A report of 30 unrecorded bacterial species in Korea, isolated from marine ecosystems in 2021

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To obtain unrecorded bacterial species in Korea, various marine samples were collected from Jeollanam-do Province, Korea in 2021. After plating the samples on marine agar and marine R2A agar, and incubating aerobically and anaerobically, approximately 1200 bacterial strains were isolated and identified using 16S rRNA gene sequences. A total of 30 strains showed ≥98.7% 16S rRNA gene sequence similarity with validly published bacterial species but not reported in Korea, indicating that they are unrecorded bacterial species in Korea. The unrecorded bacterial strains belonged to 4 phyla, 7 classes, 13 orders, 19 families, and 22 genera, which were assigned to Azospirillum, Loktanella, and Pseudovibrio of the class Alphaproteobacteria; Grimontia, Halomonas, Marinobacter, Microbulbifer, Photobacterium, Pseudoalteromonas, Pseudidiomarina, Ferrimonas, Shewanella, Simiduia, Thalassotalea, and Vibrio of the class Gammaproteobacteria; Priestia and Enterococcus of the class Bacilli; Persicobacter of the class Cytophagia; Aureivirga of the class Flavobacteria; Propionigenium and Psychrilyobacter of the class Fusobacteria; and Tepidibacter of the class Clostridia. The details of the unreported species including Gram reaction, colony and cell morphology, biochemical characteristics, and phylogenetic position are also provided in the description of the strains.

Keywords: 16S rRNA, anaerobic bacteria, islands, seawater, tidal-flat sediment, unrecorded bacterial species

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as new records for bacterial species in Korea, for which taxonomic information and phenotypic characteristics are reported.

**Materials and Methods**

Various marine samples were collected from seawater, tidal flat, and shrimp farms in 2021 and more explained in Island Bioresource total Information System (IBIS; https://ibis.hnibr.re.kr). Using a spread plating technique on agar media, an aliquot (100 μL) of the seawater samples was directly spread onto Marine agar (BD Diagnostics) and aerobically incubated at 20°C for 7 days. Bacterial strains were purified as single colonies and the pure cultures were preserved at −80°C in 20% (v/v) glycerol suspension, as well as lyophilized ampoules. On the other hand, the tidal flat samples were collected using a 30 cm long and 2 cm diameter stainless-steel soil sampler and sub-samples taken at 15 cm depth were immediately transported to the laboratory in an anaerobic jar (Mitsubishi Gas Chemical). After transporting to the laboratory, the samples were placed in a vinyl anaerobic chamber (Coy Laboratory Products) filled with N2 : H2 : CO2 (90 : 5 : 5). Using a homogenizer (IKA), 1 g of the sub-sample was thoroughly mixed with 100 mL of sterile seawater. An aliquot (100 μL) of the homogenized sample was spread onto R2A agar in aged seawater (marine R2A) and anaerobically incubated in an anaerobic jar at 20°C for 7 days. Details on the strains are shown in Table 1.

For the determination of colony morphology, bacterial colonies were observed after reaching the stationary phase on agar plates. Cellular morphology, including cell shape, presence of flagella, and cell size, was examined by transmission electron microscopy (CM200; Philips) after staining with 2% (w/v) uranyl acetate, and a scanning electron microscope (S-4800; Hitachi). Gram staining was performed using a Gram-staining kit (bioMérieux). Catalase and oxidase activities were examined using 3% hydrogen peroxide and oxidase reagent (bioMérieux), respectively. API 20NE galleries (bioMérieux) were employed for additional biochemical characterization. In API 20NE, the strains were tested according to the manufacturer’s instructions except 2% NaCl API AUX medium and 1% L-cysteine added therein for anaerobic cultivation.

For the determination of phylogenetic position of the strains isolated herein, bacterial DNA extraction, PCR amplification, and 16S rRNA gene sequencing were performed using the standard procedures as previously described (Yang and Cho, 2008). The 16s rRNA gene sequences were obtained using the primers 518F and 800R. The resultant 16S rRNA gene sequences were initially compared with those of other bacterial strains with validly published names using the EzBioCloud (Yoon et al., 2017) and the NIBR database. A sequence similarity of 98.7% was used as the cut-off value for bacterial species demarcation (Chun et al., 2018). Therefore, the bacterial strains exhibiting ≥98.7% 16S rRNA gene sequence similarities with validly published species, but never reported in Korea were determined as unreported bacterial species. For determining phylogenetic position, multiple sequence alignments between the 16S rRNA gene sequences of 30 strains and those of the unreported species were performed using ClustalW, which was implemented in MEGA X (Kumar et al., 2018). Using the unambiguously aligned 16S rRNA gene sequences, phylogenetic trees based on the neighbor-joining method were reconstructed. The robustness of the inferred phylogenetic trees was evaluated by bootstrap analyses based on 1000 random re-samplings (Felsenstein, 1985).

**Results and Discussion**

The 16S rRNA gene sequence analyses using approximately 1200 bacterial strains obtained herein revealed that many strains belonged to novel species or previously unreported species in Korea. Of these, a total of 30 strains showed ≥98.7% 16S rRNA gene sequence similarities with unrecorded bacterial species in Korea. The strain information, identification, taxonomic assignment from species to classes, isolation source and sequence accession numbers including the HNIBR and GenBank are listed in Table 1. Phylogenetic assignment of the strains to established bacterial species based on 16S rRNA gene sequence similarity was confirmed by the phylogenetic tree analysis (Figs. 1 and 2). All strains identified as unrecorded species formed a robust clade with the type strains of each corresponding species with high bootstrap values. The 30 unrecorded bacterial species were phylogenetically diverse, belonging to 4 phyla, 7 classes, 13 orders, 19 families, and 22 genera (Table 1). At the generic level, the unreported species were assigned to Azospirillum, Loktanella, and Pseudovibrio of the class Alphaproteobacteria; Grimontia, Halomonas, Marinobacter, Microbulbifer, Photobacterium, Pseudalteromonas, Pseudomonas, Ferrimonas, Shewanella, Simidvia, Thalasasotaea, and Vibrio of the class Gammaproteobacteria; Priestia and Enterococcus of the class Bacilli; Pseuobacter of the class Cytophaga; Aureivirga of the class Flavobacteria; Propionigenium and Psychrilyobacter of the class Fusobacteria; and Tepidibacter of the class Clostridia.

The 30 unrecorded bacterial species identified in this study were Gram-staining-negative or positive, flagellated or non-flagellated, short- or straight-rod or coccolid-shaped bacteria (Fig. 3). Detailed morphological, physiological, and biochemical characteristics of the un-
Table 1. Summary of strains isolated and their taxonomic affiliations.

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<tr>
<th>Class</th>
<th>Order</th>
<th>Family</th>
<th>Strain ID</th>
<th>Accession number</th>
<th>Closest species</th>
<th>Similarity (%)</th>
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Fig. 1. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences showing the relationship between the strains isolated in this study and their closest bacterial species in the class Gammaproteobacteria. Bootstrap values over 70% are shown.
recorded bacterial species are elucidated in the following strain descriptions.

**Description of Priestia taiwanensis GHH55**

Cells are Gram-stain-positive, flagellated, and rod-shaped. Colonies are circular, flat, smooth, and cream yellow-colored after incubation for 3 days on MA at 20°C. Positive for esculin hydrolysis and cytochrome oxidase; but negative for nitrates reduction, indole production, glucose fermentation, arginine hydrolysis, and \(\beta\)-galactosidase in API 20NE. L-arabinose, D-mannose, D-mannitol, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid are not utilized as a sole carbon source. Strain GHH55 (=HNIBRBA38) was isolated from seawater collected off Goha-do (34°45'55"N, 126°22'23"E), Mokpo, Jeollanam-do, Korea. The GenBank accession number of the 16S rRNA gene sequence of strain GHH55 is OL742661.

**Description of Pseudoalteromonas amylolytica GHH101**

Cells are Gram-stain-negative, flagellated, and rod-shaped. Colonies are circular, convex, smooth, and brown-colored after incubation for 3 days on MA at 20°C. Positive for urease, gelatin hydrolysis, and cytochrome oxidase; but negative for nitrates reduction, indole production, glucose fermentation, arginine dihydrolase, esculin hydrolysis, and \(\beta\)-galactosidase in API 20NE. 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 as a sole carbon source. Strain GHH101 (=HNIBRBA54) was isolated from seawater collected off Goha-do (34°45'55"N, 126°22'23"E), Mokpo, Jeollanam-do, Korea. The GenBank accession num-

![Fig. 2. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences showing the relationship between the strains isolated in this study and their closest bacterial species in classes Alphaproteobacteria, Bacilli, Cytophagia, Flavobacteriia, Fusobacteriia, and Clostridia. Bootstrap values over 70% are shown.](image-url)
The 16S rRNA gene sequence of strain GHH101 is OL742662.

**Description of *Persicobacter psychrovividus* HN9**

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies are circular, convex, entire, and orange-colored after incubation for 3 days on MA at 20°C. Positive for urease, esculin hydrolysis, β-galactosidase, and cytochrome oxidase; but negative for nitrates reduction, indole production, glucose fermentation, arginine dihydrodrolase, and gelatin hydrolysis in API 20NE. **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 as a sole carbon source. Strain HN9 (= HNIBRBA100) was isolated from seawater collected off Songho (34°18'55"N, 126°31'07"E), Haenam, Jeollanam-do, Korea. The GenBank accession number of the 16S rRNA gene sequence of strain HN9 is OL742663.

**Description of *Vibrio furnissii* GHR53**

Cells are Gram-stain-negative, flagellated, and rod-shaped. Colonies are circular, convex, entire, and yellow-colored after incubation for 3 days on MA at 20°C. Positive for nitrates reduction, indole production, glucose fermentation, arginine dihydrolase, gelatin hydrolysis, **adipic acid**, **malic acid**, **trisodium citrate**, and **phenylacetic acid** are not utilized as a sole carbon source. Strain HN9 (= HNIBRBA100) was isolated from seawater collected off Songho (34°18'55"N, 126°31'07"E), Haenam, Jeollanam-do, Korea. The GenBank accession number of the 16S rRNA gene sequence of strain HN9 is OL742663.
\( \beta \)-galactosidase, and cytochrome oxidase; but negative for urease and esculin hydrolysis in API 20NE. \( \beta \)-Glucose, \( \beta \)-arabinose, \( \beta \)-mannose, \( \beta \)-mannitol, \( \beta \)-acetyl-glucosamine, \( \beta \)-maltose, potassium gluconate, capric acid, malic acid, and trisodium citrate are utilized as a sole carbon source; but not \( \beta \)-acetyl-glucosamine and phenylacetic acid. Strain JNT22 is not utilized as a sole carbon source; but not \( \beta \)-glucose, \( \beta \)-arabinose, \( \beta \)-mannose, potassium gluconate, capric acid, adipic acid, trisodium citrate, and phenylacetic acid. Strain JNT22 (= HNIBRBA189) was isolated from tidal flat in Amatae-do (34°51'44"N, 126°08'06"E), Shinan, Jeollanam-do, Korea. The GenBank accession number of the 16S rRNA gene sequence of strain JNT22 is OL742668.

Description of Vibrio vulnificus ND14

Cells are Gram-stain-negative, flagellated, and rod-shaped. Cells are irregular, convex, entire, and yellow-colored after incubation for 3 days on MA at 20°C. Positive for nitrates reduction, indole production, glucose fermentation, arginine dihydrolase, urease, and esculin hydrolysis in API 20NE. \( \beta \)-Glucose, \( \beta \)-arabinose, \( \beta \)-mannose, \( \beta \)-mannitol, \( \beta \)-acetyl-glucosamine, \( \beta \)-maltose, potassium gluconate, capric acid, adipic acid, malic acid, and trisodium citrate are utilized as a sole carbon source; but not \( \beta \)-glucose, \( \beta \)-arabinose, \( \beta \)-mannose, potassium gluconate, capric acid, adipic acid, trisodium citrate, and phenylacetic acid. Strain ND14 (= HNIBRBA220) was isolated from seawater collected off Nokdong (34°31'56"N, 127°07'18"E), Goheung, Jeollanam-do, Korea. The GenBank accession number of the 16S rRNA gene sequence of strain ND14 is OL742666.

Description of Vibrio mexicanus ND47

Cells are Gram-stain-negative, flagellated, and rod-shaped. Cells are circular, convex, entire, and yellow-colored after incubation for 3 days on MA at 20°C. Positive for nitrates reduction, indole production, glucose fermentation, esculin hydrolysis, \( \beta \)-galactosidase, and cytochrome oxidase; but negative for arginine dihydrolase, urease, and gelatin hydrolysis in API 20NE. \( \beta \)-Mannitol, \( \beta \)-acetyl-glucosamine, \( \beta \)-maltose and malic acid are utilized as a sole carbon source; but not \( \beta \)-glucose, \( \beta \)-arabinose, \( \beta \)-mannose, potassium gluconate, capric acid, adipic acid, trisodium citrate, and phenylacetic acid. Strain ND47 (= HNIBRBA244) was isolated from seawater collected off Nokdong (34°31'56"N, 127°07'18"E), Goheung, Jeollanam-do, Korea. The GenBank accession number of the 16S rRNA gene sequence of strain ND47 is OL742667.

Description of Vibrio nigripulchritudo JNT22

Cells are Gram-stain-negative, flagellated, and rod-shaped. Cells are circular, convex, entire, and black-colored after incubation for 3 days on MA at 20°C. Positive for glucose fermentation, gelatin hydrolysis, \( \beta \)-galactosidase, and cytochrome oxidase; but negative for nitrates reduction, indole production, arginine dihydrolase, and esculin hydrolysis in API 20NE. \( \beta \)-Mannose, \( \beta \)-maltose and malic acid are utilized as a sole carbon source; but not \( \beta \)-glucose, \( \beta \)-arabinose, \( \beta \)-mannitol, \( \beta \)-acetyl-glucosamine, \( \beta \)-maltose, potassium gluconate, capric acid, adipic acid, trisodium citrate and phenylacetic acid. Strain JNT22 (= HNIBRBA255) was isolated from aquaculture water collected from a shrimp farm (34°32'11"N, 126°20'41"E), Jindo, Jeollanam-do, Korea. The GenBank accession number of the 16S rRNA gene sequence of strain JNT22 is OL742668.

Description of Pseudidiomarina aquimaris JNT52

Cells are Gram-stain-negative, flagellated, and rod-shaped. Cells are circular, convex, entire, and yellow-colored after incubation for 3 days on MA at 20°C. Positive for nitrates reduction, arginine dihydrolase, urease, esculin hydrolysis, and cytochrome oxidase; but negative for indole production glucose fermentation, gelatin hydrolysis, and \( \beta \)-galactosidase in API 20NE. \( \beta \)-Glucose, \( \beta \)-arabinose, \( \beta \)-mannose, \( \beta \)-mannitol, \( \beta \)-acetyl-glucosamine, malic acid, and trisodium citrate are utilized as a sole carbon source; but not \( \beta \)-glucose, \( \beta \)-arabinose, \( \beta \)-mannose, \( \beta \)-acetyl-glucosamine, \( \beta \)-maltose, potassium gluconate, capric acid, adipic acid, trisodium citrate and phenylacetic acid. Strain JNT52 (= HNIBRBA270) was isolated from aquaculture water collected from a shrimp farm (34°32'11"N, 126°20'41"E), Jindo, Jeollanam-do, Korea. The GenBank accession number of the 16S rRNA gene sequence of strain JNT52 is OL742669.

Description of Azospirillum massiliensis GHA1

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Cells are circular, convex, entire, and yellow-colored after incubation for 3 days on R2A at 20°C. Positive for nitrates reduction, arginine dihydrolase, urease, esculin hydrolysis, and cytochrome oxidase; but negative for inducible glucose fermentation, gelatin hydrolysis, and \( \beta \)-galactosidase in API 20NE. \( \beta \)-Glucose, \( \beta \)-arabinose, \( \beta \)-mannose, \( \beta \)-mannitol, \( \beta \)-acetyl-glucosamine, \( \beta \)-maltose, potassium gluconate, capric acid, adipic acid, trisodium citrate, and phenylacetic acid. Strain JNT52 (= HNIBRBA255) was isolated from aquaculture water collected from a shrimp farm (34°32'11"N, 126°20'41"E), Jindo, Jeollanam-do, Korea. The GenBank accession number of the 16S rRNA gene sequence of strain JNT52 is OL742668.
ase, esculin hydrolysis, gelatin hydrolysis, β-galactosidase, and cytotoxic oxidase; but negative for indole production and glucose fermentation in API 20NE. d-Glucose, d-mannose, N-acetyl-glucosamine, d-maltose, and malic acid are utilized as a sole carbon source; but not D-arabinose, potassium gluconate, capric acid, adipic acid, trisodium citrate, and phenylacetic acid. Strain GHA1 (= HNIBRBA272) was isolated from aquaculture water collected from a shrimp farm (34°41'00"N, 126°02'18"E), Shinan, Jeollanam-do, Korea. The GenBank accession number of the 16S rRNA gene sequence of strain GHA1 is OL742670.

**Description of Enterococcus sulfuresus GHA5**

Cells are Gram-stain-positive, non-flagellated, and cocci-shaped. Colonies are circular, convex, entire, and yellow-colored after incubation for 3 days on R2A at 20°C. Positive for glucose fermentation, esculin hydrolysis, gelatin hydrolysis, and β-galactosidase; but negative for nitrates reduction, indole production, arginine dihydrolase, urease, and cytochrome oxidase in API 20NE. d-Glucose are utilized as a sole carbon source; but not D-arabinose, D-mannose, D-mannitol, N-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain GHA5 (= HNIBRBA274) was isolated from aquaculture water collected from a shrimp farm (34°41'29"N, 126°22'21"E), Haenam, Jeollanam-do, Korea. The GenBank accession number of the 16S rRNA gene sequence of strain GHA5 is OL742671.

**Description of Thalassotalea marina JDF44**

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies are circular, convex, smooth, and yellow-colored after incubation for 3 days on MA at 20°C. Positive for esculin hydrolysis, β-galactosidase, and cytochrome oxidase; but negative for nitrates reduction, indole production, glucose fermentation, arginine dihydrolase, urease, and gelatin hydrolysis in API 20NE. 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 as a sole carbon source. Strain JDF44 (= HNIBRBA350) was isolated from aquaculture water collected from a shrimp farm (34°32'08"N, 126°20'43"E), Jindo, Jeollanam-do, Korea. The GenBank accession number of the 16S rRNA gene sequence of strain JDF44 is OL742672.

**Description of Simiduia agrarivorans BK30**

Cells are Gram-stain-negative, non-flagellated, and cocci-shaped. Colonies are circular, convex, entire, and yellow-colored after incubation for 3 days on MA at 20°C. Positive for nitrates reduction, gelatin hydrolysis, and cytochrome oxidase; but negative for indole production, glucose fermentation, arginine, urease, esculin hydrolysis, and β-galactosidase in API 20NE. d-Maltose are utilized as a sole carbon source; but not D-glucose, L-arabinose, D-mannose, D-mannitol, N-acetyl-glucosamine, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain BK30 (= HNIBRBA370) was isolated from the seawater collected off Jaeun-do (34°55'8.59"N, 126°03'37.26"E), Shinan, Jeollanam-do, Korea. The GenBank accession number of the 16S rRNA gene sequence of strain BK30 is OL742673.

**Description of Aureivirga marina PJ35**

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies are circular, convex, entire, and brown-colored after incubation for 3 days on MA at 20°C. Positive for nitrates reduction, urease, and cytochrome oxidase; but negative for indole production, glucose fermentation, arginine dihydrolase, esculin hydrolysis, gelatin hydrolysis, and β-galactosidase in API 20NE. 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 as a sole carbon source. Strain PJ35 (= HNIBRBA397) was isolated from seawater collected off Jaeun-do (34°55'8.59"N, 126°03'37.26"E), Shinan, Jeollanam-do, Korea. The GenBank accession number of the 16S rRNA gene sequence of strain PJ35 is OL742674.

**Description of Vibrio caribbeanicus PJ47**

Cells are Gram-stain-negative, flagellated, and rod-shaped. Colonies are translucent, convex, smooth, and cream-colored after incubation for 3 days on MA at 20°C. Positive for arginine dihydrolase, urease, gelatin hydrolysis, and cytochrome oxidase; but negative for nitrates reduction, indole production, glucose fermentation, esculin hydrolysis, and β-galactosidase in API 20NE. d-Glucose, N-acetyl-glucosamine and malic acid are utilized as a sole 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, and phenylacetic acid. Strain PJ47 (= HNIBRBA406) was isolated from seawater collected off Jaeun-do (34°55'8.59"N, 126°03'37.26"E), Shinan, Jeollanam-do, Korea. The GenBank accession number of the 16S rRNA gene sequence of strain PJ47 is OL742675.

**Description of Shewanella submarina KY46**

Cells are Gram-stain-negative, flagellated, and rod-shaped. Colonies are translucent, convex, entire, and cream-colored after incubation for 3 days on MA at 20°C. Positive for nitrates reduction, arginine dihydrolase, urease, esculin hydrolysis, gelatin hydrolysis, and cy-
tochrome oxidase; but negative for indole production, glucose fermentation, and β-galactosidase in API 20NE. d-Mannose, N-acetyl-glucosamine and d-maltose are utilized as a sole carbon source; but not d-glucose, l-arabinose, d-mannitol, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain KY46 (=HNIIBRA506) was isolated from the seawater collected off Myo-do (34°53’00”N, 127°44’52”E), Kwangyang, Jeollanam-do, Korea. The GenBank accession number of the 16S rRNA gene sequence of strain KY46 is OL742676.

**Description of Grimontia sedimenti KG16**

Cells are Gram-stain-negative, flagellated, and rod-shaped. Colonies are circular, entire, opaque, and cream-colored after incubation for 3 days on MA at 20°C. Positive for nitrates reduction, indole production, glucose fermentation, β-galactosidase, and cytochrome oxidase; but negative for arginine dihydrodase, urease, esculin hydrolysis, and β-galactosidase in API 20NE. d-Glucose, d-mannose, N-acetyl-glucosamine, and malic acid are utilized as a sole carbon source; but not l-arabinose, d-mannitol, d-maltose, potassium gluconate, capric acid, adipic acid, trisodium citrate, and phenylacetic acid. Strain KG16 (=HNIIBRA506) was isolated from seawater collected off Geumgap (34°23’46”N, 126°16’32”E), Jindo, Jeollanam-do, Korea. The GenBank accession number of the 16S rRNA gene sequence of strain KG16 is OL742677.

**Description of Ferrimonas futtsuensis KJ05**

Cells are Gram-stain-negative, flagellated, and rod-shaped. Colonies are circular, entire, opaque, and brown-colored after incubation for 3 days on MA at 20°C. Positive for nitrates reduction, arginine dihydrodase, urease, β-galactosidase, and cytochrome oxidase; but negative for indole production, glucose fermentation, esculin hydrolysis, gelatin hydrolysis, and β-galactosidase in API 20NE. 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 as a sole carbon source. Strain KJ05 (=HNIIBRA601) was isolated from seawater collected off Daegu (34°31’32”N, 126°47’23”E), Gagnjin, Jeollanam-do, Korea. The GenBank accession number of the 16S rRNA gene sequence of strain KJ05 is OL742678.

**Description of Vibrio halioticoli SK37**

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies are circular, entire, and yellow-colored after incubation for 3 days on MA at 20°C. Positive for nitrates reduction, arginine dihydrodase, urease, esculin hydrolysis, gelatin hydrolysis, β-galactosidase, and cytochrome oxidase; but negative for arginine dihydrodase, urease, esculin hydrolysis, and β-galactosidase in API 20NE. 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 as a sole carbon source. Strain SK37 (=HNIIBRA666) was isolated from seawater collected off the Wando Port (34°19’33”N, 126°45’01”E), Wando, Jeollanam-do, Korea. The GenBank accession number of the 16S rRNA gene sequence of strain SK37 is OL742679.

**Description of Vibrio anguillarum SK53**

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies are circular, convex, entire, and yellow-colored after incubation for 3 days on MA at 20°C. Positive for nitrates reduction, indole production, glucose fermentation, arginine dihydrodase, urease, esculin hydrolysis, gelatin hydrolysis, β-galactosidase, and cytochrome oxidase in API 20NE. N-Acetyl-glucosamine, d-maltose, potassium gluconate, and malic acid are utilized as a sole carbon source; but not d-glucose, l-arabinose, d-mannose, d-mannitol, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain SK53 (=HNIIBRA682) was isolated from seawater collected off the Wando Port (34°19’33”N, 126°45’01”E), Wando, Jeollanam-do, Korea. The GenBank accession number of the 16S rRNA gene sequence of strain SK53 is OL742680.

**Description of Loktanella agnita SK54**

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies are irregular, convex, smooth, and cream-colored after incubation for 3 days on MA at 20°C. Positive for nitrates reduction, arginine dihydrodase, urease, β-galactosidase, and cytochrome oxidase; but negative for indole production, glucose fermentation, esculin hydrolysis, and gelatin hydrolysis in API 20NE. d-Glucose, l-arabinose, d-mannose, d-mannitol, capric acid, adipic acid, malic acid, potassium gluconate, and malic acid are utilized as a sole carbon source; but not d-glucose, l-arabinose, d-mannose, d-mannitol, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain SK54 (=HNIIBRA683) was isolated from seawater collected off the Wando Port (34°19’33”N, 126°45’01”E), Wando, Jeollanam-do, Korea. The GenBank accession number of the 16S rRNA gene sequence of strain SK54 is OL742681.

**Description of Shewanella kaireitica SK55**

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies are entire, semitranslucent, smooth, and pink-colored after incubation for 3 days on MA at 20°C. Positive for nitrates reduction, arginine dihydrodase, urease, esculin hydrolysis, gelatin hydrolysis, β-galactosidase, and cytochrome oxidase; but negative for...
indole production and glucose fermentation in API 20NE. 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 as a sole carbon source. Strain SK55 (=HNIBRBA684) was isolated from seawater collected off the Wando Port (34°19'33"N, 126°45'01"E), Wando, Jeollanam-do, Korea. The GenBank accession number of the 16S rRNA gene sequence of strain SK55 is OL742682.

**Description of Photobacterium sanguinicancrri SK56**

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies are circular, convex, entire, and cream-colored after incubation for 3 days on MA at 20°C. Positive for nitrates reduction, glucose fermentation, arginine dihydrolase, urease, β-galactosidase, and cytochrome oxidase; but negative for indole production, esculin hydrolysis, and gelatin hydrolysis in API 20NE. 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 as a sole carbon source. Strain SK56 (=HNIBRBA685) was isolated from seawater collected off the Wando Port (34°19'33"N, 126°45'01"E), Wando, Jeollanam-do, Korea. The GenBank accession number of the 16S rRNA gene sequence of strain SK56 is OL742683.

**Description of Vibrio ezurae SK59**

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies are circular, convex, entire, and yellow-colored after incubation for 3 days on MA at 20°C. Positive for nitrates reduction, indole production, glucose fermentation, and cytochrome oxidase; but negative for arginine dihydrolase, urease, esculin hydrolysis, gelatin hydrolysis, and β-galactosidase in API 20NE. 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 as a sole carbon source. Strain SK59 (=HNIBRBA688) was isolated from seawater collected off the Wando Port (34°19'33"N, 126°45'01"E), Wando, Jeollanam-do, Korea. The GenBank accession number of the 16S rRNA gene sequence of strain SK59 is OL742684.

**Description of Pseudovibrio stylochi KHSW6**

Cells are Gram-stain-negative, flagellated, and rod-shaped. Colonies are circular, convex, smooth, and yellow-colored after incubation for 3 days on MA at 20°C. Positive for nitrates reduction and cytochrome oxidase; but negative for indole production, glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis, gelatin hydrolysis, and β-galactosidase in API 20NE. d-Glucose, and d-mannose are utilized as a sole carbon source; but not l-arabinose, d-mannitol, N-acetyl-glucosamine, d-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain KHSW6 (=HNIBRBA773) was isolated from seawater collected off Jungsan (34°43'50.03"N, 127°19'33.95"E), Goeheung, Jeollanam-do, Korea. The GenBank accession number of the 16S rRNA gene sequence of strain KHSW6 is OL742685.

**Description of Marinobacter xestospongiae SSB41**

Cells are Gram-stain-negative, flagellated, and rod-shaped. Colonies are circular, convex, smooth, and cream-colored after incubation for 3 days on MA at 20°C. Positive for nitrates reduction and cytochrome oxidase; but negative for indole production, glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis, gelatin hydrolysis, and β-galactosidase in API 20NE. Malic acid and trisodium citrate are utilized as a sole carbon source; but not d-glucose, d-arabinose, d-mannose, d-mannitol, N-acetyl-glucosamine, d-maltose, potassium gluconate, capric acid, adipic acid, and phenylacetic acid. Strain SSB41 (=HNIBRBA833) was isolated from seawater collected off Jaeun-do (34°51'51"N, 125°59'59"E), Shian, Jeollanam-do, Korea. The GenBank accession number of the 16S rRNA gene sequence of strain SSB41 is OL742686.

**Description of Psychrilyobacter atlanticus GHS7**

Cells are Gram-stain-negative, non-flagellated, and coccic-shaped. Colonies are circular, convex, entire, and white-colored after anaerobic incubation for 7 days on marine R2A at 20°C. Positive for esculin hydrolysis; but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis, gelatin hydrolysis, β-galactosidase, and cytochrome oxidase in API 20NE. 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 as a sole carbon source. Strain GHS7 (=HNIBRBA853) was isolated from tidal flat collected off Goha-do (34°45'34.91"N, 126°21'53.67"E), Mokpo, Jeollanam-do, Korea. The GenBank accession number of the 16S rRNA gene sequence of strain GHS7 is OL742687.

**Description of Propionigenium maris GHS9**

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies are circular, convex, entire, and white-
colored after anaerobic incubation for 7 days on marine R2A at 20°C. Positive for indole production, glucose fermentation, arginine dihydrolase, and cytochrome oxidase; but negative for nitrate reduction, urease, esculin hydrolysis, gelatin hydrolysis, and β-galactosidase in API 20NE. 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 as a sole carbon source. Strain GHS9 (=HNIBRBA855) was isolated from tidal flat collected off Goha-do (34°45′34.91″N, 126°21′53.67″E), Mokpo, Jeollanam-do, Korea. The GenBank accession number of the 16S rRNA gene sequence of strain GHS9 is OL742689.

**Description of Tepidibacter mesophilus GHS20**

Cells are Gram-stain-positive, non-flagellated, and rod-shaped. Colonies are circular, convex, entire, and white-colored after anaerobic incubation for 7 days on marine R2A at 20°C. Negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis, gelatin hydrolysis, β-galactosidase, and cytochrome oxidase in API 20NE. 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 as a sole carbon source. Strain GHS20 (=HNIBRBA866) was isolated from tidal flat collected off Goha-do (34°45′34.91″N, 126°21′53.67″E), Mokpo, Jeollanam-do, Korea. The GenBank accession number of the 16S rRNA gene sequence of strain GHS20 is OL742689.

**Description of Halomonas lactosivorans KEMB43-101**

Cells are Gram-stain-negative, non-flagellated, and cocci-shaped. Colonies are circular, convex, entire, and yellow-colored after incubation for 3 days on MA at 20°C. Positive for arginine dihydrolase, urease, and cytochrome oxidase; but negative for nitrate reduction, indole production, glucose fermentation, esculin hydrolysis, gelatin hydrolysis, and β-galactosidase in API 20NE. Malic acid and trisodium citrate are utilized as a sole carbon source but not d-glucose, L-arabinose, D-mannose, D-mannitol, N-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, and phenylacetic acid are not utilized as a sole carbon source. Strain KEMB43-101 (=HNIBRBA1036) was isolated from tidal flat collected off Goha-do (34°45′34.91″N, 126°21′53.67″E), Mokpo, Jeollanam-do, Korea. The GenBank accession number of the 16S rRNA gene sequence of strain KEMB43-101 is OL742690.

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**References**


