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

© 2019 National Institute of Biological Resources DOI:10.12651/JSR.2019.8.2.161

INTRODUCTION

Proteobacteria is the largest bacteria phylum of gramnegative 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: Caulobacterales, Emcibacterales, Iodidimonadales, Kiloniellales, Kordiimonadales, Magnetococcales, Micropepsales, Parvularculales, Pelagibacterales, 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, Desulfarculales, 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 galleries (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 rodshaped, 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, *Burk-holderiales*, *Neisseriales*, and *Rhodocyclales*, of the class *Betaproteobacteria*. Seven strains belonged to three fam-

Image:	Class/phylum	Order	Family	Genus	Strain ID	NIBR ID	Most closely related species	Similarity (%)	Isolation source	Medium	Incubation conditions	
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NesiotobacterHMF8042VYWGBAC00000189Nesiotobacter exalbescens100Salt pondMAParacoccusKYW1385VYWGBAC00000109Paracoccus itbetensis99.0SawaterMARoseobacterBMW10VYWGBAC00000106Roseobacter litoralis99.4SeawaterMAGenmobacterIMCC34207VYWGBAC00000106Roseobacter litoralis99.9SandR2A agarThioclavaGH1-7VYWGBAC00000102Roseibacter linvuensis99.9SandRA agarRoseibacteriumHMF8205VYWGBAC00000192Roseibacterium beinensis99.6Salt pondMARoseibacteriumHMF8205VYWGBAC00000192Roseibacterium beinensis99.6Salt pondMAPalleroniaHMF846VYWGBAC00000192Roseibacter lutimaris99.6Salt pondMARoseibacteriumHMF846VYWGBAC00000192Roseibacter lutimaris99.6Salt pondMARoseomonasHMF8486VYWGBAC00000192Roseibacter lutimaris99.1Salt pondMARoseomonasHMF7612VYWGBAC00000193Roseomonas vinacea100Tidal flatMARoseomonasHMF7612VYWGBAC00000125Talassospira lucentensis99.5Salt pondMARoseomonasHMF7612VYWGBAC00000125Roseomonas vinacea100TreeR2A agarRoseomonasHMF7612VYWGBAC00000025Roseomonas vinacea99.5SandR2A agarRoseomonasMMS17-GI036VYWGBAC00000025<		Rhodobacterales	Hyphomonadaceae	Litorimonas	IMCC34185	VYWGBAC00000119		98.8	Tidal flat	R2A agar (seawater)	25°C, 3d	
ParacoccusKYW1385VYWGBAC00000150Paracoccus tibetensis99.0SeawaterMARoseobacterBMW10VYWGBAC00000160Roseobacter litoralis99.4SeawaterMAGenunobacterIMCC34207VYWGBAC00000160Roseobacter litoralis99.9SeawaterMAThioclavaGH1-7VYWGBAC00000192Roseobacter litoralis99.9SeawaterMAThioclavaGH1-7VYWGBAC00000192Roseobacter litoralis99.9Salt pondMARosebacteriumHMF8435VYWGBAC00000192Roseobacter lutinatis99.9Salt pondMAPalleroniaHMF8435VYWGBAC00000192Roseobacter lutinatis99.0Salt pondMAPalleroniaHMF8435VYWGBAC00000192Roseobacter lutinatis99.1Salt pondMARoseonorusHMF8435VYWGBAC00000192Roseonarsminoris99.1Salt pondMARoseonorusHMF8435VYWGBAC00000135Roseonarsminoris99.1Salt pondMARoseonorusHMF7612VYWGBAC00000135Roseonarsminoris99.1Salt pondMARoseonorusHMF7612VYWGBAC00000125Roseonarsminoris99.5SandR2A agarRoseonorusHMF7612VYWGBAC00000125Roseonarswinacea100TreeR2ARoseonorusIMCC34233VYWGBAC00000125Ralassospira lucentensis99.0SoilISP 2 agarRoseonorusStC2VYWGBAC000000356Rythrobacter longus99.0<			Rhodobacteraceae	Nesiotobacter	HMF8042	VYWGBAC00000189	Nesiotobacter exalbescens	100	Salt pond	MA	30°C. 3d	
RoseobacterBMW10VYWGBAC00000160Roseobacter litoralis99.4SeawaterMAGennobacterIMCC34207VYWGBAC00000118Gennobacter lanyuensis99.9SandR2A agarThioclavaGH1-7VYWGBAC00000192Roseobacter lanyuensis99.8Tidal flatMARoseibacteriumHMF8205VYWGBAC00000192Roseibacterium beibuensis99.6Salt pondMARoseibacteriumHMF8456VYWGBAC00000192Roseibacterium beibuensis99.1Salt pondMAPalleroniaHMF8456VYWGBAC00000192Roseibacter lutimatis99.1Salt pondMAAmylibacterF-mm3VYWGBAC00000192Roseomoras99.1Salt pondMARoseomonasHMF7612VYWGBAC00000193Roseomoras vinacea100TreeR2A agarRoseomonasHMF7612VYWGBAC00000123Roseomoras vinacea100TreeR2A agarRoseomonasHMF7612VYWGBAC00000123Roseomoras vinacea100TreeR2A agarRoseomonasHMF7613VYWGBAC00000123Roseomoras vinacea99.5SandR2A agarRoseomorasIMCC34233VYWGBAC00000123Roseomoras vinacea99.5SandR2A agarRoseomorasIMCC34233VYWGBAC000000238Rowinstinosus99.5SandR2A agarRoseomorasIMCC34233VYWGBAC000000238Rquilinus timosus99.0SoilISP 2 agarRoseomorasStC2VYWGBAC00000356Rythrobacter longus<				Paracoccus	KYW1385	VYWGBAC00000159	Paracoccus tibetensis	0.66	Seawater	MA	25°C, 3d	
GenumobacterIMCC34207VYWGBAC00000118Genumobacter lanyuensis99.9SandR2A agarThioclavaGH1-7VYWGBAC00000192Roseibacterium beibuensis99.8Tidal flatMARoseibacteriumHMF8205VYWGBAC00000192Roseibacterium beibuensis99.999.1Salt pondMAPalleroniaHMF8465VYWGBAC00000192Roseibacterium beibuensis99.1Salt pondMAPalleroniaHMF8465VYWGBAC00000192Roseibacter lutimaris90.1Salt pondMAPalleroniaHMF8465VYWGBAC00000192Roseomonas99.1Salt pondMAAmylibacterF-mm3VYWGBAC00000193Roseomonas vinacea100TiceR2A agarRoseomonasHMF7612VYWGBAC00000125Thalassospira lucentensis99.5SandR2A agarIndustrisIMCC34233VYWGBAC00000125Thalassospira lucentensis99.5SandR2A agarIndustrisIMCC34233VYWGBAC00000125Thalassospira lucentensis99.5SandR2A agarIndustrisIMCC34233VYWGBAC00000125Thalassospira lucentensis99.5SandR2A agarIndustrisIMCC34233VYWGBAC00000125Thalassospira lucentensis99.5SandR2A agarIndustrisIMCC34233VYWGBAC000000228Inquilinus linosus99.0SoilISP 2 agarIndustrisStC2VYWGBAC00000350Atterrythrobacter ishigakiensis99.1Red algaeMAIndustris <td></td> <td></td> <td></td> <td>Roseobacter</td> <td>BMW10</td> <td>VYWGBAC00000160</td> <td>Roseobacter litoralis</td> <td>99.4</td> <td>Seawater</td> <td>MA</td> <td>25°C, 5d</td>				Roseobacter	BMW10	VYWGBAC00000160	Roseobacter litoralis	99.4	Seawater	MA	25°C, 5d	
Thioclava $HhF305$ VYWGBAC0000064Thioclava allantica98.8Tidal flatMARoseibacteriumHMF8205VYWGBAC00000192Roseibacterium beibuensis99.6Salt pondMAPalleroniaHMF843VYWGBAC00000194Palleronia abyssalis99.6Salt pondMAPalleroniaHMF846VYWGBAC00000195Palleronia abyssalis99.1Salt pondMAPalleroniaHMF846VYWGBAC00000195Palleronia abyssalis99.1Salt pondMAAmylibacterF-mm3VYWGBAC00000195Ravenia marisminoris99.1Salt pondMARoseononasHMF7612VYWGBAC00000183Roseononas vinacea100TreeR2AIndussospirIMC234233VYWGBAC00000125Thalassospira lucentensis99.5Sand(Seawater)IndustinusIMC23423VYWGBAC00000125Industinus limosus99.0SoilR2A agarIndustinusIMS17-GJ036VYWGBAC00000228Inquilinus limosus99.0SoilR2A agarInquilinusSt2VYWGBAC00000350Alterrythrobacter longus99.1Red algaeMAIndustinusSt2VYWGBAC00000356Alterrythrobacter longus99.1Red algaeMAIndustinusSt2VYWGBAC00000356Alterrythrobacter longus99.1Red algaeMAIndustinusSt2VYWGBAC00000356Novosphingobium guang-funense99.1Red algaeMAIndustinusSt1VYWGBAC00000354Novosphingob				Gemmobacter	IMCC34207	VYWGBAC000000118	Gemmobacter lanyuensis	6.66	Sand	R2A agar (seawater)	25°C, 3d	
RoseibacteriumHMF8205VYWGBAC00000192Roseibacterium beibuensis99.8Salt pondMAPalleroniaHMF8483VYWGBAC00000194Palleronia abyssalis99.6Salt pondMAPalleroniaHMF8486VYWGBAC00000195Palleronia abyssalis99.1Salt pondMAAmylibacterF-mm3VYWGBAC00000195Palleronia marisminoris99.1Salt pondMAAmylibacterF-mm3VYWGBAC00000183Roseomonas vinacea100TreeR2ARoseomonasIMF7612VYWGBAC00000183Roseomonas vinacea100TreeR2AInalassospirIMCC34233VYWGBAC00000125Thalassospira lucentensis99.5SandR2AInquilinusMMS17-GJ036VYWGBAC00000125Thalassospira lucentensis99.0SoilR2A agarInquilinusMMS17-GJ036VYWGBAC000000258Inquilinus limosus99.0SoilR2A agarInquilinusMMS17-GJ036VYWGBAC000000356Arterrythrobacter longus99.1Red algaeMAInquilinusSc2VYWGBAC00000356Alterrythrobacter longus99.1Red algaeMAInvosphingobiumHMF7644VYWGBAC00000356Alterrythrobacter lingus99.2TreeR2AInvosphingobiumS-1VYWGBAC00000356Marinobacter salsaginis99.2TreeR2A				Thioclava	GH1-7	VYWGBAC00000064	Thioclava atlantica	98.8	Tidal flat	MA	30°C, 5d	
PalleroniaHMF843VYWGBAC00000194Palleronia abyssalis99.6Salt pondMAPalleroniaHMF8486VYWGBAC00000195Palleronia marisminoris99.1Salt pondMAAmylibacterF-mm3VYWGBAC00000346Amylibacter lutimaris100Tidal flatMARoseomonasHMF7612VYWGBAC00000183Roseomonas vinacea100TireeR2AIndussospirIMCC34233VYWGBAC00000125Thalassospira lucentensis99.5SandR2AIndustrosoIMCC34233VYWGBAC00000125Thalassospira lucentensis99.5SandR2AInquilinusMMS17-GJ036VYWGBAC00000228Inquilinus limosus99.0SoilR2A agarErythrobacterGH1-10VYWGBAC00000055Erythrobacter longus99.0SoilR2 agarAltererythrobacterSC2VYWGBAC00000350Altererythrobacter longus99.1Red algaeMAPaltererythrobacterS-1VYWGBAC00000345Marinobacter solsuginis99.2TreeR2				Roseibacterium	HMF8205	VYWGBAC00000192	Roseibacterium beibuensis	8.66	Salt pond	MA	30°C, 3d	
FalleronuaHMF8456VYWGBAC00000195Palleronua marisminoris99.1Salt pondMAAmylibacterF-mm3VYWGBAC00000346Amylibacter lutimaris100Tidal flatMARoseomonasHMF7612VYWGBAC00000183Roseomonas vinacea100TreeR2AThalassospirIMCC34233VYWGBAC00000125Thalassospira lucentensis99.5SandR2A agarInquilinusMMS17-GJ036VYWGBAC00000125Thalassospira lucentensis99.5SandR2A agarInquilinusMMS17-GJ036VYWGBAC000000228Inquilinus limosus99.0SoilISP2 agarErythrobacterGH1-10VYWGBAC00000055Erythrobacter longus98.8Tidal flatMAAltererythrobacterStorVYWGBAC00000055Altererythrobacter isligakiensis99.1Red algaeMAPatrobacterS-1VYWGBAC00000354Marinobacter salsuginis99.2TreeR2AMarinobacterS-1VYWGBAC00000354Marinobacter salsuginis90.2TreeR2A				Palleronia	HMF8483	VYWGBAC00000194	Palleronia abyssalis	9.66 200	Salt pond	MA	30°C, 3d	
RoseomonasHMF7612VYWGBAC00000183Roseomonas vinacea100TreeR2AThalassospirIMCC34233VYWGBAC00000125Thalassospira lucentensis99.5SandR2A agarInquilinusIMCC34233VYWGBAC00000125Thalassospira lucentensis99.5SandR2A agarInquilinusMMS17-GJ036VYWGBAC000000228Inquilinus timosus99.0SoilISP2 agarErythrobacterGH1-10VYWGBAC00000055Erythrobacter longus99.1Red algaeMAAltererythrobacterStC2VYWGBAC00000350Altererythrobacter istigatiensis99.1Red algaeMAP NovosphingobiumHMF7644VYWGBAC00000344Novosphingobium guangzhouense99.2TreeR2AMarinobacterS-1VYWGBAC00000345Marinobacter salsaginis100Marine algaeMA				Palleronia Amylibacter	HMF8486 F-mm3	VYWGBAC000000346 VYWGBAC000000346	Palleronta martsmunorts Amylibacter lutimaris	1.66 100	Salt pond Tidal flat	MA MA	30°C, 3d 30°C, 2d	
ThalassospirIMCC34233VYWGBAC00000125Thalassospira lucentensis99.5SandR2A agarInquitinusMMS17-GJ036VYWGBAC00000228Inquitinus limosus99.0SoilISP2 agarErythrobacterGH1-10VYWGBAC00000055Erythrobacter longus98.8Tidal flatMAAltererythrobacterStC2VYWGBAC00000350Altererythrobacter ishigakiensis99.1Red algaeMAeNovosphingobiumHMF7644VYWGBAC00000344Novosphingobium guangzhouense99.2TreeR2AMarinobacterS-1VYWGBAC00000345Marinobacter salsaginis100Marine algaeMA		Rhodospirillales	Acetobacteraceae	Roseomonas	HMF7612	VYWGBAC00000183	Roseomonas vinacea	100	Tree	R2A	30°C, 3d	
Inquitinus MMS17-GJ036 VYWGBAC00000228 Inquitinus limosus 99.0 Soil ISP2 agar Erythrobacter GH1-10 VYWGBAC0000065 Erythrobacter longus 98.8 Tidal flat MA Altererythrobacter StC2 VYWGBAC00000350 Altererythrobacter longus 99.1 Red algae MA P Novosphingobium HMF7644 VYWGBAC00000184 Novosphingobium guangzhouense 99.2 Tree R2A Marinobacter S-1 VYWGBAC00000345 Marinobacter salsaginis 100 Marine algae MA			Rhodospirillaceae	Thalassospir	IMCC34233	VYWGBAC00000125	Thalassospira lucentensis	99.5	Sand	R2A agar	25°C, 3d	
ErythrobacterGH1-10VYWGBAC00000065Erythrobacter longus98.8Tidal flatMAAltererythrobacterStC2VYWGBAC00000350Altererythrobacter ishigakiensis99.1Red algaeMA?NovosphingobiumHMF7644VYWGBAC00000184Novosphingobium guangzhouense99.2TreeR2AMarinobacterS-1VYWGBAC00000345Marinobacter salsuginis100Marine algaeMA				Inquilinus	MMS17-GJ036	VYWGBAC000000228	Inquilinus limosus	0.66	Soil	ISP 2 agar	30°C, 3d	
HMF7644 VYWGBAC00000184 Novosphingobium guangzhouense 99.2 Tree R2A S-1 VYWGBAC00000345 Marinobacter salsuginis 100 Marine algae MA		Sphingomonadales	Erythrobacteraceae	Erythrobacter Altererythrobacter	GH1-10 StC2	VYWGBAC00000065 VYWGBAC000000350		98.8 99.1	Tidal flat Red algae	MA MA	30°C, 5d 30°C, 3d	
			Sphingomonadaceae	Novosphingobium Marinobacter	HMF7644 S-1	VYWGBAC00000184 VYWGBAC000000345	Novosphingobium guangzhouense Marinobacter salsuginis		Tree Aarine algae	R2A MA	30°C, 3d 30°C, 3d	

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Class/phylum	Order	Family	Genus	Strain ID	NIBR ID	Most closely related species	Similarity (%)	Isolation source	Medium	Incubation conditions
Betaproteobacteria Burkholderiales Burkholderiaceae	Burkholderiales	Burkholderiaceae	Burkholderia Parahurkholderi	WD42 kw_8	VYWGBAC00000148 VYWGBAC00000004	VYWGBAC00000148 Burkholderia dabaoshanensis VYWGBAC00000094 Parahurkholderia tronica	0.99 8 80	Soil Mud	R2A R7A	25°C, 2d 30°C 4d
			Paraburkholderia	MMS17-GJ039		VYWGBAC00000242 Paraburkholderia hospita	8.66	Soil	ISP 2 agar	30°C, 3d
			Paraburkholderia	Gsoil 096	VYWGBAC000000002	VYWGBAC00000002 Paraburkholderia sartisoli	99.8	Soil	R2A	30°C, 2d
			Burkholderia	HMF7693	VYWGBAC00000185 Burkholderia peredens	Burkholderia peredens	98.8	Tree	R2A	30°C, 3d
		Oxalobacteraceae	Massilia	JMn9	VYWGBAC00000143 Massilia timonae	Massilia timonae	99.2	Tidal flat	R2A	25°C, 3d
		Ralstoniaceae	Ralstonia	BR3409	VYWGBAC00000172 Ralstonia pickettii	Ralstonia pickettii	7.66	Sangulttuk Nabi	R2A	37°C
	Neisseriales	Neisseriaceae	Neisseria	HMF7346	VYWGBAC00000182 Neisseria perflava	Neisseria perflava	8.66	Soil	R2A	30°C, 4d
			Amantichitinum	HMF7887	VYWGBAC00000188	VYWGBAC00000188 Amantichitinum ursilacus	6.66	Tree	R2A	30°C, 3d
	Rhodocyclales	Rhodocyclaceae	Uliginosibacterium HMF4721	HMF4721	VYWGBAC00000180	VYWGBAC00000180 Uliginosibacterium paludis	9.66	Wetland	R2A	30°C, 3d
Deltaproteobacteria	Desulfovibrionales	Deltaproteobacteria Desulfovibrionales Desulfovibrionaceae Halodesulfovibrio		LPB0172	VYWGBAC00000030	VYWGBAC00000030 Halodesulfovibrio marinisediminis	99.1	Seawater	MA	30°C, 3d
Epsilonproteobacteria	1 Campylobacterales	Epsilonproteobacteria Campylobacterales Campylobacteraceae Arcobacter	Arcobacter	LPB0305	VYWGBAC00000046 Arcobacter bivalviorum	Arcobacter bivalviorum	9.66	Seawater	MA	25°C, 3d

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 *Halodesulfovibrio* of the family *Desulfovibrionaceae* in the order *Desulfovibrionales* and one strain was assigned to the genus *Arcobacter* of the family *Campylobacteraceae* in the order *Campylobacterales* (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 rodshaped. 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 hydrocarboniclasticum* LPB0211

Cells are gram-staining-negative, flagellated, and rodshaped. Colonies are circular, convex, smooth, and creamcolored 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 (=VYWGBAC 000000044) was isolated from a seawater sample, Incheon, Korea.

Description of Rhizobium herbae 17J44-22

Cells are gram-staining-negative, flagellated, and rodshaped. Colonies are circular, convex, smooth, and creamcolored 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-

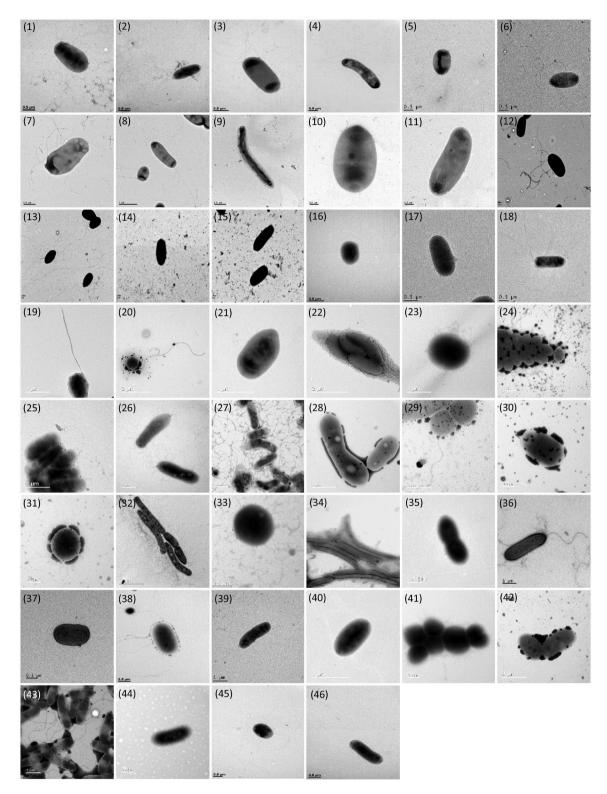


Fig. 1. Transmission electron micrographs or scanning electron micrographs of cells of the strains isolated in this study. The cells were cultured at their optimal growth conditions. Strains: 1, LPB0183; 2, LPB0211; 3, 17J44-22; 4, 17J27-16; 5, KYW1385; 6, BMW10; 7, IMCC34164; 8, IMCC34184; 9, IMCC34185; 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.

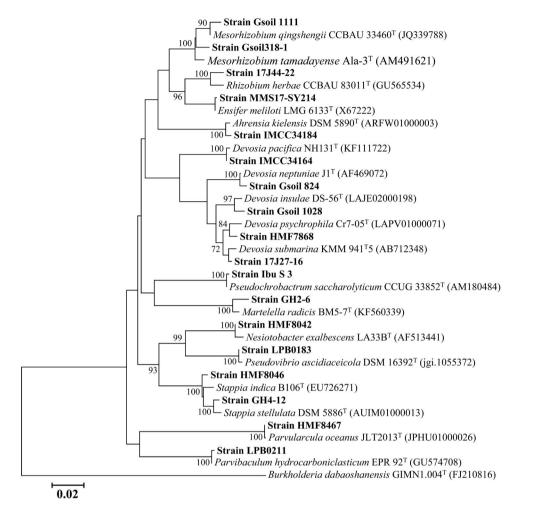


Fig. 2. Neighbor-joining phylogenetic tree, based on 16S rRNA sequences, showing the phylogenetic relationship between strains isolated in this study and their relatives in the orders *Parvularculales* and *Rhizobiales* in the class *Alphaproteobacteria*. *Burkholderia dabaoshanensis* GIMN1.004^T (FJ210816) 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 (= VYWGBAC00000379) 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, Larabinose, 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, ndole 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.

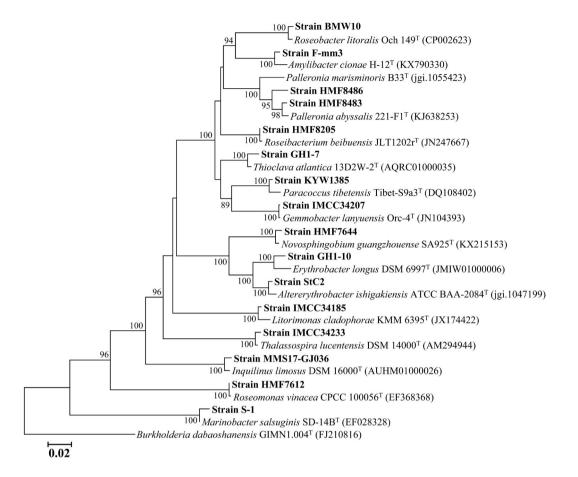


Fig. 3. Neighbor-joining phylogenetic tree, based on 16S rRNA sequences, showing the phylogenetic relationship between strains isolated in this study and their relatives in the orders *Rhodobacterales*, *Rhodospirillales*, and *Sphingomonadales* in the class *Alphaproteobacteria*. *Burkholderia dabaoshanensis* 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 litoralis BMW10

Cells are gram-staining-negative, flagellated, and ovoidshaped. 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 rodshaped. 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 (=VYWG-BAC000000116) was isolated from a tidal flat sample, Incheon, Korea.

Description of Ahrensia kielensis IMCC34184

Cells are gram-staining-negative, flagellated, and rodshaped. 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,

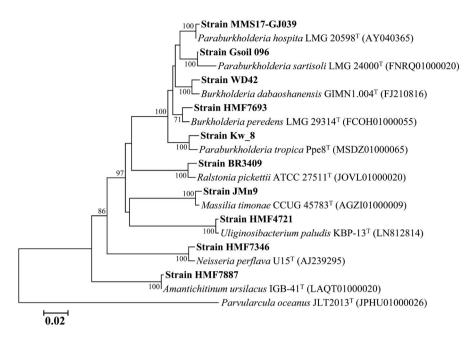


Fig. 4. Neighbor-joining phylogenetic tree, based on 16S rRNA sequences, showing the phylogenetic relationship between strains isolated in this study and their relatives in the orders *Burkholderiales*, *Neisseriales*, and *Rhodocyclales* in the class *Betaproteobacteria*. *Parvularcula oceanus* JLT2013^T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

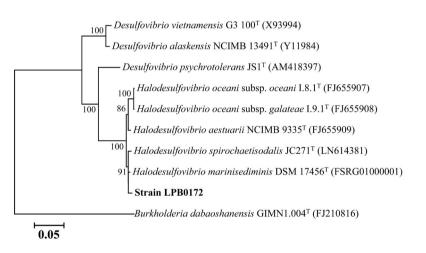


Fig. 5. Neighbor-joining phylogenetic tree, based on 16S rRNA sequences, showing the phylogenetic relationship between strain LPB0172 isolated in this study and its relatives in the order *Desulfovibrionales* in the class *Deltaproteobacteria*. *Burkholderia dabaoshanensis* GIMN1.004^T (FJ210816) was 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-BAC000000113) 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,

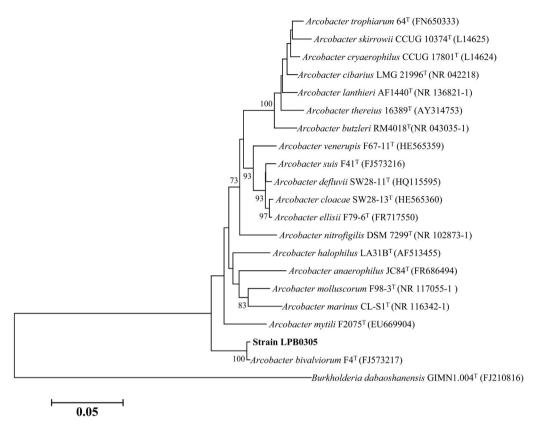


Fig. 6. Neighbor-joining phylogenetic tree, based on 16S rRNA sequences, showing the phylogenetic relationship between strain LPB0305 isolated in this study and its relatives in the order *Campylobacterales* in the class *Epsilonproteobacteria*. *Burkholderia dabaoshanensis* GIMN1.004^T (FJ210816) was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

and phenylacetic acid. Strain IMCC34185 (=VYWG-BAC00000119) 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*-ace-tyl-glucosamine, and potassium gluconate. Does not utilize D-maltose, capric acid, adipic acid, malic acid, triso-dium citrate, and phenylacetic acid. Strain IMCC34233 (=VYWGBAC00000125) 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 rodshaped. Colonies are circular, entire, convex, and creamcolored 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. 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 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 GH1-10 (=VYWGBAC000000065) was isolated from a tidal flat sample, Incheon, Korea.

Description of Martelella radicis 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 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 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 dihydrolas and urease activity. Utilizes D-Glucose, D-mannose, *N*-acetyl-glucos-amine, 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 (=VYWGBAC00000108) 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 dihydrolase, 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 rodshaped. 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 dihydrolase 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 (=VYWG-BAC000000226) was isolated from a soil sample, Gunsan, Korea.

Description of Devosia insulae Gsoil 1028

Cells are gram-staining-negative, flagellated, and ovoidshaped. 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 dihydrolase, 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 ovoidshaped. 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 (=VYWGBAC00000012) 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 (=VYWGBAC00000023) 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 (=VY-WGBAC000000008) 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 (= VYWG-BAC000000184) was isolated from a tree sample, Seoul, Korea.

Description of Devosia psychrophila HMF7868

Cells are gram-staining-negative, flagellated, and rodshaped. Colonies are circular, convex, smooth, and whitecolored 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 (=VYWGBAC 000000186) was isolated from a tree sample, Yongin, Korea.

Description of Nesiotobacter exalbescens HMF8042

Cells are gram-staining-negative, flagellated, and rodshaped. Colonies are circular, convex, smooth, and whitecolored 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 (=VYWG-BAC000000192) 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-glucosamine, potassium gluconate, adipic acid, and malic acid. Does not utilize D-maltose, capric acid, trisodium citrate, and phenylacetic acid. Strain HMF8483 (=VYWG-BAC000000194) 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 (=VYWG-BAC000000195) 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 rodshaped. 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 (*Hippoarchia autonoe*) sample, Jeju, Korea.

Description of Massilia timonae JMn9

Cells are gram-staining-negative, flagellated, and rodshaped. 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 rodshaped. 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 (=VYWGBAC00000002) 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, gelatinase, 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 rodshaped. 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 rodshaped. 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-WGBAC00000030) was isolated from a seawater sample, Incheon, Korea

Description of Arcobacter bivalviorum LPB0305

Cells are gram-staining-negative, flagellated, and rodshaped. Colonies are circular, convex, smooth, and whitecolored 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

ACKNOWLEDGEMENTS

This study was supported by the research grant "The Survey of Korean Indigenous Species" from the National Institute of Biological Resources of the Ministry of Environment in Korea.

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Submitted: July 29, 2018 Revised: December 13, 2018 Accepted: December 13, 2018