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Report of 22 unrecorded bacterial species in Korea belonging to phylum Bacteroidetes, discovered during surveys in 2018

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The phylum Bacteroidetes covers phenotypically diverse groups of Gram negative rods that do not form endospores, and currently includes 6 classes, 6 orders, 33 families and 380 genera. Members of Bacteroidetes can be aerobic and anaerobic heterotrophs, hydrogen utilizing chemolithotrophs, or methylotrophs. They can be isolated from diverse habitats including terrestrial and aquatic environments, environments with extreme physicochemical conditions, and animal and plant hosts. During a series of extensive surveys of prokaryotic species diversity in Korea, bacterial strains belonging to Bacteroidetes were isolated from various sources of aquatic and terrestrial environments. A total of 22 isolates were obtained, which represent 22 unrecorded species in Korea belonging to 14 genera of 6 families. Sixteen species among them were assigned to *Flavobacteriaceae*, two species were to *Sphingobacteriaceae*, and single species was to each of the families *Bacteroidaceae*, *Balneolaceae*, *Chitinophagaceae* and *Cytophagaceae*. At genus level, *Chryseobacterium* (5 species) and *Flavobacterium* (5 species) were the most abundant genera, and single species were obtained for the genera *Bacteroides*, *Baloneola*, *Terrimonas*, *Dyadobacter*, *Aquimarina*, *Arenibacter*, *Gillisia*, *Gilvibacter*, *Salinimicrobium*, *Winogradskyella*, *Pedobacter* and *Sphingobacterium*. The detailed descriptions of each unrecorded species are provided.

Keywords: Bacteroidetes, *Chryseobacterium*, *Flavobacteriaceae*, *Flavobacterium*, unrecorded species

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Introduction

The phylum Bacteroidetes was first proposed by Krieg *et al*. (2012) to accommodate phenotypically diverse groups of Gram negative rods that do not form endospores, and currently includes 6 classes, 6 orders, 33 families and 380 genera as of August 2019 (Euzéby, 2019).

Bacteroidetes encompasses aerobic and anaerobic heterotrophs, hydrogen utilizing chemolithotrophs and methylotrophs, and some members are capable of nitrogen fixation. Their habitats are also diverse, including terrestrial and aquatic environments, environments with extreme physicochemical conditions, and animal and plant hosts.

There have been reports of unrecorded species of this phylum in Korea, and recent studies indicate that members of the genera *Chryseobacterium*, *Flavobacterium*, *Mucilaginibacter*, and *Pedobacter* have been recovered as main taxa (Cho *et al*., 2018; Lee *et al*., 2018; Maeng *et al*., 2018).

In a series of extensive surveys on the prokaryotic diversity in Korea in the year 2018, novel strains belonging to the phylum Bacteroidetes were isolated from various environmental sources, and their taxonomic properties were analyzed. As a result, a total of 22 unrecorded species of Bacteroidetes were identified, and their taxonomic properties are presented.

Materials and Methods

A total of 24 bacterial strains assigned to the phylum Bacteroidetes were isolated from diverse environmental samples collected from mouse, seawater, seawater algae, sludge, soil, moss, and mudflat (Table 1). The samples were processed or treated separately, diluted and spread onto diverse culture media, namely R2A, marine agar (MA), tryptic soy agar (TSA), or nutrient agar (NA), and incubated at 25−30°C for 2−5 days. The designated strain IDs, sources of isolation, culture media, and incubation conditions are provided in the description and Table 1. All strains were purified as single colonies and stored as 10−20% glycerol suspension at −80°C as well as lyophilized ampoules.

Colony characteristics of the isolates were observed on the same agar media for cultivation. Cellular morphology and cell size were examined using either a transmission electron microscope or a scanning electron microscope. Gram staining was performed using standard procedures. Biochemical characteristics were tested by using API 20NE galleries (bioMérieux) according to the manufacturer's instructions.

The extraction of genomic DNA, PCR amplification of 16S rRNA gene, and sequencing were performed using the procedures as described previously (Cho *et al*., 2018; Lee *et al*., 2018; Maeng *et al*., 2018). The 16S rRNA gene sequences of the strains were compared with corresponding reference strains using the EzBioCloud (Kim *et al*., 2012), and their 16S rRNA sequences were aligned using EzEditor2 (Jeon *et al*., 2014). Phylogenetic trees were generated by Jukes-Cantor distance model (Jukes and Cantor, 1969) and neighbor-joining method (Saitou and Nei, 1987) using MEGA 7.0 (Kumar *et al*., 2016). The phylogenetic trees were evaluated using the bootstrap analysis (Felsenstein, 1985) based on 1,000 resampled datasets.

Results and Discussion

A total of 22 bacterial strains belonging to Bacteroidetes were isolated (Table 1). The strains represented 22 unrecorded species in Korea, belonging to 14 genera in 6 families. Sixteen species were assigned to *Flavobacteriaceae*, whereas two species were to *Sphingobacteriaceae*, and single species was to each of the families *Bacteroidaceae*, *Balneolaceae*, *Chitinophagaceae* and *Cytophagaceae*. At genus level, *Chryseobacterium* (5 species) and *Flavobacterium* (5 species) were the two most abundant genera, and single species were obtained for the remaining genera (Table 1). The electron microscopic images of the isolates are provided in Fig. 1, and the phylogenetic relationship between the isolates and closely related species are presented in Figs. 2 and 3. The detailed descriptions of each unrecorded species are provided as below.

Description of *Bacteroides caecimuris* LPB0213

Cells are Gram-stain-negative, non-flagellated, non-pigmented, and short rod-shaped. Colonies are circular, entire, smooth, convex, and creamy-white colored after incubation for 3 days on anaerobe basal at 30°C. Positive for Indole formation, esculin hydrolysis, but negative for urease and gelatin hydrolysis in API 20A. D-Glucose, D-lactose, D-saccharose (sucrose), D-maltose, D-xylose, D-arabinose, D-cellobiose, D-mannose, D-melezitose, D-raffinose, L-rhamnose and D-trehalose are utilized as sole carbon sources, but not D-mannitol, salicin, glycerol and D-sorbitol. Strain LBP0213 (=GFMCBAC000000229) was isolated from mouse intestine sampled at the Korea Institute of Oriental Medicine. The GenBank accession number for the 16S rRNA gene sequence of strain LBP0213 is MH997842.

Description of *Balneola alkaliphila* MaG24

Cells are Gram-stain-negative, non-flagellated, non-pigmented, and bacteriod-shaped. Colonies are round, smooth, and pink colored after incubation for 3 days on MA at 25°C. Positive for nitrate reduction, but negative for indole production, glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis, gelatin hydrolysis, and β-galactosidase in API 20NE. L-Arabinose, D-mannose, *N*-acetyl-glucosamine and malic acid are utilized as sole carbon sources, but not D-glucose, D-mannitol, potassium gluconate, capric acid, adipic acid, trisodium citrate and phenylacetic acid. Strain MaG24 (=GFMCBAC000000251) was isolated from a seawater alga sampled at Taean, Chungcheongnam-do. The GenBank accession number for the 16S rRNA gene sequence of strain MaG24 is MN258893.

Description of *Terrimonas ferruginea* Wi-47

Cells are Gram-stain-negative, non-flagellated, non-pigmented, and rod-shaped. Colonies are circular, convex, smooth, glistering, and orange colored after incubation for 2 days on R2A at 30°C. Positive for esculin hydrolysis and gelatin hydrolysis, but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, and β-galactosidase in API 20NE. L-Arabinose, *N*-acetyl-glucosamine, D-maltose and malic acid are utilized as sole carbon sources, but not D-glucose, D-mannose, D-mannitol, potassium gluconate, capric acid, adipic acid, trisodium citrate and phenylacetic acid. Strain Wi-47 (=GFMCBAC000000169) was isolated from sludge sampled at Seoul. The GenBank accession number for the 16S rRNA gene sequence of strain Wi-47

Table 1. Summary of isolated strains belonging to the class Bacteroidetes and their taxonomic affiliations.

Family	Genus	Strain ID	NIBR ID	Most closely related species	Similarity (%)	Isolation source	Medium	Incubation conditions
Bacteroidaceae	*Bacteroides*	LPB0213	GFMCBAC000000229	*Bacteroides caecimuris*	99.5%	Mouse	Anaerobe basal	30°C, 3 days
Balneolaceae	*Balneola*	MaG24	GFMCBAC000000251	*Balneola alkaliphila*	100.0%	Seawater algae	MA	25°C, 3 days
Chitinophagaceae	*Terrimonas*	Wi-47	GFMCBAC000000169	*Terrimonas ferruginea*	100.0%	Sludge	R2A	30°C, 2 days
Cytophagaceae	*Dyadobacter*	GA076	GFMCBAC000000151	*Dyadobacter alkalitolerans*	98.7%	Soil	R2A	30°C, 3 days
Flavobacteriaceae	*Aquimarina*	KYW1525	GFMCBAC000000234	*Aquimarina atlantica*	99.9%	Seawater	MA	25°C, 3 days
	Arenibacter	Ast28	GFMCBAC000000242	*Arenibacter algicola*	99.9%	Seawater algae	MA	10−30°C, 7 days
	Chryseobacterium	HMF5202	GFMCBAC000000222	*Chryseobacterium nepalense*	100.0%	Moss	R2A	30°C, 3 days
		18S4T3	GFMCBAC000000191	*Chryseobacterium carnipullorum*	98.8%	Soil	MH	30°C, 2 days
		18H1T5	GFMCBAC000000198	*Chryseobacterium rhizoplanae*	99.2%	Soil	MH	30°C, 2 days
		18H3M2	GFMCBAC000000206	*Chryseobacterium lineare*	99.4%	Soil	MH	30°C, 2 days
		BT43	GFMCBAC000000055	*Chryseobacterium profundimaris*	99.0%	Soil	R2A	25°C, 4 days
	Flavobacterium	BO204	GFMCBAC000000159	*Flavobacterium flevense*	99.8%	Soil	R2A	25°C, 3 days
		18S4P11	GFMCBAC000000192	*Flavobacterium banpakuense*	98.8%	Soil	MH	30°C, 2 days
		18H3V6	GFMCBAC000000195	*Flavobacterium branchiarum*	99.0%	Soil	MH	30°C, 2 days
		18N3G15	GFMCBAC000000197	*Flavobacterium pectinovorum*	98.8%	Soil	MH	30°C, 2 days
		18N3V8	GFMCBAC000000201	*Flavobacterium tructae*	99.6%	Soil	MH	30°C, 2 days
	Gillisia	SC115	GFMCBAC000000237	*Gillisia limnaea*	99.1%	Mud flat	MA	25°C, 5 days
	Gilvibacter	HMF9181	GFMCBAC000000224	*Gilvibacter sediminis*	99.3%	Seawater	MA	30°C, 3 days
	Salinimicrobium	SC71	GFMCBAC000000152	*Salinimicrobium flavum*	100.0%	Mud flat	MA	25°C, 3 days
	Winogradskyella	HMF9088	GFMCBAC000000106	*Winogradskyella litoriviva*	98.8%	Seawater	MA	30°C, 3 days
Sphingobacteriaceae	*Pedobacter*	BO167	GFMCBAC000000256	*Pedobacter borealis*	99.2%	Soil	R2A	25°C, 3 days
	Sphingobacterium	18SBM11	GFMCBAC000000205	*Sphingobacterium nematocida*	99.9%	Soil	MH	30°C, 2 days

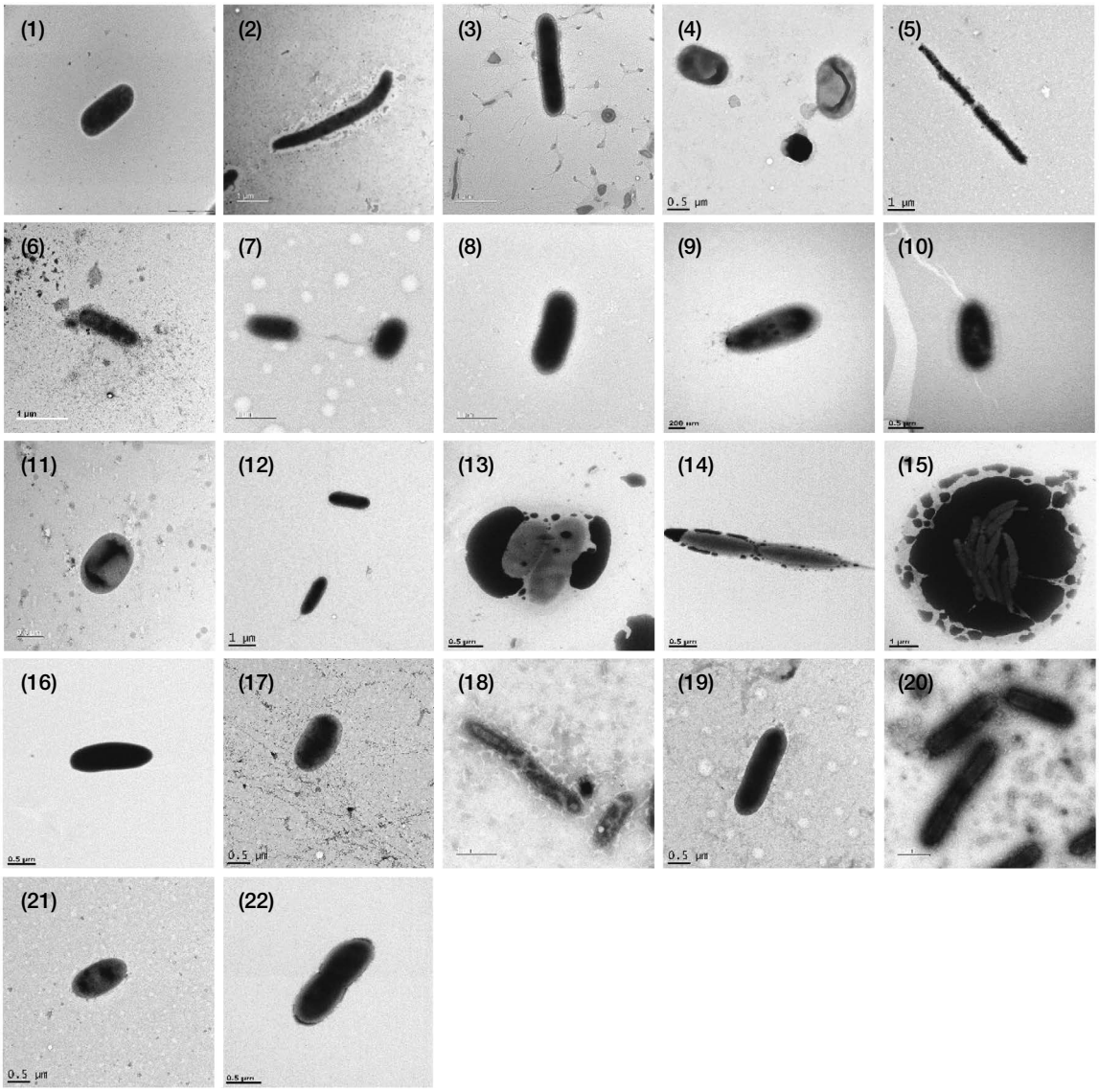

Fig. 1. Transmission electron micrographs or scanning electron micrographs of cells of the strains isolated in the study. Strains: 1, LPB0213; 2, MaG24; 3, Wi-47; 4, GA076; 5, KYW1525; 6, Ast28; 7, HMF5202; 8, 18S4T3; 9, 18H1T5; 10, 18H3M2; 11, BT43; 12, BO204; 13, 18S4P11; 14, 18H3V6; 15, 18N3G15; 16, 18N3V8; 17, SC115; 18, HMF9181; 19, SC71; 20, HMF9088; 21, BO167; 22, 18SBM11.

is MK039089.

Description of *Dyadobacter alkalitolerans* GA076

Cells are Gram-stain-negative, non-flagellated, non-pigmented, and rod-shaped. Colonies are circular, convex, smooth, glistening, and yellow colored after incubation for 3 days on R2A at 30°C. Positive for glucose fermentation, esculin hydrolysis, β-galactosidase, and cytochrome oxidase, but negative for nitrate reduction, indole production, arginine dihydrolase, urease, and gelatin hydrolysis. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine and D-maltose are utilized as sole carbon sources, but not gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. Strain GA076 (=GFMCBAC000000151) was isolated from soil sampled at Daejeon. The GenBank accession number for the 16S rRNA gene sequence of strain GA076 is MK135796.

Description of *Aquimarina atlantica* KYW1525

Cells are Gram-stain-negative, non-flagellated, non-pigmented, and rod-shaped. Colonies are circular, convex, smooth, and yellow colored after incubation for 3 days on MA at 25°C. Positive for β-galactosidase nitrate re-

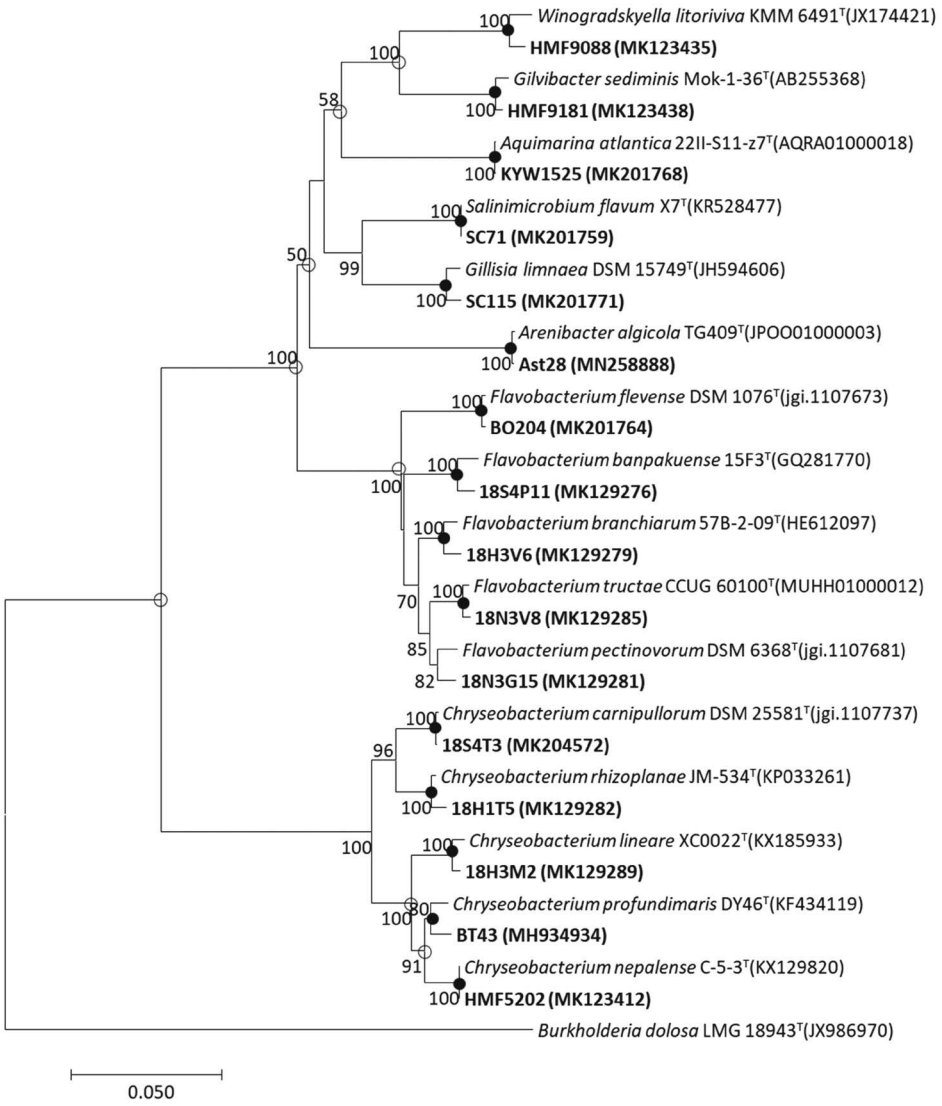

Fig. 2. Neighbor-joining phylogenetic tree, based on 16S rRNA gene sequences, showing the relationships between the strains isolated in this study and their relatives of the order *Flavobacteriales* in the class Bacteroidetes. Bootstrap values (>50%) are shown at branching points. Filled circles indicate that the corresponding nodes were also recovered in the trees generated with the maximum-likelihood and maximum-parsimony algorithms, while open circles indicate that the corresponding nodes were also recovered in the tree generated with one of these algorithms. Bar, 0.05 substitutions per nucleotide position.

duction, indole production, glucose fermentation, urease, and esculin hydrolysis, but negative for nitrate reduction, indole production, glucose fermentation, urease, esculin hydrolysis, arginine dihydrolase, and gelatin hydrolysis in API 20NE. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, malic acid, trisodium citrate, phenylacetic acid and adipic acid are not utilized as sole carbon sources. Strain KYW1525 (GFMCBAC000000234) was isolated from seawater sampled at Jeollanam-do. The GenBank accession number for the 16S rRNA gene sequence of strain KYW1525 is MK201768.

Description of *Arenibacter algicola* Ast28

Cells are Gram-stain-negative, non-flagellated, non-pigmented, and rod-shaped. Colonies are round, convex, smooth, and yellow colored after incubation for 7 days on MA at 10−30°C. Positive for nitrate reduction, glucose fermentation, gelatin hydrolysis but negative for urease, esculin hydrolysis, and β-galactosidase indole production, arginine dihydrolase, and gelatin hydrolysis in API 20NE. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, malic acid and trisodium citrate are utilized as sole carbon sources, but not capric acid, adipic acid and phenylacetic

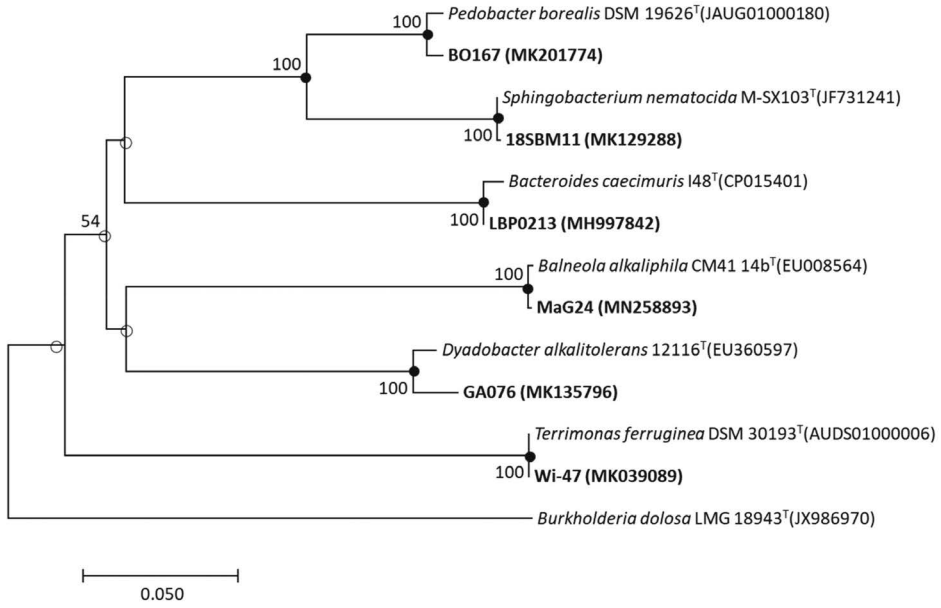

Fig. 3. Neighbor-joining phylogenetic tree, based on 16S rRNA gene sequences, showing the relationships between the strains isolated in this study and their relatives of the order *Bacteroidales*, *Balneolales*, *Chitinophagales*, *Cytophagales* and *Sphingobacteriales* in the class Bacteroidetes. Bootstrap values (>50%) are shown at branching points. Filled circles indicate that the corresponding nodes were also recovered in the trees generated with the maximum likelihood and maximum parsimony algorithms, while open circles indicate that the corresponding nodes were also recovered in the tree generated with one of these algorithms. Bar, 0.05 substitutions per nucleotide position.

acid. Strain Ast28 (=GFMCBAC000000242) was isolated from a seawater alga sampled at Chungcheongbuk-do. The GenBank accession number for the 16S rRNA gene sequence of strain Ast28 is MN258888.

Description of *Chryseobacterium nepalense* HMF5202

Cells are Gram-stain-negative, non-flagellated, non-pigmented, and rod-shaped. Colonies are circular, convex, mucoid, and yellow colored after incubation for 3 days on R2A at 30°C. Positive for esculin hydrolysis, gelatin hydrolysis, and β-galactosidase but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, and urease in API 20NE. D-Glucose, D-mannose, D-maltose, potassium gluconate and malic acid are utilized as sole carbon sources, but not L-arabinose, D-mannitol, *N*-acetyl-glucosamine, capric acid, adipic acid, trisodium citrate and phenylacetic acid. Strain HMF5202 (=GFMCBAC000000222) was isolated from a moss sampled at Daegu. The GenBank accession number for the 16S rRNA gene sequence of strain HMF5202 is MK123412.

Description of *Chryseobacterium carnipullorum* 18S4T3

Cells are Gram-stain-negative, non-flagellated, non-pigmented, and rod-shaped. Colonies are circular, convex, smooth, and yellow colored after incubation for 2 days on MH at 30°C. Positive for indole production, esculin hydrolysis, and gelatin hydrolysis, but negative for nitrate reduction, glucose fermentation, arginine dihydrolase, urease, and β-galactosidase in API 20NE. D-Glucose, D-mannose, *N*-acetyl-glucosamine, potassium gluconate, D-maltose, malic acid, trisodium citrate, adipic acid and phenylacetic acid are utilized as sole carbon sources, but not L-arabinose, D-mannitol and capric acid. Strain 18S4T3 (=GFMCBAC000000191) was isolated from soil sampled at Goyang, Gyeonggi-do. The GenBank accession number for the 16S rRNA gene sequence of strain 18S4T3 is MK204572.

Description of *Chryseobacterium rhizoplanae* 18H1T5

Cells are Gram-stain-negative, non-flagellated, non-pigmented, and rod-shaped. Colonies are circular, convex, smooth, and yellow colored after incubation for 2 days on MH at 30°C. Positive for indole production, esculin hydrolysis, gelatin hydrolysis, and β-galactosidase, but negative for nitrate reduction, arginine dihydrolase, glucose fermentation, and urease in API 20NE. D-Glucose, D-mannose, D-maltose, potassium gluconate, malic acid, and phenylacetic acid are utilized as sole carbon sources, but not L-arabinose, D-mannitol, *N*-acetyl-glucosamine, capric acid, adipic acid, and trisodium citrate. Strain 18H1T5 (=GFMCBAC000000198) was isolated from soil sampled at Hanam, Gyeonggi-do. The GenBank ac-

cession number for the 16S rRNA gene sequence of strain 18H1T5 is MK129282.

Description of *Chryseobacterium lineare* 18H3M2

Cells are Gram-stain-negative, non-flagellated, non-pigmented, and rod-shaped. Colonies are circular, convex, smooth, and yellow colored after incubation for 2 days on MH at 30°C. Positive for nitrate reduction, indole production, esculin hydrolysis, gelatin hydrolysis, and β-galactosidase, but negative for glucose fermentation, arginine dihydrolase, and urease in API 20NE. D-Glucose, L-arabinose, D-mannose, D-maltose, potassium gluconate, adipic acid and malic acid are utilized as sole carbon sources, but not *N*-acetyl-glucosamine, D-mannitol, potassium gluconate, capric acid, trisodium citrate and phenylacetic acid. Strain 18H3M2 (=GFMCBAC000000206) was isolated from stream side soil sampled at Seoul. The GenBank accession number for the 16S rRNA gene sequence of strain 18H3M2 is MK129289.

Description of *Chryseobacterium profundimaris* BT43

Cells are Gram-stain-negative, non-flagellated, non-pigmented, and rod-shaped. Colonies are circular, convex, smooth, and yellow colored after incubation for 4 days on R2A at 25°C. Positive for indole production, esculin hydrolysis, and gelatin hydrolysis, but negative for nitrate reduction, glucose fermentation, arginine dihydrolase urease, and β-galactosidase in API 20NE. D-Glucose and D-mannose are utilized as sole carbon sources, but not L-arabinose, D-maltose, *N*-acetyl-glucosamine, D-mannitol, potassium gluconate, capric acid, trisodium citrate, adipic acid, malic acid and phenylacetic acid. Strain BT43 (=GFMCBAC000000055) was isolated from soil sampled at Peongchang, Gangwon-do. The GenBank accession number for the 16S rRNA gene sequence of strain BT43 is MH934934.

Description of *Flavobacterium flevense* BO204

Cells are Gram-stain-negative, non-flagellated, non-pigmented, and rod-shaped. Colonies are circular, smooth, convex, and pale yellow colored after incubation for 3 days on R2A at 25°C. Positive for nitrate reduction, but negative for indole production, glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis, gelatin hydrolysis, and β-galactosidase. Adipic acid, malic acid, trisodium citrate and phenylacetic acid are utilized as sole carbon sources, but not D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, gluconate and capric acid. Strain BO204 (=GFMCBAC000000159) was isolated from soil sampled at Suncheon, Jeollanam-do. The GenBank accession number for the 16S rRNA gene sequence of strain BO204 is MK201764.

Description of *Flavobacterium banpakuense* 18S4P11

Cells are Gram-stain-negative, non-flagellated, non-pigmented, and rod-shaped. Colonies are circular, smooth, raised, and yellow colored after incubation for 2 days on MH at 30°C. Positive for nitrate reduction, esculin hydrolysis, and β-galactosidase, but negative for indole production, glucose fermentation, arginine dihydrolase, urease, and gelatin hydrolysis. D-Glucose, L-arabinose, D-mannose, *N*-acetyl-glucosamine and D-maltose are utilized as sole carbon sources, but not D-mannitol, gluconate. capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. Strain 18S4P11 (=GFMCBAC000000192) was isolated from soil sampled at Goyang, Gyeonggi-do. The GenBank accession number for the 16S rRNA gene sequence of strain 18S4P11 is MK129276.

Description of *Flavobacterium branchiarum* 18H3V6

Cells are Gram-stain-negative, non-flagellated, non-pigmented, and rod-shaped. Colonies are circular, smooth, raised, and yellow colored after incubation for 2 days on MH at 30°C. Positive for arginine dihydrolase and β-galactosidase, but negative for nitrate reduction, indole production, glucose fermentation, urease, esculin hydrolysis, and gelatin hydrolysis. D-Glucose, D-mannose, *N*-acetyl-glucosamine, D-maltose and trisodium citrate are utilized as sole carbon sources, but not L-arabinose, D-mannitol, gluconate, capric acid, adipic acid, malic acid and phenylacetic acid. Strain 18H3V6 (=GFMCBAC000000195) was isolated from soil sampled at Seoul. The GenBank accession number for the 16S rRNA gene sequence of strain 18H3V6 is MK129279.

Description of *Flavobacterium pectinovorum* 18N3G15

Cells are Gram-stain-negative, non-flagellated, non-pigmented, and rod-shaped. Colonies are circular, smooth, raised, and yellow colored after incubation for 2 days on MH at 30°C. Positive for arginine dihydrolase and β-galactosidase, but negative for nitrate reduction, indole production, glucose fermentation, urease, esculin hydrolysis, and gelatin hydrolysis. D-Glucose, D-mannose, D-maltose and trisodium citrate are utilized as sole carbon sources, but not L-arabinose, D-mannitol, *N*-acetyl-glucosamine, gluconate, capric acid, adipic acid, malic acid and phenylacetic acid. Strain 18N3G15 (=GFMCBAC000000197) was isolated from soil sampled at Gapyeong, Gyeonggi-do. The GenBank accession number for the 16S rRNA gene sequence of strain 18N3G15 is MK129281.

Description of *Flavobacterium tructae* 18N3V8

Cells are Gram-stain-negative, non-flagellated, non-pigmented, and rod-shaped. Colonies are circular, smooth, raised, and yellow colored after incubation for 2 days on MH at 30°C. Positive for esculin hydrolysis and β-galactosidase, but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, and gelatin hydrolysis. D-Glucose, D-mannose, *N*-acetyl-glucosamine, D-maltose, gluconate, adipic acid, malic acid and trisodium citrate are utilized as sole carbon sources, but not L-arabinose, D-mannitol, capric acid and phenylacetic acid. Strain 18N3V8 (=GFMCBAC000000201) was isolated from soil sampled at Gapyeong, Gyeonggi-do. The GenBank accession number for the 16S rRNA gene sequence of strain 18N3V8 is MK129285.

Description of *Gillisia limnaea* SC115

Cells are Gram-stain-negative, non-flagellated, non-pigmented, and rod-shaped. Colonies are circular, smooth, convex, and yellow colored after incubation for 3 days on MA at 30°C. Positive for esculin hydrolysis and β-galactosidase, but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, and gelatin hydrolysis. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid are not utilized as sole carbon sources. Strain SC115 (=GFMCBAC000000237) was isolated from soil sampled at Suncheon, Jeollanam-do. The GenBank accession number for the 16S rRNA gene sequence of strain SC115 is MK201771.

Description of *Gilvibacter sediminis* HMF9181

Cells are Gram-stain-negative, non-flagellated, non-pigmented, and rod-shaped. Colonies are circular, smooth, convex, and yellow colored after incubation for 3 days on MA at 30°C. Positive for esculin hydrolysis, gelatin hydrolysis, and β-galactosidase, but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, and urease. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid are not utilized as sole carbon sources. Strain HMF9181 (=GFMCBAC000000224) was isolated from soil sampled at Pohang, Gyeongsangbuk-do. The GenBank accession number for the 16S rRNA gene sequence of strain HMF9181 is MK123438.

Description of *Salinimicrobium flavum* SC71

Cells are Gram-stain-negative, non-flagellated, non-pigmented, and rod-shaped. Colonies are circular, smooth, convex, opaque, and yellow colored after incubation for 3 days on MA at 25°C. Positive for esculin hydrolysis, but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, gelatin hydrolysis, and β-galactosidase. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid are not utilized as sole carbon sources. Strain SC71 (=GFMCBAC000000152) was isolated from soil sampled at Suncheon, Jeollanam-do. The GenBank accession number for the 16S rRNA gene sequence of strain SC71 is MK201759.

Description of *Wingogradskyella litoriviva* HMF9088

Cells are Gram-stain-negative, non-flagellated, non-pigmented, and rod-shaped. Colonies are circular, smooth, convex, and yellow colored after incubation for 3 days on MA at 30°C. Positive for glucose fermentation, arginine dihydrolase, esculin hydrolysis, and gelatin hydrolysis, but negative for nitrate reduction, indole production, urease, and β-galactosidase. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid are not utilized as sole carbon sources. Strain HMF9088 (=GFMCBAC000000106) was isolated from soil sampled at Gangneung, Gangwon-do. The GenBank accession number for the 16S rRNA gene sequence of strain HMF9088 is MK123435.

Description of *Pedobacter borealis* BO167

Cells are Gram-stain-negative, non-flagellated, non-pigmented, and rod-shaped. Colonies are circular, smooth, convex, and pale pink colored after incubation for 3 days on R2A at 25°C. Positive for esculin hydrolysis and β-galactosidase, but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, and gelatin hydrolysis. D-Glucose, L-arabinose, D-mannose, *N*-acetyl-glucosamine and D-maltose are utilized as sole carbon sources, but not D-mannitol, gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. Strain BO167 (=GFMCBAC000000256) was isolated from soil sampled at Yeoju, Gyeonggi-do. The GenBank accession number for the 16S rRNA gene sequence of strain BO167 is MK201774.

Description of *Sphingobacterium nematocida* 18SBM11

Cells are Gram-stain-negative, non-flagellated, non-pigmented, and rod-shaped. Colonies are circular, smooth, convex, and yellow colored after incubation for 2 days

on MH at 30°C. Positive for urease, esculin hydrolysis, and β-galactosidase, but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, and gelatin hydrolysis. D-Glucose, D-mannose, *N*-acetyl-glucosamine and D-maltose are utilized as sole carbon sources, but not L-arabinose, D-mannitol, gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. Strain 19SBM11 (=GFMC-BAC000000205) was isolated from soil sampled at Yeoju, Gyeonggi-do. The GenBank accession number for the 16S rRNA gene sequence of strain 18SBM11 is MK129288.

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