A report of 23 unrecorded bacterial species belonging to the class Alphaproteobacteria

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To study the biodiversity of bacterial species, here we report indigenous prokaryotic species of Korea. A total of 23 bacterial strains affiliated to the class Alphaproteobacteria were isolated from various environmental sources including seaweeds, seawater, fresh water, wetland/marsh, tidal sediment, plant roots, sewage and soil. Considering higher than 98.8% 16S rRNA gene sequence similarities and formation of a well-defined phylogenetic clade with named species, it was confirmed that each strain belonged to the predefined bacterial species of the class Alphaproteobacteria. There is no official report of these 23 species in Korea; 20 species of 16 genera (Mameliella, Yangia, Paracoccus, Ruegeria, Loktanella, Phaeobacter, Dinoroseobacter, Tropicimonas, Litimirabelacter, Litoreibacter, Sulfitobacter, Roseivivax, Labrenzia, Hyphomonas, Maricaulis, Thalassospira) in the order Rhodobacterales and 3 species of a single genus (Brevundimonas) in the order Caulobacterales. Gram-staining, cell morphology, basic biochemical characteristics, isolation sources, optimum temperature, growth media, and strain IDs are detailed in the species description as well as Table 1.

Keywords: 16S rRNA, Alphaproteobacteria, bacterial diversity, indigenous prokaryotic species in Korea, unrecorded species

INTRODUCTION

In 2016, many novel and unreported bacterial species were isolated from different environmental samples collected in Korea. Based on the 16S rRNA gene sequence analysis, the identified bacterial species belong to the class Alphaproteobacteria. Therefore, the aim of this study is to describe the unrecorded species belonging to the class Alphaproteobacteria.

In 1987, Carl Woese (Woese, 1987) suggested that based on nucleotide sequences similarity of the bacterial genome, a large and diverse group of bacteria which were called purple bacteria should be classifies as a separate phylum within domain Bacteria. Afterwards, this phylum was established under the name Proteobacteria. The phylum Proteobacteria includes many bacterial strains that are pathogens and part of the normal human microbiota, and can be further classified into five classes: 1. Alphaproteobacteria, 2. Betaproteobacteria, 3. Gammaproteobacteria, 4. Deltaproteobacteria, and 5. Epsilonproteobacteria.

Alphaproteobacteria is the first class of phylum Proteobacteria, with many important biological characteristics. Members of this class are oligotrophs and are able to live in low-nutrient environments such as sediments, deep under-surface, deep ocean, glacial ice and soil (Krom et al., 1991; Pitta et al., 2005; DeLong et al., 2006; Thompson et al., 2013). Affiliates of the class Alphaproteobacteria are gram-
stain-negative and some parasitic members lack peptidoglycan and are thus gram variable (Brenner et al., 2005; Euzéby, 2011). Furthermore, the class Alphaproteobacteria is divided into three subdivisions: Rickettsiidae, Magnetococcoidae, and Caulobacteridae (Ferla et al., 2013). Among these subclasses, the basal class/group Magneto- coccoidae consists of a large variety of magnetotactic bacteria, in which only [Magnetococcus marinus] is described by Bazylinski et al., 2012. As such, these subdivisions of Alphaproteobacteria are comprised of diverse group of bacteria that are plant and animal pathogens, plant mutualists, photosynthetic, and also several genera metabolizing C1-compounds (Methyllobacterium) (Williams et al., 2007). However, until now, no scientist has studied the molecular or biochemical characteristics that can differentiate these bacteria from other groups.

Similarly, changes in the metabolic strategies are found in the class Alphaproteobacteria, including ammonia oxidation, nitrogen fixation, photosynthesis and methylotrophic. Different morphologies (stellate, stalked, and spiral) are also found within the members of class Alphaproteobacteria. Therefore, some developmental programs switch between cell types, and are controlled by a web of regulatory systems (Viollier and Shapiro, 2004).

A special interest has been taken in the class Alphaproteobacteria as the ancestral group for mitochondria. The most often cited subgroup of Alphaproteobacteria is Rickettsiales, from which mitochondria are inferred to have arisen from, which there is disagreement on this point (Esser et al., 2004; Wu et al., 2004; Fitzpatrick et al., 2006). Moreover, genome sequencing has revealed a well-maintained molecular marker which is characteristics of either all Alphaproteobacteria or its main orders. This suggestion provides the assignment of new bacterial species into these groups, which conveys that Alphaproteobacteria has branched off later than most other classes, with the exception of Beta- and Gammaproteobacteria (Parle, 2014; Oren and Garrity, 2014).

In the current investigation, we briefly describe 23 unrecorded bacterial species in Korea in the class Alphaproteobacteria belonging to 4 families of 2 orders. This research program was conducted and supported by NIBR Korea.

**Materials and Methods**

A total of 23 bacterial strains belong to the class Alphaproteobacteria were isolated from different environmental sources collected from plant roots, soil, tidal sediment, sea sources (including water, weeds, grasses) and freshwater (Table 1). Each environmental sample was processed separately, spread onto diverse culture media including R2A and marine agar 2216, and incubated at 20, 25, 30 and 35°C for 1–5 days (Table 1). The designated strain IDs, sources, culture media, and incubation conditions are summarized in Table 1. All strains were purified as single colonies and stored both as 10–20% glycerol suspension at −80°C and as lyophilized ampoules.

The colony morphology was studied on agar plates until the cell grew up to their stationary phase. Cell size and shape were examined either by transmission electron microscopy or scanning electron microscopy. Gram staining was performed using a Gram-staining kit (bioMérieux) or standard procedures. The biochemical characteristics were performed using API 20NE (bioMérieux) according to the manufacturer’s instructions.

Bacterial DNA extraction, PCR amplification and 16S rRNA gene sequencing were performed using the standard procedures described elsewhere. The 16S rRNA gene sequences of the strains assigned to Alphaproteobacteria were compared with the sequences held in GenBank by BLASTN and also analyzed using the EzBioCloud (https://www.ezbiocloud.net) (Kim et al., 2017). For phylogenetic analyses, multiple alignments were performed using the Clustal_X program (Thompson et al., 1997), with gaps edited in the BioEdit program (Hall, 1999). Evolutionary distances were calculated using the Kimura two-parameter model (Kimura, 1983). Phylogenetic trees were constructed using the neighbor-joining (Saitou and Nei, 1987) and maximum-parsimony (Fitch, 1971) methods with the MEGA6 (Tamura et al., 2013) with bootstrap values based on 1,000 replications (Felsenstein, 1985).

**Results and Discussion**

The 23 strains were distributed in 2 orders of Alphaproteobacteria, 20 strains in the order Rhodobacterales and 3 strains in the order Caulobacterales (Table 1). These strains were Gram-staining-negative, chemoheterotrophic, coccoid, rod and short-rod shaped bacteria, except for strain CSC-1 (23) (Fig. 1).

The strains in the order Rhodobacterales (Fig. 2) belong to 3 families and 16 genera: Mameliella (1 species), Yangia (1 species), Paracoccus (2 species), Tropicimonas (1 species), Lukimaribacter (1 species), Litoreibacter (1 species), Sulfitobacter (1 species), Roseivivax (1 species), Hyphomonas (1 species), and Thalassospira (2 species) (Fig. 2, Table 1).

Figure 3 shows phylogenetic assignment of 10 strains of the order Rhodobacterales and 3 strains belong to Bre- vundimonas of the family Caulobacteraceae.

Here we report 23 unrecorded bacterial species in Korea belonging to 4 families of 2 orders in the Alphaproteobacteria.
Table 1. The taxonomic affiliations of isolated strains belonging to the class Alphaproteobacteria.

<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 conditions</th>
</tr>
</thead>
<tbody>
<tr>
<td>Caulobacterales Caulobacteraceae</td>
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<td>Brevundimonas</td>
<td>YHD2</td>
<td>NIBRBAC00498430</td>
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<td>R2A</td>
<td>30°C, 3d</td>
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<td>T4-2</td>
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<td>ZOD2-5</td>
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<td>NIBRBAC00498470</td>
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<td>99.6</td>
<td>Fresh water</td>
<td>MA</td>
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</tr>
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</table>
Description of *Mameliella phaeodactyli* FIL 61

Cells are Gram-staining-negative, non-flagellated, diffusible pigmented and short rod. Colonies are circular, convex and ivory colored after 2 days of incubation on MA at 30°C. Positive for nitrate reduction, urease and esculin hydrolysis in API 20NE; but negative for gelatinase, β-galactosidase, indole production, glucose fermentation and arginine dihydrolase. Utilizes D-glucose, L-arabinose, D-mannose, D-mannitol, N-acetyl-glucosamine, D-maltose, potassium gluconate and malic acid. Does not utilize capric acid, adipic acid, trisodium citrate and phenylacetic acid. Strain FIL 61 (= NIBRBA000498407) was isolated from tidal water, Chungcheongnam-do, Korea.

Description of *Yangia pacifica* T4-2

Cells are Gram-staining-negative, non-flagellated, non-pigmented and rod-shaped. Colonies are circular, raised, entire and pale-yellow colored after 2 days of incubation on MA at 30°C. Positive for hydrolysis of esculin, gelatin, glucose fermentation, and β-galactosidase; and negative for nitrate reduction, arginine dihydrolase, urease and indole production. Utilizes D-glucose, L-arabinose, D-mannose, D-mannitol, D-maltose, N-acetyl-glucosamine, trisodium citrate and malic acid; but does not utilize capric acid, adipic acid, phenylacetic acid and potassium gluconate. Strain T4-2 (= NIBRBA000498427) was isolated from seashore sand, Chungcheongnam-do, Korea.
Description of *Paracoccus aminovorans* YH6C

Cells are Gram-staining-negative, non-flagellated, non-pigmented and coccoid-rod shaped. Colonies are punctiform, smooth and red orange colored after 3 days of incubation on R2A agar medium at 30°C. In API 20NE, positive for nitrate reduction, glucose fermentation, arginine dihydrolase, esculin hydrolysis, gelatinase and β-galactosidase; but negative for urease and indole production. Utilizes D-glucose, L-arabinose, D-mannose, D-mannitol, N-acetyl-glucosamine, D-maltose, potassium gluconate, malic acid, trisodium citrate and phenylacetic acid. Does not utilize capric acid and adipic acid. Strain YH6C (=NIBRBAC000498429) was isolated from sewage treatment plant, Busan, Korea.

Description of *Brevundimonas bullata* YHD2

Cells are Gram-reaction-negative, non-flagellated, non-pigmented and rod-shaped. Colonies grown on R2A agar plates are ivory, circular, raised and entire after 3 days of incubation at 30°C. In API 20NE, positive for nitrate...
reduction and urease; but negative for gelatinase, esculin hydrolysis, glucose fermentation, \( \beta \)-galactosidase, indole production and arginine dihydrolase. Does not utilize D-glucose, D-mannitol, \( N \)-acetyl-glucosamine, capric acid, malic acid, adipic acid, L-arabinose, D-maltose and trisodium citrate. Utilizes potassium gluconate and phenylacetic acid. Strain YDH2 (\( =\) NIBRBC000498430) was isolated from sewage treatment plant, Busan, Korea.

Description of *Brevundimonas variabilis* HMF4573

Cells are Gram-staining-negative, non-spore-forming, flagellated and non-pigmented rods. Colonies are circular, raised, entire and orange colored on R2A agar medium after 3 days of incubation at 25°C. In API 20NE, positive for esculin and \( \beta \)-galactosidase; but negative for nitrate reduction, urease, gelatinase, arginine dihydrolase, indole production and glucose fermentation. Utilize D-glucose, D-maltose, capric acid, adipic acid, malic acid and phenylacetic acid. Utilizes L-arabinose, D-mannose, \( N \)-acetyl-glucosamine, D-Mannitol, trisodium citrate and potassium gluconate. Strain HMF4573 (\( =\) NIBRBC000498442) was isolated from wetland/marsh, Yongin, Korea.

Description of *Brevundimonas staleyi* HMF4667

Cells are Gram-staining-negative, non-spore-forming,
flagellated, pigmented and rod-shaped. Colonies are circular, convex, entire and yellow colored after 3 days of incubation on R2A agar medium at 25°C. In API 20NE, positive for esculin hydrolysis; but negative for nitrate reduction, urease, indole production, glucose fermentation, arginine dihydrolase, gelatinase and β-galactosidase. Does not utilize L-arabinose, capric acid, trisodium citrate, potassium gluconate, D-mannose and N-acetyl-glucosamine but D-glucose, D-maltose, adipic acid, D-mannitol and phenyl-acetic acid are utilized. Strain HMF4667 (=NIBRBAC000498446) was isolated from wetland/marsh, Yongin, Korea.

**Description of *Maricaulis maris* HMF6043**

Cells are Gram-staining-negative, flagellated and rod or fusiform-shaped. Colonies are circular, drop-like, entire and beige colored after 3 days of incubation on MA medium at 25°C. Negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease and β-galactosidase; but positive for esculin hydrolysis and gelatinase. Does not utilize D-glucose, L-arabinose, D-mannose, citric acid, N-acetyl-glucosamine, D-maltose, malic acid and trisodium citrate, D-mannitol, potassium gluconate, capric acid, adipic acid and phenyl-acetic acid. **Strain HMF6043 (=NIBRBAC000498449)** was isolated from seaweed, Boseong-gun, Jeollanam-do, Korea.

**Description of *Labrenzia alba* SFD13**

Cells are Gram-staining-negative, non-flagellated, pigmented and rod-shaped. Colonies are opaque, circular, smooth, convex and pinkish-beige colored after 5 days of incubation on R2A at 25°C. In API 20NE positive for arginine dihydrolase; weakly positive for esculin hydrolysis; and negative for nitrate reduction, urease, indole production, glucose fermentation, gelatinase, β-galactosidase, D-glucose, L-arabinose, D-maltose, D-mannitol, D-mannose, potassium gluconate, malic acid, trisodium citrate, N-acetyl-glucosamine, capric acid, adipic acid and phenylacetic acid. **Strain SFD13 (=NIBRBAC000498470)** was isolated from a gulfweed sample, Jeju Island, Korea.

**Description of *Ruegeria atlantica* SF30**

Cells are Gram-staining-negative, non-flagellated, non-pigmented and rod-shaped. Colonies are circular and beige colored after 3 days on MA at 25°C. Positive for nitrate reduction, esculin hydrolysis and β-galactosidase in API 20NE. Negative for indole production, arginine dihydrolase, urease, gelatinase and glucose fermentation. Potassium gluconate and malic acid are utilized. Does not utilize L-arabinose N-acetyl-glucosamine, citrate, capric acid, adipic acid, malic acid, D-glucose, D-mannose, D-maltose, D-mannitol, trisodium citrate and phenylacetic acid. **Strain SF30 (=NIBRBAC000498476)** was isolated from a gulfweed sample, Jeju Island, Korea.

**Description of *Loktanella rosea* ZOD2-5**

Cells are Gram-staining-negative, non-flagellated, non-pigmented and rod-shaped. Colonies are pink colored, opaque, circular, entire, convex, and smooth after 3 days of incubation on MA at 25°C. Positive for esculin hydrolysis and β-galactosidase in API 20NE; but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease and gelatinase. Does not utilize D-mannitol, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate D-glucose, L-arabinose, D-mannose, N-acetyl-glucosamine, D-maltose and phenylacetic acid. **Strain ZOD2-5 (=NIBRBAC000498479)** was isolated from seagrass, Seosan, Chungnam, Korea.

**Description of *Phaeobacter inhibens* EC2**

Cells are Gram-staining-negative, non-flagellated, non-pigmented, and rod-shaped. Colonies are opaque, circular, smooth, convex and brown colored after 3 days of incubation on MA medium at 25°C. Positive for esculin hydrolysis; but negative for nitrate reduction, indole production, urease, glucose fermentation, arginine dihydrolase, gelatinase and β-galactosidase. Does not utilize D-glucose, capric acid, N-acetyl-glucosamine, L-arabinose, D-mannose, D-mannitol, D-maltose, D-maltose, potassium gluconate, trisodium citrate, adipic acid and phenyl acetic acid. **Strain EC2 (=NIBRBAC000498481)** was isolated from seaweed Jeonnam, Yeosu, Korea.

**Description of *Dinoroseobacter shibae* GLB36**

Cells are Gram-staining-negative, non-flagellated, non-pigmented and rod-shaped. Colonies are opaque, circular, smooth, convex and wine-red colored after 5 days of incubation on MA at 25°C. In API 20NE, positive for nitrate reduction, esculin hydrolysis, β-galactosidase, D-glucose and D-mannose. Negative for glucose fermentation, arginine dihydrolase, urease, gelatinase, indole production, L-arabinose, D-mannitol, N-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. **Strain GLB36 (=NIBRBAC000498483)** was isolated from a grilled scallop sample, Sokcho, Gangwon-do, Korea.

**Description of *Labrenzia aggregata* EC2D15**

Cells are Gram-staining-negative, non-flagellated, non-pigmented and rod-shaped. Colonies are opaque, circular, smooth, flat, and beige colored after 3 days on MA at 25°C. In API 20NE, positive for nitrate reduction, esculin hydrolysis and β-galactosidase; but negative for indole produc
production, arginine dihydrolase, urease, glucose fermentation and gelatinase. Does not utilize D-glucose, D-mannose, L-arabinose and N-acetyl-glucosamine. D-Mannitol, potassium gluconate, capric acid, malic acid, trisodium citrate, D-maltose, adipic acid and phenylactic acid are utilized. Strain EC2D15 (=NIBRBAC000498485) was isolated from a seaweed (Gamuta) sample, Jeonnam, Yeosu, Korea.

Description of Tropicimonas sediminicola CAU 1140

Cells are Gram-staining-negative, non-flagellated, non-pigmented and rod-shaped. Colonies are circular, convex and cream colored after 3 days of incubation on MA at 30°C. In API 20NE, positive for nitrate reduction, esculin hydrolysis, urease and β-galactosidase; but negative for arginine dihydrolase, gelatinase, glucose fermentation and indole production. Utilizes L-arabinose, D-maltose and D-mannitol. Does not utilize D-glucose, D-mannose, malic acid, trisodium citrate, N-acetyl-glucosamine, potassium gluconate, capric acid, adipic acid and phenylactic acid. Strain CAU 1140 (= NIBRBAC000498503) was isolated from reclaimed soil, Incheon, Korea.

Description of Lutimaribacter saemankumensis CAU 1340

Cells are Gram-staining-negative, non-flagellated and non-pigmented rods. Colonies grown on MA agar medium are circular, raised, entire and cream colored after 3 days at 35°C. In API 20NE, negative for β-galactosidase, esculin, indole production, glucose fermentation, arginine dihydrolase, urease and gelatinase; but positive for nitrate reduction. Utilizes D-glucose, potassium gluconate and adipic acid. Does not utilize D-mannose, D-mannitol, N-acetyl-glucosamine, capric acid, phenylactic acid, trisodium citrate, D-maltose and malic acid. Strain CAU 1340 (= NIBR BAC000498508) was isolated from a sea soil sample, Incheon, Korea.

Description of Litoreibacter albidus LPB0157

Cells are Gram-staining-negative, non-flagellated and long rods. Colonies are circular, convex, entire and beige colored after 1 day of incubation on MA at 25°C. In API 20NE, only positive for nitrate reduction; but negative for esculin hydrolysis, β-galactosidase, indole production, gelatinase, glucose fermentation, arginine dihydrolase, urease, L-arabinose, D-mannose, D-mannitol, N-acetyl-glucosamine, potassium gluconate, capric acid, trisodium citrate, phenylactic acid, D-glucose, adipic acid, D-maltose and malic acid. Strain LPB0157 (= NIBRBAC000498528) was isolated from seashore sand, Jebu Island, Korea.

Description of Sulfitobacter mediterraneus LPB0162

Cells are Gram-staining-negative, flagellated and rod-shaped. Colonies are circular, convex, entire and beige colored after 1 day of incubation on MA at 25°C. Positive for nitrate reduction and arginine dihydrolase in API 20NE. Negative for esculin hydrolysis, indole production, β-galactosidase, glucose fermentation, urease and gelatinase. Does not utilize L-arabinose, D-mannitol, potassium gluconate, capric acid, adipic acid, trisodium citrate, phenylactic acid, D-glucose, D-mannose, N-acetyl-glucosamine, D-maltose and malic acid. Strain LBP0162 (= NIBRBAC000498532) was isolated from seashore sand, Jebu Island, Korea.

Description of Thalassospira profundimaris IMCC25636

Cells are Gram-staining-negative, non-flagellated and rod-shaped. Colonies are circular, convex, entire and white colored after 3 days on MA at 20°C. In API 20NE, negative for all kind of substrates such as arginine dihydrolase, urease, esculin hydrolysis, nitrate reduction, indole production, glucose fermentation, gelatinase, β-galactosidase, L-arabinose, D-mannose, D-mannitol, N-acetyl-glucosamine, potassium gluconate, capric acid, trisodium citrate, malic acid, phenylactic acid, D-glucose, D-maltose and adipic acid. Strain IMCC25636 (= NIBRBAC000498553) was isolated from plant roots, Incheon, Korea.

Description of Hyphomonas jannaschiana IMCC25644

Cells are Gram-staining-negative, non-flagellated and rod-shaped. Colonies are circular, convex, entire and white colored after 3 days of incubation on MA at 20°C. Strain IMCC25644 is negative for nitrate reduction, β-galactosidase, glucose fermentation, arginine dihydrolase, esculin hydrolysis, indole production, urease, gelatinase, D-mannose, D-mannitol, N-acetyl-glucosamine, D-maltose, potassium gluconate, malic acid, trisodium citrate, phenylactic acid, capric acid, adipic acid, D-glucose and L-arabinose in API 20NE. Strain IMCC25644 (= NIBRBAC000498543) was isolated from plant roots, Incheon, Korea.

Description of Roseivivax pacificus IMCC25645

Cells are Gram-staining-negative, non-flagellated, diffusible pigmented and rod-shaped. Colonies are circular, convex, entire and white colored after 3 days on MA at 20°C. In API 20NE, negative for nitrate reduction, indole production, gelatinase, urease and β-galactosidase; but positive for esculin hydrolysis, arginine dihydrolase and glucose fermentation. D-Glucose, L-arabinose, D-mannose, D-mannitol, N-acetyl-glucosamine, D-maltose, pa-
positive for nitrate reduction and urease; but negative for glucose fermentation, arginine dihydrolase, urease, β-galactosidase, indole production and gelatinase but positive for nitrate reduction and esculin hydrolysis in API 20NE. Does not utilize D-glucose, L-arabinose, D-mannose, D-maltose, malic acid, L-arabinose, D-mannose, adipic acid and malic acid, D-mannitol, N-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, trisodium citrate and phenylacetic acid. Strain IMCC25646 (= NIBRBA001948545) was isolated from fresh water, Incheon, Korea.

**Description of Thalassospira tepidiphila IMCC25646**

Cells are Gram-staining-negative, non-flagellated and rod-shaped. Colonies grown on MA agar medium are circular, convex, entire and white colored after 3 days of incubation at 20°C. Negative for esculin hydrolysis, arginine dihydrolase, urease, β-galactosidase, indole production and gelatinase but positive for nitrate reduction and esculin hydrolysis in API 20NE. Does not utilize D-glucose, L-arabinose, D-mannose, D-maltose, malic acid, L-arabinose, D-mannose, potassium gluconate, capric acid, trisodium citrate and phenylacetic acid. Strain IMCC25646 (= NIBRBA001948545) was isolated from fresh water, Incheon, Korea.

**Description of Paracoccus seriniphilus JHR-13**

Cells are Gram-staining-negative, non-flagellated and rod or oval-shaped. Colonies are punctiform, convex, entire and white colored after 3 days of incubation on R2A at 25°C. Positive for nitrate reduction, glucose fermentation and β-galactosidase; but negative for esculin hydrolysis, arginine dihydrolase, urease, indole production and gelatinase. Does not utilize D-glucose, L-arabinose, D-mannitol, N-acetyl-glucosamine, D-maltose and potassium gluconate. D-Mannose, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid are utilized. Strain JHR-13 (= NIBRBA001948633) was isolated from seawater, Jeju Island, Korea.

**Description of Paracoccus yeei CSC-1**

Cells are Gram-staining-positive, non-flagellated and circular-shaped. Colonies are irregular and beige colored after 3 days of incubation on R2A at 25°C. In API 20NE, positive for nitrate reduction and urease; but negative for indole production, glucose fermentation, β-galactosidase, arginine dihydrolase, gelatinase, and esculin hydrolysis. Does not utilize capric acid and phenylacetic acid but D-glucose, D-maltose, malic acid, L-arabinose, D-mannose, D-mannitol, N-acetyl-glucosamine, potassium gluconate, adipic acid and trisodium citrate are utilized. Strain CSC-1 (= NIBRBA00498638) was isolated from freshwater, Jeonju, Jeollabuk-do, Korea.

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**References**


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