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# A report of 21 unrecorded bacterial species of Korea belonging to the phylum *Bacteroidota* isolated in 2021

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During screening for indigenous prokaryotic species in Republic of Korea in 2021, a total of 21 bacterial strains assigned to the phylum *Bacteroidota* were isolated from a variety of environmental habitats including pine cone, seaweed, soil, sea sediment, brackish water and moss. Based on the 16S rRNA gene sequence similarity value of more than 98.7% and formation of a robust phylogenetic clade with the type strain of the closest bacterial species, it was found that the 21 strains belong to independent and recognized bacterial species. There has been no official report that the identified 21 species have been isolated in Republic of Korea up to date. Therefore, 16 species in six genera of two families in the order *Flavobacteriales*, two species in two genera of two families in the order *Cytophagales*, one species in one genus of one family in the order *Chitinophagales* and two species in one genus of one family in the order *Sphingobacteriales* are proposed as unrecorded species of the phylum *Bacteroidota* isolated in Republic of Korea. Their 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: 16S rRNA gene, *Bacteroidota*, prokaryote, prokaryotic diversity, unrecorded species

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## Introduction

Microorganisms estimated to occupy more than approximately 60% of total biomass on earth have been known to be important for ecological system. They have also been utilized extensively as the most valuable resources in various biotechnological fields and demands of novel and useful microorganisms are estimated to increase in the futures due to their high economic value. Nevertheless, a majority of microorganisms present in nature is known to be uncultured in laboratory, because the current methods can cultivate only small fraction (<0.1%) of microbial cells (Delong *et al*., 1989; Giovannoni *et al*., 1990). Since the value on microbial diversity is becoming increasingly important, many attempts have been made to find novel microorganisms that have not been yet discovered (Connon and Giovannoni, 2002; Cho and Giovannoni, 2004; Yoon *et al*., 2011).

During screening indigenous prokaryotic species from a variety of habitats at Republic of Korea in 2021, we isolated a number of novel bacterial strains belonging to unrecorded bacterial species. The identified bacterial strains were assigned to the phyla *Actinomycetota*, *Bacillota*, *Bacteroidota* and *Pseudomonadota*. Of these bacterial isolates, the present study focuses on the descriptions of unrecorded species belonging to the phylum *Bacteroidota*. The phylum *Bacteroidota* has been recently presented newly as the corrected name of *Bacteroidetes* (Oren and Garrity, 2021). The phylum *Bacteroidota* encompasses phenotypically diverse group of Gram-negative and non-endospore-forming bacteria (Krieg *et al*., 2010). Members of the phylum *Bacteroidota* have been described from a variety of habitats including terrestrial, marine and aquatic environments, gastrointestinal tract and others

(Thomas *et al*., 2011; Sun *et al*., 2016). It this study, we report 21 unrecorded bacterial species, isolated in 2021 from Republic of Korea, belonging to 10 genera of six families of four orders in the phylum *Bacteroidota*.

## Materials and Methods

A total of 21 bacterial strains were isolated from environmental samples including pine cone, seaweed, soil, sea sediment, brackish water and moss (Table 1). Each sample was processed separately, spread onto several culture media including R2A agar (R2A), marine agar 2216 (MA) or trypticase soy agar (TSA), and incubated at 25 or 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 after streaking and maintained at −80°C in a glycerol solution (20%, w/v) as well as lyophilized ampoules for long-term preservation.

Colony morphology of isolated strains was observed on agar plates after their cells were grown up to stationary phase. Cellular morphology and cell size were examined by light microscopy or transmission 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. The 16S rRNA gene sequences of the strains assigned to the phylum *Bacteroidota* 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 CLUSTALW software (Thompson *et al*., 1994). Phylogenetic tree was inferred by using the neighbor-joining algorithm (Saitou and Nei, 1987) 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 resamplings 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 *Bacteroidota*

On the basis of 16S rRNA gene sequence comparisons and phylogenetic analyses, a total of 21 strains were assigned to the phylum *Bacteroidota*. The 21 strains were assigned to four orders of the phylum *Bacteroidota*; 16 strains in the *Flavobacteriales*, two strain in the *Cytophagales*, one strain in the *Chitinophagales* and one strain in the *Sphingobacteriales* (Table 1). These strains were Gram-staining-negative, chemoheterotrophic and rod-shaped bacteria (Fig. 1). Colony color, colony morphology, and other phenotypic characteristics are shown in the species descriptions.

A total of 16 strains assigned to the order *Flavobacteriales* belong to the families *Flavobacteriaceae* and *Weeksellaceae* (Fig. 2; Table 1). The nine strains assigned to the family *Flavobacteriaceae* belonged to the genera *Flavobacterium*, *Lacinutrix*, *Maribacter* and *Wenyingzhuangia*, and were isolated from soil, sea sediment and seaweed (Fig. 2, Table 1). Phylogenetic analyses based on 16S rRNA gene sequences showed that the 16 strains were identified as members of the following species: *Flavobacterium arsenatis* (Ao *et al*., 2014), *Flavobacterium johnsoniae* subsp. *aurantiacum* (García-López *et al*., 2019), *Flavobacterium oncorhynchi* (Zamora *et al*., 2012), *Flavobacterium panici* (Kämpfer *et al*., 2020), *Flavobacterium psychroterrae* (Králová *et al*., 2018), *Hanstruepera neustonica* (Hameed *et al*., 2015), *Lacinutrix mariniflava* (Nedashkovskaya *et al*., 2008), *Maribacter vaceletii* (Jackson *et al*., 2015) and *Wenyingzhuangia aestuarii* (Yoon and Kasai, 2016). The seven strains assigned to the family *Weeksellaceae* belonged to the genus *Chryseobacterium* and were isolated from brackish water and soil (Fig. 2; Table 1). Phylogenetic analyses based on 16S rRNA gene sequences showed that the seven strains were identified as members of the following species: *Chryseobacterium aquaticum* subsp. *aquaticum* (García-López *et al*., 2019), *Chryseobacterium candidae* (Indu *et al*., 2020), *Chryseobacterium joostei* (Hugo *et al*., 2003), *Chryseobacterium nakagawai* (Holmes *et al*., 2013), *Chryseobacterium oranimense* (Hantsis-Zacharov *et al*., 2008), *Chryseobacterium vietnamense* (Li and Zhu, 2012) and *Chryseobacterium vrystaatense* (de Beer *et al*., 2005).

One strain (HMG2945) assigned to the family *Hymenobacteraceae* of the order *Cytophagales* belongs to the genus *Hymenobacter* and was isolated from a pine cone (Fig. 2; Table 1). One strain (GJ41-1) assigned to the family *Spirosomaceae* of the order *Cytophagales* belongs to the genus *Arcticibacterium* and was isolated from a seaweed (Fig. 2; Table 1). From phylogenetic analysis based on 16S rRNA gene sequences, strains HMG2945 and GJ41-1 were identified as members of *Hymenobacter polaris* (Dahal *et al*., 2020) and *Arcticibacterium luteifluviistationis* (Li *et al*., 2017), respectively.

One strain (MMS21-SHT2) assigned to the family *Chitinophagaceae* of the order *Chitinophagales* belongs to the genus *Chitinophaga* and was isolated from a soil (Fig. 2; Table 1). From phylogenetic analysis based on 16S rRNA gene sequences, strain MMS21-SHT2 was iden-

**Table 1.** Summary of isolates belonging to the phylum *Bacteroidota* and their taxonomic affiliations, isolations sources and culture conditions.

| Order | Family | Genus | Strain no. | NIBR ID | Closest species | 16S rRNA gene sequence similarity (%) | Isolation source | Medium for incubation | Condition for incubation |
|---|---|---|---|---|---|---|---|---|---|
| *Cytophagales* | *Hymenobacteraceae* | *Hymenobacter* | HMG2945 | NIBRBAC000508762 | *Hymenobacter polaris* | 99.24 | Pine cone | R2A | 30°C, 3d |
| | *Spirosomaceae* | *Arcticibacterium* | GJ41-1 | NIBRBAC000508962 | *Arcticibacterium luteifluviistationis* | 99.44 | Seaweed | MA | 30°C, 3d |
| *Chitinophagales* | *Chitinophagaceae* | *Chitinophaga* | MMS21-SHT2 | NIBRBAC000508736 | *Chitinophaga varians* | 99.59 | Soil | TSA | 30°C, 3d |
| *Flavobacteriales* | *Flavobacteriaceae* | *Flavobacterium* | 16_S3_A3 | NIBRBAC000508801 | *Flavobacterium arsenatis* | 99.56 | Soil | R2A | 30°C, 2–3d |
| | | *Flavobacterium* | 18_S2_G9 | NIBRBAC000508802 | *Flavobacterium johnsoniae* subsp. *aurantiacum* | 99.65 | Soil | R2A | 30°C, 2–3d |
| | | *Flavobacterium* | 16_N3_V7 | NIBRBAC000508803 | *Flavobacterium oncorhynchi* | 99.44 | Soil | R2A | 30°C, 2–3d |
| | | *Flavobacterium* | BT759 | NIBRBAC000508879 | *Flavobacterium panici* | 99.14 | Soil | R2A | 25°C, 3d |
| | | *Flavobacterium* | 18_H3_G4 | NIBRBAC000508804 | *Flavobacterium psychroterrae* | 99.26 | Soil | R2A | 30°C, 4–5d |
| | | *Hanstruepera* | CAU 1656 | NIBRBAC000508836 | *Hanstruepera neustonica* | 99.66 | Sea sediment | MA | 30°C, 3–5d |
| | | *Lacinutrix* | 15G1-1 | NIBRBAC000508958 | *Lacinutrix mariniflava* | 99.86 | Seaweed | MA | 25°C, 3d |
| | | *Maribacter* | D2-5 | NIBRBAC000508961 | *Maribacter vaceletii* | 98.83 | Seaweed | MA | 30°C, 2d |
| | | *Wenyingzhuangia* | G1-8 | NIBRBAC000508960 | *Wenyingzhuangia aestuarii* | 99.72 | Seaweed | MA | 30°C, 3d |
| | *Weeksellaceae* | *Chryseobacterium* | 17_H6_F1 | NIBRBAC000508793 | *Chryseobacterium aquaticum* subsp. *aquaticum* | 99.65 | Brackish water | R2A | 30°C, 2–3d |
| | | *Chryseobacterium* | 16_H1_V15 | NIBRBAC000508794 | *Chryseobacterium candidae* | 99.93 | Soil | R2A | 30°C, 2–3d |
| | | *Chryseobacterium* | 19_H2_S6 | NIBRBAC000508795 | *Chryseobacterium joostei* | 99.10 | Soil | R2A | 30°C, 2–3d |
| | | *Chryseobacterium* | 16_S2_M1 | NIBRBAC000508796 | *Chryseobacterium nakagawai* | 98.81 | Soil | R2A | 30°C, 2–3d |
| | | *Chryseobacterium* | 18_N3_T14 | NIBRBAC000508797 | *Chryseobacterium oranimense* | 98.75 | Soil | R2A | 30°C, 2–3d |
| | | *Chryseobacterium* | 16_H2_M3 | NIBRBAC000508798 | *Chryseobacterium vietnamense* | 99.28 | Soil | R2A | 30°C, 2–3d |
| | | *Chryseobacterium* | 16_S3_M10 | NIBRBAC000508799 | *Chryseobacterium vrystaatense* | 99.86 | Soil | R2A | 30°C, 2–3d |
| *Sphingobacteriales* | *Sphingobacteriaceae* | *Mucilaginibacter* | HMG3142 | NIBRBAC000508766 | *Mucilaginibacter kameinonensis* | 99.65 | Soil | R2A | 30°C, 3d |
| | | *Mucilaginibacter* | HMG3746 | NIBRBAC000508769 | *Mucilaginibacter terrenus* | 99.86 | Moss | R2A | 30°C, 3d |

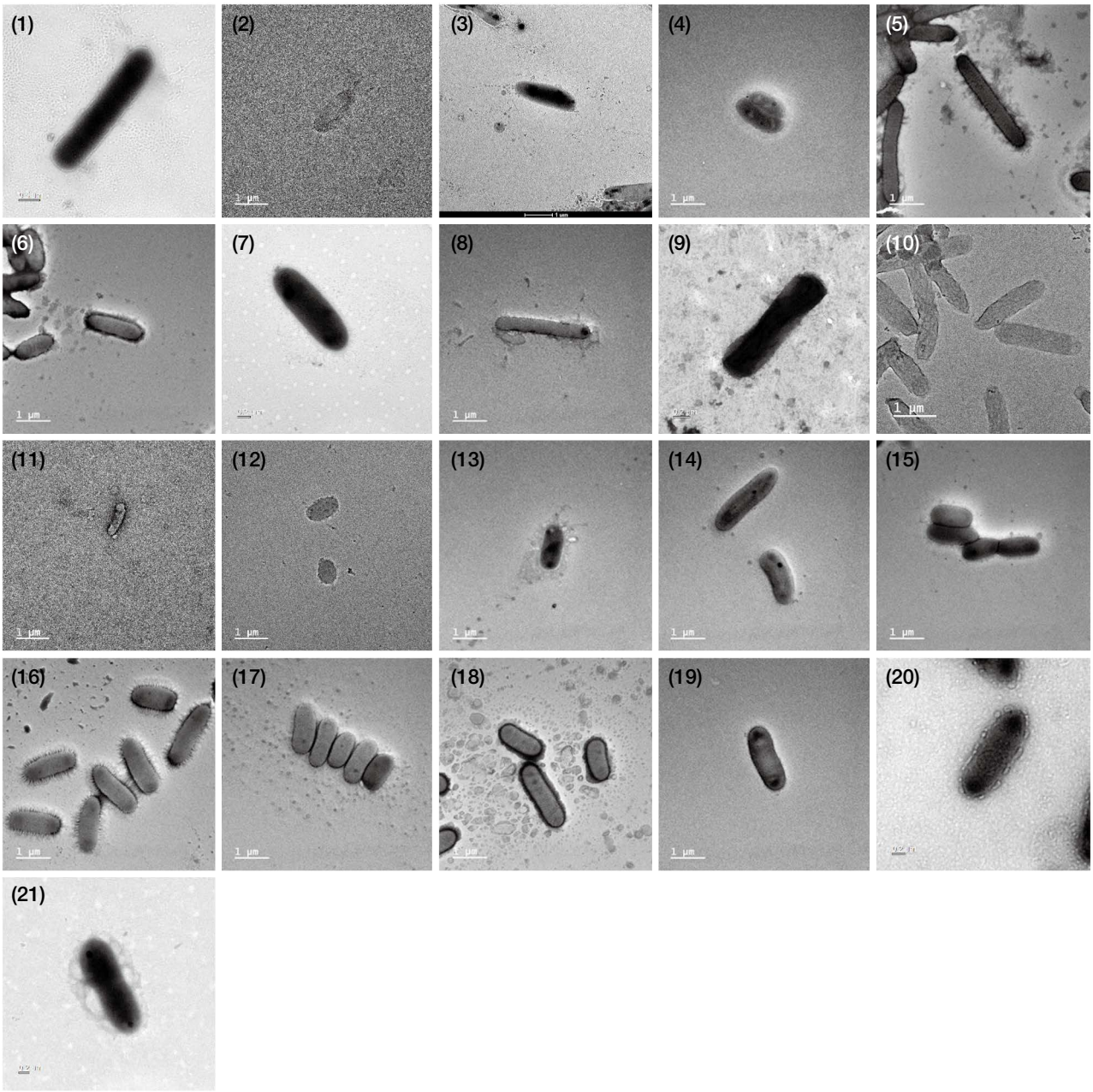


**Fig. 1.** Transmission electron micrographs of cells of the strains isolated in this study. Strains: (1), HMG2945; (2), GJ41-1; (3), MMS21-SHT2; (4), 16_S3_A3; (5), 18_S2_G9; (6), 16_N3_V7; (7), BT759; (8), 18_H3_G4; (9), CAU 1656; (10), 15G1-1; (11), D2-5; (12), G1-8; (13), 17_H6_F1; (14), 16_H1_V15; (15), 19_H2_S6; (16), 16_S2_M1; (17), 18_N3_T14; (18), 16_H2_M3; (19), 16_S3_M10; (20), HMG3142; (21), HMG3746.

tified as a member of *Chitinophaga varians* (Lv *et al*., 2018).

Two strains (HMG3142 and HMG3746) assigned to the family *Sphingobacteriaceae* of the order *Sphingobacteriales* belongs to the genus *Mucilaginibacter* and were isolated from soil (Fig. 2; Table 1). From phylogenetic analysis based on 16S rRNA gene sequences, strains HMG3142 and HMG3746 were identified as members of *Mucilaginibacter kameinonensis* (Urai *et al*., 2008) and *Mucilaginibacter terrenus* (Zhou *et al*., 2019), respectively.

In conclusion, there are no official reports that above-mentioned 21 species have been isolated in Republic of Korea up to date; therefore, 16 species in six genera of two families in the order *Flavobacteriales*, two species in two genera of two families in the order *Cytophagales*,

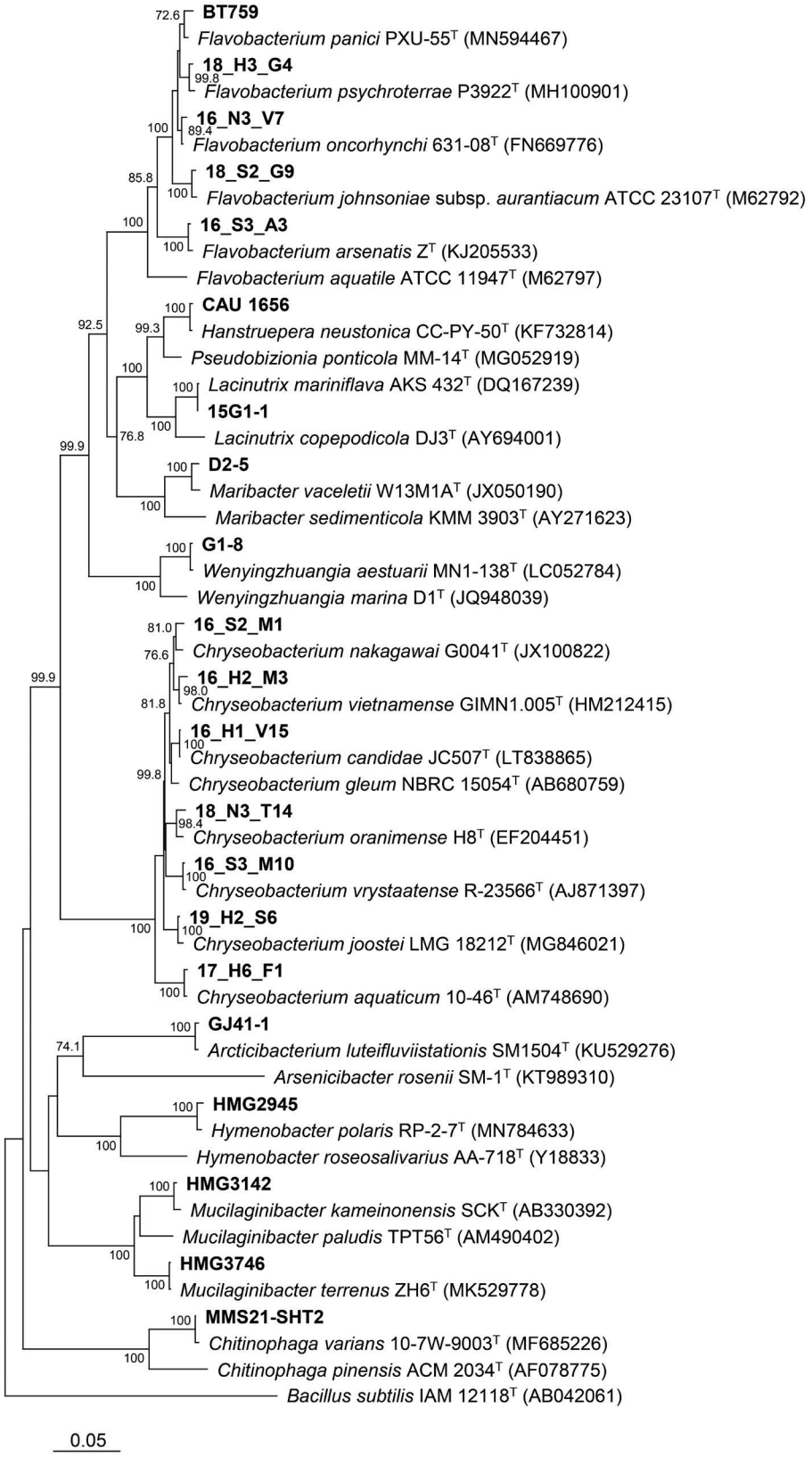


**Fig. 2.** Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences showing the relationships between bacterial strains isolated in this study and their relatives in the phylum *Bacteroidota*. Only bootstrap values greater than 70% are shown at branching points. *Bacillus subtilis* IAM 12118$^T$ (GenBank accession no. AB042061) was used as an outgroup. Bar, 0.05 substitutions per nucleotide position.

one species in one genus of one family in the order *Chitinophagales* and two species in one genus of one family in the order *Sphingobacteriales* are proposed as unrecorded species of the phylum *Bacteroidota* found in Republic of Korea.

**Description of *Hymenobacter polaris* HMG2945**

Cells are Gram-staining-negative, non-flagellated and rod shaped. Colonies are circular, convex, smooth and pale red colored after aerobic incubation for three days on R2A at 30°C. In the API 20NE system, positive reaction for esculin hydrolysis, gelatin hydrolysis, β-galactosidase activity and oxidase activity. In the API 20NE system, 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*-acetylglucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. Strain HMG2945 (=NIBR BAC000508762) was isolated from a pine cone from Yongin, Gyeonggi-do, Korea.

**Description of *Arcticibacterium luteifluviistationis* GJ41-1**

Cells are Gram-staining-negative, flagellated and rod shaped. Colonies are circular and light yellow colored after aerobic incubation for three days on marine agar 2216 (MA) at 30°C. In the API 20NE system, positive reaction for oxidase activity, indole production, glucose fermentation, urease activity, esculin hydrolysis, gelatin hydrolysis, β-galactosidase activity, and utilization of D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetylglucosamine, D-maltose, potassium gluconate, adipic acid, malic acid, trisodium citrate and phenylacetic acid. In the API 20NE system, negative reaction for nitrate reduction, arginine dihydrolase, and utilization of capric acid. Strain GJ41-1 (=NIBRBAC000508962) was isolated from a seaweed from Yangyang, Gangwon-do, Korea.

**Description of *Chitinophaga varians* MMS21-SHT2**

Cells are Gram-staining-negative, non-flagellated and rod shaped. Colonies are circular, convex, entire and orange colored after aerobic incubation for three days on TSA at 30°C. In the API 20NE system, positive reaction for oxidase activity, utilization of L-arabinose, D-mannose, D-mannitol, *N*-acetylglucosamine, D-maltose, potassium gluconate and phenylacetic acid. In the API 20NE system, negative reaction for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease activity, esculin hydrolysis, gelatin hydrolysis, β-galactosidase activity and utilization of D-glucose, capric acid, adipic acid, malic acid and trisodium citrate. Strain MMS21-SHT2 (=NIBRBAC000508736) was isolated from soil from Gongju, Chungcheongnam-do, Korea.

**Description of *Flavobacterium arsenatis* 16_S3_A3**

Cells are Gram-staining-negative, non-flagellated and rod shaped. Colonies are circular, raised, smooth and yellow colored after aerobic incubation for 2−3 days on R2A at 30°C. In the API 20NE system, positive reaction for oxidase activity, nitrate reduction, esculin hydrolysis, and utilization of D-glucose, D-mannose and D-maltose. In the API 20NE system, negative reaction for indole production, glucose fermentation, arginine dihydrolase, urease activity, gelatin hydrolysis, β-galactosidase activity, and utilization of L-arabinose, D-mannitol, *N*-acetylglucosamine, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. Strain 16_S3_A3 (=NIBRBAC000508801) was isolated from a soil around the Hangang River in Seoul, Korea.

**Description of *Flavobacterium johnsoniae* subsp. *aurantiacum* 18_S2_G9**

Cells are Gram-staining-negative, non-flagellated and rod shaped. Colonies are circular, raised, smooth and yellow colored after aerobic incubation for 2−3 days on R2A at 30°C. In the API 20NE system, positive reaction for nitrate reduction, esculin hydrolysis, gelatin hydrolysis, β-galactosidase activity and utilization of D-glucose, L-arabinose, D-mannose, *N*-acetylglucosamine, D-maltose, adipic acid and malic acid. In the API 20NE system, negative reaction for oxidase activity, indole production, glucose fermentation, arginine dihydrolase, urease activity, and utilization of D-mannitol, potassium gluconate, capric acid, trisodium citrate and phenylacetic acid. Strain 18_S2_G9 (=NIBRBAC000508802) was isolated from a soil around the Hangang River in Seoul, Korea.

**Description of *Flavobacterium oncorhynchi* 16_N3_V7**

Cells are Gram-staining-negative, non-flagellated and rod shaped. Colonies are circular, raised, smooth and yellow colored after aerobic incubation for 2−3 days on R2A at 30°C. In the API 20NE system, positive reaction for nitrate reduction, esculin hydrolysis, β-galactosidase activity, and utilization of D-glucose, L-arabinose, D-mannose, D-mannitol, D-maltose and potassium gluconate. In the API 20NE system, negative reaction for oxidase activity, indole production, glucose fermentation, arginine dihydrolase, urease activity, gelatin hydrolysis, and utilization of *N*-acetylglucosamine, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. Strain 16_N3_V7 (=NIBRBAC000508803) was isolated from a soil around the Hangang River in Seoul, Korea.

**Description of *Flavobacterium panici* BT759**

Cells are Gram-staining-negative, non-flagellated and rod shaped. Colonies are circular, convex, glistening and yellow colored after aerobic incubation for three days on R2A at 25°C. In the API 20NE system, positive reaction for esculin hydrolysis, gelatin hydrolysis, β-galactosidase activity, and utilization of D-glucose, L-arabinose (weak), D-mannose, *N*-acetylglucosamine and D-maltose. In the API 20NE system, negative reaction for oxidase activity, nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease activity, and utilization of D-mannitol, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. Strain BT759 (=NIBRBAC000508879) was isolated from soil from Jeju island, Korea.

**Description of *Flavobacterium psychroterrae* 18_H3_G4**

Cells are Gram-staining-negative, non-flagellated and rod shaped. Colonies are circular, raised, smooth and yellow colored after aerobic incubation for 4−5 days on R2A at 30°C. In the API 20NE system, positive reaction for oxidase activity, nitrate reduction, esculin hydrolysis, gelatin hydrolysis, β-galactosidase activity, and utilization of D-glucose, L-arabinose, D-mannose, *N*-acetylglucosamine, D-maltose and trisodium citrate. In the API 20NE system, negative reaction for indole production, glucose fermentation, arginine dihydrolase, urease activity, and utilization of D-mannitol, potassium gluconate, capric acid, adipic acid, malic acid and phenylacetic acid. Strain 18_H3_G4 (=NIBRBAC000508804) was isolated from a soil around the Hangang River in Seoul, Korea.

**Description of *Hanstruepera neustonica* CAU 1656**

Cells are Gram-staining-negative, non-flagellated and rod shaped. Colonies are circular, entire, convex, smooth, translucent and yellowish orange colored after aerobic incubation for 3−5 days on marine agar 2216 (MA) at 30°C. In the API 20NE system, positive reaction for oxidase activity, esculin hydrolysis and β-galactosidase activity. In the API 20NE system, positive reaction for oxidase activity, esculin hydrolysis, and utilization of D-glucose, D-mannose, D-maltose and phenylacetic acid. In the API 20NE system, negative reaction for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease activity, gelatin hydrolysis and utilization of L-arabinose, D-mannitol, *N*-acetylglucosamine, potassium gluconate, capric acid, adipic acid, malic acid and trisodium citrate. Strain CAU 1656 (=NIBRBAC000508836) was isolated from sea sediment from Incheon, Gyeonggi-do, Korea.

**Description of *Lacinutrix mariniflava* 15G1-1**

Cells are Gram-staining-negative, non-flagellated and rod shaped. Colonies are circular and yellow colored after aerobic 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 gelatin hydrolysis. In the API 20NE system, 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*-acetylglucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. Strain 15G1-1 (=NIBRBAC 000508958) was isolated from a seaweed at Goseong, Gangwon-do, Korea.

**Description of *Maribacter vaceletii* D2-5**

Cells are Gram-staining-negative, non-flagellated and rod shaped. Colonies are circular and yellow colored after aerobic incubation for two days on marine agar 2216 (MA) at 30°C. In the API 20NE system, positive reaction for esculin hydrolysis, and utilization of D-glucose, L-arabinose, D-mannose, *N*-acetylglucosamine, D-maltose, malic acid and trisodium citrate. In the API 20NE system, negative reaction for oxidase activity, nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease activity, gelatin hydrolysis, β-galactosidase activity, and utilization of D-mannitol, potassium gluconate, capric acid, adipic acid and phenylacetic acid. Strain D2-5 (=NIBRBAC000508961) was isolated from seaweed from Yeongdeok, Gyeongsangbuk-do, Korea.

**Description of *Wenyingzhuangia aestuarii* G1-8**

Cells are Gram-staining-negative, non-flagellated and rod shaped. Colonies are circular and pale yellow colored after aerobic incubation for three days on marine agar 2216 (MA) at 30°C. In the API 20NE system, positive reaction for oxidase activity, urease activity, esculin hydrolysis, β-galactosidase activity, and utilization of D-mannose. In the API 20NE system, negative reaction for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, gelatin hydrolysis and utilization of D-glucose, L-arabinose, D-mannitol, *N*-acetylglucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. Strain G1-8 (=NIBRBAC000508960) was isolated from seaweed from Goseong, Gangwon-do, Korea.

**Description of *Chryseobacterium aquaticum* subsp. *aquaticum* 17_H6_F1**

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

rod shaped. Colonies are circular, convex, smooth and yellow orange colored after aerobic incubation for 2−3 days on R2A agar at 30°C. In the API 20NE system, positive reaction for oxidase activity, esculin hydrolysis and gelatin hydrolysis. In the API 20NE system, 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*-acetylglucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. Strain 17_H6_F1 (=NIBRBAC000508793) was isolated from brackish water from Seoul, Korea.

**Description of *Chryseobacterium candidae* 16_H1_V15**

Cells are Gram-staining-negative, non-flagellated and rod shaped. Colonies are circular, convex, smooth and yellow orange colored after aerobic incubation for 2−3 days on R2A agar at 30°C. In the API 20NE system, positive reaction for esculin hydrolysis and gelatin hydrolysis. In the API 20NE system, negative reaction for oxidase activity, 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*-acetylglucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. Strain 16_H1_V15 (=NIBRBAC000508794) was isolated from soil from Hanam, Gyeonggi-do, Korea.

**Description of *Chryseobacterium joostei* 19_H2_S6**

Cells are Gram-staining-negative, non-flagellated and rod shaped. Colonies are circular, convex, smooth and yellow orange colored after aerobic incubation for 2−3 days on R2A agar at 30°C. In the API 20NE system, positive reaction for esculin hydrolysis and gelatin hydrolysis. In the API 20NE system, negative reaction for oxidase activity, 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*-acetylglucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. Strain 19_H2_S6 (=NIBRBAC000508795) was isolated from soil from Guri, Gyeonggi-do, Korea.

**Description of *Chryseobacterium nakagawai* 16_S2_M1**

Cells are Gram-staining-negative, non-flagellated and rod shaped. Colonies are circular, convex, smooth and yellow orange colored after aerobic incubation for 2−3 days on R2A agar at 30°C. In the API 20NE system, positive reaction for esculin hydrolysis and gelatin hydrolysis. In the API 20NE system, negative reaction for oxidase activity, 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*-acetylglucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. Strain 16_S2_M1 (=NIBRBAC000508796) was isolated from soil from Chungju, Chungcheongbuk-do, Korea.

**Description of *Chryseobacterium oranimense* 18_N3_T14**

Cells are Gram-staining-negative, non-flagellated and rod shaped. Colonies are circular, convex, smooth and yellow orange colored after aerobic incubation for 2−3 days on R2A agar at 30°C. In the API 20NE system, positive reaction for esculin hydrolysis and gelatin hydrolysis. In the API 20NE system, negative reaction for oxidase activity, 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*-acetylglucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. Strain 18_N3_T14 (=NIBRBAC000508797) was isolated from soil from Gapyeong, Gyeonggi-do, Korea.

**Description of *Chryseobacterium vietnamense* 16_H2_M3**

Cells are Gram-staining-negative, non-flagellated and rod shaped. Colonies are circular, convex, smooth and yellow orange colored after aerobic incubation for 2−3 days on R2A agar at 30°C. In the API 20NE system, positive reaction for esculin hydrolysis and gelatin hydrolysis. In the API 20NE system, negative reaction for oxidase activity, 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*-acetylglucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. Strain 16_H2_M3 (=NIBRBAC000508798) was isolated from soil from Guri, Gyeonggi-do, Korea.

**Description of *Chryseobacterium vrystaatense* 16_S3_M10**

Cells are Gram-staining-negative, non-flagellated and rod shaped. Colonies are circular, convex, smooth and yellow orange colored after aerobic incubation for 2−3 days on R2A agar at 30°C. In the API 20NE system, positive

reaction for esculin hydrolysis and gelatin hydrolysis. In the API 20NE system, negative reaction for oxidase activity, 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*-acetylglucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. Strain 16_S3_M10 (=NIBRBAC000508799) was isolated from soil from Yeoju, Gyeonggi-do, Korea.

**Description of *Mucilaginibacter kameinonensis* HMG3142**

Cells are Gram-staining-negative, non-flagellated and rod shaped. Colonies are circular, convex, smooth, mucoid and pale pink colored after aerobic incubation for three days on R2A agar 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, L-arabinose, D-mannose, *N*-acetylglucosamine and D-maltose. In the API 20NE system, negative reaction for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease activity, and utilization of D-mannitol, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. Strain HMG3142 (=NIBRBAC000508766) was isolated from soil from Yongin, Gyeonggi-do, Korea.

**Description of *Mucilaginibacter terrenus* HMG3746**

Cells are Gram-staining-negative, non-flagellated and rod shaped. Colonies are circular, convex, smooth and orange colored after aerobic incubation for three days on R2A agar 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, L-arabinose, D-mannose, *N*-acetylglucosamine and D-maltose. In the API 20NE system, negative reaction for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease activity, and utilization of D-mannitol, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. Strain HMG3746 (=NIBRBAC000508769) was isolated from moss from Yongin, Gyeonggi-do, Korea.

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