

# A report of 28 unrecorded bacterial species, phylum *Bacteroidetes*, in Korea

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In order to investigate indigenous prokaryotic species diversity in Korea, various environmental samples from diverse ecosystems were examined. Isolated bacterial strains were identified based on 16S rRNA gene sequences, and those exhibiting at least 98.7% sequence similarity with known bacterial species, but not reported in Korea, were selected as unrecorded species. 28 unrecorded bacterial species belonging to the phylum *Bacteroidetes* were discovered from various habitats including wastewater, freshwater, freshwater sediment, wet land, reclaimed land, plant root, bird feces, seawater, sea sand, tidal flat sediment, a scallop, marine algae, and seaweed. The unrecorded species were assigned to 18 different genera in five families: *Flavobacterium*, *Epilithonimonas*, *Dokdonia*, *Gillisia*, *Flavicella*, *Chryseobacterium*, *Algibacter*, *Aquimarina*, *Lacinutrix*, *Gaetbulibacter*, *Cellulophaga*, *Tenacibaculum*, and *Maribacter* of *Flavobacteriaceae*, *Dyadobacter* of *Cytophagaceae*, *Draconibacterium* of *Draconibacterium\_f*, *Sunxiuqinia* of *Prolixibacteraceae*, and *Fulvivirga* of *Fulvivirga\_f*. The selected isolates were subjected to further taxonomic characterization including analysis of Gram reaction, cellular and colonial morphology, biochemical activities, and phylogenetic trees. Descriptive information of the 28 unrecorded species is provided.

Keywords: *Bacteroidetes*, *Bacteroidia*, *Cytophagia*, *Flavobacteriia*, *Sphingobacteria*, unrecorded bacterial species

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## INTRODUCTION

The phylum *Bacteroidetes* encompasses a phenotypically diverse group of Gram-reaction-negative rods that do not form endospores (Krieg *et al.*, 2010; Euzéby, 2012). This phylum contains a diverse set of members in terms of morphology, physiology, and metabolic capability. This phenotypic versatility enabled members of this phylum to colonize a wide array of ecological niches. Members of the phylum *Bacteroidetes* are found in a

wide range of both terrestrial and aquatic environments, as well as in the gastrointestinal tract and skin of animals (Thomas *et al.*, 2011).

According to the Bergey's Manual of Systematic Bacteriology, the phylum *Bacteroidetes* comprises four classes: *Flavobacteriia*, *Bacteroidia*, *Cytophagia*, and *Sphingobacteria* (Krieg *et al.*, 2010). The class *Flavobacteriia* is the largest group but includes only the order *Flavobacteriales*. Members of this class include organisms with a wide range of basic physiology, from

strict anaerobes to strict aerobes. Cells are non-motile or exhibit gliding motility and colonies are yellow or orange due to the production of carotenoid and/or flexirubin-type pigments. Many marine members require NaCl or other sea salts for growth, but the *Bacteroidetes* are widely distributed in soil or fresh water. Some species are endosymbiotic (Bernardet, 2015). The class *Bacteroidia* presently contains one order, *Bacteroidales*. This class includes many anaerobic species that are the dominant species of normal flora of the gastrointestinal tract of mammalian, vertebrate, and invertebrate hosts. The majority of *Bacteroidetes* are commensals or symbionts, but some are known pathogens. Most members are saccharolytic, although proteins and other substrates may be used for energy (Krieg, 2015). The class *Sphingobacteriia* is composed of a single order of aerobic or facultatively anaerobic bacteria that are capable of producing a high concentration of sphingophospholipids as cellular lipid components. Members of this class are commonly found in marine and soil environments (Kämpfer, 2015). The members of the class *Cytophagia* are chemo-organotrophic, motile by gliding or flagella, or non-motile, and usually strictly aerobic. Colonies are yellow, orange, pink, or red owing to carotenoids and/or flexirubin-type pigments. This class is observed in a wide range of natural environments (Nakagawa, 2015).

In this study, bacteria belonging to the phylum *Bacteroidetes* were isolated from various sources including terrestrial, limnic, and marine environments, as well as animals and plants. A phylogenetic analysis using 16S rRNA gene sequences revealed 28 species that were unrecorded in Korea.

## MATERIALS AND METHODS

Bacterial strains were isolated from various terrestrial and marine environmental sources including wastewater, freshwater, freshwater sediment, wet land, reclaimed land, plant root, bird feces, seawater, sea sand, tidal flat sediment, a scallop, marine algae, and seaweed. Each environmental sample was processed separately. Bacterial strains were cultured in R2A or marine agar 2216 (MA) media at 20–30°C for 1–5 days. The designation of strains, source of isolation, culture media, and incubation conditions are summarized in Table 1. All strains were purified as single colonies and stored in 10–20% glycerol suspension at –80°C and as lyophilized ampoules.

Bacterial DNA extraction, PCR amplification, and gene sequencing were performed using standard procedures. Primers 27F (5'-AGAGTTTGATCMTGGCTCAG-3') and 1492R (5'-TACGGYTACCTTGTTACGACTT-3') were used for PCR and sequencing of the 16S rRNA gene. The 16S sequences were compared with other bac-

terial species with published names using the EzTaxon-e server (Yoon *et al.*, 2017). A cutoff value of 98.7% sequence similarity was employed for identification. Strains exhibiting 98.7% or higher sequence similarity with known bacterial species but not reported in Korea were identified as unrecorded species. For phylogenetic analyses, sequence alignments between the 16S rRNA gene sequences of the isolates and those of the reference type strains were carried out using EzEditor (Jeon *et al.*, 2014). Evolutionary distances were calculated using the Kimura two-parameter model and the phylogenetic trees were constructed by using the neighbor-joining and maximum-likelihood algorithms implemented in MEGA 6.0 (Tamura *et al.*, 2013). The robustness of the inferred trees was evaluated by bootstrap analysis based on 1,000 re-samplings.

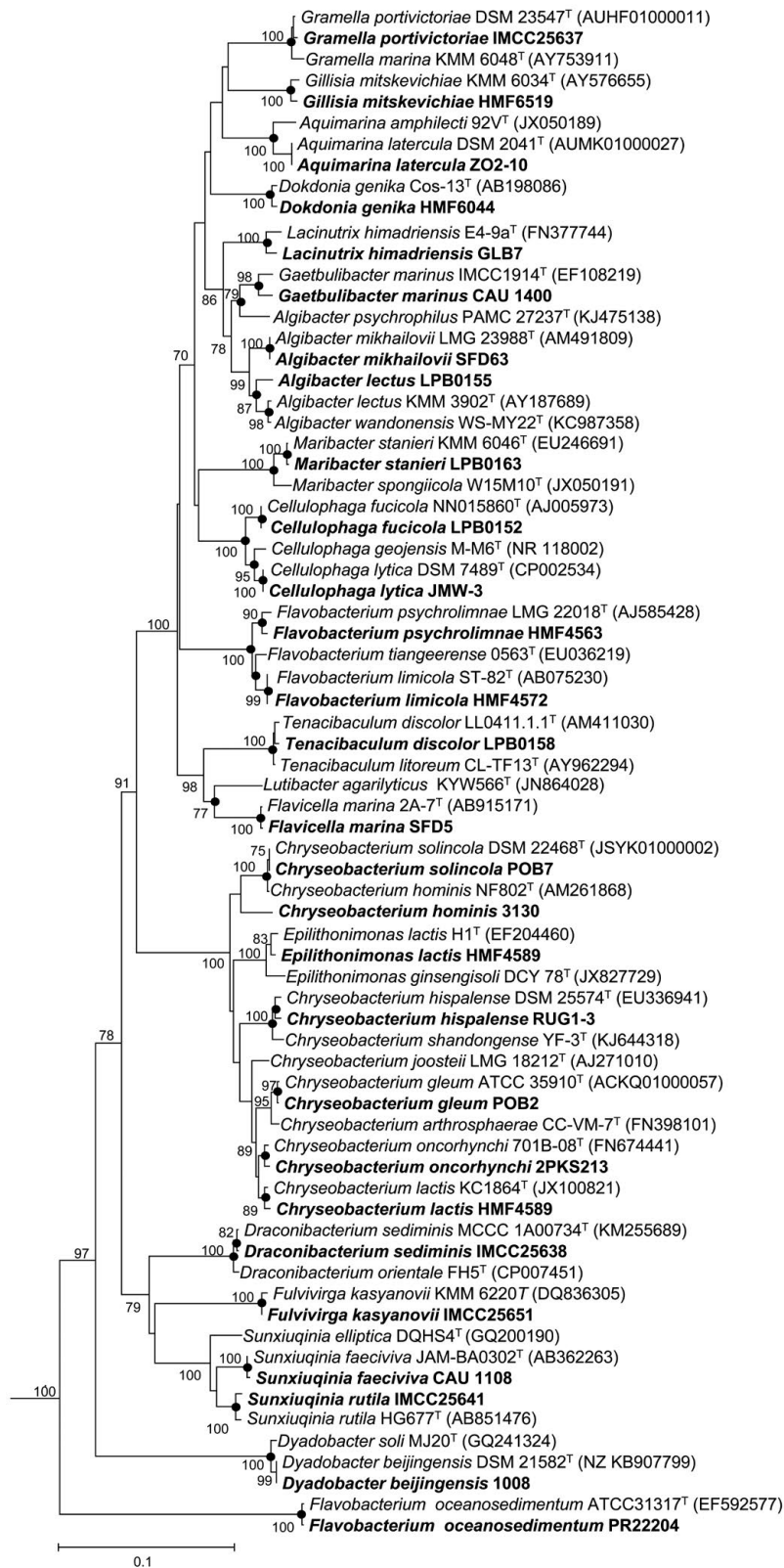
Colonial morphology was observed on agar plates after the cells were cultivated to their stationary phase. Cellular morphology and cell size were examined by either transmission electron microscopy or scanning electron microscopy. Gram staining was performed using a Gram-staining kit or the standard procedures. Biochemical characteristics were tested by using API 20NE galleries (bioMérieux) according to the manufacturer's instructions.

## RESULTS AND DISCUSSION

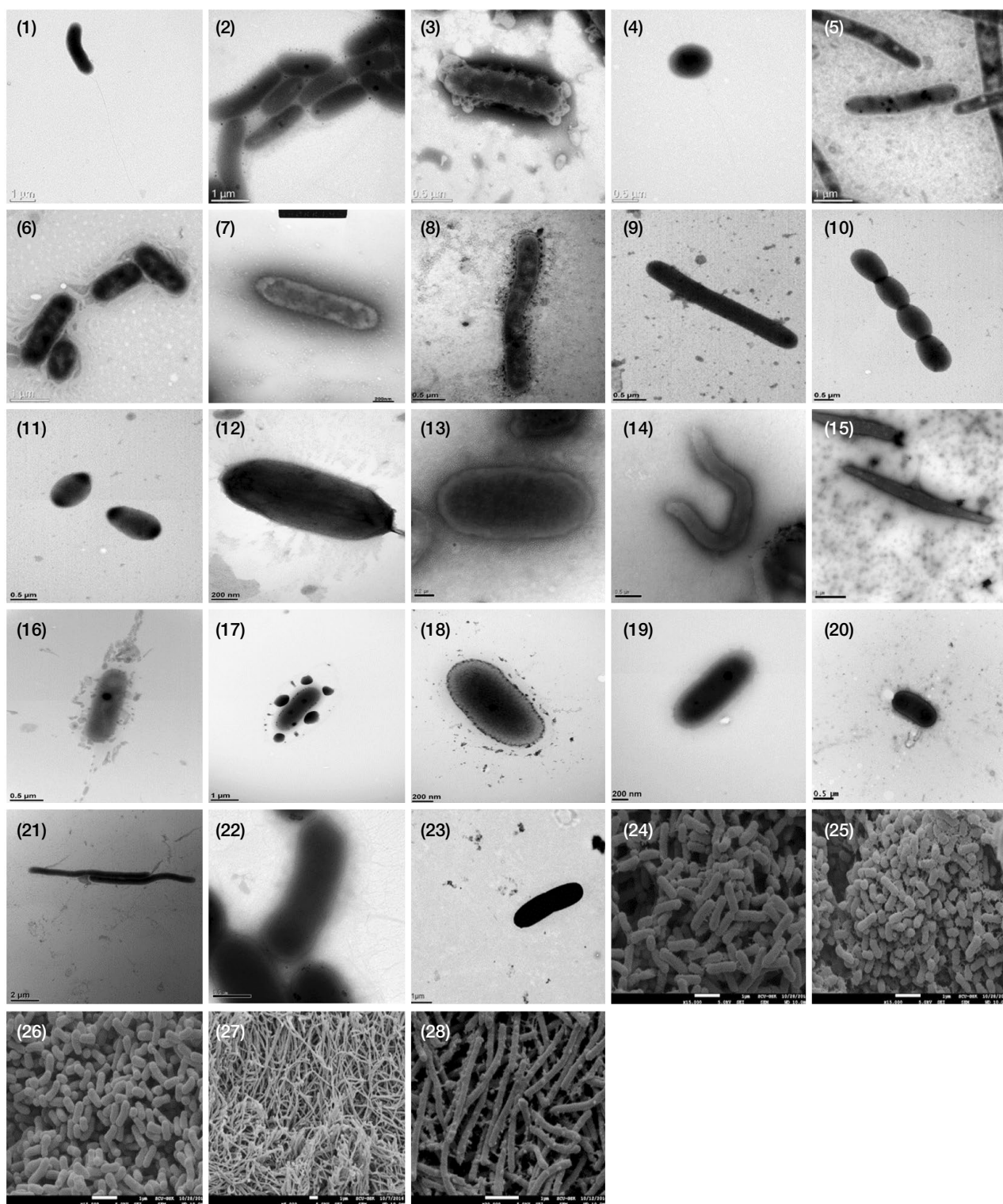
Based on the 16S rRNA gene sequence similarities, 28 isolates were identified as members of the phylum *Bacteroidetes*. The taxonomic composition and identification results are summarized in Table 1. One strain belonged to the family *Draconibacterium\_f* and two strains belonged to the *Prolixibacteraceae* of the (order *Bacteroidales*). One strain belonged to the family *Fulvivirga\_f* and another to the *Cytophagaceae* (order *Cytophagales*). The other 23 strains were assigned to the family *Flavobacteriaceae* in the order *Flavobacteriales*. At the genus level, the strains belong to 18 different genera: *Flavobacterium* (3 species), *Epilithonimonas* (1 species), *Dokdonia* (1 species), *Gillisia* (1 species), *Gramella* (1 species), *Flavicella* (1 species), *Chryseobacterium* (6 species), *Algibacter* (2 species), *Aquimarina* (1 species), *Lacinutrix* (1 species), *Gaetbulibacter* (1 species), *Cellulophaga* (2 species), *Tenacibaculum* (1 species), *Maribacter* (1 species), *Draconibacterium* (1 species), *Sunxiuqinia* (2 species), *Fulvivirga* (1 species), and *Dyadobacter* (1 species). The identification of the isolates based on sequence similarity was supported by the phylogenetic trees. The neighbor-joining and maximum likelihood trees were almost identical in their tree topologies showing the close relationship between the isolates and type strains of published species (Fig. 1).

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

Order	Family	Genus	Strain ID	NIBR ID	Most closely related species	Similarity (%)	Isolation source	Medium	Incubation condition
Flavobacteriales	Flavobacteriaceae	<i>Flavobacterium</i>	HMF4563	NIBRBAC000498440	<i>Flavobacterium psychrolimnae</i>	99.4	Wet land	R2A	25°C, 3d
			HMF4572	NIBRBAC000498441	<i>Flavobacterium limicola</i>	99.9	Wet land	R2A	25°C, 3d
			PR2204	NIBRBAC000498391	<i>Flavobacterium oceanosedimentum</i>	99.3	Feces of <i>Platalea minor</i>	R2A	20°C, 2d
		<i>Epilithonimonas</i>	HMF4589	NIBRBAC000498443	<i>Epilithonimonas lactis</i>	99.7	Wet land	R2A	25°C, 3d
		<i>Dokdonia</i>	HMF6044	NIBRBAC000498450	<i>Dokdonia genika</i>	99.7	Seawater	MA	25°C, 3d
		<i>Gillisia</i>	HMF6519	NIBRBAC000498452	<i>Gillisia mitskevichiae</i>	99.4	Sea sand	MA	25°C, 3d
		<i>Gramella</i>	IMCC25637	NIBRBAC000498536	<i>Gramella portivictoriae</i>	99.1	Tidal flat sediment	MA	20°C, 3d
		<i>Flavicella</i>	SFD5	NIBRBAC000498468	<i>Flavicella marina</i>	99.9	Gulfweed	MA	25°C, 3d
			POB2	NIBRBAC000498469	<i>Chryseobacterium gleum</i>	99.7	Wastewater	R2A	25°C, 2d
			POB7	NIBRBAC000498471	<i>Chryseobacterium solincola</i>	99.9	Wastewater	R2A	25°C, 3d
<i>Chryseobacterium</i>		RUG1-3	NIBRBAC000498561	<i>Chryseobacterium hispidense</i>	99.5	Wet land	R2A	30°C, 2d	
		3130	NIBRBAC000498566	<i>Chryseobacterium hominis</i>	98.9	Freshwater sediment	R2A	30°C, 2d	
		6024	NIBRBAC000498573	<i>Chryseobacterium lactis</i>	99.3	Freshwater sediment	R2A	30°C, 2d	
		2PKS213	NIBRBAC000498639	<i>Chryseobacterium oncofynchii</i>	98.9	Freshwater	2 × R2A	25°C, 4d	
		SFD63	NIBRBAC000498474	<i>Algibacter mikhalovii</i>	99.6	Gulfweed	MA	25°C, 3d	
<i>Algibacter</i>		LPB0155	NIBRBAC000498526	<i>Algibacter lectus</i>	98.8	Tidal flat sediment	MA	25°C, 1d	
	<i>Aquimarina</i>	ZO2-10	NIBRBAC000498477	<i>Aquimarina latercula</i>	99.7	Seaweed	MA	25°C, 3d	
	<i>Lacinutrix</i>	GLB7	NIBRBAC000498482	<i>Lacinutrix himadriensis</i>	98.8	<i>Patinopecten yessoensis</i>	MA	25°C, 5d	
	<i>Gaetbulibacter</i>	CAU 1400	NIBRBAC000498507	<i>Gaetbulibacter marinus</i>	99.0	Sea sand	MA, pH8.5	30°C, 4d	
	<i>Cellulophaga</i>	LPB0152	NIBRBAC000498524	<i>Cellulophaga fucicola</i>	99.8	Tidal flat sediment	MA	25°C, 1d	
		JMW-3	NIBRBAC000498663	<i>Cellulophaga lytica</i>	99.9	Marine algae	MA	30°C, 4d	
	<i>Tenacibaculum</i>	LPB0158	NIBRBAC000498529	<i>Tenacibaculum discolor</i>	99.3	Tidal flat sediment	MA	25°C, 1d	
	<i>Maribacter</i>	LPB0163	NIBRBAC000498533	<i>Maribacter stanieri</i>	99.9	Tidal flat sediment	MA	25°C, 1d	
	<i>Bacteroidales</i>	<i>Draconibacterium_f</i>	IMCC25638	NIBRBAC000498537	<i>Draconibacterium sediminis</i>	99.9	Tidal flat sediment	MA	20°C, 3d
			IMCC25641	NIBRBAC000498540	<i>Sunxiuqinia rutila</i>	99.5	Tidal flat sediment	MA	20°C, 3d
CAU 1108			NIBRBAC000498506	<i>Sunxiuqinia faeciviva</i>	99.9	Reclaimed land	MA, pH6.0	30°C, 3d	
<i>Cytophagales</i>	<i>Fulvivirga_f</i>	IMCC25651	NIBRBAC000498550	<i>Fulvivirga kasyanovii</i>	99.0	Plant roots	MA	20°C, 3d	
		1008	NIBRBAC000498563	<i>Dyadobacter beijingensis</i>	99.1	Freshwater sediment	R2A	30°C, 2d	



**Fig. 1.** Neighbor-joining tree based on 16S rRNA gene sequences showing the phylogenetic relationships between the strains isolated in this study and their relatives in the phylum Bacteroidetes. *Escherichia coli* ATCC 11775<sup>T</sup> (X80725) was used as an outgroup. Filled circles indicate the nodes were also recovered in maximum-likelihood tree. Bootstrap values (> 70%) are shown above nodes. Scale bar, 0.1 substitutions per nucleotide.



**Fig. 2.** Transmission electron micrographs or scanning electron micrographs of cells of the strains isolated in this study. Strains: 1. PR22204; 2. HMF4563; 3. HMF4572; 4. HMF4589; 5. HMF6044; 6. HMF6519; 7. SFD5; 8. CAU 1400; 9. LPB0152; 10. LPB0155; 11. LPB0158; 12. LPB0163; 13. IMCC25638; 14. IMCC25641; 15. IMCC25651; 16. RUG1-3; 17. 1008; 18. 3130; 19. 6024; 20. 2PKS213; 21. CAU 1108; 22. IMCC25637; 23. JMW-3; 24. POB2; 25. POB7; 26. SFD63; 27. ZO2-10; 28. GLB7.

The 28 isolates were Gram-staining-negative, rod- or oval-shaped bacteria (Fig. 2). Detailed morphological and physiological characteristics are given in the strain descriptions.

This study contributes to the understanding of the diversity of bacterial species in Korean ecosystems, and reports previously unreported species for Korea. The 28 isolates all belong in the phylum *Bacteroidetes*, and their phenotypic characteristics were examined through a polyphasic taxonomic study. Accordingly, the following 28 species are reported as unrecorded species in Korea.

#### **Description of *Flavobacterium oceanosedimentum* PR22204**

Cells are Gram-staining-negative, flagellated, and rod-shaped. Colonies are circular, flat, dry, and saffron colored after 2 days on R2A agar at 20°C. Positive for oxidase, esculin, and  $\beta$ -galactosidase activities. Negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, or gelatinase activities. Uses D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, and potassium gluconate, but not capric acid, adipic acid, malic acid, trisodium citrate, or phenyl acetic acid as a carbon source. Strain PR22204 (=NIBRBA000498391) was isolated from a feces of Black-faced Spoonbill *Platalea minor*, Korea.

#### **Description of *Flavobacterium psychrolimnae* HMF4563**

Cells are Gram-staining-negative, non-flagellated, and rod-shaped. Colonies are circular, convex with entire margin and yellow colored after 3 days on R2A agar at 25°C. Positive for oxidase, esculin hydrolysis, and  $\beta$ -galactosidase. Negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, or gelatin hydrolysis. Uses D-glucose, D-mannose, and D-maltose, but not L-arabinose, D-mannitol, *N*-acetyl-glucosamine, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, or phenyl acetic acid as a carbon source. Strain HMF4563 (=NIBRBA 000498440) was isolated from a wet land sample, Yongin-si, Korea.

#### **Description of *Flavobacterium limicola* HMF4572**

Cells are Gram-staining-negative, non-flagellated, and rod-shaped. Colonies are circular with entire margin, convex, and yellow colored after 3 days on R2A agar at 25°C. Positive for oxidase and esculin hydrolysis. Negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, gelatin hydrolysis, and  $\beta$ -galactosidase. Uses D-glucose and D-maltose,

but not L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, or phenyl-acetic acid as a carbon source. Strain HMF4572 (=NIBRBA 000498441) was isolated from a wet land sample, Yongin-si, Korea.

#### **Description of *Epilithonimonas lactis* HMF4589**

Cells are Gram-staining-negative, flagellated, and rod or oval-shaped. Colonies are circular, convex with entire margin, and yellow colored after 3 days on R2A agar at 25°C. Positive for oxidase, glucose fermentation, esculin hydrolysis, gelatin hydrolysis, and  $\beta$ -galactosidase. Negative for nitrate reduction, indole production, arginine dihydrolase, and urease. Uses D-glucose, L-arabinose, D-mannose, and D-maltose, but not D-mannitol, *N*-acetyl-glucosamine, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, or phenyl-acetic acid as a carbon source. Strain HMF4589 (=NIBRBA 000498443) was isolated from a wet land sample, Yongin-si, Korea.

#### **Description of *Dokdonia genika* HMF6044**

Cells are Gram-staining-negative, non-flagellated, and rod-shaped. Colonies are circular, convex with entire margin, and yellow colored after 3 days on marine agar at 25°C. Positive for oxidase, esculin hydrolysis, and  $\beta$ -galactosidase. Negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, and gelatin hydrolysis. Uses *N*-acetyl-glucosamine, but not D-glucose, L-arabinose, D-mannose, D-mannitol, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, or phenyl-acetic acid as a carbon source. Strain HMF6044 (=NIBRBA 000498450) was isolated from seawater, Korea.

#### **Description of *Gillsia mitskevichiae* HMF6519**

Cells are Gram-staining-negative, non-flagellated, and rod-shaped. Colonies are circular, convex with entire margin and yellow colored after 3 days on marine agar at 25 °C. Positive for oxidase, esculin hydrolysis, and  $\beta$ -galactosidase. Negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, and gelatin hydrolysis. Does not use D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, or phenyl-acetic acid as a carbon source. Strain HMF6519 (=NIBRBA 000498452) was isolated from sea sand, Korea.

#### **Description of *Flavicella marina* SFD5**

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

rod-shaped. Colonies are transparent, circular, smooth, flat, and yellow colored after 3 days on marine agar at 25°C. Positive for esculin hydrolysis and  $\beta$ -galactosidase. Negative for oxidase, nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, and gelatin hydrolysis. Does not use D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, or phenyl-acetic acid as a carbon source. Strain SFD5 (=NIBRBA 000498468) was isolated from a gulfweed, Jeju Island, Korea.

#### **Description of *Chryseobacterium gleum* POB2**

Cells are Gram-staining-negative, non-flagellated, and rod-shaped. Colonies are transparent, circular, smooth, convex, and yellow colored after 2 days on R2A agar at 25°C. Positive for esculin hydrolysis and gelatin hydrolysis. Negative for oxidase, nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, and  $\beta$ -galactosidase. Does not use D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, or phenyl-acetic acid as a carbon source. Strain POB2 (=NIBRBAC 000498469) was isolated from wastewater, Korea.

#### **Description of *Chryseobacterium solincola* POB7**

Cells are Gram-staining-negative, non-flagellated, and rod-shaped. Colonies are translucent, circular smooth, convex, and light yellow colored after 3 days on R2A agar at 25°C. Positive for oxidase and esculin hydrolysis. Negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, gelatin hydrolysis, and  $\beta$ -galactosidase. Does not use D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, or phenyl-acetic acid as a carbon source. Strain POB7 (=NIBRBAC 000498471) was isolated from wastewater, Korea.

#### **Description of *Algibacter mikhailovii* SFD63**

Cells are Gram-staining-negative, non-flagellated, and rod-shaped. Colonies are circular, opaque, smooth, convex, and yellow colored after 3 days on marine agar at 25°C. Positive for oxidase, glucose fermentation, and  $\beta$ -galactosidase. Negative for nitrate reduction, indole production, arginine dihydrolase, urease, esculin hydrolysis, and gelatin hydrolysis. Does not use D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, or phenyl-acetic

acid as a carbon source. Strain SFD63 (=NIBRBAC 000498474) was isolated from a gulfweed, Korea.

#### **Description of *Aquimarina latercula* ZO2-10**

Cells are Gram-staining-negative, non-flagellated, and long-rod-shaped. Colonies are transparent, circular, smooth, convex, and orange colored after 3 days on marine agar at 25°C. Positive for oxidase, esculin hydrolysis, and gelatin hydrolysis. Negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, and  $\beta$ -galactosidase. Does not use D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, or phenyl-acetic acid as a carbon source. Strain ZO2-10 (=NIBRBAC000498477) was isolated from a seaweed of the family *Zosteraceae*, Korea.

#### **Description of *Lacinutrix himadriensis* GLB7**

Cells are Gram-staining-negative, non-flagellated, and rod-shaped. Colonies are opaque, circular, smooth, convex with entire margin, and yellow colored after 5 days on marine agar at 25°C. Positive for oxidase and gelatin hydrolysis. Negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, and urease. Weakly positive for esculin hydrolysis and  $\beta$ -galactosidase. Uses D-mannitol as a carbon source, but not D-glucose, L-arabinose, D-mannose, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, or phenyl-acetic acid. Strain GLB7 (=NIBRBAC000498482) was isolated from a yessoensis *Patinopecten yessoensis*, Korea.

#### **Description of *Gaetbulibacter marinus* CAU 1400**

Cells are Gram-staining-negative, non-flagellated, and rod-shaped. Colonies are circular, sticky, glistening, convex, and deep-yellow colored after 4 days on marine agar with pH 8.5 at 30°C. Positive for esculin hydrolysis and  $\beta$ -galactosidase. Negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, and gelatin hydrolysis. Uses D-mannose, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, trisodium citrate, and phenyl-acetic acid as a carbon source, but not D-glucose, L-arabinose, D-mannitol, capric acid, adipic acid, or malic acid. Strain CAU 1400 (=NIBRBAC000498507) was isolated from a sea sand, Incheon, Korea.

#### **Description of *Cellulophaga fucicola* LPB0152**

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

rod-shaped. Colonies are circular, convex with entire margin, and yellowish-orange colored after 1 day on marine agar at 25°C. Positive for oxidase, esculin hydrolysis, and  $\beta$ -galactosidase. Negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, and gelatin hydrolysis. Does not use D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, or phenyl-acetic acid as a carbon source. Strain LPB0152 (=NIBRBAC000498524) was isolated from tidal flat sediment, Jebudo Island, Korea.

#### **Description of *Algibacter lectus* LPB0155**

Cells are Gram-staining-negative, non-flagellated, and rod-shaped. Colonies are circular, convex with entire margin, and yellow colored after 1 day on marine agar at 25°C. Positive for oxidase and esculin hydrolysis. Negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, gelatin hydrolysis, and  $\beta$ -galactosidase. Does not use D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, or phenyl-acetic acid as a carbon source. Strain LPB0155 (=NIBRBA C000498526) was isolated from tidal flat sediment, Jebudo Island, Korea.

#### **Description of *Tenacibaculum discolor* LPB0158**

Cells are Gram-staining-negative, non-flagellated, and rod-shaped. Colonies are circular, convex with entire margin, and yellow colored after 1 day on marine agar at 25°C. Positive for oxidase and esculin hydrolysis. Negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, gelatin hydrolysis, and  $\beta$ -galactosidase. Does not use D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, or phenyl-acetic acid as a carbon source. Strain LPB0158 (=NIBRBAC 000498529) was isolated from tidal flat, Jebudo Island, Korea.

#### **Description of *Maribacter stanieri* LPB0163**

Cells are Gram-staining-negative, flagellated, and rod-shaped. Colonies are circular, convex with entire margin, and yellow colored after 1 day on marine agar at 25°C. Positive for oxidase, esculin hydrolysis, and gelatin hydrolysis. Negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis, and  $\beta$ -galactosidase. Does not use D-glucose, L-arabinose, D-mannose, D-mannitol,

*N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, or phenyl-acetic acid as a carbon source. Strain LPB0163 (=NIBRBAC000498533) was isolated from tidal flat sediment, Jebudo Island, Korea.

#### **Description of *Draconibacterium sediminis* IMCC25638**

Cells are Gram-staining-negative, non-flagellated, and rod-shaped. Colonies are circular, convex with entire margin, and white colored after 3 days on marine agar at 20°C. Positive for gelatin hydrolysis. Negative for oxidase, nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis, and  $\beta$ -galactosidase. Does not use D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, or phenyl-acetic acid as a carbon source. Strain IMCC25638 (=NIBRBAC 000498537) was isolated from tidal flat sediment, Yeongjongdo Island, Korea.

#### **Description of *Sunxiuqinia rutila* IMCC25641**

Cells are Gram-staining-negative, non-flagellated, and rod-shaped. Colonies are circular, convex with entire margin, and red colored after 3 days on marine agar at 20°C. Positive for gelatin hydrolysis. Negative for oxidase, nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis, and  $\beta$ -galactosidase. Uses D-glucose as a carbon source, but not L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, or phenyl-acetic acid. Strain IMCC25641 (=NIBRBAC 000498540) was isolated from tidal flat sediment, Yeongjongdo Island, Korea.

#### **Description of *Fulvivirga kasyanovii* IMCC25651**

Cells are Gram-staining-negative, non-flagellated, and rod-shaped. Colonies are circular, convex with entire margin, and red colored after 3 days on marine agar at 20°C. Positive for gelatin hydrolysis and  $\beta$ -galactosidase. Negative for oxidase, nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, and esculin hydrolysis. Uses D-glucose, L-arabinose, D-mannitol, and trisodium citrate as a carbon source, but not D-mannose, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, and phenyl-acetic acid. Strain IMCC25651 (=NIBRBAC000498550) was isolated from a plant root, Yeongjongdo Island, Korea.



**Description of *Chryseobacterium hispalense* RUG1-3**

Cells are Gram-staining-negative, non-flagellated, and rod-shaped. Colonies are smooth, raised, circular with entire margin, and yellow colored after 2 days on R2A agar at 30°C. Positive for esculin hydrolysis and gelatin hydrolysis. Negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, and  $\beta$ -galactosidase. Uses D-glucose, L-arabinose, D-mannose, D-maltose, and adipic acid as a carbon source, but not D-mannitol, *N*-acetyl-glucosamine, potassium gluconate, capric acid, malic acid, trisodium citrate, or phenyl-acetic acid. Strain RUG1-3 (=NIBRBAC 000498561) was isolated from a wet land sample, Gochang-gun, Korea.

**Description of *Dyadobacter beijingensis* 1008**

Cells are Gram-staining-negative, non-flagellated, and rod-shaped. Colonies are smooth, raised, circular with entire margin, and yellow colored after 2 days on R2A agar at 30°C. Positive for esculin hydrolysis and  $\beta$ -galactosidase. Negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, and gelatin hydrolysis. Uses D-glucose, D-mannose, *N*-acetyl-glucosamine, and D-maltose as a carbon source, but not L-arabinose, D-mannitol, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, or phenyl-acetic acid. Strain 1008 (=NIBRBAC 000498563) was isolated from a freshwater sediment, Han River, Korea.

**Description of *Chryseobacterium hominis* 3130**

Cells are Gram-staining-negative, non-flagellated, and rod-shaped. Colonies are smooth, raised, circular with entire margin, and white colored after 2 days on R2A agar at 30°C. Positive for esculin hydrolysis and gelatin hydrolysis. Negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, and  $\beta$ -galactosidase. Uses D-glucose, D-mannose, and D-maltose as a carbon source, but not L-arabinose, D-mannitol, *N*-acetyl-glucosamine, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, or phenyl-acetic acid. Strain 3130 (=NIBRBAC 000498566) was isolated from a freshwater sediment, Han River, Korea.

**Description of *Chryseobacterium lactis* 6024**

Cells are Gram-staining-negative, non-flagellated, and rod-shaped. Colonies are smooth, raised, circular with entire margin, and yellow colored after 2 days on R2A agar at 30°C. Positive for indole production, urease, esculin hydrolysis, gelatin hydrolysis, and  $\beta$ -galactosi-

dase. Negative for oxidase, nitrate reduction, glucose fermentation, and arginine dihydrolase. Uses D-glucose, D-mannose, D-mannitol, D-maltose, and trisodium citrate as a carbon source, but not L-arabinose, *N*-acetyl-glucosamine, potassium gluconate, capric acid, adipic acid, malic acid, or phenyl-acetic acid. Strain 6024 (=NIBRBAC 000498573) was isolated from a freshwater sediment, Han River, Korea.

**Description of *Chryseobacterium oncorhynchi* 2PKS213**

Cells are Gram-staining-negative, non-flagellated, and oval-shaped. Colonies are circular, slightly convex, and yellow colored after 4 days on 2×R2A agar at 25°C. Positive for nitrate reduction, indole production, urease, esculin hydrolysis, and gelatin hydrolysis. Negative for glucose fermentation, arginine dihydrolase, and  $\beta$ -galactosidase. Uses D-glucose, D-maltose as a carbon source, but not L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, or phenyl-acetic acid. Strain 2PKS213 (=NIBRBAC000498639) was isolated from fresh water, Jeonju-si, Korea.

**Description of *Sunxiuqinia faeciviva* CAU 1108**

Cells are Gram-staining-negative, non-flagellated, and rod-shaped. Colonies are circular, sticky, glistening, convex, and orange colored after 3 days on marine agar with pH6.0 at 30°C. Positive for esculin hydrolysis and  $\beta$ -galactosidase. Negative for indole production, glucose fermentation, arginine dihydrolase, urease, and gelatin hydrolysis. Uses L-arabinose and adipic acid as a carbon source, but not D-glucose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, malic acid, trisodium citrate, or phenyl-acetic acid. Strain CAU 1108 (=NIBRBAC000498506) was isolated from reclaimed land, Incheon, Korea.

**Description of *Gramella portivictoriae* IMCC25637**

Cells are Gram-staining-negative, non-flagellated, and rod-shaped. Colonies are circular, convex with entire margin, and yellow colored after 3 days on marine agar at 20°C. Negative for oxidase, nitrate reduction, glucose fermentation, indole production, arginine dihydrolase, urease, esculin hydrolysis, gelatin hydrolysis, and  $\beta$ -galactosidase. Does not use D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, or phenyl-acetic acid as a carbon source. Strain IMCC25637 (=NIBRBAC000498536) was isolated from tidal flat sediment, Yeongjongdo Island, Korea.

### Description of *Cellulophaga lytica* JMW-3

Cells are Gram-staining-negative, non-flagellated, and rod-shaped. Colonies are circular, flat with entire margin, and yellow colored after 4 days on marine agar at 30°C. Positive for nitrate reduction, urease, and  $\beta$ -galactosidase. Negative for oxidase, indole production, glucose fermentation, arginine dihydrolase, esculin hydrolysis, and gelatin hydrolysis. Does not use D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, or phenyl-acetic acid as a carbon source. Strain JMW-3 (=NIBRBAC 000498663) was isolated from a marine algae, Jejudo Island, Korea.

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