Report of 29 unrecorded bacterial species from the phylum *Proteobacteria*

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Our study aimed to discover indigenous prokaryotic species in Korea. A total of 29 bacterial species in the phylum *Proteobacteria* were isolated from freshwater and sediment of rivers and brackish zones in Korea. From the high 16S rRNA gene sequence similarity (≥98.8%) and formation of a robust phylogenetic clade with the closest species, it was determined that each strain belonged to an independent and predefined bacterial species. To our knowledge, there is no official report or publication that has previously described these 29 species in Korea. Specifically, we identified 10, 12, and seven species of eight, 12, and seven genera that belong to classes *Alphaproteobacteria*, *Betaproteobacteria*, and *Gammaproteobacteria*, respectively; all are reported as previously unrecorded bacterial species in Korea. The Gram reaction, colony and cell morphology, basic biochemical characteristics, isolation source, and strain IDs for each are also described.

Keywords: 16S rRNA gene, *Proteobacteria*, unrecorded species

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**INTRODUCTION**

*Proteobacteria* (Stackebrandt *et al.*, 1988; Garrity *et al.*, 2005) is the largest phylum of bacteria, containing over 500 genera. *Proteobacteria* constitutes the most diverse phylogenetic lineage with regard to phenotypic, physiological, and metabolic characteristics. Members of the phylum *Proteobacteria* have been observed in various environmental habitats ranging from aquatic and terrestrial environments to mammals (Costello *et al.*, 2009; Joung *et al.*, 2014; Pascault *et al.*, 2014). Based on 16S rRNA gene sequences, the phylum *Proteobacteria* is further divided into six classes: *Alphaproteobacteria*, *Betaproteobacteria*, *Gammaproteobacteria*, *Deltaproteobacteria*, *Epsilonproteobacteria*, and *Zetaproteobacteria*. Previously, it was reported that the six classes of *Proteobacteria* showed significant differences in distribution based on environment: *Alphaproteobacteria* and *Betaproteobacteria* were enriched in the freshwater environment, *Gammaproteobacteria* and *Zetaproteobacteria* in the marine environment, *Gammaproteobacteria* and *Epsilonproteobacteria* in the intertidal zone, and *Deltaproteobacteria* were found in all environments (Emerson *et al.*, 2007; Wang *et al.*, 2012).

In 2015-16, we collected freshwater samples from the major rivers (Han, Nakdong, and Seomjin Rivers) in Korea and isolated myriads of novel and unrecorded bacterial species. Here, we report 29 previously unrecorded bacterial species in Korea from the phylum *Proteobacteria*, especially the classes *Alphaproteobacteria*, *Betaproteobacteria*, and *Gammaproteobacteria*.

**MATERIALS AND METHODS**

A total of 29 bacterial strains from the phylum *Proteobacteria* were isolated from environmental samples including freshwater, brackish water, and sediment. Each environmental sample was processed separately, spread onto various culture media, including R2A agar, marine agar 2216, and nutrient agar, and incubated at 15-25°C for 2-3 weeks. All the strains were purified as single colonies and stored in a 10-20% glycerol suspension at −80°C. The designated strain IDs, isolation sources, culture media, and incubation conditions are summarized in Table 1.

Bacterial DNA preparation, PCR amplification, and 16S rRNA gene sequencing were carried out as previ-
Table 1. Summary of strains belonging to the phylum *Proteobacteria* and their taxonomic affiliations.

<table>
<thead>
<tr>
<th>Class</th>
<th>Family</th>
<th>Genus</th>
<th>Strain ID</th>
<th>NNIBR ID</th>
<th>Most closely related species</th>
<th>Similarity (%)</th>
<th>Isolation source</th>
<th>Medium</th>
<th>Incubation conditions</th>
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<td><strong>Alphaproteobacteria</strong></td>
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<td>Sediment</td>
<td>R2A</td>
<td>30°C, 3d</td>
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<td><em>Arenimonas</em></td>
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<td>99.9</td>
<td>Sediment</td>
<td>R2A</td>
<td>25°C, 3d</td>
</tr>
</tbody>
</table>
ously described (Chun & Goodfellow, 1995). The 16S rRNA gene sequences of the related taxa were obtained from the EzTaxon-e server (Kim et al., 2012). The 16S rRNA gene sequences were aligned in the SILVA aligner version 1.2.1.11 (http://www.arb-silva.de/aligner; Pruesse et al., 2012). Phylogenetic trees were reconstructed by neighbor-joining (NJ) (Saitou & Nei, 1987), maximum-parsimony (MP) (Fitch, 1971), and maximum-likelihood (ML) (Felsenstein, 1981) algorithms using the MEGA software version 6 (Tamura et al., 2013). For the neighbor-joining analysis, the evolutionary distances between sequences were calculated using the Jukes-cantor distance (Jukes & Cantor, 1969), and the tree topology was evaluated with 1,000 replicates of bootstrap resampling (Felsenstein, 1985).

The colony morphology of the strains was observed on agar plates with a magnifying glass after cells grew to stationary phase. Cellular morphology and cell size were examined by transmission electron microscopy (Fig. 1). Gram staining was performed using a Gram Staining Kit (Sigma). Biochemical characteristics were tested using the API 20 NE galleries (bioMérieux) according to the manufacturer’s instructions.

RESULTS AND DISCUSSION

Based on 16S rRNA gene sequence comparisons and phylogenetic analyses, a total 29 strains were identified as previously unrecorded bacterial species in Korea. These strains were gram-negative and rod-shaped bacteria, except for strains AS5-06 and ES1-46 which had either a coccoid or oval shape (Fig. 1). The 29 unrecorded bacterial species belonged to three classes, 10 orders, 17 families, and 27 genera. They were assigned to 10 species of Alphaproteobacteria, 12 species of Betaproteobacteria, and seven species of Gammaproteobacteria. Fig. 2 shows the phylogenetic assignments of these strains within the class Alphaproteobacteria; these species were identified as the species Sphingomonas abaci (Busse et al., 2005), S. endophytica (Huang et al., 2012), S. yunnanensis (Zhang et al., 2005), and Blastomonas aquatica (Xiao et al., 2015) of the order Sphingomonadales; Tardiphaga robiniae (De Mayer et al., 2012), Afipia massiliensis (La Scola et al., 2002), and Methylobacterium bullatum (Hoppe et al., 2011) of the order Rhizobiales; Pseudorhodobacter ferrugineus (Uchino et al., 2002) and Pseudooceanicola nanhaiensis (Lai et al., 2015) of the order Rhodobacterales; and Belnapia moabensis (Reddy et al., 2006) of the order Rhodospirillales. In the class Betaproteobacteria, 12 strains were assigned to the three orders Burkholderiales, Rhodocyclales, and Neisseriales (Fig. 3). The strains were identified as the species Ideonella dechloratans (Malmqvist et al., 1994), Kinneretia asaccharophila (Gomila et al., 2010), Hydrogenophaga atypica (Kämpfer et al., 2005), Inhella inkyongensis (Chen et al., 2012), Polynucleobacter necessarius subsp. symbiobius (Hahn et al., 2016), Rhizobacter dauci (Goto & Kuwata, 1988), Piscinibacter aquaticus (Stackebrandt et al., 2009), Malikia gronosa (Spring et al., 2005), and Herminiimonas contaminans (Kämpfer et al., 2013) of the order Burkholderiales; Dechloromonas hortensis (Wolterink et al., 2005) and Thauera aminoaeromatica (Mechichi et al., 2002) of the order Rhodocyclales; and Chitinibacter tainanensis (Chen et al., 2004) of the order Neisseriales. Fig. 4 shows the phylogenetic assignments of seven species of the orders Xanthomonadales, Alteromonadales, Neisseriales, and Pseudomonadales within the class Gammaproteobacteria. Lyso bacter brunescens (Christensen & Cook, 1978), Thermomonas carbonis (Wang et al., 2014), and Arenimonas subflava (Makk et al., 2015) of the order Xanthomonadales; Rheinheimera aquatica (Chen et al., 2010) and Pseudoalteromonas tunicata (Holmström et al., 1998) of the order Alteromonadales; Nevisia ramosa (Famintzin, 1892) of the order Neisseriales; and Pseudomonas avellanae (Janse et al., 1996) of the order Pseudomonadales were identified.

In conclusion, we have described 29 previously unrecorded bacterial species from the phylum Proteobacteria, which were isolated from freshwater environments in Korea.

Description of Sphingomonas abaci SS1-08

Cells are gram-staining-negative, non-flagellated and rod-shaped. Colonies are circular, shiny, leathery, dry and yellow-colored after 3 days on R2A agar at 25°C. Positive for esculin hydrolysis, gelatinase and β-galactosidase, but negative for oxidase, nitrate reduction, indole production, glucose fermentation, arginine dihydrolase and urease. D-Glucose, L-arabinose, D-mannose, D-maltose, potassium gluconate, malic acid and trisodium citrate are utilized. Weakly utilize N-acetyl-glucosamine. Dose not utilize D-mannitol, capric acid, adipic acid and phenylacetic acid. The strain SS1-08 (= NNIBRBA 3) was isolated from sediment of the Nakdong River, Gyeongcheon-island, Sangju, Korea.

Description of Sphingomonas endophytica SS1-17

Cells are gram-staining-negative, non-flagellated and rod-shaped. Colonies are circular, convex, opaque and yellow-colored after 3 days on R2A agar at 25°C. Positive for esculin hydrolysis and β-galactosidase, weakly positive for gelatinase, but negative for oxidase, nitrate reduction, indole production, glucose fermentation, arginine dihydrolase and urease. D-Glucose, L-arabinose, D-mannose, N-acetyl-glucosamine, D-maltose and malic
Fig. 1. Transmission electron micrographs of the strains isolated in this study. Strains: 1, S1-08; 2, SS1-17; 3, SS1-22; 4, SH33; 5, BK16-1; 6, SH41; 7, BES-63; 8, ES2-15; 9, AS5-06; 10, CS4-36; 11, BK-22; 12, BK-77; 13, BK-179; 14, SS1-70; 15, SS2-102; 16, BK-176; 17, SJ55; 18, BK-182; 19, BK-210; 20, ES1-46; 21, BK-219; 22, BK-438; 23, BK-128; 24, BK-213; 25, GS1-30; 26, 04KS1-07; 27, CS4-45; 28, BES3-108; 29, KS1-13.
acid are utilized. Do not utilize D-mannitol, potassium gluconate, capric acid, adipic acid, trisodium citrate and phenylacetic acid. The strain SS1-17 (\(=\)NNIBRBA 5) was isolated from sediment of the Nakdong River, Gyeongcheon-island, Sangju, Korea.

Description of *Sphingomonas yunnanensis* SS1-22

Cells are gram-staining-negative, non-flagellated and rod-shaped. Colonies are circular, convex, opaque and yellow-colored after 3 days on R2A agar at 25°C. Positive for oxidase, esculin hydrolysis, gelatinase and \(\beta\)-galactosidase, but negative for nitrate reduction, indole.
Fig. 3. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences, showing the relationship between 12 unrecorded bacterial species and other representatives of the class Betaproteobacteria. Bootstrap values (>70%) based on 1000 resamplings are shown at branching points. Filled circles indicate that the corresponding nodes were recovered by all treeing methods. Open circles indicate that the corresponding nodes were recovered by the neighbour-joining and maximum-likelihood methods. *Escherichia coli* NCTC9001$^T$ (LN831047) was used as an outgroup (not shown). Bar, 0.02 substitutions per nucleotide position.
production, glucose fermentation, arginine dihydrolase and urease. D-Glucose, L-arabinose, D-mannose, N-acetyl-glucosamine, D-maltose, potassium gluconate and malic acid are utilized. Dose not utilize D-mannitol, capric acid, adipic acid, trisodium citrate and phenylacetic acid. The strain SS1-22 (= NNIBRBA 6) was isolated from a sediment of the Nakdong River, Gyeongcheon-island, Sangju, Korea.

Description of Tardiphaga robiniae BK16-1

Cells are gram-staining-negative, non-flagellated and
rod-shaped. Colonies are circular, convex with entire edge and white-colored after 3 days on R2A agar at 25 °C. Positive for oxidase, urease and esculin hydrolysis, but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, gelatinase and β-galactosidase. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, N-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. The strain BK16-1 (= NIBRBA 43) was isolated from freshwater of the Geomyeongso (origin of Han River), Taebaek, Korea.

**Description of *Pseudorhodobacter ferrugineus* BES-63**

Cells are gram-staining-negative, non-flagellated, rod-shaped. Colonies are circular, convex with entire edge and yellow-colored after 3 days on MA at 25°C. Positive for oxidase, esculin hydrolysis and β-galactosidase but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease and gelatinase. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, N-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. The strain BES-63 (= NIBRBA 48) was isolated from freshwater, Eulsuk-island at the end of the Nakdong River, Busan, Korea.

**Description of *Blastomonas aquatica* SH33**

Cells are gram-staining-negative, non-flagellated, rod-shaped. Colonies are circular, convex with entire edge and yellow-colored after 3 days on R2A agar at 25°C. Positive for oxidase, esculin hydrolysis and gelatinase, but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease and β-galactosidase. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, N-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. The strain SH33 (= NIBRBA 41) was isolated from freshwater of the Sohan-stream, Samcheok, Korea.

**Description of *Afipia massiliensis* SH41**

Cells are gram-staining-negative, non-flagellated, rod-shaped. Colonies are circular, convex with entire edge and white-colored after 3 days on R2A agar at 25°C. Positive for oxidase, arginine dihydrolase and urease, but negative for nitrate reduction, indole production, glucose fermentation, esculin hydrolysis, gelatinase and β-galactosidase. Adipic acid and malic acid are utilized. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, N-acetyl-glucosamine, D-maltose, potassium gluconate, D-maltose, potassium gluconate, capric acid, trisodium citrate and phenylacetic acid. The strain SH41 (= NIBRBA 42) was isolated from freshwater of the Sohan-stream, Samcheok, Korea.

**Description of *Belnapia moabensis* AS5-06**

Cells are gram-staining-negative, non-flagellated, coccus-shaped. Colonies are convex, round, rough and red-pink colored after 3 days on R2A agar at 30°C. Positive for oxidase and urease, but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, esculin hydrolysis, gelatinase and β-galactosidase. L-Arabinose, potassium gluconate and adipic acid are utilized. Does not utilize D-glucose, D-mannose, D-mannitol, N-acetyl-glucosamine, D-maltose, capric acid, malic acid, trisodium citrate and phenylacetic acid. The strain AS5-06 (= NIBRBA 60) was isolated from sediment of the Seobu-dock, Andong, Korea.

**Description of *Methylobacterium bullatum* CS4-36**

Cells are gram-staining-negative, non-flagellated, rod-shaped. Colonies are circular, convex, smooth and red-pink colored after 3 days on R2A agar at 30°C. Positive for oxidase, nitrate reduction, urease and esculin hydrolysis, but negative for indole production, glucose fermentation, arginine dihydrolase, gelatinase and β-galactosidase. Potassium gluconate, adipic acid and malic acid are utilized. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, N-acetyl-glucosamine, D-maltose, capric acid, trisodium citrate and phenylacetic acid. The strain CS4-36 (= NIBRBA 67) was isolated from sediment of the Changnyeong-Haman weir, Changnyeong, Korea.

**Description of *Pseudoocceanica nanhaiensis* ES2-15**

Cells are gram-staining-negative, non-flagellated, rod-shaped. Colonies are circular, convex, smooth and faint yellow-colored after 3 days on MA at 25°C. Positive for oxidase, arginine dihydrolase and urease, but negative for nitrate reduction, indole production, glucose fermentation, esculin hydrolysis, and activity of β-galactosidase and gelatinase. D-Glucose, L-arabinose, D-mannitol, malic acid and adipic acid are utilized. Does not utilize D-mannose, D-maltose, N-acetyl-glucosamine, potassium gluconate, capric acid, trisodium citrate and phenylacetic acid. The strain ES2-15 (= NIBRBA 64) was isolated from sediment of the Eulsuk-island, Busan, Korea.

**Description of *Ideonella dechloratans* BK-22**

Cells are gram-staining-negative non-flagellated and rod-shaped. Colonies are convex entire margins, mucoid
and cream-colored after 2 days on R2A agar at 30°C. Positive for oxidase, urease and esculin hydrolysis, but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, gelatinase and β-galactosidase. D-Glucose, L-arabinose, D-mannose, D-mannitol, N-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid are not utilized. The strain BK-176 (= NNIBRBA 19) was isolated from freshwater of the Nakdong River, Sangju, Korea.

**Description of Kinneretia asaccharophila BK-77**

Cells are gram-staining-negative non-flagellated and rod-shaped. Colonies are translucent, irregular, margins and cream-colored after 3 days on R2A agar at 25°C. Positive for oxidase, nitrate reduction, esculin hydrolysis and gelatinase, but negative for indole production, glucose fermentation, arginine dihydrolase, urease and β-galactosidase. D-Glucose, L-arabinose, D-mannose, D-mannitol, N-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid are not utilized. The strain BK-77 (= NNIBRBA 22) was isolated from freshwater of the Nakdong River, Sangju, Korea.

**Description of Hydrogenophaga atypica BK-176**

Cells are gram-staining-negative non-flagellated and rod-shaped. Colonies are circular, regular and cream-colored after 3 days on R2A agar at 25°C. Positive for oxidase, nitrate reduction, urease and esculin hydrolysis, but negative for indole production, glucose fermentation, arginine dihydrolase, gelatinase and β-galactosidase. D-Glucose, L-arabinose, D-mannose, D-mannitol, N-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid are not utilized. The strain BK-176 (= NNIBRBA 27) was isolated from freshwater of the Nakdong River, Sangju, Korea.

**Description of Inhella inkyongensis BK-179**

Cells are gram-staining-negative non-flagellated and shot rod-shaped. Colonies are circular, convex, smooth and cream-colored after 3 days on R2A agar at 15°C. Positive for oxidase, esculin hydrolysis, gelatinase and β-galactosidase, but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase and urease. D-Glucose, L-arabinose, D-mannose, D-mannitol, N-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid are not utilized. The strain BK-179 (= NNIBRBA 28) was isolated from freshwater of the Nakdong River, Sangju, Korea.

**Description of Polynucleobacter necessarius subsp. Asymbioticus BK-182**

Cells are gram-staining-negative non-flagellated and shot rod-shaped. Colonies are circular, convex, smooth and cream-colored after 3 days on R2A agar at 30°C. Positive for oxidase, but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis, gelatinase and β-galactosidase. D-Glucose, L-arabinose, D-mannose, D-mannitol, N-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid are not utilized. The strain BK-182 (= NNIBRBA 29) was isolated from freshwater of the Nakdong River, Sangju, Korea.

**Description of Dechloromonas hortensis BK-210**

Cells are gram-staining-negative non-flagellated and rod-shaped. Colonies are circular, regular and yellow-colored after 3 days on R2A agar at 30°C. Positive for oxidase and esculin hydrolysis, but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, gelatinase and β-galactosidase. D-Glucose, L-arabinose, D-mannose, D-mannitol, N-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid are not utilized. The strain BK-210 (= NNIBRBA 30) was isolated from freshwater of the Nakdong River, Sangju, Korea.

**Description of Chitinibacter tainanensis BK-219**

Cells are gram-staining-negative non-flagellated and rod-shaped. Colonies are circular, entire, convex and milky white-colored after 4 days on NA at 30°C. Positive for oxidase, glucose fermentation, esculin hydrolysis and gelatinase, but negative for nitrate reduction, indole production, arginine dihydrolase, urease and β-galactosidase. D-Mannose is utilized. Dose not utilize D-glucose, L-arabinose, D-mannitol, N-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. The strain BK-219 (= NNIBRBA 33) was isolated from freshwater of the Nakdong River, Sangju, Korea.

**Description of Rhizobacter dauci SS1-70**

Cells are gram-staining-negative non-flagellated and rod-shaped. Colonies are circular, tough and lemon-colored after 3 days on R2A agar at 25°C. Positive for oxidase, nitrate reduction and β-galactosidase, weakly positive for urease, but negative for indole production, glucose fermentation, arginine dihydrolase, urease and gelatinase. D-Maltose is utilized. Dose not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, N-acetyl-
glucosamine, potassium gluconate, capric acid, adipic acid, D-malic acid, trisodium citrate and phenylacetic acid. The strain SS1-70 (= NNRBRA 11) was isolated from riverside sediment of the Nakdong River, Gyeongcheon-island, Sangju, Korea.

Description of *Piscinibacter aquaticus* SS2-102

Cells are gram-staining-negative non-flagellated and rod-shaped. Colonies are circular, smooth with entire margins and beige-colored after 3 days on R2A agar at 25°C. Positive for oxidase, nitrate reduction, urease, gelatinase and β-galactosidase, weakly positive for esculin hydrolysis, but negative for indole production, glucose fermentation and arginine dihydrolase. D-Glucose, D-mannitol and D-maltose are utilized. Dose not utilize L-arabinose, D-mannose, N-acetyl-glucosamine, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. The strain SS2-102 (= NNRBRA 17) was isolated from riverside sediment of the Nakdong River, Gyeongcheon-island, Sangju, Korea.

Description of *Malikia granosa* SJ55

Cells are gram-staining-negative non-flagellated and rod-shaped. Colonies are circular, convex with entire edge and white-colored after 3 days on R2A agar at 25°C. Positive for oxidase, nitrate reduction, urease, esculin hydrolysis, gelatinase and β-galactosidase, but negative for indole production, glucose fermentation and arginine dihydrolase. D-Glucose, D-mannose and D-mannitol are utilized. Dose not utilize L-arabinose, D-mannose, N-acetyl-glucosamine, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. The strain SJ55 (= NNRBRA 37) was isolated from brackish water of the Seomjin River, Gwangyang, Korea.

Description of *Herminiimonas contaminans* BK-438

Cells are gram-staining-negative non-flagellated and rod-shaped. Colonies are circular, convex with entire edge and white-colored after 3 days on R2A agar at 35°C. Positive for oxidase, nitrate reduction, esculin hydrolysis, gelatinase and β-galactosidase, but negative for indole production, glucose fermentation, arginine dihydrolase and urease. D-Glucose, L-arabinose, D-mannose, D-mannitol, N-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid are not utilized. The strain BK-127 (= NNRBRA 25) was isolated from freshwater of the Nakdong River, Gyeongcheon-island, Sangju, Korea.

Description of *Nevskia ramosa* BK-213

Cells are gram-staining-negative non-flagellated and shot rod-shaped. Colonies are convex with entire margins and greenish-yellow colored after 2 days on R2A agar at 35°C. Positive for oxidase, esculin hydrolysis, gelatinase and β-galactosidase, but negative for indole production, glucose fermentation, arginine dihydrolase and urease. D-Glucose, L-arabinose, D-mannose, D-mannitol, N-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid are not utilized. The strain BK-213 (= NNRBRA 31) was isolated from freshwater of the Nakdong River, Gyeongcheon-island, Sangju, Korea.

Description of *Lysobacter brunescens* GS1-30

Cells are gram-staining-negative non-flagellated and rod-shaped. Colonies are circular, convex, smooth and light-yellow colored after 3 days on R2A agar at 25°C. Positive for oxidase, esculin hydrolysis and β-galactosidase, but negative for nitrate reduction, indole production, arginine dihydrolase and gelatinase. D-Glucose, L-arabinose, D-mannose, D-mannitol, D-maltose and potassium gluconate are utilized. Dose not utilize N-acetyl-glucosamine, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. The strain ES1-46 (= NNRBRA 63) was isolated from brackish marsh sediment of Eulsook-island at the end of the Nakdong River, Busan, Korea.
citrate and phenylacetic acid are not utilized. The strain GS1-30 (= NIBR BA 52) was isolated from riverside sediment of the Nakdong River, Gumi, Korea.

**Description of Pseudoalteromonas tunicata BES3-108**

Cells are gram-staining negative non-flagellated and rod-shaped. Colonies are circular, convex, smooth and ivory-colored after 3 days on R2A agar at 25°C. Positve for oxidase, nitrate reduction, glucose fermentation, esculin hydrolysis, gelatinase and β-galactosidase, but negative for indole production, arginine dihydrolase and urease. D-Glucose, D-mannose, N-acetylglucosamine and D-maltose are utilized. L-Arabinose, D-mannitol, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid are not utilized. The strain BES3-108 (= NIBR BA 49) was isolated from brackish marsh sediment of the Eulsuk-island at the end of the Nakdong River, Busan, Korea.

**Description of Thermomonas carbonis 04KS1-07**

Cells are gram-staining negative, non-flagellated, rod-shaped. Colonies are circular, convex, smooth and yellowish-white colored after 3 days on R2A agar at 30°C. Positive for oxidase, esculin hydrolysis, gelatinase and β-galactosidase, but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, and urease. D-Mannitol is utilized. Weakly utilize D-maltose. Does not utilize D-glucose, L-arabinose, D-mannose, N-acetylglucosamine, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. The strain 04KS1-07 (= NIBR BA 57) was isolated from freshwater sediment of the Geomryeongso (origin of Han River), Taebaek, Korea.

**Description of Arenimonas subflava CS4-45**

Cells are gram-staining-negative, non-flagellated, rod-shaped. Colonies are circular, convex, smooth, and yellowish-white colored after 3 days on R2A agar at 25°C. Positive for oxidase, and gelatinase, but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis and β-galactosidase. Does not utilize 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. The strain CS4-45 (= NIBR BA 68) was isolated from sediment of the Nakdong River, Changnyeong, Korea.

**Description of Pseudomonas avellanae KS1-13**

Cells are gram-staining-negative, non-flagellated, rod-shaped. Colonies are circular, glistening, mucoid and cream-colored after 3 days on R2A agar at 25°C. Positive for oxidase, nitrate reduction and arginine dihydrolase, weakly positive for esculin hydrolysis, but negative for, indole production, glucose fermentation, urease, gelatinase and β-galactosidase. D-Glucose, D-mannose, D-mannitol, N-acetylglucosamine, potassium gluconate, capric acid, malic acid and trisodium citrate are utilized. Does not utilize L-arabinose, D-maltose, adipic acid and phenylacetic acid. The strain KS1-13 (= NIBR BA 56) was isolated from sediment of the Eulsuk-island, Busan, Korea.

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