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Identification of 24 previously unrecorded bacterial species from Korean coastal islands in 2025

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Island-associated coastal waters constitute environmentally heterogeneous habitats that can support diverse bacterial assemblages, yet microbial diversity in many Korean island regions remains insufficiently documented. In this study, bacterial strains were isolated from coastal seawater samples collected in 2025 from eight Korean islands: Daecheongdo, Gyodongdo, Jangbongdo, Pungdo, Seokmodo, Sido, Somaemuldo, and Yeonpyeongdo. Using conventional dilution plating techniques, approximately 800 bacterial isolates were recovered, and their taxonomic affiliations were assessed based on 16S rRNA gene sequence analysis. Among these isolates, 24 strains exhibited ≥98.7% sequence similarity to validly published bacterial species that had not previously been recorded in Korea and were therefore designated as newly recorded bacterial species. The newly recorded strains encompassed a broad taxonomic range, representing three phyla, four classes, six orders, 11 families, and 20 genera. These taxa were assigned to the classes *Alphaproteobacteria*, *Gammaproteobacteria*, *Bacteroidia*, and *Campylobacteria*. Phylogenetic analyses confirmed that each isolate formed a well-supported clade with its closest related type strain. Detailed morphological, biochemical, and phylogenetic characteristics of these newly recorded species are presented. This study expands the current inventory of bacterial species recorded from Korea and highlights island-associated coastal waters as important reservoirs of previously undocumented microbial diversity.

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

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Introduction

Coastal waters surrounding islands represent environmentally complex systems shaped by the interaction of terrestrial runoff, oceanic circulation, and localized hydrodynamic processes. In such settings, seawater properties are continuously modified by inputs from adjacent landmasses, sediment resuspension, and variable nutrient fluxes, resulting in pronounced spatial heterogeneity. Around the Korean Peninsula, island-associated coastal environments are extensive along the western and southern coasts, where shallow bathymetry and irregular shorelines further enhance environmental variability. These characteristics are expected to generate diverse ecological niches and impose selective pressures that promote microbial diversification within island coastal waters (Losos and Ricklefs, 2009; Davison *et al*., 2018).

Despite the ecological relevance of island-associated coastal systems, microbial diversity in many Korean island regions remains insufficiently documented. Previous investigations in Korean marine environments have frequently emphasized open coastal waters or nearshore sites, whereas systematic surveys targeting island-associated coastal habitats have been comparatively limited (Yang *et al*., 2016; Lim *et al*., 2023). Island coastal environments are inherently dynamic, experiencing fluctuations in salinity, nutrient

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availability, and water mass exchange, all of which contribute to high environmental heterogeneity (Li *et al*., 2020). High-throughput sequencing surveys of Korean coastal and island-influenced waters have also reported pronounced temporal and spatial variation in microbial community composition, indicating that island-associated systems are likely to harbor diverse bacterial assemblages that remain incompletely represented (Oktavitri *et al*., 2021).

Coordinated surveys are essential for establishing baseline knowledge of microbial diversity in island and coastal ecosystems and for identifying bacterial taxa not yet recorded at the national level. In this context, the Honam National Institute of Biological Resources (HNIBR) launched the "Survey of Island - Coastal Indigenous Organisms (Prokaryotes)" program in 2022 to systematically document prokaryotic diversity across Korean island and coastal environments. Studies conducted under this program as well as comparable national biodiversity survey programs have reported multiple bacterial species previously unrecorded in Korea (Joung *et al*., 2018; 2019; Kim *et al*., 2021; Cho *et al*., 2023; Lim *et al*., 2024), emphasizing the continuing value of culture-based isolation combined with taxonomic characterization for expanding national microbial resources.

As part of the ongoing HNIBR initiative, the present study focuses on the isolation and taxonomic identification of bacterial strains obtained from coastal seawater collected in 2025 from eight Korean islands: Daecheongdo, Gyodongdo, Jangbongdo, Pungdo, Seokmodo, Sido, Somaemuldo, and Yeonpyeongdo. Using culture-based approaches and 16S rRNA gene sequence analysis, 24 bacterial strains were identified as species not previously recorded in Korea. These strains span multiple taxonomic groups within the classes *Alphaproteobacteria*, *Gammaproteobacteria*, *Bacteroidia*, and *Campylobacteria*. Here, we provide phylogenetic, morphological, and biochemical characterizations of these newly recorded bacterial species, thereby contributing to the ongoing documentation of microbial diversity in Korean island-associated coastal environments.

Materials and Methods

In 2025, seawater samples were obtained from multiple island locations, including Daecheongdo, Gyodongdo, Jangbongdo, Pungdo, Seokmodo, Sido, Somaemuldo, and Yeonpyeongdo. Immediately after collection, samples were kept refrigerated and transported to the laboratory within six hours. Each seawater sample was serially diluted (1/10, 1/50, and 1/100), and 200 μL aliquots from each dilution were spread onto five types of culture media: marine agar 2216 (MA; BD Difco, USA), MA containing 8% (w/v) NaCl, ISP2 agar (BD Difco, USA), M-R2A (R2A agar prepared with aged seawater), and a 1/10 dilution of M-R2A. To recover anaerobic or facultatively anaerobic bacteria, MA plates were also incubated under anaerobic conditions in an anaerobic chamber (Coy Laboratory Products, USA) filled with $N_2 : H_2 : CO_2$ (80 : 10 : 10). Plates were incubated at 20−25°C for 3−7 days. Distinct colonies recovered from all plates were subcultured on MA under aerobic conditions to obtain pure isolates. Colonies recovered from MA plates incubated anaerobically were further examined for aerobic growth; isolates capable of aerobic growth were maintained aerobically for subsequent characterization. In total, 801 bacterial strains were isolated and purified. Pure cultures were preserved at −80°C in 20% (v/v) glycerol stocks and were also lyophilized for long-term storage. Detailed strain information and sampling sites are provided in Table 1.

Colony morphology was recorded during the stationary growth phase under low magnification. Cellular characteristics (size, shape, and flagellar presence) were examined by transmission electron microscopy (CM200; Philips, Germany) after negative staining with 1% (w/v) uranyl acetate. The Gram reaction was evaluated using a commercial Gram-staining kit (bioMérieux, France) and verified using the KOH string test. Physiological and biochemical characteristics were analyzed with API 20NE strips (bio Mérieux, France) according to the manufacturer's instructions.

Genomic DNA was extracted from each strain, and 16S rRNA gene sequences ($\geq$1,350 bp) were amplified using universal primers 27F and 1492R (Weisburg *et al*., 1991). Amplicons were sequenced using primers 518F and 805R. Resulting sequences were compared against validly published named species in the EzBioCloud database (Chalita *et al*., 2024). Species-level identification was assigned using a similarity threshold of 98.7% (Chun *et al*., 2018). Isolates sharing $\geq$98.7% sequence identity with known taxa but not previously recorded in Korea were recognized as new national records. Sequence alignments were generated using the SILVA Incremental Aligner in the ARB platform (Pruesse *et al*., 2007). Phylogenetic trees were inferred using maximum-likelihood, neighbor-joining, and minimum-evolution methods with 1,000 bootstrap replicates in MEGA 12 (Kumar *et al*., 2024) based on aligned 16S rRNA gene sequences exported from ARB.

Results and Discussion

Analysis of 16S rRNA gene sequences obtained from 801 bacterial isolates resulted in the identification of 24 strains that showed sequence similarities of $\geq$98.7% to validly published bacterial species. As none of these taxa had previously been documented from Korea, the strains were designated as newly recorded bacterial species.

Table 1. Taxonomic affiliation of 24 bacterial strains isolated from coastal seawater samples collected around Korean islands in 2025.

Class	Order	Family	Genus	Strain ID	HNIBR ID	Accession number	Closest species	16S rRNA similarity	Isolation source	Isolation medium
Alphaproteobacteria	*Rhizobiales*	*Stappiaceae*	*Roseibium*	IMCC44501	HNIBRBA17225	PX515345	*Roseibium sediminis*	99.7	Seawater	3M-R2A
	Rhodobacterales	*Rhodobacteraceae*	*Pseudophaeobacter*	IMCC46094	HNIBRBA17242	PX515362	*Pseudophaeobacter profundi*	99.9	Seawater	MA (8% NaCl)
Gammaproteobacteria	*Enterobacterales*	*Alteromonadaceae*	*Bowmanella*	IMCC45450	HNIBRBA17227	PX515347	*Bowmanella yangjiangensis*	99.1	Seawater	3M-R2A
		Erwiniaceae	*Winslowiella*	IMCC46074	HNIBRBA17241	PX515361	*Winslowiella iniecta*	99.4	Seawater	MA (8% NaCl)
		Moritellaceae	*Moritella*	IMCC45969	HNIBRBA17237	PX515357	*Moritella viscosa*	99.7	Seawater	MA
		Shewanellaceae	*Ferrimonas*	IMCC46039	HNIBRBA17239	PX515359	*Ferrimonas kyonanensis*	99.2	Seawater	MA (Anaerobic)
		Vibrionaceae	*Photobacterium*	IMCC45839	HNIBRBA17231	PX515351	*Photobacterium marinum*	99.2	Seawater	MA (Anaerobic)
				IMCC45825	HNIBRBA17230	PX515350	*Photobacterium alginatilyticum*	99.0	Seawater	MA (Anaerobic)
			Vibrio	IMCC45319	HNIBRBA17223	PX515343	*Vibrio marisflavi*	99.2	Seawater	3M-1/10R2A
				IMCC45955	HNIBRBA17234	PX515354	*Vibrio sagamiensis*	99.7	Seawater	ISP2
				IMCC45168	HNIBRBA17220	PX515340	*Vibrio agarivorans*	99.8	Seawater	MA
				IMCC45262	HNIBRBA17221	PX515341	*Vibrio quintilis*	100.0	Seawater	3M-R2A
	Pseudomonadales	*Marinobacteraceae*	*Marinobacter*	IMCC46103	HNIBRBA17243	PX515363	*Marinobacter vinifirmus*	99.9	Seawater	MA (8% NaCl)
		Marinomonadaceae	*Marinomonas*	IMCC45766	HNIBRBA17228	PX515348	*Marinomonas vaga*	99.4	Seawater	ISP2
Bacteroidia	*Flavobacteriales*	*Flavobacteriaceae*	*Algitalea*	IMCC45296	HNIBRBA17222	PX515342	*Algitalea ulvae*	100.0	Seawater	3M-R2A
			Aquibacter	IMCC44520	HNIBRBA17236	PX558117	*Aquibacter zeaxanthinifaciens*	99.5	Seawater	3M-1/10R2A
			Aquimarina	IMCC44024	HNIBRBA17224	PX515344	*Aquimarina algiphila*	99.9	Seawater	MA
			Arenibacter	IMCC45435	HNIBRBA17226	PX515346	*Arenibacter amylolyticus*	99.6	Seawater	3M-1/10R2A
			Dokdonia	IMCC45995	HNIBRBA17238	PX515358	*Dokdonia pacifica*	99.7	Seawater	3M-1/10R2A
			Polaribacter	IMCC45965	HNIBRBA17235	PX515355	*Polaribacter septentrionalilitoris*	99.2	Seawater	MA
			Salegentibacter	IMCC45849	HNIBRBA17232	PX515352	*Salegentibacter holothuriorum*	99.6	Seawater	MA (8% NaCl)
			Winogradskyella	IMCC46052	HNIBRBA17240	PX515360	*Winogradskyella arenosi*	99.4	Seawater	MA
Campylobacteria	*Campylobacterales*	*Arcobacteraceae*	*Arcobacter*	IMCC45772	HNIBRBA17229	PX515349	*Arcobacter roscoffensis*	98.9	Seawater	ISP2
			Poseidonibacter	IMCC45854	HNIBRBA17233	PX515353	*Poseidonibacter lekithochrous*	99.8	Seawater	MA

All strains were incubated at 20°C for 3 days.

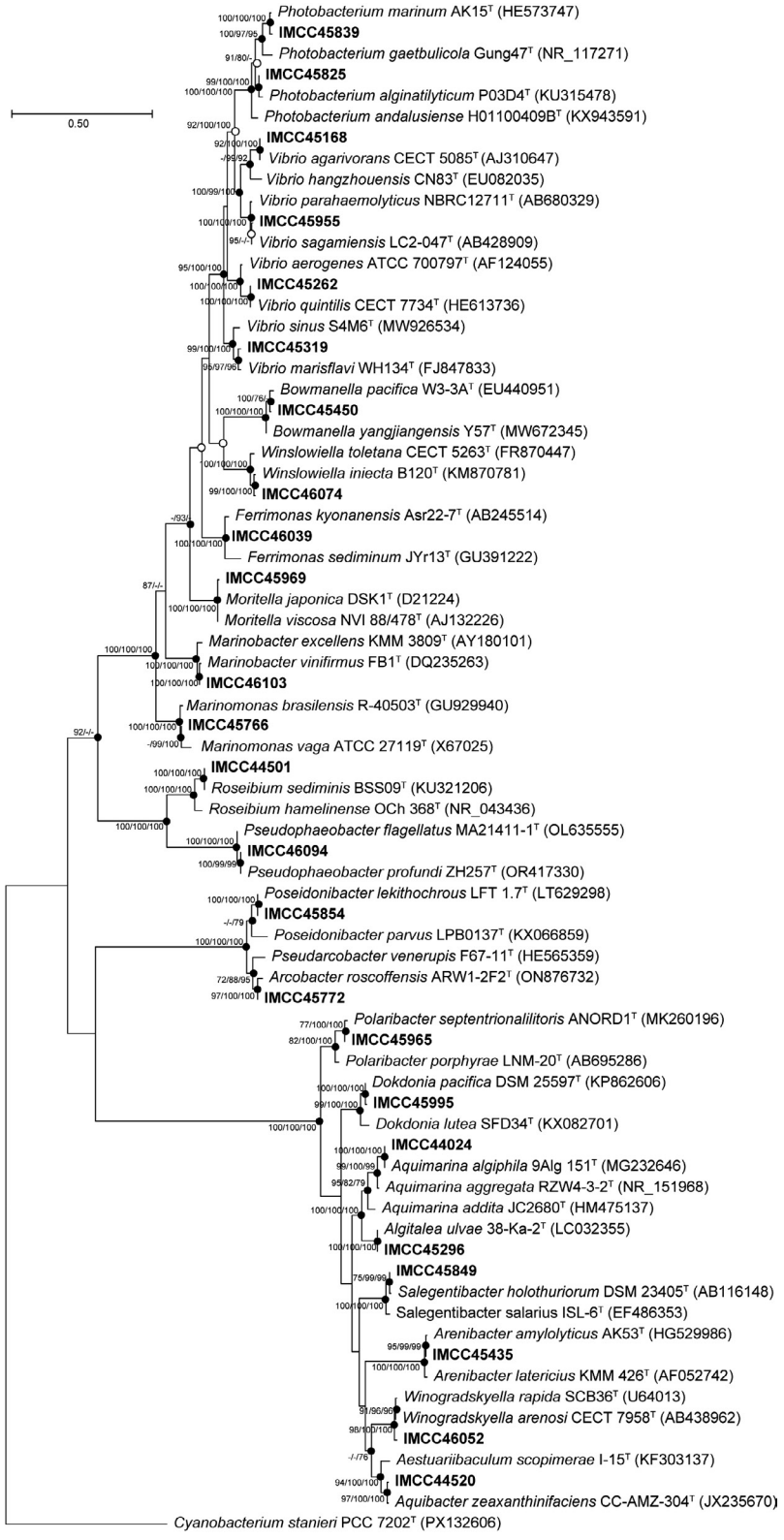


Fig. 1. Maximum-likelihood (ML) phylogenetic tree constructed from 16S rRNA gene sequences, showing the relationships between the 24 bacterial strains isolated in this study and their closest validly published species. The tree was rooted using *Cyanobacterium stanieri* PCC 7202^T as an outgroup. Bootstrap support values above 70% are indicated at nodes in the order ML/neighbor-joining (NJ)/minimum evolution (ME); "−" denotes values below 70%. Filled circles represent nodes supported by both NJ and ME analyses, while open circles indicate support from only one of the two methods. The scale bar represents 0.05 nucleotide substitutions per site.

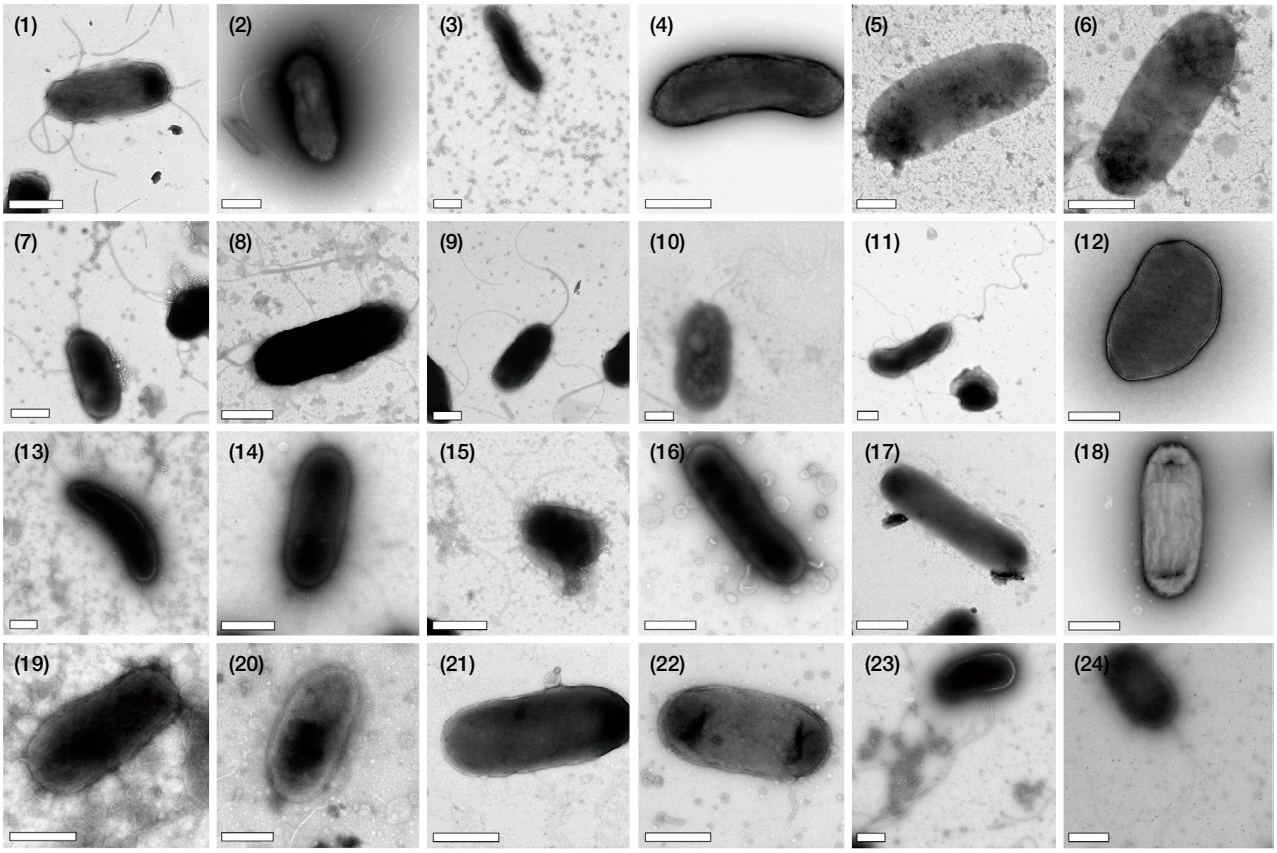


Fig. 2. Transmission electron micrographs of the 24 bacterial strains isolated in this study. Strain numbers correspond to the following isolates: 1, IMCC44501; 2, IMCC46094; 3, IMCC45450; 4, IMCC46074; 5, IMCC45969; 6, IMCC44520; 7, IMCC46039; 8, IMCC45839; 9, IMCC45825; 10, IMCC45319; 11, IMCC45955; 12, IMCC45168; 13, IMCC45262; 14, IMCC46103; 15, IMCC45766; 16, IMCC45296; 17, IMCC44024; 18, IMCC45435; 19, IMCC45995; 20, IMCC45965; 21, IMCC45849; 22, IMCC46052; 23, IMCC45772; 24, IMCC45854. Scale bars = 0.5 μm.

Detailed information for each strain, including isolation source, taxonomic assignment, and accession numbers deposited in both the HNIBR collection and GenBank, is summarized in Table 1.

Phylogenetic affiliations of the newly recorded strains were examined using 16S rRNA gene-based analyses with multiple tree reconstruction methods, including maximum-likelihood, neighbor-joining, and minimum-evolution approaches. Across all analyses, each isolate consistently clustered with the type strain of its closest related species, supported by high bootstrap values (typically 99–100%), indicating stable phylogenetic placement (Fig. 1). Concordance among tree topologies generated by different algorithms further supports the reliability of the taxonomic assignments presented.

The 24 newly recorded bacterial species collectively represent a broad taxonomic spectrum, encompassing three phyla, four classes, six orders, 11 families, and 20 genera (Table 1). Alphaproteobacterial members were assigned to the genera *Roseibium* and *Pseudophaeobacter*. The class *Gammaproteobacteria* exhibited the highest genus-level diversity and included representatives of the genera *Bowmanella*, *Winslowiella*, *Moritella*, *Ferrimonas*, *Photobacterium*, *Vibrio*, *Marinobacter*, and *Marinomonas*. Within the class *Bacteroidia*, newly recorded taxa belonged to *Algitalea*, *Aquibacter*, *Aquimarina*, *Arenibacter*, *Dokdonia*, *Polaribacter*, *Salegentibacter*, and *Winogradskyella*. Two additional genera, *Arcobacter* and *Poseidonibacter* were affiliated with the class *Campylobacteria* (Table 1).

Phenotypic characterization revealed variability among the newly recorded isolates with respect to Gram reaction, cell morphology, and flagellation (Fig. 2). Detailed morphological, physiological, and biochemical characteristics of each strain are presented in the individual species descriptions.

Description of *Roseibium sediminis* IMCC44501

Cells are Gram-stain-negative, aerobic, flagellated, and rod-shaped. Colonies are circular, convex, entire, and beige-colored after incubation for 3 days on MA at 20°C.

Positive for nitrate reduction and glucose fermentation, but negative for indole production, 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 sole carbon sources. Strain IMCC44501 (=HNIBRBA17225) was isolated from a coastal seawater sample, Jangbongdo, Incheon, Korea (37°31′41.9″N, 126°20′49.0″E).

Description of *Pseudophaeobacter profundi* IMCC46094

Cells are Gram-stain-negative, aerobic, flagellated, and short rod-shaped. Colonies are circular, convex, entire, and white-colored after incubation for 3 days on MA at 20°C. Positive for nitrate reduction, esculin hydrolysis, and gelatin hydrolysis, but negative for indole production, glucose fermentation, arginine dihydrolase, urease, β-galactosidase, and cytochrome oxidase in API 20NE. D-Maltose is utilized as sole carbon source, while D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid are not. Strain IMCC46094 (=HNIBRBA17242) was isolated from a coastal seawater sample, Daecheongdo, Incheon, Korea (37°50′51.9″N, 124°42′25.6″E).

Description of *Bowmanella yangjiangensis* IMCC45450

Cells are Gram-stain-negative, aerobic, flagellated, and rod-shaped. Colonies are irregular, raised, undulate, and creamy white-colored after incubation for 3 days on MA 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 sole carbon sources. Strain IMCC45450 (=HNIBRBA17227) was isolated from a coastal seawater sample, Gyodongdo, Incheon, Korea (37°45′29.772″N, 126°14′29.328″E).

Description of *Winslowiella iniecta* IMCC46074

Cells are Gram-stain-negative, aerobic, non-flagellated, and rod-shaped. Colonies are circular, convex, entire, and white-colored after incubation for 3 days on MA at 20°C. Positive for glucose fermentation, esculin hydrolysis, and β-galactosidase, but negative for nitrate reduction, indole production, arginine dihydrolase, urease, gelatin hydrolysis, and cytochrome oxidase in API 20NE. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, malic acid, potassium gluconate, capric acid, adipic acid, D-maltose, and trisodium citrate are utilized as sole carbon sources, while phenylacetic acid is not. Strain IMCC46074 (=HNIBRBA17241) was isolated from a coastal seawater sample, Daecheongdo, Incheon, Korea (37°50′35.5″N, 124°42′09.8″E).

Description of *Moritella viscosa* IMCC45969

Cells are Gram-stain-negative, aerobic, flagellated, and rod-shaped. Colonies are circular, entire, and pale yellow-colored after incubation for 3 days on MA at 20°C. Positive for nitrate reduction and gelatin hydrolysis, but negative for indole production, glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis, β-galactosidase, and cytochrome oxidase in API 20NE. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, malic acid, potassium gluconate, capric acid, adipic acid, D-maltose, trisodium citrate, and phenylacetic acid are not utilized as sole carbon sources. Strain IMCC45969 (=HNIBRBA17237) was isolated from a coastal seawater sample, Daecheongdo, Incheon, Korea (37°50′51.9″N, 124°42′25.6″E).

Description of *Ferrimonas kyonanensis* IMCC46039

Cells are Gram-stain-negative, aerobic, flagellated, and rod-shaped. Colonies are circular, convex, entire, and beige-colored after incubation for 3 days on MA at 20°C. Positive for nitrate reduction, glucose fermentation, esculin hydrolysis, gelatin hydrolysis, and cytochrome oxidase, but negative for indole production, arginine dihydrolase, urease, and β-galactosidase in API 20NE. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, malic acid, potassium gluconate, capric acid, adipic acid, D-maltose, trisodium citrate, and phenylacetic acid are not utilized as sole carbon sources. Strain IMCC46039 (=HNIBRBA17239) was isolated from a coastal seawater sample, Daecheongdo, Incheon, Korea (37°50′51.9″N, 124°42′25.6″E).

Description of *Photobacterium marinum* IMCC45839

Cells are Gram-stain-negative, aerobic, flagellated, and rod-shaped. Colonies are circular, convex, entire, and beige-colored after incubation for 3 days on MA at 20°C. Positive for nitrate reduction, glucose fermentation, esculin hydrolysis, and gelatin hydrolysis, but negative for indole production, arginine dihydrolase, urease, β-galactosidase, and cytochrome oxidase in API 20NE. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, malic acid, potassium gluconate, capric acid, adipic acid, D-maltose, trisodium citrate, and phenylacetic acid are not utilized

as sole carbon sources. Strain IMCC45839 (=HNIBRBA 17231) was isolated from a coastal seawater sample, Seokmodo, Incheon, Korea (37°39′01.1″N, 126°20′01.7″E).

Description of *Photobacterium alginatilyticum* IMCC45825

Cells are Gram-stain-negative, aerobic, flagellated, and rod-shaped. Colonies are circular, convex, entire, and beige-colored after incubation for 3 days on MA at 20°C. Positive for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, esculin hydrolysis, and gelatin hydrolysis, but negative for urease, β-galactosidase, and cytochrome oxidase in API 20NE. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, malic acid, potassium gluconate, capric acid, adipic acid, D-maltose, trisodium citrate, and phenylacetic acid are not utilized as sole carbon sources. Strain IMCC45825 (=HNIBRBA17230) was isolated from a coastal seawater sample, Seokmodo, Incheon, Korea (37°43′41.0″N, 126° 17′11.7″E).

Description of *Vibrio marisflavi* IMCC45319

Cells are Gram-stain-negative, aerobic, flagellated, and short rod-shaped. Colonies are circular, convex, entire, and white-colored after incubation for 3 days on MA at 20°C. Positive for nitrate reduction, arginine dihydrolase, esculin hydrolysis, gelatin hydrolysis, β-galactosidase, glucose fermentation, and cytochrome oxidase, but negative for indole production and urease in API 20NE. D-Glucose, D-mannose, *N*-acetyl-glucosamine, malic acid, potassium gluconate, adipic acid, and D-maltose are utilized as sole carbon sources, while L-arabinose, D-mannitol, capric acid, trisodium citrate, and phenylacetic acid are not. Strain IM CC45319 (=HNIBRBA17223) was isolated from a coastal seawater sample, Somaemuldo, Korea (34°37′48.0″N, 128° 33′07.5″E).

Description of *Vibrio sagamiensis* IMCC45955

Cells are Gram-stain-negative, aerobic, flagellated, and rod-shaped. Colonies are circular, convex, entire, and beige-colored after incubation for 3 days on MA 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, malic acid, potassium gluconate, capric acid, adipic acid, D-maltose, trisodium citrate, and phenylacetic acid are not utilized as sole carbon sources. Strain IMCC45955 (=HNIBRBA17234) was isolated from a coastal seawater sample, Pungdo, Korea (37° 6′34.5″N, 126°23′37.1″E).

Description of *Vibrio agarivorans* IMCC45168

Cells are Gram-stain-negative, aerobic, non-flagellated, and rod-shaped. Colonies are circular, entire, and ivory-colored after incubation for 3 days on MA at 20°C. Positive for nitrate reduction, glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis, gelatin hydrolysis, and β-galactosidase, but negative for indole production and cytochrome oxidase in API 20NE. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, malic acid, potassium gluconate, capric acid, adipic acid, D-maltose, trisodium citrate, and phenylacetic acid are not utilized as sole carbon sources. Strain IMCC45168 (=HNIBRBA 17220) was isolated from a coastal seawater sample, Somaemuldo, Korea (34°37′45.084″N, 128°32′52.836″E).

Description of *Vibrio quintilis* IMCC45262

Cells are Gram-stain-negative, aerobic, flagellated, and curved rod-shaped. Colonies are circular, convex, entire, and white-colored after incubation for 3 days on MA at 20°C. Positive for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, and gelatin hydrolysis, but negative for urease, esculin hydrolysis, β-galactosidase, and cytochrome oxidase in API 20NE. D-Glucose, D-mannose, D-mannitol, and trisodium citrate are utilized as sole carbon sources, while L-arabinose, *N*-acetyl-glucosamine, malic acid, potassium gluconate, capric acid, adipic acid, D-maltose, and phenylacetic acid are not. Strain IMCC45262 (=HNIBRBA17221) was isolated from a coastal seawater sample, Somaemuldo, Korea (34°37′45.084″N, 128°32′52.836″E).

Description of *Marinobacter vinifirmus* IMCC46103

Cells are Gram-stain-negative, aerobic, non-flagellated, and short rod-shaped. Colonies are circular, convex, entire, and white-colored after incubation for 3 days on MA at 20°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-Maltose and phenylacetic acid are utilized as sole carbon sources, while D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, malic acid, potassium gluconate, capric acid, adipic acid, and trisodium citrate are not. Strain IMCC46103 (=HNIBRBA17243) was isolated from a coastal seawater sample, Daecheongdo, Korea (37°49′ 33.0″N, 124°42′58.0″E).

Description of *Marinomonas vaga* IMCC45766

Cells are Gram-stain-negative, aerobic, flagellated, and oval-shaped. Colonies are circular, convex, entire, and white-colored after incubation for 3 days on MA 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, malic acid, potassium gluconate, capric acid, adipic acid, D-maltose, trisodium citrate, and phenylacetic acid are not utilized as sole carbon sources. Strain IMCC45766 (=HNIBRBA17228) was isolated from a coastal seawater sample, Seokmodo, Korea (37°39′01.1″N, 126°20′01.7″E).

Description of *Algitalea ulvae* IMCC45296

Cells are Gram-stain-negative, aerobic, 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 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-Maltose and trisodium citrate are utilized as sole carbon sources, while D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, malic acid, potassium gluconate, capric acid, adipic acid, and phenylacetic acid are not. Strain IMCC45296 (=HNIBRBA17222) was isolated from a coastal seawater sample, Somaemuldo, Korea (34°37′48.0″N, 128°33′07.5″E).

Description of *Aquibacter zeaxanthinifaciens* IMCC44520

Cells are Gram-stain-negative, aerobic, non-flagellated, and rod-shaped. Colonies are circular, entire, and yellow-colored after incubation for 3 days on MA at 20°C. Positive for glucose fermentation and gelatin hydrolysis, but negative for nitrate reduction, indole production, arginine dihydrolase, urease, esculin hydrolysis, β-galactosidase, and cytochrome oxidase in API 20NE. D-Glucose, L-arabinose, D-mannose, *N*-acetyl-glucosamine, and D-maltose are utilized as sole carbon sources, while D-mannitol, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid are not. Strain IMCC44520 (=HNIBRBA17236) was isolated from a coastal seawater sample, Jangbongdo, Incheon, Korea (37°31′41.9″N, 126°20′49.0″E).

Description of *Aquimarina algiphila* IMCC44024

Cells are Gram-stain-negative, aerobic, 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 nitrate reduction, esculin hydrolysis, gelatin hydrolysis, and β-galactosidase, but negative for indole production, glucose fermentation, arginine dihydrolase, urease, and cytochrome oxidase in API 20NE. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, malic acid, potassium gluconate, capric acid, adipic acid, D-maltose, trisodium citrate, and phenylacetic acid are not utilized as sole carbon sources. Strain IMCC44024 (=HNIBRBA17224) was isolated from a coastal seawater sample, Yeonpyeongdo, Korea (37°40′09.4″N, 125°41′04.2″E).

Description of *Arenibacter amylolyticus* IMCC45435

Cells are Gram-stain-negative, aerobic, non-flagellated, and rod-shaped. Colonies are circular, entire, and yellow-colored after incubation for 3 days on MA at 20°C. Positive for β-galactosidase, but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis, gelatin hydrolysis, and cytochrome oxidase in API 20NE. Trisodium citrate is utilized as sole carbon source, while D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, malic acid, potassium gluconate, capric acid, adipic acid, D-maltose, and phenylacetic acid are not. Strain IMCC45435 (=HNIBRBA17226) was isolated from a coastal seawater sample, Gyodongdo, Incheon, Korea (37°45′29.772″N, 126°14′29.328″E).

Description of *Dokdonia pacifica* IMCC45995

Cells are Gram-stain-negative, aerobic, non-flagellated, and rod-shaped. Colonies are circular, convex, entire, and pale yellow-colored after incubation for 3 days on MA at 20°C. Positive for urease, esculin hydrolysis, and β-galactosidase, but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, gelatin hydrolysis, and cytochrome oxidase in API 20NE. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, malic acid, potassium gluconate, capric acid, adipic acid, D-maltose, trisodium citrate, and phenylacetic acid are not utilized as sole carbon sources. Strain IMCC45995 (=HNIBRBA17238) was isolated from a coastal seawater sample, Pungdo, Korea (37°6′52.4″N, 126°22′57.0″E).

Description of *Polaribacter septentrionalilitoris* IMCC45965

Cells are Gram-stain-negative, aerobic, non-flagellated, and rod-shaped. Colonies are circular and convex, and yellow-colored after incubation for 3 days on MA at 20°C. Positive for glucose fermentation, esculin hydrolysis, gelatin hydrolysis, and cytochrome oxidase, but negative for nitrate reduction, indole production, arginine dihydrolase, urease, and β-galactosidase in API 20NE. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, malic acid, potassium gluconate, capric acid, adipic acid, D-maltose, trisodium citrate, and phenylacetic acid are

not utilized as sole carbon sources. Strain IMCC45965 (=HNIBRBA17235) was isolated from a coastal seawater sample, Daecheongdo, Korea (37°50′51.9″N, 124°42′25.6″E).

Description of *Salegentibacter holothuriorum* IMCC45849

Cells are Gram-stain-negative, aerobic, non-flagellated, and short rod-shaped. Colonies are circular, convex, entire, and yellow-colored after incubation for 3 days on MA at 20°C. Positive for glucose fermentation, esculin hydrolysis, gelatin hydrolysis, and β-galactosidase, but negative for nitrate reduction, indole production, arginine dihydrolase, urease, and cytochrome oxidase in API 20NE. D-Glucose, D-mannose, *N*-acetyl-glucosamine, and malic acid are utilized as sole carbon sources, while L-arabinose, D-mannitol, potassium gluconate, capric acid, adipic acid, D-maltose, trisodium citrate, and phenylacetic acid are not. Strain IMCC45849 (=HNIBRBA17232) was isolated from a coastal seawater sample, Sido, Korea (37°31′20.8″N, 126°25′29.5″E).

Description of *Winogradskyella arenosi* IMCC46052

Cells are Gram-stain-negative, aerobic, 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 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, malic acid, potassium gluconate, capric acid, adipic acid, D-maltose, trisodium citrate, and phenylacetic acid are not utilized as sole carbon sources. Strain IMCC46052 (=HNIBRBA17240) was isolated from a coastal seawater sample, Daecheongdo, Korea (37°49′33.0″N, 124°42′58.0″E).

Description of *Arcobacter roscoffensis* IMCC45772

Cells are Gram-stain-negative, aerobic, flagellated, and rod-shaped. Colonies are circular, convex, entire, and white-colored after incubation for 3 days on MA at 20°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, malic acid, potassium gluconate, capric acid, adipic acid, D-maltose, trisodium citrate, and phenylacetic acid are not utilized as sole carbon sources. Strain IMCC45772 (=HNIBRBA17229) was isolated from a coastal seawater sample, Seokmodo, Korea (37°39′01.1″N, 126°20′01.7″E).

Description of *Poseidonibacter lekithochrous* IMCC45854

Cells are Gram-stain-negative, aerobic, flagellated, and short rod-shaped. Colonies are circular, convex, entire, and beige-colored after incubation for 3 days on MA at 20°C. Positive for nitrate reduction, but negative for 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, malic acid, potassium gluconate, capric acid, adipic acid, D-maltose, trisodium citrate, and phenylacetic acid are not utilized as sole carbon sources. Strain IMCC45854 (=HNIBRBA17233) was isolated from a coastal seawater sample, Seokmodo, Korea (37°43′41.0″N, 126°17′11.7″E).

Conflicts of Interest

The authors of this paper have no affiliation with any interests and are solely responsible for the paper.

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