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A report of 20 unrecorded bacterial species isolated from the coastal area of Korean islands in 2022

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Bacterial communities inhabiting islands play a vital role in the functioning and formation of a unique, isolated ecosystem. Nevertheless, there has been a lack of systematic research on the indigenous microbiological resources of the islands in Korea. To excavate microbial resources for further studies on the metabolism and biotechnological potential, a standard dilution plating was applied to coastal seawater samples collected from islands along the west coast of the Korean Peninsula, including Deokjeokdo, Baengnyeongdo, and Daebudo in 2022. A total of 2,007 bacterial strains were isolated from the samples as single colonies and identified using 16S rRNA gene sequence analyses. A total of 20 strains, with $\geq$98.7% 16S rRNA gene sequence similarity to bacterial species having validly published names but not reported in Korea, were designated as unrecorded bacterial species in Korea. The unrecorded bacterial strains were phylogenetically diverse and belonged to four phyla, five classes, 12 orders, 17 families, and 18 genera. The unreported species were assigned to *Algimonas*, *Amylibacter*, *Notoacmeibacter*, *Roseibium*, and *Terasakiella* of the class *Alphaproteobacteria*; *Alteromonas*, *Congregibacter*, *Marinagarivorans*, *Marinicella*, *Oceanospirillum*, *Psychromonas*, *Thalassotalea*, *Umboniibacter*, and *Vibrio* of the class *Gammaproteobacteria*; *Lutibacter* and *Owenweeksia* of the class *Flavobacteriia*; *Paenibacillus* of the class *Bacilli*; and *Pelagicoccus* of the class *Opitutae*. The taxonomic characteristics of the unreported species, including morphology, biochemistry, and phylogenetic position are provided in detail.

Keywords: 16S rRNA, coast, island, prokaryote, seawater, unrecorded bacterial species

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Introduction

The Korean Peninsula has a complex coastline with approximately 3,400 islands scattered along its shores. Islands are characterized by their diverse ecosystems, including marine, coastal, and soil ecosystems and each of these ecosystems has its own distinct characteristics. In addition, islands and coasts are known to have high biodiversity because they act as a bridge between terrestrial and marine ecosystems (Li *et al*., 2020b). Despite the high level of biodiversity present on Korean islands and coastlines, relatively few studies have focused on the diversity of endemic bacterial species in these areas.

The Honam National Institute of Biological Resources (HNIBR) initiated the 'Survey of island-coastal indigenous organisms (Prokaryotes)' research program in 2022 in response to a need for microbial diversity studies. As demonstrated in prior studies on freshwater ecosystems (i.e., Joung *et al*., 2018; 2019; Kim *et al*., 2021), this research program has resulted in the discovery of previously unrecorded bacterial species from the Korean islands. The ocean, which makes up 70% of the Earth's surface and contains approximately 1.2×10^{29} cells of prokaryotes, plays a significant role in the global carbon cycle and climate regulation (Whitman *et al*., 1998). As islands are surrounded by the sea and also have unique terrestrial ecosystems, the microbial community residing on the coasts of the islands is expected to be one of key factors in establishing the unique ecosystem of each island.

This study, which is part of a research program supported by the HNIBR, focuses on the isolation of previously unrecorded bacterial species from various island and coastal habitats. In 2022, we attempted to isolate such bacterial species in coastal seawater samples collected from four different islands: Deokjeokdo, Baengnyeongdo, Daebudo, and small islands off the coast of Mokpo. Based on the

16S rRNA gene-based phylogenetic analyses, 20 bacterial strains assigned to the classes *Alphaproteobacteria*, *Gammaproteobacteria*, *Flavobacteriia*, *Bacilli*, and *Opitutae* were identified as new records for bacterial species in Korea, for which taxonomic information and phenotypic characteristics are reported.

Materials and Methods

Various coastal seawater samples were collected from selected islands on the southwest side of Korea, including Deokjeokdo, Baengnyeongdo, Daebudo, and several small islands off the coast of Mokpo in 2022. The collected samples were kept refrigerated and transported to the laboratory within six hours for further analysis.

Seawater samples were serially diluted and 200 µL was taken and plated on three different media: marine agar 2216 (MA; Difco), R2A agar (Difco) based on aged seawater (M-R2A), and 1/10-diluted M-R2A agar. After being aerobically incubated for 3−7 days at 20−25°C, colonies were isolated and maintained on MA media. A total of 2,007 strains were purified as single colonies after subsequent cultivation, and the pure cultures were preserved at −80°C in a 20% (v/v) glycerol suspension. Lyophilized ampoules were additionally prepared for the selected 20 unrecorded strains to ensure their stable preservation. The designation of the selected strains and source of isolation are listed in Table 1.

Colony morphology was observed using a magnifying glass on agar plates with bacterial colonies that had reached stationary phase. Cellular morphologies including cell size, cell shape, and the presence of flagella were verified using a transmission electron microscope (CM200; Philips) after staining with 1% (w/v) uranyl acetate. Gram staining was performed using a Gram-staining kit (bio Mérieux) and the KOH method. Biochemical characteristics were investigated by using API 20NE galleries (bio Mérieux) with an artificial seawater medium (Li *et al*., 2020a) as the basal culture medium.

The phylogenetic position of the strains was determined by performing standard procedures of bacterial DNA extraction, PCR amplification, and 16S rRNA gene sequencing. The universal primers 27F and 1492R were used to amplify 16S rRNA genes (Weisburg *et al*., 1991), and the primers 518F and 805R were used to obtain sequences using Sanger sequencing method. The resulting 16S rRNA gene sequences were initially compared with those of other bacterial strains with validly published names using the EzTaxon-e server (Kim *et al*., 2012). The 16S rRNA gene sequence similarity of 98.7% was used as the cut-off value for bacterial species demarcation (Chun *et al*., 2018). The strains exhibiting ≥98.7% 16S rRNA gene sequence similarities with validly published species but never reported in Korea were determined to be unreported bacterial species.

For phylogenetic analysis, the 16S rRNA gene sequence was aligned using the SILVA Incremental Aligner implemented in ARB software (Pruesse *et al*., 2007). Phylogenetic trees were reconstructed using the maximum-likelihood, neighbor-joining, and minimum-evolution algorithms with bootstrap analyses of 1,000 replicates by MEGA X software (Kumar *et al*., 2018) using the pre-aligned sequences exported from ARB.

Results and Discussion

The 16S rRNA gene sequence analyses of approximately 2,000 bacterial strains revealed that many of the strains belonged to unreported bacterial species in Korea. Of these, a total of 20 strains were identified as unrecorded bacterial species in Korea. The strain information, identification, taxonomic assignment from species to classes, and sequence accession numbers including HNIBR and GenBank are listed in Table 1. The phylogenetic assignment of the strains to established bacterial species based on 16S rRNA gene sequence similarity was confirmed by phylogenetic tree analysis (Fig. 1). All strains identified as unrecorded species formed a robust clade with the type strains of each corresponding species with high bootstrap values (Fig. 1).

The 20 unrecorded bacterial species were phylogenetically diverse, belonging to four phyla, five classes, 12 orders, 17 families, and 18 genera (Table 1). At the generic level, the unreported species were assigned to *Algimonas*, *Amylibacter*, *Notoacmeibacter*, *Roseibium*, and *Terasakiella* of the class *Alphaproteobacteria*; *Alteromonas*, *Congregibacter*, *Marinagarivorans*, *Marinicella*, *Oceanospirillum*, *Psychromonas*, *Thalassotalea*, *Umboniibacter*, and *Vibrio* of the class *Gammaproteobacteria*; *Lutibacter* and *Owenweeksia* of the class *Flavobacteriia*; *Paenibacillus* of the class *Bacilli*; and *Pelagicoccus* of the class *Opitutae*.

The 20 unrecorded bacterial species identified in this study were Gram-staining-negative or positive, flagellated or non-flagellated, short- or straight-rod or coccoid-shaped bacteria (Fig. 2). Detailed morphological, physiological, and biochemical characteristics of these unrecorded bacterial species are provided in the following strain description sections.

Description of *Owenweeksia hongkongensis* IMCC43116

Cells are Gram-stain-negative, aerobic, non-flagellated, and rod-shaped. Colonies are circular, convex, entire, and orange colored after incubation for three days on MA at 25°C. Positive for nitrate reduction, indole production,

Table 1. Summary of bacterial strains isolated from coastal sea water habitats of islands and their taxonomic affiliations.

Class	Order	Family	Genus	Strain ID	HNIBR ID	Accession number	Closest species	16S rRNA similarity (%)	Isolation source	Isolation medium	Incubation conditions
Alphaproteobacteria	*Caulobacterales*	*Hyphomonadaceae*	*Algimonas*	IMCC43225	HNIBRBA4497	OP672400	*Algimonas arctica*	98.99	Sea water	M-R2A	25°C, 3 days
	Hyphomicrobiales	*Stappiaceae*	*Roseibium*	IMCC43670	HNIBRBA4512	OP672415	*Roseibium polysiphoniae*	98.90	Sea water	MA	25°C, 3 days
		Notoacmeibacteraceae	*Notoacmeibacter*	IMCC33673	HNIBRBA4504	OP672407	*Notoacmeibacter marinus*	99.93	Sea water	M-1/10R2A	25°C, 3 days
	Rhodobacterales	*Roseobacteraceae*	*Amylibacter*	IMCC43586	HNIBRBA4503	OP672406	*Amylibacter marinus*	98.85	Sea water	M-1/10R2A	25°C, 3 days
	Rhodospirillales	*Terasakiellaceae*	*Terasakiella*	IMCC43666	HNIBRBA4511	OP672414	*Terasakiella brassicae*	98.80	Sea water	MA	25°C, 3 days
Gammaproteobacteria	*Alteromonadales*	*Alteromonadaceae*	*Alteromonas*	IMCC43657	HNIBRBA4510	OP672413	*Alteromonas abrolhosensis*	99.09	Sea water	M-1/10R2A	25°C, 3 days
		Colwelliaceae	*Thalassotalea*	IMCC43617	HNIBRBA4508	OP672411	*Thalassotalea sediminis*	99.93	Sea water	MA	25°C, 3 days
		Psychromonadaceae	*Psychromonas*	IMCC43240	HNIBRBA4498	OP672401	*Psychromonas aquimarina*	99.52	Sea water	M-R2A	25°C, 3 days
				IMCC33772	HNIBRBA4505	OP672408	*Psychromonas marina*	98.85	Sea water	MA	25°C, 3 days
				IMCC33842	HNIBRBA4506	OP672409	*Psychromonas ossibalaenae*	98.98	Sea water	M-1/10R2A	25°C, 3 days
	Cellvibrionales	*Cellvibrionaceae*	*Umboniibacter*	IMCC43252	HNIBRBA4499	OP672402	*Umboniibacter marinipuniceus*	99.79	Sea water	M-R2A	25°C, 3 days
			Marinagarivorans	IMCC33788	HNIBRBA4513	OP672416	*Marinagarivorans algicola*	99.66	Sea water	M-R2A	25°C, 3 days
		Halieaceae	*Congregibacter*	IMCC43200	HNIBRBA4496	OP672399	*Congregibacter litoralis*	98.76	Sea water	M-1/10R2A	25°C, 3 days
	Marinicella	*Marinicella*	*Marinicella*	IMCC43261	HNIBRBA4502	OP672405	*Marinicella litoralis*	98.84	Sea water	M-1/10R2A	25°C, 3 days
	Oceanospirillales	*Oceanospirillaceae*	*Oceanospirillum*	IMCC43611	HNIBRBA4507	OP672410	*Oceanospirillum sanctuarii*	98.84	Sea water	MA	25°C, 3 days
	Vibrionales	*Vibrionaceae*	*Vibrio*	IMCC43655	HNIBRBA4509	OP672412	*Vibrio japonicus*	99.43	Sea water	M-1/10R2A	25°C, 3 days
Flavobacteriia	*Flavobacteriales*	*Flavobacteriaceae*	*Lutibacter*	IMCC33805	HNIBRBA4514	OP672417	*Lutibacter holmesii*	99.86	Sea water	M-1/10R2A	25°C, 3 days
		Schleiferiaceae	*Owenweeksia*	IMCC43116	HNIBRBA4495	OP672398	*Owenweeksia hongkongensis*	99.45	Sea water	M-R2A	25°C, 3 days
Bacilli	*Caryophanales*	*Paenibacillaceae*	*Paenibacillus*	IMCC43345	HNIBRBA4501	OP672404	*Paenibacillus hispanicus*	99.24	Sea water	M-1/10R2A	25°C, 3 days
Opitutae	*Puniceicoccales*	*Puniceicoccaceae*	*Pelagicoccus*	IMCC43266	HNIBRBA4500	OP672403	*Pelagicoccus litoralis*	99.11	Sea water	MA	25°C, 3 days

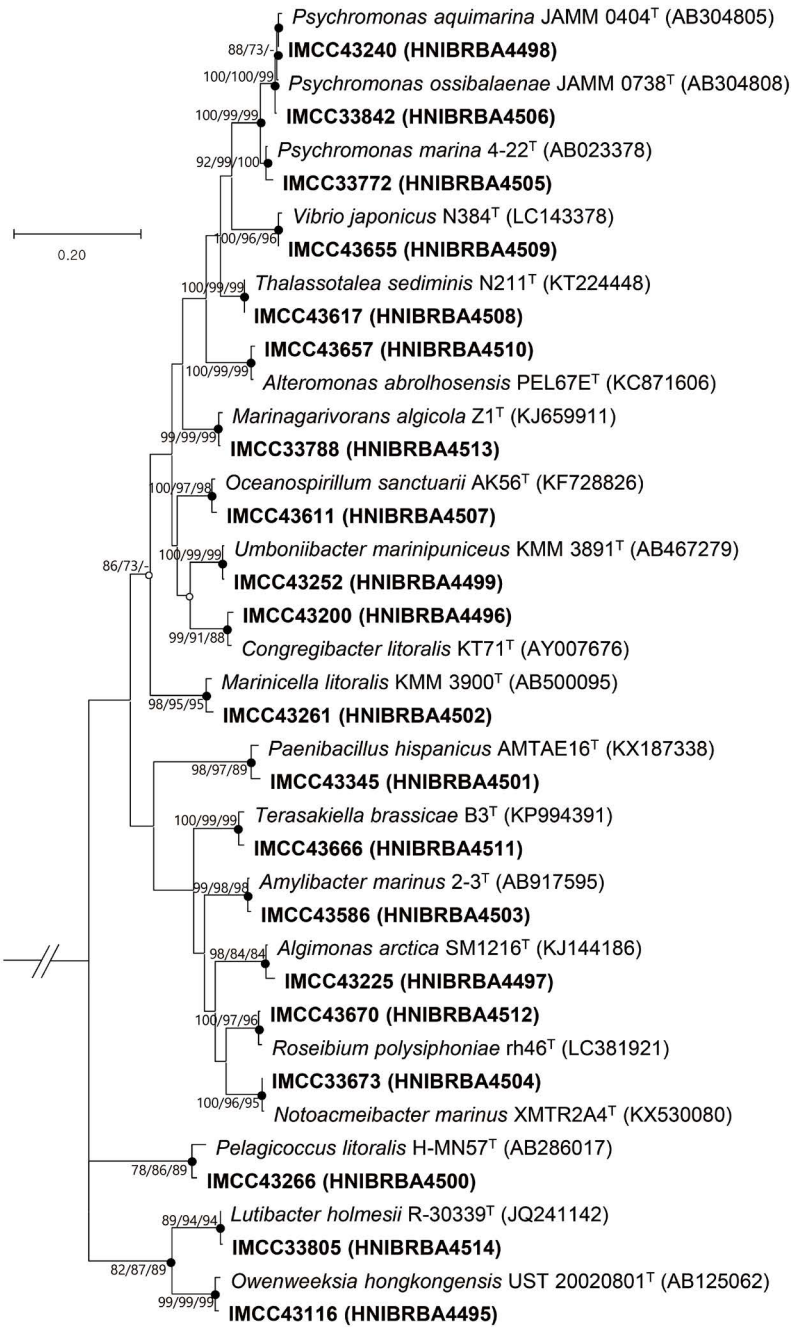

Fig. 1. The maximum-likelihood (ML) phylogenetic tree based on 16S rRNA gene sequences showing the relationship between the strains isolated in this study and their closest bacterial species. Bootstrap values over 70% are shown at nodes for ML, neighbor-joining (NJ), and minimum evolution (ME) methods, respectively (ML/NJ/ME; −, less than 70%). Tree was rooted with *Dehalococcoides mccartyi* KCTC 15142^T (not shown; GenBank accession no. AX814128). Filled circles indicate that the corresponding node was also recovered in the trees reconstructed with both the NJ and ME algorithms, while open circles indicate that the corresponding node was recovered in the tree generated with only one of these algorithms. Scale bar = 0.05 substitutions per nucleotide position.

esculin hydrolysis, and cytochrome oxidase; but negative for glucose fermentation, arginine dihydrolase, urease, 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 sole carbon sources. Strain IMCC43116 (=HNIBRBA4495) was isolated from a coastal seawater sample, Gurido, Mokpo, Jeollanam-do, Korea.

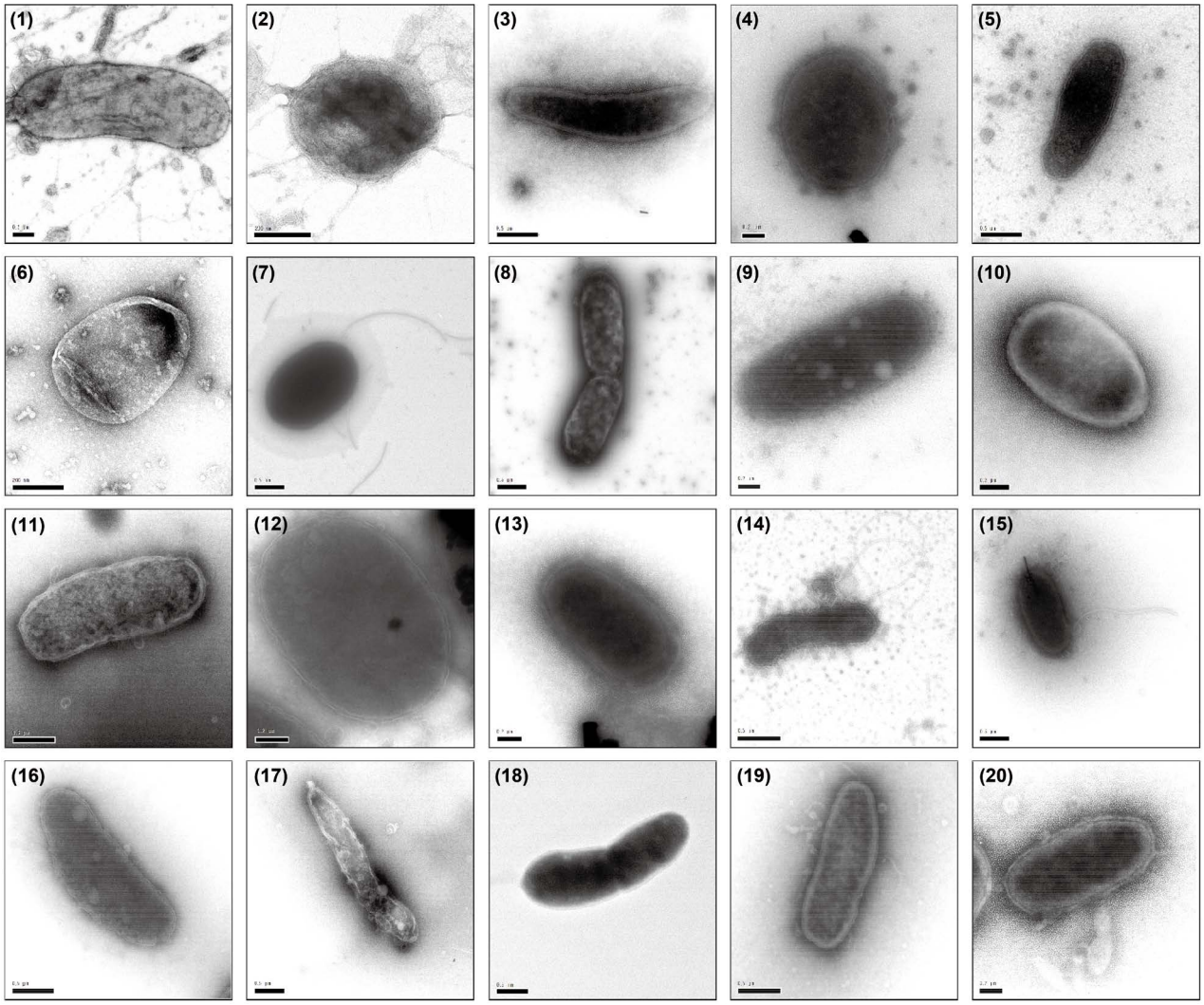

Fig. 2. Transmission electron micrographs of cells of the strains isolated in this study. Strains: 1. IMCC43116 (0.2 μm); 2. IMCC43200 (0.2 μm); 3. IMCC43225 (0.5 μm); 4. IMCC43240 (0.2 μm); 5. IMCC43252 (0.5 μm); 6. IMCC43266 (0.2 μm); 7. IMCC43345 (0.5 μm); 8. IMCC43261 (0.5 μm); 9. IMCC43586 (0.2 μm); 10. IMCC33673 (0.2 μm); 11. IMCC33772 (0.5 μm); 12. IMCC33842 (0.2 μm); 13. IMCC43611 (0.2 μm); 14. IMCC43617 (0.5 μm); 15. IMCC43655 (0.5 μm); 16. IMCC43657 (0.5 μm); 17. IMCC43666 (0.5 μm); 18. IMCC43670 (0.5 μm); 19. IMCC33788 (0.5 μm); 20. IMCC33805 (0.2 μm). Scale bars are indicated in parenthesis after strain ID.

Description of *Congregibacter litoralis* IMCC43200

Cells are Gram-stain-negative, aerobic, non-flagellated, and coccus-shaped. Colonies are circular, convex, entire, and brown colored after incubation for three days on MA at 25°C. Positive for esculin hydrolysis and β-galactosidase; but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, gelatin hydrolysis, 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 sole carbon sources. Strain IMCC43200 (=HNIBRBA4496) was isolated from a coastal seawater sample, Halmido, Mokpo, Jeollanam-do, Korea.

Description of *Algimonas arctica* IMCC43225

Cells are Gram-stain-negative, aerobic, non-flagellated, and rod-shaped. Colonies are circular, raised, entire, and orange colored after incubation for three days on MA at 25°C. Positive for nitrate reduction, indole production, esculin hydrolysis, β-galactosidase, and cytochrome oxidase; but negative for 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 sole carbon sources. Strain IMCC43225 (=HNIBRBA4497) was isolated from a coastal seawater sample, Aphaedo, Mokpo, Jeollanam-do, Korea.

Description of *Psychromonas aquimarina* IMCC43240

Cells are Gram-stain-negative, aerobic, non-flagellated, and coccus-shaped. Colonies are circular, flat, entire, and white colored after incubation for three days on MA at 25°C. Positive for nitrate reduction, indole production, esculin hydrolysis, and cytochrome oxidase; but negative for glucose fermentation, arginine dihydrolase, urease, 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 sole carbon sources. Strain IMCC43240 (=HNIBRBA4498) was isolated from a coastal seawater sample, Seopori Beach in Deokjeokdo, Ongjin-gun, Incheon, Korea.

Description of *Umboniibacter marinipuniceus* IMCC43252

Cells are Gram-stain-negative, aerobic, non-flagellated, and rod-shaped. Colonies are circular, convex, entire, and beige colored after incubation for three days on MA at 25°C. Positive for esculin hydrolysis, β-galactosidase, and cytochrome oxidase; but negative for nitrate 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 sole carbon sources. Strain IMCC 43252 (=HNIBRBA4499) was isolated from a coastal seawater sample, Seopori Beach in Deokjeokdo, Ongjin-gun, Incheon, Korea.

Description of *Pelagicoccus litoralis* IMCC43266

Cells are Gram-stain-negative, aerobic, non-flagellated, and rod-shaped. Colonies are circular, flat, entire, and white colored after incubation for three days on MA at 25°C. Positive for esculin hydrolysis, β-galactosidase, and cytochrome oxidase; but negative for nitrate 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 sole carbon sources. Strain IMCC 43266 (=HNIBRBA4500) was isolated from a coastal seawater sample, Seopori Beach in Deokjeokdo, Ongjin-gun, Incheon, Korea.

Description of *Paenibacillus hispanicus* IMCC43345

Cells are Gram-stain-positive, aerobic, flagellated, and short rod-shaped. Colonies are circular, flat, entire, and white colored after incubation for three days on MA at 25°C. Positive for esculin hydrolysis, β-galactosidase, and cytochrome oxidase; but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, and gelatin hydrolysis in API 20NE. Malic acid is utilized; but D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, potassium gluconate, capric acid, adipic acid, trisodium citrate, and phenylacetic acid are not utilized. Strain IMCC43345 (=HNIBRBA 4501) was isolated from a coastal seawater sample, Batjileum Beach in Deokjeokdo, Ongjin-gun, Incheon, Korea.

Description of *Marinicella litoralis* IMCC43261

Cells are Gram-stain-negative, aerobic, non-flagellated, and rod-shaped. Colonies are circular, convex, entire, and white colored after incubation for three days on MA at 25°C. Positive for esculin hydrolysis and cytochrome oxidase; but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, 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 sole carbon sources. Strain IMCC 43261 (=HNIBRBA4502) was isolated from a coastal seawater sample, Seopori Beach in Deokjeokdo, Ongjin-gun, Incheon, Korea.

Description of *Amylibacter marinus* IMCC43586

Cells are Gram-stain-negative, aerobic, non-flagellated, and rod-shaped. Colonies are circular, raised, entire, and beige colored after incubation for three days on MA at 25°C. Positive for β-galactosidase and cytochrome oxidase; but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, 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 sole carbon sources. Strain IMCC 43586 (=HNIBRBA4503) was isolated from a coastal seawater sample, Igae Beach in Deokjeokdo, Ongjin-gun, Incheon, Korea.

Description of *Notoacmeibacter marinus* IMCC33673

Cells are Gram-stain-negative, aerobic, non-flagellated,

and short rod-shaped. Colonies are circular, raised, entire, and red colored after incubation for three days on MA at 25°C. Positive for nitrate reduction, indole production, arginine dihydrolase, esculin hydrolysis, β-galactosidase, and cytochrome oxidase; but negative for glucose fermentation, 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 sole carbon sources. Strain IMCC33673 (=HNIBRBA4504) was isolated from a coastal seawater sample, Gobong Port in Baengnyeongdo, Ongjin-gun, Incheon, Korea.

Description of *Psychromonas marina* IMCC33772

Cells are Gram-stain-positive, aerobic, non-flagellated, and rod-shaped. Colonies are circular, flat, entire, and white colored after incubation for three days on MA at 25°C. Positive for nitrate reduction, glucose fermentation, urease, esculin hydrolysis, and cytochrome oxidase; but negative for indole production, arginine dihydrolase, β-galactosidase, 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 sole carbon sources. Strain IMCC 33772 (=HNIBRBA4505) was isolated from a coastal seawater sample, Junghwa Port in Baengnyeongdo, Ongjin-gun, Incheon, Korea.

Description of *Psychromonas ossibalaenae* IMCC33842

Cells are Gram-stain-negative, aerobic, non-flagellated, and rod-shaped. Colonies are circular, raised, entire, and beige colored after incubation for three days on MA at 25°C. Positive for nitrate reduction, glucose fermentation, esculin hydrolysis, β-galactosidase, and cytochrome oxidase; but negative for indole production, 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 sole carbon sources. Strain IMCC 33842 (=HNIBRBA4506) was isolated from a coastal seawater sample, Simcheonggak in Baengnyeongdo, Ongjin-gun, Incheon, Korea.

Description of *Oceanospirillum sanctuarii* IMCC43611

Cells are Gram-stain-negative, aerobic, non-flagellated, and rod-shaped. Colonies are circular, convex, entire, and white colored after incubation for three days on MA at 25°C. Positive for nitrate reduction, arginine dihydrolase, esculin hydrolysis, gelatin hydrolysis, and cytochrome oxidase; but negative for indole production, glucose fermentation, urease, 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 sole carbon sources. Strain IMCC 43611 (=HNIBRBA4507) was isolated from a coastal seawater sample, Nogari Beach in Daebudo, Ongjin-gun, Incheon, Korea.

Description of *Thalassotalea sediminis* IMCC43617

Cells are Gram-stain-negative, aerobic, flagellated, and rod-shaped. Colonies are circular, convex, entire, and beige colored after incubation for three days on MA at 25°C. Positive for nitrate reduction, indole production, esculin hydrolysis, β-galactosidase and cytochrome oxidase; but negative for 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 sole carbon sources. Strain IMCC43617 (=HNIBRBA4508) was isolated from a coastal seawater sample, Nogari Beach in Daebudo, Ongjin-gun, Incheon, Korea.

Description of *Vibrio japonicus* IMCC43655

Cells are Gram-stain-negative, aerobic, flagellated, and rod-shaped. Colonies are circular, convex, entire, and beige colored after incubation for three days on MA at 25°C. Positive for nitrate reduction, indole production, esculin hydrolysis, and β-galactosidase, and cytochrome oxidase; but negative for 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 sole carbon sources. Strain IMCC43655 (=HNIBRBA4509) was isolated from a coastal seawater sample, Nogari Beach in Daebudo, Ongjin-gun, Incheon, Korea.

Description of *Alteromonas abrolhosensis* IMCC43657

Cells are Gram-stain-negative, aerobic, non-flagellated, and rod-shaped. Colonies are circular, convex, entire, and beige colored after incubation for three days on MA at 25°C. Positive for esculin hydrolysis, gelatin hydrolysis, β-galactosidase, and cytochrome oxidase; but negative for nitrate reduction, indole production, glucose fermen-

tation, arginine dihydrolase, and urease 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 sole carbon sources. Strain IMCC43657 (=HNIBRBA4510) was isolated from a coastal seawater sample, Nogari Beach in Daebudo, Ongjin-gun, Incheon, Korea.

Description of *Terasakiella brassicae* IMCC43666

Cells are Gram-stain-negative, aerobic, non-flagellated, and rod-shaped. Colonies are circular, raised, entire, and beige colored after incubation for three days on MA at 25°C. Positive for nitrate reduction, esculin hydrolysis, and cytochrome oxidase; but negative for indole production, glucose fermentation, arginine dihydrolase, urease, 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 sole carbon sources. Strain IMCC43666 (=HNIBRBA4511) was isolated from a coastal seawater sample, Nogari Beach in Daebudo, Ongjin-gun, Incheon, Korea.

Description of *Roseibium polysiphoniae* IMCC43670

Cells are Gram-stain-negative, aerobic, non-flagellated, and rod-shaped. Colonies are circular, convex, entire, and white colored after incubation for three days on MA at 25°C. Positive for nitrate reduction, indole production, urease, esculin hydrolysis, and cytochrome oxidase; but negative for glucose fermentation, arginine dihydrolase, 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 sole carbon sources. Strain IMCC43670 (=HNIBRBA4512) was isolated from a coastal seawater sample, Nogari Beach in Daebudo, Ongjin-gun, Incheon, Korea.

Description of *Marinagarivorans algicola* IMCC33788

Cells are Gram-stain-negative, aerobic, non-flagellated, and rod-shaped. Colonies are circular, flat, entire, and white colored after incubation for three days on MA at 25°C. Positive for nitrate reduction, indole production, esculin hydrolysis, gelatin hydrolysis, and cytochrome oxidase; but negative for glucose fermentation, arginine dihydrolase, urease, 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 sole carbon sources. Strain IMCC33788 (=HNIBRBA4513) was isolated from a coastal seawater sample, Junghwa Port in Baengnyeongdo, Ongjin-gun, Incheon, Korea.

Description of *Lutibacter holmesii* IMCC33805

Cells are Gram-stain-negative, aerobic, non-flagellated, and rod-shaped. Colonies are circular, convex, entire, and yellow colored after incubation for three days on MA at 25°C. Positive for esculin hydrolysis; but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, 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 sole carbon sources. Strain IMCC 33805 (=HNIBRBA4514) was isolated from a coastal seawater sample, Junghwa Port in Baengnyeongdo, Ongjin-gun, Incheon, Korea.

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