A report of 24 unrecorded bacterial species in Korea belonging to the Phyla Proteobacteria and Bacteroidetes isolated in 2020

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In 2020, 24 bacterial strains were isolated from algae, kudzu leaf, mud, pine cone, seashore sand, seawater, soil, tidal flat, and wetland from the Republic of Korea. 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 highlighted as unrecorded species. These isolates were allocated to the phyla Bacteroidetes and Proteobacteria as unrecorded species in Korea. The four Bacteroidetes strains were classified into the families Chitinophagaceae, Flavobacteriaceae, and Sphingobacteriaceae (of the orders Chitinophagales, Flavobacteriales, and Sphingobacteriales, respectively). The 20 Proteobacteria strains belonged to the Aeromonadaceae, Marinobacter, Microbulbiferaceae, Enterobacteriaceae, Erwiniaeaceae, Morganellaceae, Yersiniaceae, Lysobacteraceae, Halomonadaceae, Moraxellaceae, Pseudomonadaceae, Steroidobacteraceae, Xanthomonadaceae, and Myxococcaceae (of the orders Aeromonadales, Alteromonadales, Cellvibrionales, Enterobacterales, Lysobacterales, Oceanospirillales, Pseudomonadales, Steroidobacter, Xanthomonadales, and Myxococcales). This study focused on the description of 24 unreported bacterial species in Korea in the phyla Bacteroidetes and Proteobacteria belonging to six classes.

Keywords: 16S rRNA, Bacteria, bacterial diversity, unreported species

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INTRODUCTION

In 2020, 24 unrecorded bacterial species were isolated from environmental samples collected in Korea and identified as members of Bacteroidetes and Proteobacteria. The Bacteroidetes species are all Gram-stain-negative heterotrophs, mainly rod-shaped, and do not form endospores (Krieg et al., 2010). They are known to play important roles in the biogeochemical processes such as the decomposition of peptides and polysaccharides (Russell et al., 2014; Hahnke et al., 2016). The phylum Proteobacteria constitutes the largest phylogenetic lineage (Kersters et al., 2006) that contains pathogenic bacteria. Gammaproteobacteria has the taxonomic rank of class within the phylum Proteobacteria (Garrity et al., 2005). Gammaproteobacteria includes a large and diverse group of bacteria that exhibits wide variation in term of phenotypes, morphologies, metabolic capabilities, and trophism (phototrophs and chemolithotrophs). Members of the class Gammaproteobacteria are Gram-staining-negative with different morphologies including rods, cocci, spirilla, and filaments, and isolated from wide range of
environments. The isolated bacteria species belong to the class Chitinophagia, Flavobacteria, Sphingobacteria, Gammaproteobacteria and Delta proteobacteria. In this study, we focused on the description of 24 unreported strains.

**MATERIALS AND METHODS**

A total of 24 bacterial strains isolated from algae, kudzu leaf, mud, pine cone, seashore sand, sea water, soil, tidal flat, and wetland samples collected in Korea. The samples were serially diluted in distilled water and the aliquot was spread onto R2A and MA medium, incubated at 25–37°C for 2–3 days. The strain IDs, growth media, isolation sources, and incubation conditions are summarized in Table 1. All strains were purified as single strain and stored using 20% glycerol suspension at −80°C as well as freeze-dried ampoules. Morphology of strains was examined by transmission electron microscopy (JEOL, JEM1010) using cells grown for 2–3 days on R2A and MA media. Transmission electron microgram of the strains are shown in Fig. 1. Gram staining tests were performed using a commercial kit, according to the manufacturer’s instruction (bioMérieux). Biochemical characteristics were evaluated using Biolog Microstation with GEN III microplate system, API 20NE strips according to manufacturer’s instruction (bioMérieux). Genomic DNA was extracted and 16S rRNA gene was amplified by PCR with 9F and 1492R universal bacterial primers (Weisburg et al., 1991). The 16S rRNA gene sequences of the closely related strains were obtained from EzBioCloud (https://www.ezbiocloud.net) and edited using the BioEdit program (Hall, 1999). Multiple alignments were performed with the Clustal X program (Thompson et al., 1997). Using the two-parameter model (Kimura, 1983) the evolutionary distances were calculated. Phylogenetic trees were constructed using the neighbor-joining method (Saitou and Nei, 1987) in the MEGA7 program (Kumar et al., 2016) with bootstrap values based on 1,000 replications (Felsenstein, 1985).

**RESULTS AND DISCUSSION**

Four strains of Bacteroidetes were distributed into three orders: one strain in Chitinophagales, one strain in Flavobacteriales and two strains in Sphingobacteriales. A total of 20 strains were classified into nine orders of Gammaproteobacteria: two strains in Aeromonadales, one strain in Alteromonadales, one strain in Cellvibrionales, four strains in Enterobacteriales, three strains in Lysobacteriales, one strain in Oceanospirillales, five strains in Pseudomonadales, one strain in Steroidobacter, and one strain in Xanthomonadales. Also, one strain was classified into the order Delta proteobacteria: one strain in Myxococcales (Table 1). All strains were Gram-staining-negative and one strain was coccus shaped and 23 strains were rod shaped (Fig. 1). In the class of Bacteroidetes, one strain was assigned to the genus Flavihumibacter of the family Chitinophagaceae in the order Chitinophagales and one strain was assigned to the genus Aquimarina of the family Flavobacteriales. Two strains in the order Sphingobacteriales in the order Sphingobacteriales belonged to two genera: Pedobacter (one strain) and Pedobacter (one strain) (Fig. 2). In the class of Proteobacteria, 20 strains were distributed into 10 orders, Aeromonadales, Alteromonadales, Cellvibrionales, Enterobacteriales, Lysobacteriales, Oceano spirillales, Pseudomonadales, Steroidobacter, Xanthomonadales and Myxococcales. Two strains in Aeromonadales, one strain in Marinobacter, one strain in Microbulbiferaceae, four strains in the order Enterobacteriales were separated into four families: Enterobacteriaceae (one strain), Erwiniaceae (one strain), Morganellaceae (one strain), Yersiniaceae (one strain), three strains in the order Lysobacteriales in the family Lysobacteraceae, one strain in Halomonadales, five strains in the order Pseudomonadales were separated into two families: Moravellaceae (one strain), Pseudomonadales (four strains), one strain in Steroidobacteraceae, one strain in Xanthomonadales, and one strain in Myxococcales. These strains were Gram-stain-negative and rod-shaped except for the strain L1_34_Aci, which was coccus-shaped (Fig. 1). The identification of the 24 strains based on sequence similarity was supported by the phylogenetic trees. The neighbor-joining trees inferred close relationships of the species and type strains of validly published species. The detailed morphological and physiological characteristics are given in the strain descriptions.

**Description of Flavihumibacter petaseus SM8**

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies are yellow-colored after 3 days of incubation on R2A at 30°C. In API 20NE test, positive for esculin hydrolysis; but negative for potassium gluconate, reduction of nitrates (NO3) to nitrite (NO2−), reduction of nitrates (NO3) to nitrogen (N2), indole production on tryptophan, glucose fermentation, arginine dihydrolase, urease, and gelatin hydrolysis. d-Glucose, l-arabinose, d-mannose, and d-maltose were utilized; whereas adipic acid, d-mannitol, N-acetyl-d-glucosamine, capric acid, malic acid, trisodium citrate, and phenylacetic acid were not utilized. Strain SM8 (= NIBRBA000506148) was isolated from a soil sample from Ecological Park in Godeok-dong, Gangdong-gu, Seoul, Korea.
<table>
<thead>
<tr>
<th>Order</th>
<th>Family</th>
<th>Strain ID</th>
<th>NIBRBAC</th>
<th>Most closely related species</th>
<th>16S rRNA similarity</th>
<th>Isolation source</th>
<th>Medium</th>
</tr>
</thead>
<tbody>
<tr>
<td>Chitinophagales</td>
<td>Chitinophagaceae</td>
<td>SM8</td>
<td>NIBRBAC000506148</td>
<td>Flavihuminibacter petaseus</td>
<td>99.8%</td>
<td>Wetland</td>
<td>R2A at 30°C, 3 days</td>
</tr>
<tr>
<td>Flavobacteria</td>
<td>Flavobacteriaceae</td>
<td>KYW2188</td>
<td>NIBRBAC000506233</td>
<td>Aquimaria aggregata</td>
<td>99.9%</td>
<td>Sea water</td>
<td>MA at 25°C, 3 days</td>
</tr>
<tr>
<td>Sphingobacteria</td>
<td>Sphingobacteriaceae</td>
<td>HMG1331</td>
<td>NIBRBAC000506261</td>
<td>Pedobacter aquatilis</td>
<td>99.9%</td>
<td>Seashore sand</td>
<td>R2A at 25°C, 3 days</td>
</tr>
<tr>
<td></td>
<td></td>
<td>HMG2653</td>
<td>NIBRBAC000506268</td>
<td>Mucilaginibacter ximonensis</td>
<td>99.3%</td>
<td>Pine cone</td>
<td>R2A at 25°C, 3 days</td>
</tr>
<tr>
<td>Aeromonadales</td>
<td>Aeromonadaceae</td>
<td>JHSTF-R13</td>
<td>NIBRBAC000506395</td>
<td>Tolunonas osononis</td>
<td>99.8%</td>
<td>Tidal flat</td>
<td>R2A at 25°C, 2 days</td>
</tr>
<tr>
<td></td>
<td></td>
<td>HMG1343</td>
<td>NIBRBAC000506262</td>
<td>Oceanisphaera arctica</td>
<td>99.3%</td>
<td>Seashore sand</td>
<td>R2A at 25°C, 3 days</td>
</tr>
<tr>
<td>Alteromonadales</td>
<td>Marinobacter_f</td>
<td>CAU 1621</td>
<td>NIBRBAC000506279</td>
<td>Marinobacter mobilis</td>
<td>100%</td>
<td>Mud</td>
<td>MA at 30°C, 3–5 days</td>
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<td>Cellvibrionales</td>
<td>Microbulbiferaceae</td>
<td>BDTF-M8</td>
<td>NIBRBAC000506391</td>
<td>Microbulbiffer elongatus</td>
<td>99.04%</td>
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<td>Enterobacteriales</td>
<td>Enterobacteriaceae</td>
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<td>NIBRBAC000506143</td>
<td>Citrobacter pasteurii</td>
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<td>Wetland</td>
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<td>Erwiniaceae</td>
<td>HMG2551</td>
<td>NIBRBAC000506267</td>
<td>Pantoea wallisii</td>
<td>99.9%</td>
<td>Kudzu leaf</td>
<td>R2A at 25°C, 3 days</td>
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<td></td>
<td>Morganellaceae</td>
<td>LW_53_Sal</td>
<td>NIBRBAC000506411</td>
<td>Providencia burhodogramaria</td>
<td>99.4%</td>
<td>Soil</td>
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<td>Versiniaceae</td>
<td>SO215</td>
<td>NIBRBAC000506239</td>
<td>Serratia oryzae</td>
<td>99.9%</td>
<td>Soil</td>
<td>R2A at 25°C, 2 days</td>
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<tr>
<td>Lysobacteriales</td>
<td>Lysobacteraceae</td>
<td>AsT1</td>
<td>NIBRBAC000506373</td>
<td>Maritimibacter alkaliphilus</td>
<td>99.8%</td>
<td>Algae</td>
<td>MA at 30°C, 3 days</td>
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<tr>
<td></td>
<td></td>
<td>L1_74_Sal</td>
<td>NIBRBAC000506406</td>
<td>Stenotrophomonas pavanii</td>
<td>99.0%</td>
<td>Soil</td>
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<td></td>
<td>BT648</td>
<td>NIBRBAC000506193</td>
<td>Lysobacter psychrotolerans</td>
<td>100%</td>
<td>Soil</td>
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<tr>
<td>Oceanospirillales</td>
<td>Halomonadaceae</td>
<td>KYW1991</td>
<td>NIBRBAC000506237</td>
<td>Halomonas axialenis</td>
<td>100%</td>
<td>Sea water</td>
<td>MA at 25°C, 3 days</td>
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<td>Pseudomonadales</td>
<td>Moraxellaceae</td>
<td>L1_34_Aci</td>
<td>NIBRBAC000506405</td>
<td>Acinetobacter seifertii</td>
<td>99.9%</td>
<td>Soil</td>
<td>R2A at 37°C, 3 days</td>
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<tr>
<td></td>
<td>Pseudomonadaceae</td>
<td>JHSTF-R6</td>
<td>NIBRBAC000506393</td>
<td>Pseudomonas composti</td>
<td>98.9%</td>
<td>Tidal flat</td>
<td>R2A at 25°C, 3 days</td>
</tr>
<tr>
<td></td>
<td></td>
<td>L1_104_Sal</td>
<td>NIBRBAC000506407</td>
<td>Pseudomonas asiatica</td>
<td>100%</td>
<td>Soil</td>
<td>R2A at 37°C, 3 days</td>
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<tr>
<td></td>
<td></td>
<td>LW_92_Aci</td>
<td>NIBRBAC000506410</td>
<td>Pseudomonas saponiphil</td>
<td>99.8%</td>
<td>Soil</td>
<td>R2A at 37°C, 3 days</td>
</tr>
<tr>
<td></td>
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<td>DM7</td>
<td>NIBRBAC000506145</td>
<td>Azotobacter brýphylí</td>
<td>99.8%</td>
<td>Wetland</td>
<td>R2A at 30°C, 3 days</td>
</tr>
<tr>
<td>Steroidobacter_o</td>
<td>Steroidobacteraceae</td>
<td>HMG1413</td>
<td>NIBRBAC000506264</td>
<td>Steroidobacter agariperforans</td>
<td>99.1%</td>
<td>Soil</td>
<td>R2A at 25°C, 3 days</td>
</tr>
<tr>
<td>Xanthomonadales</td>
<td>Xanthomonadaceae</td>
<td>MA7</td>
<td>NIBRBAC000506142</td>
<td>Stenotrophomonas bentonitica</td>
<td>99.9%</td>
<td>Wetland</td>
<td>R2A at 30°C, 3 days</td>
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<tr>
<td>Myxococcales</td>
<td>Myxococceae</td>
<td>17bor-14</td>
<td>NIBRBAC000501349</td>
<td>Simulacicoccus ruber</td>
<td>99.45%</td>
<td>Soil</td>
<td>R2A at 30°C, 3 days</td>
</tr>
</tbody>
</table>
Description of *Aquimarina aggregata* KYW2188

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies are yellow-colored after 3 days of incubation on MA at 25°C. In API 20NE test, positive for esculin hydrolysis; but negative for potassium gluconate, reduction of nitrates (NO$_3^-$) to nitrite (NO$_2^-$), reduction of nitrates (NO$_3^-$) to nitrogen (N$_2$), indole production on tryptophan, glucose fermentation, arginine dihydrolase, urease, and gelatin hydrolysis. D-Glucose, L-arabinose, D-mannose, N-acetyl-D-glucosamine, D-maltose, adipic acid, D-mannitol, capric acid, malic acid, trisodium citrate, and phenylacetic acid were not utilized. Strain KYW2188 (=NIBRBAC000506233) was isolated from a soil sample from Gwangyang Bay, Gwangyang-si, Jeollanam-do, Korea.

Description of *Pedobacter aquatilis* HMG1331

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies are yellow-colored after 3 days of incubation on MA at 25°C. In API 20NE test, positive for esculin hydrolysis; but negative for potassium gluconate, reduction of nitrates (NO$_3^-$) to nitrite (NO$_2^-$), reduction of nitrates (NO$_3^-$) to nitrogen (N$_2$), indole production on tryptophan, glucose fermentation, arginine dihydrolase, urease, and gelatin hydrolysis. D-Glucose, L-arabinose, D-mannose, N-acetyl-D-glucosamine, D-maltose, adipic acid, D-mannitol, capric acid, malic acid, trisodium citrate, and phenylacetic acid were not utilized. Strain KYW2188 (=NIBRBAC000506233) was isolated from a soil sample from Gwangyang Bay, Gwangyang-si, Jeollanam-do, Korea.
shaped. Colonies are pale pink-colored after 3 days of incubation on R2A at 25°C. In API 20NE test, positive for esculin hydrolysis; but negative for reduction of nitrates (NO₃⁻) to nitrite (NO₂⁻), reduction of nitrates (NO₃⁻) to nitrogen (N₂), indole production on tryptophan, glucose fermentation, arginine dihydrolase, gelatin hydrolysis, urease, and potassium gluconate. D-Glucose, L-arabinose, D-mannose, N-acetyl-D-glucosamine, and D-maltose were utilized; whereas adipic acid, malic acid, trisodium citrate, D-mannitol, capric acid, and phenylacetic acid were not utilized. Strain HMG1331 (= NIBRBAC000506261) was isolated from a soil sample from Jumunjin Beach, Jumunjin-eup, Gangneung-si, Gangwon-do, Korea.

Description of Mucilaginibacter ximonensis HMF2653

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies are pale yellow-colored after 3 days of incubation on R2A at 25°C. In API 20NE test, positive for esculin hydrolysis; but negative for reduction of nitrates (NO₃⁻) to nitrite (NO₂⁻), reduction of nitrates (NO₃⁻) to nitrogen (N₂), indole production on tryptophan, glucose fermentation, arginine dihydrolase, urease, and potassium gluconate. D-Glucose, L-arabinose, D-mannose, D-maltose, adipic acid, malic acid, trisodium citrate, D-mannitol, N-acetyl-D-glucosamine, capric acid, and phenylacetic acid were not utilized. Strain HMF2653 (= NIBRBAC000506268) was isolated from a soil sample from Jumunjin Beach, Jumunjin-eup, Gangneung-si, Gangwon-do, Korea.

Description of Tolumonas osonensis JHSTF-R13

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies are white-colored after 2 days of incubation on R2A at 25°C. In API 20NE test, positive for reduction of nitrates (NO₃⁻) to nitrite (NO₂⁻), and esculin hydrolysis; but negative for reduction of nitrates (NO₃⁻) to nitrogen (N₂), indole production on tryptophan, glucose fermentation, arginine dihydrolase, urease, potassium gluconate, and gelatin hydrolysis. D-Glucose, L-arabinose, D-mannose, D-maltose, adipic acid, malic acid, trisodium citrate, D-mannitol, N-acetyl-D-glucosamine, capric acid, and phenylacetic acid were not utilized. Strain JHSTF-R13 (= NIBRBAC000506395) was isolated from a soil sample from Seocheon-gun, Chungcheongnam-do, Korea.

Description of Oceanisphaera arctica HMG1343

Cells are Gram-stain-negative, flagellated, and rod-shaped. Colonies are beige-colored after 3 days of incubation on R2A at 25°C. In API 20NE test, positive for urease and esculin hydrolysis; but negative for potassium gluconate, reduction of nitrates (NO₃⁻) to nitrite (NO₂⁻), reduction of nitrates (NO₃⁻) to nitrogen (N₂), indole production on tryptophan, glucose fermentation, arginine dihydrolase, and gelatin hydrolysis. D-Mannitol, malic acid, trisodium citrate, and phenylacetic acid were utilized; whereas D-glucose, L-arabinose, D-mannose, D-maltose, adipic acid, malic acid, trisodium citrate, and phenylacetic acid were not utilized. Strain HMG1343 (= NIBRBAC000506262) was isolated from a soil sample from Jumunjin Beach, Jumunjin-eup, Gangneung-si, Gangwon-do, Korea.

Fig. 2. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences shows the relationship between the strains isolated in this study and their relatives of the genus Pedobacter HMG1331, Mucilaginibacter HMG2653, Aquimarrina KYW2188, and Flavihumibacter SM8. Bootstrap values (> 70%) are shown above nodes for the neighbor-joining methods. Bar: 0.01 and 0.05 substitutions per nucleotide position, respectively.
Description of *Marinobacter mobilis* CAU 1621s

Cells are Gram-stain-negative, flagellated, and rod-shaped. Colonies are creamy white-colored after 3–5 days of incubation on MA at 30°C. In API 20NE test, weekly positive for esculin hydrolysis; but negative for reduction of nitrates (NO₃) to nitrite (NO₂), reduction of nitrates (NO₃) to nitrogen (N₂), indole production on tryptophan, glucose fermentation, arginine dihydrolase, urease, potassium gluconate, and gelatin hydrolysis. α-Glucose, β-arabinose, α-mannose, α-maltose, adipic acid, malic acid, tricarboxylic acid, α-mannitol, N-acetyl-α-glucosamine, capric acid, and phenylacetic acid were not utilized. Strain CAU 1621s (=NIBRBAC000506279) was isolated from a soil sample from Sindo of Woongjin-gun, Incheon, Korea.

Description of *Microbulbifer elongatus* BDTF-M8

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies are moderate yellow-colored after 3 days of incubation on MA at 25°C. In API 20NE test, reduction of nitrates (NO₃) to nitrogen (N₂), esculin hydrolysis, gelatin hydrolysis.
Description of *Citrobacter pasteurii* MA20

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies are cream-colored after 3 days of incubation on R2A at 30°C. In API 20NE test, positive for reduction of nitrates (NO3⁻) to nitrite (NO2⁻), urease, indole production on tryptophan, glucose fermentation, and arginine dihydrolase. d-Glucose, l-arabinose, d-mannose, d-maltose, adic acid, malic acid, trisodium citrate, d-mannitol, N-acetyl-d-glucosamine, capric acid, and phenylacetic acid were not utilized. Strain BDTF-M8 (=NIBRBAC000506391) was isolated from a soil sample from Buldo, Ansan-si, Gyeonggi-do, Korea.

Description of *Bacillus* LW_53_Sal

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies are cream-colored after 3 days of incubation on R2A at 25°C. In API 20NE test, positive for reduction of nitrates (NO3⁻) to nitrogen (N₂), glucose fermentation, esculin hydrolysis, gelatin hydrolysis; but negative for indole production on tryptophan, arginine dihydrolase, and gelatin hydrolysis. d-Glucose, l-arabinose, d-mannose, d-mannitol, N-acetyl-d-glucosamine, d-maltose, capric acid, malic acid, trisodium citrate, and phenylacetic acid were utilized; whereas adipic acid was not utilized. Strain LW_53_Sal (=NIBRBAC000506411) was isolated from a soil sample from Cheoingu, Yongin-si, Gyeonggi-do, Korea.

Description of *Serratia oryzae* SO215

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies are white-colored after 2 days of incubation on R2A at 25°C. In API 20NE test, positive for potassium gluconate, esculin hydrolysis, reduction of nitrates (NO3⁻) to nitrite (NO2⁻), reduction of nitrates (NO3⁻) to nitrogen (N₂), glucose fermentation, and gelatin hydrolysis; but negative for indole production on tryptophan, arginine dihydrolase, and urease. d-Glucose, l-arabinose, d-mannose, d-maltose, malic acid, trisodium citrate, d-mannitol, N-acetyl-d-glucosamine, and phenylacetic acid were utilized; whereas capric acid and adipic acid were not utilized. Strain SO215 (=NIBRBAC000506239) was isolated from a soil sample from Sunchon National University, Suncheon-si, Jeollanam-do, Korea.

Description of *Maritimibacter alkaliphilus* AsT1

Cells are Gram-stain-negative, non-flagellated, and short rod-shaped. Colonies are white yellow-colored after 3 days of incubation on MA at 30°C. In API 20NE test, positive for urease, potassium gluconate, esculin hydrolysis, reduction of nitrates (NO3⁻) to nitrite (NO2⁻), reduction of nitrates (NO3⁻) to nitrogen (N₂), and arginine dihydrolase; but negative for indole production on tryptophan, glucose fermentation, and gelatin hydrolysis. d-Glucose, l-arabinose, d-mannose, d-maltose, adic acid, malic acid, trisodium citrate, d-mannitol, N-acetyl-d-glucosamine, capric acid, and phenylacetic acid were utilized. Strain AsT1 (=NIBRBAC000506373) was isolated from a soil sample from Taean Coast, Chunccheongbuk-do, Korea.

Description of *Providencia burhodogranariea* LW_53_Sal

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies are white-colored after 3 days of incubation on R2A at 37°C. In API 20NE test, positive for urease, esculin hydrolysis, reduction of nitrates (NO3⁻) to nitrite (NO2⁻), reduction of nitrates (NO3⁻) to nitrogen (N₂), indole production on tryptophan, glucose fermentation, arginine dihydrolase, and arginine dihydrolase; but negative for gelatin hydrolysis and potassium gluconate. d-Glucose, d-mannose, d-maltose, malic acid, trisodium citrate, d-mannitol, N-acetyl-d-glucosamine, capric acid, and phenylacetic acid were utilized; whereas l-arabinose and adipic acid were not utilized. Strain LW_53_Sal (=NIBRBAC000506391) was isolated from a soil sample from Cheoingu, Yongin-si, Gyeonggi-do, Korea.
BAC000506406) was isolated from a soil sample from Cheoin-gu, Yongin-si, Gyeonggi-do, Korea.

**Description of Lysobacter psychrotolerans BT648**

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies are light yellow-colored after 3 days of incubation on R2A at 25°C. In API 20NE test, positive for reduction of nitrates (NO₃⁻) to nitrite (NO₂⁻), reduction of nitrates (NO₃⁻) to nitrogen (N₂), indole production on tryptophan, esculin hydrolysis, and gelatin hydrolysis; but negative for glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis, gelatin hydrolysis, and potassium gluconate. d-Glucose, l-arabinose, d-mannose, d-mannitol, N-acetyl-d-glucosamine, d-maltose, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid were not utilized. Strain BT648 (= NIBRBAC000506193) was isolated from a soil sample from Hwam-myeon, Jeongseon-gun, Gangwon-do, Korea.

**Description of Halomonas axialisensis KYW9191**

Cells are Gram-stain-negative, flagellated, and rod-shaped. Colonies are cream-colored after 3 days of incubation on MA at 25°C. In API 20NE test, positive for reduction of nitrates (NO₃⁻) to nitrite (NO₂⁻), reduction of nitrates (NO₃⁻) to nitrogen (N₂), and esculin hydrolysis; but negative for indole production on tryptophan, glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis, gelatin hydrolysis, and potassium gluconate. d-Maltose, adipic acid, and malic acid were utilized; whereas d-glucose, l-arabinose, d-mannose, d-mannitol, N-acetyl-d-glucosamine, capric acid, trisodium citrate, and phenylacetic acid were not utilized. Strain KYW9191 (= NIBRBAC000506237) was isolated from a soil sample from Gwangyang Bay, Gwangyang-si, Jeollanam-do, Korea.

**Description of Acinetobacter seifertii L1_34_Aci**

Cells are Gram-stain-negative, non-flagellated, and coccus-shaped. Colonies are white colored after 3 days of incubation on R2A at 37°C. In API 20NE test, positive for glucose fermentation, urease, esculin hydrolysis, and potassium gluconate; but negative for reduction of nitrates (NO₃⁻) to nitrite (NO₂⁻), reduction of nitrates (NO₃⁻) to nitrogen (N₂), indole production on tryptophan, arginine dihydrolase, esculin hydrolysis, gelatin hydrolysis, and potassium gluconate. d-Glucose, l-arabinose, d-mannose, d-mannitol, N-acetyl-d-glucosamine, capric acid, trisodium citrate, and phenylacetic acid were not utilized. Strain L1_34_Aci (= NIBRBAC000506407) was isolated from a soil sample from Cheoin-gu, Yongin-si, Gyeonggi-do, Korea.

**Description of Pseudomonas asiatica L1_104_Sal**

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies are white-colored after 3 days of incubation on R2A at 37°C. In API 20NE test, positive for arginine dihydrolase, urease, esculin hydrolysis, and potassium gluconate; but negative for reduction of nitrates (NO₃⁻) to nitrite (NO₂⁻), reduction of nitrates (NO₃⁻) to nitrogen (N₂), indole production on tryptophan, glucose fermentation, and gelatin hydrolysis. d-Glucose, l-arabinose, d-mannose, d-mannitol, N-acetyl-d-glucosamine, d-maltose, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid were utilized. Strain L1_104_Sal (= NIBRBAC000506407) was isolated from a soil sample from Cheoin-gu, Yongin-si, Gyeonggi-do, Korea.

**Description of Pseudomonas saponiphila LW_92_Aci**

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies are white-colored after 3 days of incubation on R2A at 37°C. In API 20NE test, positive for indole production on tryptophan, glucose fermentation, arginine dihydrolase, esculin hydrolysis, and potassium gluconate; but negative for reduction of nitrates (NO₃⁻) to nitrite (NO₂⁻), reduction of nitrates (NO₃⁻) to nitrogen (N₂), urease, and gelatin hydrolysis. d-Glucose, d-mannose, d-mannitol, N-acetyl-d-glucosamine, capric acid, malic acid, trisodium citrate, and phenylacetic acid were utilized; whereas l-arabinose, d-maltose, and adipic acid were not utilized. Strain LW_92_Aci (= NIBRBAC000506410) was isolated from a soil sample from Cheoin-gu, Yongin-si, Gyeonggi-do, Korea.

**Description of Azotobacter bryophylli DM7**

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies are pale yellow colored after 3 days of incubation on R2A at 30°C. In API 20NE test, positive for reduction of nitrates (NO₃⁻) to nitrite (NO₂⁻), reduction of nitrates (NO₃⁻) to nitrogen (N₂), urease, gelatin hydrolysis, and potassium gluconate; but negative for indole produc-
Description of *Steroidobacter agariperforans* HMG1413

Cells are Gram-stain-negative, flagellated, and rod-shaped. Colonies are yellow-colored after 3 days of incubation on R2A at 25°C. In API 20NE test, positive for reduction of nitrates (NO₃⁻) to nitrite (NO₂⁻), reduction of nitrates (NO₃⁻) to nitrogen (N₂), esculin hydrolysis, gelatin hydrolysis, and potassium gluconate; but negative for indole production on tryptophan, glucose fermentation, arginine dihydrolase, and urease. d-Glucose, l-arabinose, N-acetyl-d-glucosamine, d-maltose, malic acid, and trisodium citrate were utilized; whereas d-mannose, d-mannitol, capric acid, adipic acid, and phenylacetic acid were not utilized. Strain HMG1413 (=NIBRBAC000506264) was isolated from a soil sample from Hankuk University of Foreign Studies, Cheoin-gu, Yongin-si, Gyeonggi-do, Korea.

Description of *Stenotrophomonas bentonitica* MA7

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies are cream-colored after 3 days of incubation on R2A at 30°C. In API 20NE test, positive for esculin hydrolysis and gelatin hydrolysis; but negative for reduction of nitrates (NO₃⁻) to nitrite (NO₂⁻), reduction of nitrates (NO₃⁻) to nitrogen (N₂), indole production on tryptophan, glucose fermentation, arginine dihydrolase, urease, and potassium gluconate. d-Glucose, d-mannose, N-acetyl-d-glucosamine, d-maltose, malic acid, and trisodium citrate were utilized; whereas l-arabinose, d-mannitol, capric acid, adipic acid, and phenylacetic acid were not utilized. Strain MA7 (=NIBRBAC000506142) was isolated from a soil sample from Ecological Park in Godeok-dong, Gangdong-gu, Seoul, Korea.

Description of *Simulacricoccus ruber* 17bor-14

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies are pink-colored after 3 days of incubation on R2A at 30°C. In API 20NE test, positive for urease; but negative for reduction of nitrates (NO₃⁻) to nitrite (NO₂⁻), reduction of nitrates (NO₃⁻) to nitrogen (N₂), esculin hydrolysis, gelatin hydrolysis, indole production on tryptophan, potassium gluconate, glucose fermentation, and arginine dihydrolase. d-Glucose, l-arabinose, d-mannose, d-maltose, adipic acid, malic acid, and trisodium citrate were utilized; whereas N-acetyl-d-glucosamine, d-mannitol, capric acid, and phenylacetic acid were not utilized. Strain 17bor-14 (=NIBRBAC000501349) was isolated from a soil sample from Gongneung-dong, Nowon-gu, Seoul, Korea.

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**References**


