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 *Draconibacteriaceae* and *Sunxiuqinia* of *Prolixibacteraceae*, and *Fulvivirga* of *Fulvivirgaceae*. 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 Bacillales 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 Sphingobacteria 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, 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 bacterial 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 Prolibacteraceae of the (order Bacteroidales). One strain belonged to the family Fulvivirga_f and another to the Cytophagaceae (order Cytophaga). 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), Sunxiaquinia (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.

<table>
<thead>
<tr>
<th>Order</th>
<th>Family</th>
<th>Genus</th>
<th>Strain ID</th>
<th>NIBR ID</th>
<th>Most closely related species</th>
<th>Similarity (%)</th>
<th>Isolation source</th>
<th>Medium</th>
<th>Incubation condition</th>
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<td>Flavobacteriales</td>
<td>Flavobacteriaceae</td>
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<td>HMF4563</td>
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<td><em>Flavobacterium psychrolophile</em></td>
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<td>IMCC25651</td>
<td>NIBRBAC000498550</td>
<td><em>Fulvivirga kasyanovii</em></td>
<td>99.0</td>
<td>Plant roots</td>
<td>MA</td>
<td>20°C, 3d</td>
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<td>NIBRBAC000498563</td>
<td><em>Dyadobacter beijingensis</em></td>
<td>99.1</td>
<td>Freshwater sediment</td>
<td>R2A</td>
<td>30°C, 2d</td>
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<td><em>Dyadobacter beijingensis</em></td>
<td>99.1</td>
<td>Freshwater sediment</td>
<td>R2A</td>
<td>30°C, 2d</td>
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</table>
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\(^T\) (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 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 β-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 β-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 (= NIBRBA000498440) was isolated from a wet land sample, Yong-in-si, Korea.

Description of Flavobacterium limicola HMF4572

Cells are Gram-staining-negative, non-flagellated, and rod-shaped. Colonies are circular with entire margin, and yellow colored after 3 days on R2A agar at 25°C. Positive for oxidase, esculin hydrolysis, and β-galactosidase. Negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, or gelatin hydrolysis. 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 (= NIBRBA000498441) was isolated from a wet land sample, Yong-in-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 β-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 (= NIBRBA000498443) was isolated from a wet land sample, Yong-in-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 β-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 (= NIBRBA000498450) was isolated from seawater, Korea.

Description of Gillisia 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 β-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 (= NIBRBA000498452) 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 β-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 wastewater, 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 β-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 (= NIBRBA 000498469) was isolated from wastewater, Korea.

Description of Chryseobacterium solinicola POB7

Cells are Gram-staining-negative, non-flagellated, and rod-shaped. Colonies are transparent, 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 β-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 (= NIBRBA 000498477) was isolated from seaweed, 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 β-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 (= NIBRBA 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 β-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 (= NIBRBA000498477) 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 β-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 (= NIBRBA000498482) was isolated from a yessoensis Patinopecten yessoensis, Korea.

Description of Gaethulibacter 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 β-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 (= NIBRBA000498507) 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 β-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 β-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 (= NIBRBAC000498526) 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 β-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 (= NIBRBAC000498529) was isolated from tidal flat sediment, 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 β-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 β-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 (= NIBRBAC000498537) 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 β-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 (= NIBRBAC000498540) 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 β-galactosidase. Negative for oxidase, nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, and esculin hydrolysis. Uses D-glucose, L-arabinose, D-mannose, 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 β-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 3130 (= NIBRBAC 000498563) was isolated from a freshwater sediment, Han River, 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 β-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 β-galactosidase. Uses D-glucose, D-mannose, 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 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 β-galactosidase. 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 β-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 β-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 β-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 β-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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References


