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A report of 17 unrecorded bacterial species of Korea belonging to the phylum *Bacteroidetes*

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While screening indigenous prokaryotic species in Republic of Korea in 2017, a total of 17 bacterial strains assigned to the phylum *Bacteroidetes* were isolated from a variety of environmental habitats including water of fountain, tidal flat, plant root, soil, the gut of Russian grayling butterfly, ginseng field, seawater, lagoon and seashore sand. From the 16S rRNA gene sequence similarity of more than 98.7% and the formation of a robust phylogenetic clade with the closest species, it was found that the 17 strains belong to independent and recognized bacterial species. There has been no official report that the identified 17 species have been previously isolated in the Republic of Korea. Thus, 15 species in 10 genera of one family in the order *Flavobacteriales*, one species in one genus of one family in the order *Cytophagales*, and one species in one genus of one family in the order *Sphingobacteriales* are proposed as unrecorded species of the phylum *Bacteroidetes* found in the Republic of Korea. Gram reaction, colony and cell morphology, basic phenotypic characteristics, isolation source, taxonomic status, strain ID and other information are described in the species descriptions.

Keywords: prokaryote, 16S rRNA gene, *Bacteroidetes*, unrecorded species, prokaryotic diversity

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Introduction

Microorganisms, including prokaryotes, have been estimated to occupy more than approximately 60% of the total biomass on earth and are known to play important roles in sustaining ecological system. Microorganisms are arguably the most valuable resources in biotechnology, and thus the demand for novel and useful microorganisms is expected to increase in the future due to their high economic value. Nevertheless, the majority of microorganisms in nature have not been cultured in the laboratory, because the current methods can cultivate only a small fraction ($< 0.1\%$) of microbial cells (Delong *et al*., 1989; Giovannoni *et al*., 1990). Since the value of microbial diversity is becoming increasingly important, a good deal of effort has been dedicated to discover novel microorganisms that have not been yet discovered (Connon and Giovannoni, 2002; Cho and Giovannoni, 2004; Yoon *et al*., 2011).

While screening indigenous prokaryotic species from a variety of environmental samples in the Republic of Korea in 2017, we isolated a number of novel and unrecorded bacterial species. The identified bacterial species belonged to the classes/phyla *Proteobacteria*, *Bacteroidetes*, *Firmicutes* and *Actinobacteria*. Of these bacterial species, the present study focuses on the descriptions of unrecorded species belonging to the phylum *Bacteroidetes*. The phylum *Bacteroidetes* encompasses a pheno-

typically diverse group of Gram-negative and non-endospore-forming bacteria (Krieg *et al*., 2010). Members of the phylum *Bacteroidetes* have been described from a variety of habitats including terrestrial, marine and aquatic environments, gastrointestinal tracts of animals and other environments (Thomas *et al*., 2011; Sun *et al*., 2016). It this study, we report 17 unrecorded bacterial species, isolated from Republic of Korea, belonging to three families in three orders in the phylum *Bacteroidetes*.

Materials and Methods

A total of 17 bacterial strains were isolated from diverse environmental samples including water of fountain, tidal flat, plant root, soil, gut of Russian grayling butterfly, ginseng field, seawater, lagoon and seashore sand (Table 1). Each sample was processed separately, spread onto diverse culture media including R2A, marine agar 2216 (MA; Difco), trypticase soy agar (TSA; Difco) or seawater agar, and incubated at 25-30°C for 2-5 days (Table 1). The designated strain ID, taxonomic information, isolation sources, culture media and incubation conditions are summarized in 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 morphology of isolated strains was observed on agar plates after their cells were grown to stationary phase. Cellular morphology and cell size were examined by light microscopy, transmission electron microscopy or scanning electron microscopy. Gram staining was performed using a Gram-staining kit or the standard procedures. Phenotypic characteristics were tested by using API 20NE galleries (bioMérieux) according to the manufacturer's instructions.

DNA extraction, PCR amplification of 16S rRNA gene and 16S rRNA gene sequencing were performed using the standard procedures described elsewhere (Yoon *et al*., 2012). The 16S rRNA gene sequences of the strains assigned to the phylum *Bacteroidetes* were compared with those of other bacterial species with validly published names using the EzBioCloud database (Yoon *et al*., 2017). For phylogenetic analyses, alignment of sequences was carried out with CLUSTAL W software (Thompson *et al*., 1994). Phylogenetic trees were inferred by using three tree-making algorithms: the neighbor-joining (Saitou and Nei, 1987), maximum-likelihood (Felsenstein, 1981) and maximum-parsimony (Kluge and Farris, 1969) methods implemented within the PHYLIP package (Felsenstein, 1993). Evolutionary distance matrices for the neighbor-joining method were calculated by using the algorithm of Jukes and Cantor (1969) with the program DNADIST. The stability of relationships was assessed by bootstrap analysis based on 1000 re-samplings of the neighbor-joining dataset by using the programs SEQBOOT, DNADIST, NEIGHBOR and CONSENSE of the PHYLIP package.

Results and Discussion

Strains assigned to the phylum *Bacteroidetes*

On the basis of 16S rRNA gene sequence comparisons and phylogenetic analyses, a total of 17 strains were assigned to the phylum *Bacteroidetes*. The 17 strains were distributed in three orders of the phylum *Bacteroidetes*; 15 strains in the *Flavobacteriales*, one strain in the *Cytophagales*, and one strain in the *Sphingobacteriales* (Table 1). These strains were Gram-staining-negative, chemoheterotrophic, and rod-shaped bacteria (Fig. 1). Colony size, morphology, and phenotypic characteristics are shown in the species descriptions.

A total of 15 strains assigned to the order *Flavobacteriales* belonged to the family *Flavobacteriaceae* (Fig. 2, Table 1). The strains assigned to the family *Flavobacteriaceae* belonged to the genera *Bizionia*, *Chryseobacterium*, *Cellulophaga*, *Dokdonia*, *Flavimarina*, *Flavobacterium*, *Maribacter*, *Mesoflavibacter*, *Salegentibacter* and *Zobellia*, and were isolated mainly from a variety of habitats (Fig. 2, Table 1). Phylogenetic analyses based on 16S rRNA gene sequences showed that the 15 strains are members of the following species: *Bizionia paragorgiae* (Nedashkovskaya *et al*., 2005a), *Chryseobacterium culicis* (Kämpfer *et al*., 2010), *Chryseobacterium formosense* (Young *et al*., 2005), *Chryseobacterium sediminis* (Kämpfer *et al*., 2015), *Chryseobacterium shandongense* (Yang *et al*., 2015), *Chryseobacterium viscerum* (Zamora *et al*., 2012), *Cellulophaga lytica* (Johansen *et al*., 1999), *Dokdonia diaphoros* (Yoon *et al*., 2012), *Flavimarina pacifica* (Nedashkovskaya *et al*., 2014), *Flavobacterium hibernum* (McCammon *et al*., 1998), *Maribacter spongiicola* (Jackson *et al*., 2015), *Mesoflavibacter zeaxanthinifaciens* (Asker *et al*., 2007), *Salegentibacter echinorum* (Xia *et al*., 2013), *Salegentibacter mishustinae* (Nedashkovskaya *et al*., 2005b) and *Zobellia russellii* (Nedashkovskaya *et al*., 2004).

One strain (JH2) assigned to the family *Cytophagaceae* of the order *Cytophagales* belonged to the genus *Runella* and was isolated from a water of fountain (Fig. 2, Table 1). From phylogenetic analysis based on 16S rRNA gene sequences, strain JH2 was identified as a member of *Runella slithyformis* (Larkin and Williams, 1978).

One strain (Amx_S_17) assigned to the family *Chitinophagaceae* of the order *Sphingobacteriales* belonged

Table 1. Summary of isolates belonging to the phylum *Bacteroidetes* and their taxonomic affiliations.

Order	Family	Genus	Strain no.	NIBR ID	Closest species	16S rRNA gene sequence similarity (%)	Isolation source	Medium for incubation	Condition for incubation
Cytophagales	*Cytophagaceae*	*Runella*	JH2	VYWGBAC000000145	*Runella slithyformis*	99.3	Water of fountain	R2A	25°C, 3d
Flavobacteriales	*Flavobacteriaceae*	*Bizionia*	GH1-5	VYWGBAC000000063	*Bizionia paragorgiae*	99.8	Tidal flat	MA	30°C, 5d
		Chryseobacterium	HMF7877	VYWGBAC000000187	*Chryseobacterium culicis*	98.9	Plant root	R2A	30°C, 3d
		Chryseobacterium	17J42-12	VYWGBAC000000378	*Chryseobacterium formosense*	99.2	Soil	R2A	25°C, 4d
		Chryseobacterium	BT2401	VYWGBAC000000162	*Chryseobacterium sediminis*	99.6	Gut of Russian grayling butterfly	TSA	20°C
		Chryseobacterium	JH4	VYWGBAC000000146	*Chryseobacterium shandongense*	99.9	Water of fountain	R2A	25°C, 3d
		Chryseobacterium	r2a108d329	VYWGBAC000000101	*Cryseobacterium viscerum*	99.0	Soil of ginseng field	R2A	30°C, 2d
		Cellulophaga	IMCC34136	VYWGBAC000000115	*Cellulophaga lytica*	99.9	Tidal flat	R3A seawater agar	25°C, 3d
		Dokdonia	BMW36	VYWGBAC000000157	*Dokdonia diaphoros*	99.9	Seawater	MA	25°C, 3d
		Flavimarina	IMCC34176	VYWGBAC000000117	*Flavimarina pacifica*	99.9	Tidal flat	R11A seawater agar	25°C, 3d
		Flavobacterium	HMF9511	VYWGBAC000000199	*Flavobacterium hibernum*	99.9	Lagoon	R2A	30°C, 3d
		Maribacter	BMW32	VYWGBAC000000156	*Maribacter spongiicola*	99.2	Seawater	MA	25°C, 3d
		Mesoflavibacter	IMCC34232	VYWGBAC000000120	*Mesoflavibacter zeaxanthinifaciens*	99.8	Seashore sand	R18A seawater agar	25°C, 3d
		Salegentibacter	IMCC34139	VYWGBAC000000124	*Salegentibacter echinorum*	99.3	Tidal flat	R6A seawater agar	25°C, 3d
		Salegentibacter	LPB0187	VYWGBAC000000039	*Salegentibacter mishustinae*	99.5	Seawater	MA	25°C, 3d
		Zobellia	IMCC34137	VYWGBAC000000130	*Zobellia russellii*	100	Tidal flat	R4A seawater agar	25°C, 3d
Sphingobacteriales	*Chitinophagaceae*	*Terrimonas*	Amx_S_17	VYWGBAC000000105	*Terrimonas rubra*	99.4	Soil	R2A	30°C, 2d

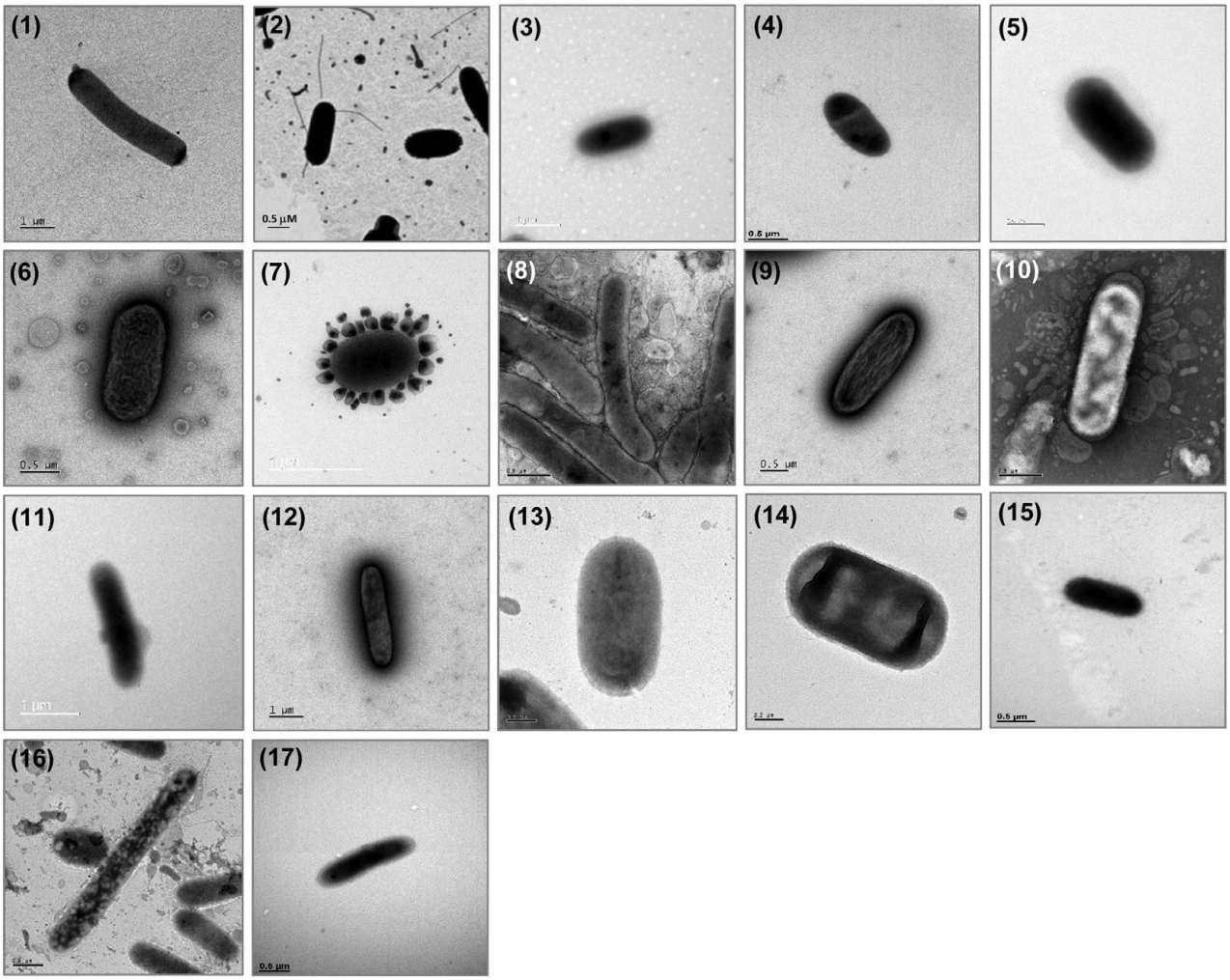

Fig. 1. Electron micrographs of cells of the strains isolated in this study. Strains: 1, JH2; 2, GH1-5; 3, HMF7877; 4, 17J42-12; 5, BT2401; 6, JH4; 7, r2a108d329; 8, IMCC34136; 9, BMW36; 10, IMCC34176; 11, HMF9511; 12, BMW32; 13, IMCC34232; 14, IMCC34139; 15, LPB0187; 16, IMCC34137; 17, Amx_S_17.

to the genus *Terrimonas*, and was isolated from soil (Fig. 2, Table 1). From phylogenetic analysis based on 16S rRNA gene sequences, strain Amx_S_17 was identified as a member of *Terrimonas rubra* (Zhang *et al*., 2012).

There has been no official report that above-mentioned 17 species have been isolated in the Republic of Korea; therefore, 15 species in 10 genera of one family in the order *Flavobacteriales*, one species in one genus of one family in the order *Cytophagales*, and one species in one genus of one family in the order *Sphingobacteriales* are proposed as unrecorded species of the phylum *Bacteroidetes* found in Republic of Korea.

Description of *Runella slithyformis* JH2

Cells are Gram-staining-negative, aerobic, non-flagellated and rodshaped. Colonies are circular, convex, smooth, entire and pale pinkcolored after incubation for 3 days on R2A at 25°C. In the API 20NE system, positive reaction for oxidase activity, esculin hydrolysis and β-galactosidase activity, but negative reaction for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease activity, gelatin hydrolysis and utilization of 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 JH2 (=VYWGBAC000000145) was isolated from a water of fountain at Suncheon, Korea.

Description of *Bizionia paragorgiae* GH1-5

Cells are Gram-staining-negative, aerobic, non-flagellated and rodshaped. Colonies are irregular, convex,

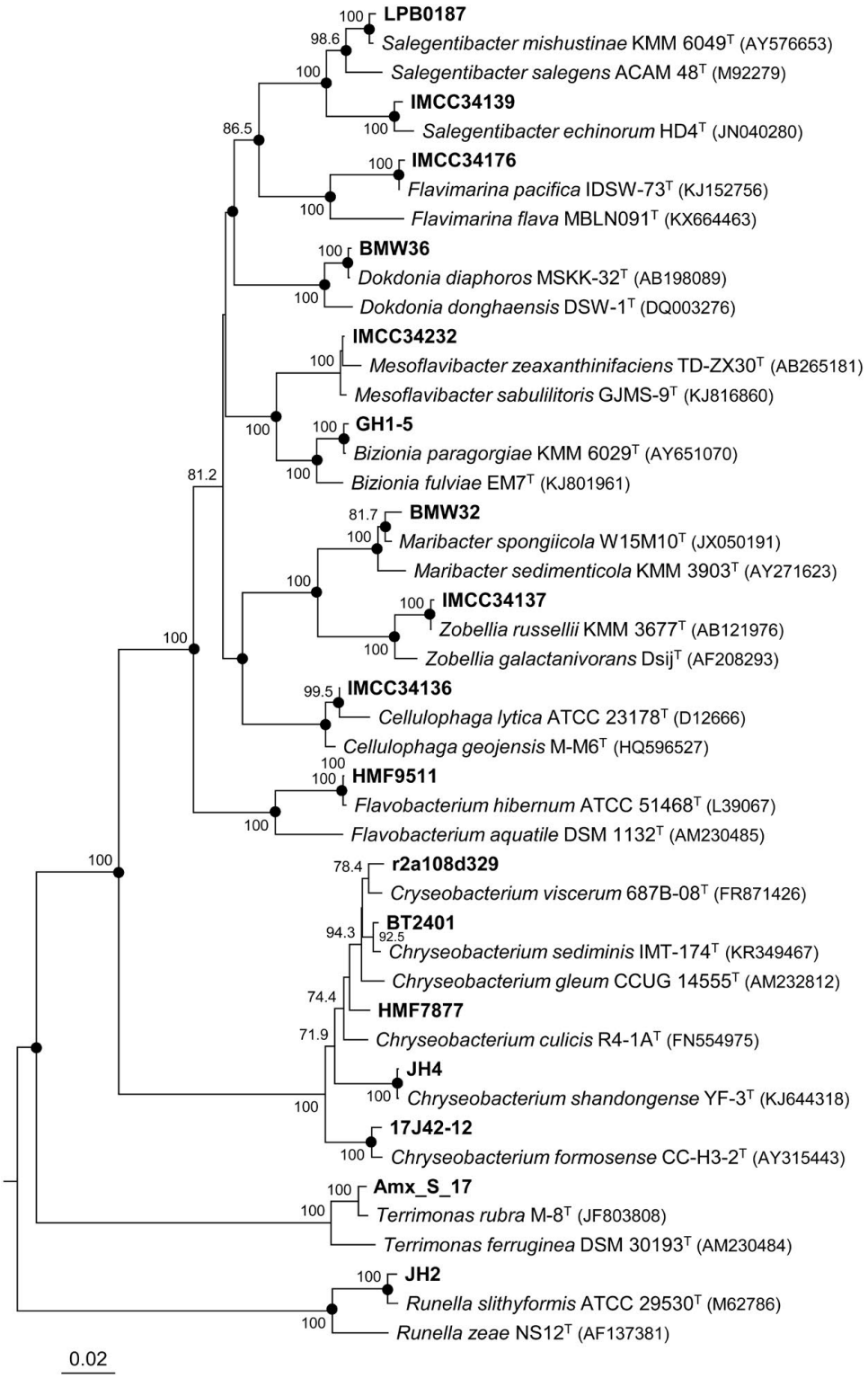

Fig. 2. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences showing the relationships between bacterial strains isolated in this study and their relatives in the phylum *Bacteroidetes*. Only bootstrap values greater than 70% are shown at branching points. Filled circles indicate that the corresponding nodes were also recovered in the trees generated with the maximum-likelihood and maximum-parsimony algorithms. *Escherichia coli* ATCC 11775^T (GenBank accession no. X80725) was used as an outgroup. Bar, 0.02 substitutions per nucleotide position.

undulate and yellowcolored after incubation for 5 days on marine agar 2216 (MA) at 30°C. In the API 20NE system, positive reaction for oxidase activity and gelatin hydrolysis (weak), but negative reaction for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease activity, esculin hydrolysis, β-galactosidase activity and utilization of 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 GH1-5 (=VYWGBAC000000063) was isolated from a tidal flat at Ganghwa, Korea.

Description of *Chryseobacterium culicis* HMF7877

Cells are Gram-staining-negative, aerobic, non-flagellated and rodshaped. Colonies are circular, convex, smooth and whitecolored after incubation for 3 days on R2A at 30°C. In the API 20NE system, positive reaction for oxidase activity, indole production, gelatin hydrolysis and utilization of D-glucose, but negative reaction for nitrate reduction, glucose fermentation, arginine dihydrolase, urease activity, esculin hydrolysis, β-galactosidase activity and utilization of 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 HMF7877 (=VYWGBAC000000187) was isolated from a plant root at Boseong, Korea.

Description of *Chryseobacterium formosense* 17J42-12

Cells are Gram-staining-negative, aerobic, non-flagellated and rodshaped. Colonies are circular, convex, smooth and orangecolored after incubation for 4 days on R2A at 25°C. In the API 20NE system, positive reaction for arginine dihydrolase, urease activity, esculin hydrolysis, gelatin hydrolysis, β-galactosidase activity and utilization of D-glucose, D-mannose, D-maltose, potassium gluconate, malic acid and phenylacetic acid, but negative reaction for nitrate reduction, indole production, glucose fermentation and utilization of L-arabinose, D-mannitol, *N*-acetyl-glucosamine, capric acid, adipic acid and trisodium citrate. Strain 17J42-12 (=VYWGBAC000000378) was isolated from a soil at Jeju island, Korea.

Description of *Chryseobacterium sediminis* BT2401

Cells are Gram-staining-negative, aerobic, non-flagellated and rodshaped. Colonies are circular, convex and yellowcolored after incubation on TSA at 20°C. In the API 20NE system, positive reaction for urease activity, esculin hydrolysis, gelatin hydrolysis, β-galactosidase activity and utilization of D-glucose, L-arabinose, D-mannose, D-maltose, potassium gluconate, adipic acid, malic acid, trisodium citrate and phenylacetic acid, but negative reaction for oxidase activity, nitrate reduction, indole production, glucose fermentation, arginine dihydrolase and utilization of D-mannitol, *N*-acetyl-glucosamine and capric acid. Strain BT2401 (=VYWGBAC000000162) was isolated from a gut of Russian grayling butterfly, Korea.

Description of *Chryseobacterium shandongense* JH4

Cells are Gram-staining-negative, aerobic, non-flagellated and rodshaped. Colonies are circular, convex, smooth, opaque and yellowcolored after incubation for 3 days on R2A at 25°C. In the API 20NE system, positive reaction for oxidase activity, esculin hydrolysis, gelatin hydrolysis and utilization of D-glucose, but negative reaction for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease activity, β-galactosidase activity and utilization of 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 JH4 (=VYWGBAC000000146) was isolated from a water of fountain at Suncheon, Korea.

Description of Cryseobacterium viscerum r2a108d329

Cells are Gram-staining-negative, aerobic, non-flagellated and rodshaped. Colonies are circular, smooth and yellowcolored after incubation for 2 days on R2A at 30°C. In the API 20NE system, positive reaction for oxidase activity, nitrate reduction, urease activity, esculin hydrolysis, gelatin hydrolysis, β-galactosidase activity and utilization of D-glucose, D-mannose, *N*-acetyl-glucosamine, D-maltose, capric acid, malic acid and trisodium citrate, but negative reaction for indole production, glucose fermentation, arginine dihydrolase and utilization of L-arabinose, D-mannitol, potassium gluconate, adipic acid and phenylacetic acid. Strain r2a108d329 (=VYWGBAC000000101) was isolated from a soil of ginseng field at Anseong, Korea.

Description of *Cellulophaga lytica* IMCC34136

Cells are Gram-staining-negative, aerobic, non-flagellated and rodshaped. Colonies are irregular, undulate, flat and yellowcolored after incubation for 3 days on "R3A" seawater agar at 25°C. In the API 20NE system, positive reaction for esculin hydrolysis, gelatin hydrolysis and β-galactosidase activity, but negative reaction for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease activity and utilization of 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 IMCC34136 (=VYWGBAC000000115) was isolated from a tidal flat at Jangbong island of Incheon, Korea.

Description of *Dokdonia diaphoros* BMW36

Cells are Gram-staining-negative, aerobic, non-flagellated and rodshaped. Colonies are circular, convex, smooth, opaque and yellowcolored after incubation for 3 days on marine agar 2216 (MA) at 25°C. In the API 20NE system, positive reaction for oxidase activity, esculin hydrolysis and β-galactosidase activity, but negative reaction for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease activity, gelatin hydrolysis and utilization of 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 BMW36 (=VYWGBAC000000157) was isolated from a seawater at Jangheung, Korea.

Description of *Flavimarina pacifica* IMCC34176

Cells are Gram-staining-negative, aerobic, non-flagellated and rodshaped. Colonies are circular, entire, raised and yellowcolored after incubation for 3 days on "R11A" seawater agar at 25°C. In the API 20NE system, positive reaction for esculin hydrolysis and β-galactosidase activity, but negative reaction for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease activity, gelatin hydrolysis and utilization of 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 IMCC34176 (=VYWGBAC000000117) was isolated from a tidal flat at Jangbong island of Incheon, Korea.

Description of *Flavobacterium hibernum* HMF9511

Cells are Gram-staining-negative, aerobic, non-flagellated and rodshaped. Colonies are circular, convex, smooth and yellowcolored after incubation for 3 days on R2A at 30°C. In the API 20NE system, positive reaction for oxidase activity, nitrate reduction, esculin hydrolysis, β-galactosidase activity and utilization of malic acid, but negative reaction for indole production, glucose fermentation, arginine dihydrolase, urease activity, gelatin hydrolysis and utilization of D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, trisodium citrate and phenylacetic acid. Strain HMF9511 (=VYWGBAC000000199) was isolated from a lagoon at Gangneung, Korea.

Description of *Maribacter spongiicola* BMW32

Cells are Gram-staining-negative, aerobic, non-flagellated and rodshaped. Colonies are circular, convex, smooth, entire and orangecolored after incubation for 3 days on marine agar 2216 (MA) at 25°C. In the API 20NE system, positive reaction for oxidase activity, esculin hydrolysis and β-galactosidase activity, but negative reaction for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease activity, gelatin hydrolysis and utilization of 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 BMW32 (=VYWGBAC000000156) was isolated from seawater at Jangheung, Korea.

Description of *Mesoflavibacter zeaxanthinifaciens* IMCC34232

Cells are Gram-staining-negative, aerobic, non-flagellated and rodshaped. Colonies are circular, entire, raised and yellowcolored after incubation for 3 days on "R18A" seawater agar at 25°C. In the API 20NE system, positive reaction for esculin hydrolysis and gelatin hydrolysis, but negative reaction for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease activity, β-galactosidase activity and utilization of 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 IMCC34232 (=VYWGBAC000000120) was isolated from a seashore sand at Wando, Korea.

Description of *Salegentibacter echinorum* IMCC34139

Cells are Gram-staining-negative, aerobic, non-flagellated and rodshaped. Colonies are circular, entire, convex and yellowcolored after incubation for 3 days on "R6A" seawater agar at 25°C. In the API 20NE system, positive reaction for nitrate reduction, arginine dihydrolase, urease activity, esculin hydrolysis and β-galactosidase activity, but negative reaction for indole production, glucose fermentation, gelatin hydrolysis and utilization of 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 IMCC34139 (=VYWGBAC000000124) was isolated from a tidal flat at Jangbong island of Incheon, Korea.

Description of *Salegentibacter mishustinae* LPB0187

Cells are Gram-staining-negative, aerobic, non-flag-

ellated and rodshaped. Colonies are circular, convex, smooth and yellowcolored after incubation for 3 days on marine agar 2216 (MA) at 25°C. In the API 20NE system, positive reaction for oxidase activity and esculin hydrolysis, but negative reaction for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease activity, gelatin hydrolysis, β-galactosidase activity and utilization of 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 LPB0187 (=VYWGBAC000000039) was isolated from a seawater at Jeju island, Korea.

Description of *Zobellia russellii* IMCC34137

Cells are Gram-staining-negative, aerobic, non-flagellated and rodshaped. Colonies are circular, entire, raised and orange yellowcolored after incubation for 3 days on "R4A" seawater agar at 25°C. In the API 20NE system, positive reaction for nitrate reduction, esculin hydrolysis and β-galactosidase activity, but negative reaction for indole production, glucose fermentation, arginine dihydrolase, urease activity, gelatin hydrolysis and utilization of 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 IMCC34137 (=VYWGBAC000000130) was isolated from a tidal flat at Jangbong island of Incheon, Korea.

Description of *Terrimonas rubra* Amx_S_17

Cells are Gram-staining-negative, aerobic, non-flagellated and rodshaped. Colonies are circular and deep saffroncolored after incubation for 2 days on R2A at 30°C. In the API 20NE system, positive reaction for oxidase activity, esculin hydrolysis, gelatin hydrolysis, β-galactosidase activity and utilization of D-glucose, D-mannose, *N*-acetyl-glucosamine and D-maltose, but negative reaction for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease activity and utilization of L-arabinose, D-mannitol, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. Strain Amx_S_17 (=VYWGBAC000000105) was isolated from a soil at Anseong, Korea.

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