase, gelatinase, and β -galactosidase activity. Utilizes D-Glucose, D-mannitol, N-acetyl-glucosamine, D-maltose, potassium gluconate and malic acid. Does not utilize L-arabinose, D-mannose, capric acid, adipic acid, trisodium citrate, and phenylacetic acid. Strain HMF4721 (= VYWG-BAC000000180) was isolated from a water sample from a wetland, Yongin, Korea

Description of *Halodesulfovibrio marinisediminis* LPB0172

Cells are gram-staining-negative, non-flagellated, and cocci-shaped. Colonies are circular, convex, smooth, and black-colored after three days of incubation at 30°C on MA. Negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease activity, esculin hydrolysis, gelatinase, and β -galactosidase activity. 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 and phenylacetic acid. Strain LPB0172 (= VY-WGBAC000000030) was isolated from a seawater sample, Incheon, Korea

Description of *Arcobacter bivalviorum* LPB0305

Cells are gram-staining-negative, flagellated, and rod-shaped. Colonies are circular, convex, smooth, and white-colored after 3 days of incubation at 25°C on MA. Positive for nitrate reduction. Negative for indole production, glucose fermentation, esculin hydrolysis and arginine dihydrolase, urease, gelatinase and β -galactosidase activity. 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, and phenylacetic acid. Strain LPB0305 (= VY-WGBAC000000046) was isolated from a seawater sample, Incheon, Korea

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REFERENCES

- Felsenstein, J. 2002. PHYLIP (phylogeny inference package), version 3.6a, Seattle: Department of genetics, University

- of Washington, Seattle, WA, USA.
- 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.
- Iino, T., M. Ohkuma, Y. Kamagata and S. Amachi. 2016. *Iodidimonas muriae* gen. nov., sp. nov., an aerobic iodide-oxidizing bacterium isolated from brine of a natural gas and iodine recovery facility, and proposals of *Iodidimonadaceae* fam. nov., *Iodidimonadales* ord. nov., *Emcibacteraceae* fam. nov. and *Emcibacterales* ord. nov. International Journal of Systematic and Evolutionary Microbiology 66:5016-5022.
- Kim, O.S., Y.J. Cho, K. Lee, S.H. Yoon, M. Kim, H. Na, S.C. Park, Y.S. Jeon, J.H. Lee, H. Yi, S. Won and J. Chun. 2012. Introducing EzTaxon-e: a prokaryotic 16S rRNA gene sequence database with phylotypes that represent uncultured species. International Journal of Systematic and Evolutionary Microbiology 62:716-721.
- 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.
- 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.
- Watanabe, T., H. Kojima and M. Fukui. 2015. *Sulfuriferula multivorans* gen. nov., sp. nov., isolated from a freshwater lake, reclassification of '*Thiobacillus plumbophilus*' as *Sulfuriferula plumbophilus* sp. nov., and description of *Sulfuricellaceae* fam. nov. and *Sulfuricellales* ord. nov. International Journal of Systematic and Evolutionary Microbiology 65:1504-1508
- 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.

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