Journal of Species Research 13(3):293-305, 2024

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A report on 36 unrecorded bacterial species isolated from Korean islands in 2023

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Various samples were collected from Korean islands in order to obtain unrecorded bacterial species in 2023. After aerobically incubating on marine agar and Reasoner's 2A agar, approximately 1,200 bacterial strains were isolated and identified using 16S rRNA gene sequences. A total of 36 strains showed ≥98.7% sequence similarity to previously published and validated bacterial species. However, these strains have not previously been reported in the Republic of Korea, indicating that they belong to Korean unrecorded bacterial species. The unrecorded bacterial species were assigned to the classes *Actinomycetes*, *Bacilli*, *Bacteroidia*, *Flavobacteriia*, *Sphingobacteriia*, *Alphaproteobacteria*, *Betaproteobacteria*, and *Gammaproteobacteria*. The information we obtained by examining the strains includes details of the Gram reactions, colony and cell morphology, biochemical characteristics, and phylogenetic positions of the unrecorded species.

Keywords: 16S rRNA gene sequence, islands, unrecorded bacterial species

DOI:10.12651/JSR.2024.13.3.293

Introduction

Islands are characterized by the presence of various endemic species, harboring ~20% of the Earth's biodiversity (Fernández-Palacios *et al*., 2021). In the Republic of Korea, 3,358 islands exist, the ecosystems of which are diverse, including marine, coastal, and soil environments. Albeit small area accounting for a mere 3.5% of Korea's land area, the Korean islands have contributed to increase the biodiversity of the Korean Peninsula. Among the 287 novel plant species reported in Korea since the 1990s, 150 were discovered on islands (Lim *et al*., 2012; National Institute of Biological Resources, 2020). In addition to plants, numerous new and unrecorded microbial species have also been discovered around islands (Kim *et al*., 2020; Shin *et al*., 2022; Cho *et al*., 2023; Shin *et al*., 2023a; Shin *et al*., 2023b). As of January 2024, 4,989 bacterial species were recorded in Korea (National List of Species of Korea, https://species.nibr.go.kr/index.do). These species have been found in diverse regions, yet only a small portion have been retrieved from islands. Microorganisms, like plants and animals, exhibit biogeographic patterns, but little is known about their distribution and functional features on and between islands (Li *et al*., 2020). Here, we tried to isolate previously unrecorded bacterial species from various Korean islands and investigate their phenotypic characteristics based on a research program supported by the Honam National Institute of Biological Resources (HNIBR). A total of 36 bacterial species belonging to the classes *Actinomycetes*, *Bacilli*, *Bacteroidia*, *Flavobacteria*, *Sphingobacteria*, *Alphaproteobacteria*, *Betaproteobacteria*, and *Gammaproteobacteria* were determined to be previously unrecorded in Korea, and their phenotypic characteristics are reported here.

Materials and Methods

Seawater, halophyte, and tidal flat sediment samples were collected from Korean islands in 2023 using a

1 L buck sampler, digging knife, and sediment sampler, respectively. The samples were transferred at 4°C and inoculated as follows. An aliquot (100 μL) of each seawater sample was spread directly onto marine agar (MA, Difco). A piece of halophyte root was washed with phosphate buffered saline (PBS) to remove residual soil and severed using sterile scissors. Using a homogenizer (IKA), 0.1 g of the sub-sample was thoroughly mixed with 1 mL of 1% PBS. The final suspension (100 μL) of the homogenized sample was spread onto MA and Reasoner's 2A agar (R2A, Difco). For tidal flat sediment, 1 g of each sample was thoroughly mixed with 100 mL of distilled water using the homogenizer. An aliquot (100 μL) of each homogenized sample was spread onto the MA and R2A. The inoculated samples were aerobically incubated at 20°C for 7 days. The bacterial strains were purified; the pure cultures were preserved in a 20% (v/v) glycerol suspension at −80°C as well as a lyophilized ampoule. Details of the strains are shown in Table 1.

To determine colony morphology, bacterial colonies that had reached the stationary phase were observed on the agar plates. Cell morphology, including cell shape, presence of flagella, and cell size, was examined using transmission electron microscopy (CM200; Philips) after staining with 2% (w/v) uranyl acetate. Gram staining was performed using a Gram staining kit (bioMérieux). Oxidase activity was examined using an oxidase reagent (bioMérieux). API 20NE galleries (bioMérieux) were employed for additional biochemical characterization. In API 20NE, the strains were tested according to the manufacturer's instructions.

To determine the phylogenetic positions of the isolated strains, bacterial DNA extraction, PCR amplification, and 16S rRNA gene sequencing were performed according to the standard procedures previously described (Yang and Cho, 2008). We obtained 16S rRNA gene sequences using primers 518F and 800R. The resultant 16S rRNA gene sequences were compared with those of other bacterial strains with validly published names using EzBioCloud (Yoon *et al*., 2017) and the NIBR database. A 16S rRNA gene sequence similarity of 98.7% was used as the cutoff value for bacterial species demarcation (Chun *et al*., 2018). Therefore, bacterial strains exhibiting ≥98.7% 16S rRNA gene sequence similarity with species that have been validly published but never reported in Korea were determined to be unrecorded species. To determine phylogenetic position, the closely related species of the 36 strains were selected based on EzBioCloud and NIBR database. Multiple sequence alignments were performed between the 16S rRNA gene sequences using ClustalW, which was implemented in version 11 of MEGA (Tamura *et al*., 2021). Using the unambiguously aligned 16S rRNA gene sequences, phylogenetic trees were reconstructed based on the neighbor-joining (Saitou and Nei, 1987), maximum-likelihood (Felsenstein, 1981), and minimum evolution (Rzhetsky and Nei, 1993) methods. The robustness of the inferred phylogenetic trees was evaluated using bootstrap analyses based on 1,000 random resamplings (Felsenstein, 1985).

Results and Discussion

Detailed information on the samples is listed in the Island Bioresource Total Information System (IBIS, https://ibis.hnibr.re.kr). We performed 16S rRNA gene sequence analyses using approximately 1,200 bacterial strains, revealing that many strains were expected to be novel species or species previously unreported in Korea. Of these 1,200 strains, 36 showed ≥98.7% 16S rRNA gene sequence similarity with species that have previously been reported, but not in Korea. Strain information and identifications, taxonomic assignments from species to classes, isolation sources, and sequence accession numbers, including HNIBR and GenBank numbers, are listed in Table 1. Phylogenetic assignments of strains to established bacterial species based on 16S rRNA gene sequence similarity were confirmed through phylogenetic tree analysis (Figs. 1, 2). All strains identified as unrecorded species formed a robust clade with the type strains of each corresponding species, with high bootstrap values.

The 36 unrecorded bacterial species were phylogenetically diverse, belonging to 4 phyla, 8 classes, 16 orders, 24 families, and 33 genera (Table 1). At the genus level, the unrecorded species were assigned to genera *Streptomyces*, *Myceligenerans*, *Gordonia*, *Nocardia*, *Mycolicibacterium*, and *Lentzea* of the class *Actinomycetes;* *Saccharibacillus* and *Paenibacillus* of the class *Bacilli*; *Mangrovibacterium* of the class *Bacteroidia; Bizionia*, *Aquimarina*, and *Kordia* of the class *Flavobacteriia*; *Sphingobacterium* of the class *Sphingobacteriia*; *Rhizobium*, *Roseibium*, *Phyllobacterium*, *Pararhodobacter*, *Pseudosulfitobacter*, *Salipiger*, *Ruegeria*, *Qipengyuania*, *Aurantiacibacter*, *Erythrobacter*, and *Sphingomonas* of the class *Alphaproteobacteria*; *Hydrogenophaga* and *Caballeronia* of the class *Betaproteobacteria*; and *Shewanella*, *Saccharospirillum*, *Halomonas*, *Salinicola*, *Atopomonas*, *Vibrio*, and *Paraphotobacterium* of the class *Gammaproteobacteria*.

The 36 unrecorded species identified in this study are Gram-negative or -positive, flagellated or non-flagellated, rod-shaped bacteria (Fig. 3). The detailed morphological, physiological, and biochemical characteristics of the unrecorded bacterial species are specified in the following strain descriptions.

Table 1. Summary of strains isolated and their taxonomic affiliations.

Phylum	Class	Order	Family	Strain ID	HNIBRBA ID	Accession number	Closest species	Similarity (%)	Source
Actinomycetota	*Actinomycetes*	*Kitasatosporales*	*Streptomycetaceae*	R23HP9	HNIBRBA5984	PP067164	*Streptomyces chumphonensis*	99.1	Halophyte root
				UCR7	HNIBRBA7025	OR564222	*Streptomyces spectabilis*	99.9	Agricultural soil
		Micrococcales	*Promicromonosporaceae*	R23HP188	HNIBRBA6729	OR863777	*Myceligenerans indicum*	99.5	Halophyte root
		Mycobacteriales	*Gordoniaceae*	22HPR-12	HNIBRBA7036	PP067163	*Gordonia mangrovi*	99.1	Halophyte root
			Nocardiaceae	KR3-23	HNIBRBA7030	OR342813	*Nocardia takedensis*	100.0	Soil
			Mycobacteriaceae	KR3-11	HNIBRBA7031	OR346158	*Mycolicibacterium fluoranthenivorans*	99.4	Soil
		Pseudonocardiales	*Pseudonocardiaceae*	R23HP317	HNIBRBA6862	OR863780	*Lentzea alba*	98.9	Halophyte root
Bacillota	*Bacilli*	*Caryophanales*	*Paenibacillaceae*	M23HP199	HNIBRBA6230	OR863772	*Saccharibacillus endophyticus*	99.2	Halophyte root
				BT773	HNIBRBA7029	OR350926	*Paenibacillus periandrae*	99.9	Soil
Bacteroidota	*Bacteroidia*	*Bacteroidales*	*Prolixibacteraceae*	M23HP108	HNIBRBA6165	OR863764	*Mangrovibacterium lignilyticum*	100.0	Halophyte root
	Flavobacteriia	*Flavobacteriales*	*Flavobacteriaceae*	M23HP44	HNIBRBA5755	OR863763	*Bizionia echini*	99.9	Halophyte root
				M23SW434	HNIBRBA6937	OR863783	*Aquimarina macrocephali*	100.0	Seawater
				DB13	HNIBRBA7141	PP079953	*Kordia ulvae*	99.3	Seawater
	Sphingobacteriia	*Sphingobacteriales*	*Sphingobacteriaceae*	M23HP145	HNIBRBA6194	OR863769	*Sphingobacterium alkalisoli*	99.5	Halophyte root
Pseudomonadota	*Alphaproteobacteria*	*Hyphomicrobiales*	*Rhizobiaceae*	M23HP171	HNIBRBA6209	OR863771	*Rhizobium sphaerophysae*	99.9	Halophyte root
				R23HP227	HNIBRBA7039	OR889344	*Rhizobium rhizolycopersici*	98.8	Halophyte root
			Stappiaceae	M23HP230	HNIBRBA6248	OR863773	*Roseibium litorale*	99.8	Halophyte root
			Phyllobacteriaceae	BU6-25	HNIBRBA7032	PP709217	*Phyllobacterium trifolii*	99.4	Soil
		Rhodobacterales	*Paracoccaceae*	M23HP266	HNIBRBA6333	OR863774	*Pararhodobacter aggregans*	99.0	Halophyte root
			Roseobacteraceae	M23HP116	HNIBRBA6169	OR863765	*Pseudosulfitobacter pseudonitzschiae*	100.0	Halophyte root
				M23SW15	HNIBRBA5793	OR863775	*Salipiger marinus*	98.7	Seawater
				WD6	HNIBRBA7027	OR535062	*Ruegeria alba*	100.0	Tidal flat
		Sphingomonadales	*Erythrobacteraceae*	M23HP119	HNIBRBA6170	OR863766	*Qipengyuania aestuarii*	99.9	Halophyte root
				M23HP134	HNIBRBA6184	OR863767	*Aurantiacibacter xanthus*	99.8	Halophyte root
				R31	HNIBRBA7140	PP079952	*Erythrobacter aurantius*	99.1	Seawater
			Sphingomonadaceae	DG1-23	HNIBRBA7033	OR342727	*Sphingomonas psychrotolerans*	99.4	Soil
	Betaproteobacteria	*Burkholderiales*	*Comamonadaceae*	M23HP170	HNIBRBA6208	OR863770	*Hydrogenophaga carboriunda*	98.8	Halophyte root
			Burkholderiaceae	DG2UV-4-2	HNIBRBA7028	OR342744	*Caballeronia arvi*	98.8	Soil
	Gammaproteobacteria	*Alteromonadales*	*Shewanellaceae*	M23SW444	HNIBRBA6943	OR863785	*Shewanella woodyi*	99.8	Seawater
		Oceanospirillales	*Saccharospirillaceae*	M23HP139	HNIBRBA6189	OR863768	*Saccharospirillum correiae*	99.4	Halophyte root
			Halomonadaceae	M23HP354	HNIBRBA6820	OR863778	*Halomonas malpeensis*	98.9	Halophyte root
				M23HP356	HNIBRBA6822	OR863779	*Salinicola socius*	99.9	Halophyte root
		Pseudomonadales	*Pseudomonadaceae*	WA2	HNIBRBA7026	OR492599	*Atopomonas hussainii*	99.9	Tidal flat
		Vibrionales	*Vibrionaceae*	M23SO83	HNIBRBA6905	OR863781	*Vibrio amylolyticus*	99.6	Tidal flat
				M23SW435	HNIBRBA6938	OR863784	*Vibrio gallaecicus*	99.5	Seawater
				M23SW448	HNIBRBA6947	OR863786	*Paraphotobacterium marinum*	100.0	Seawater

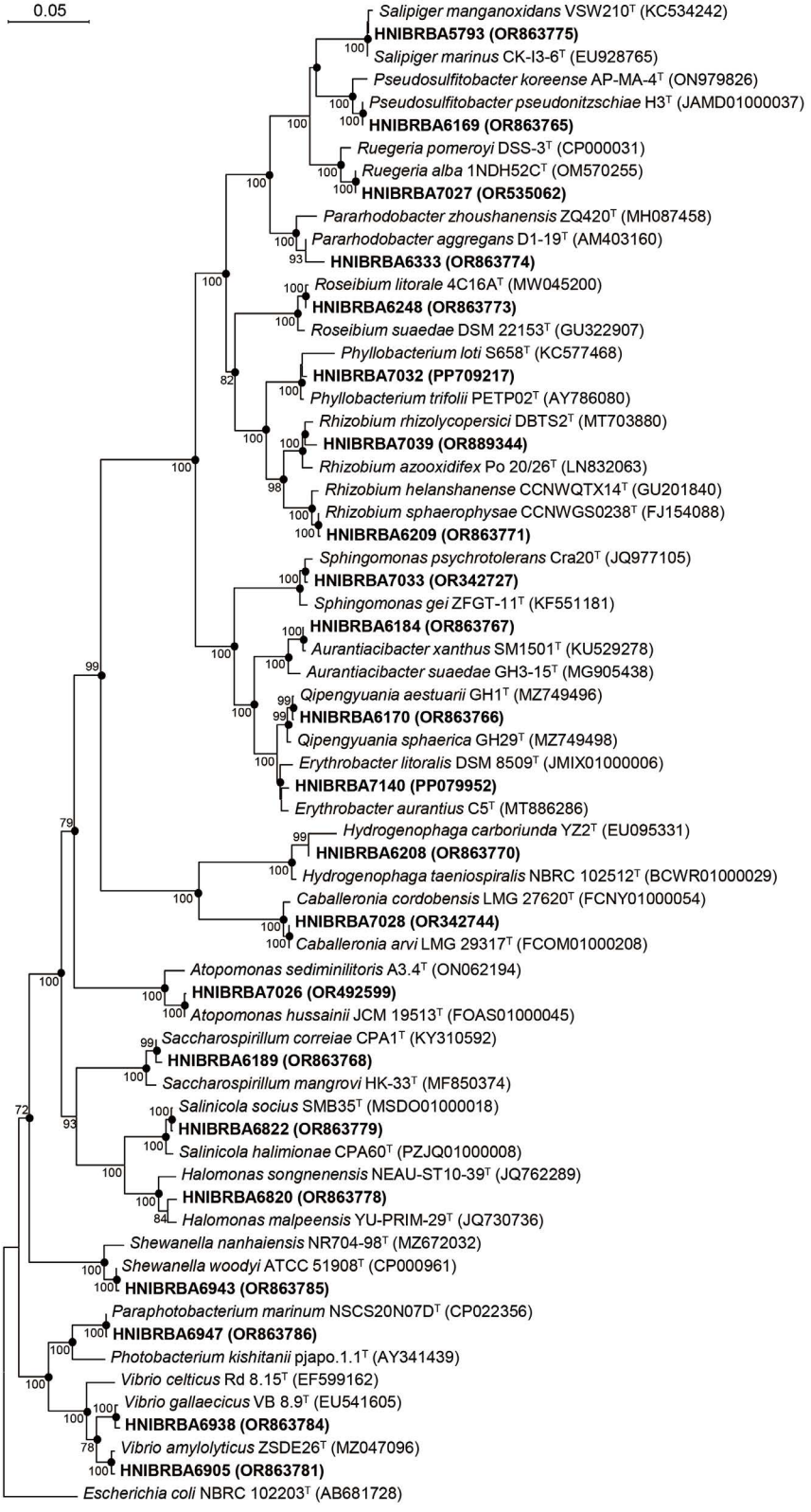

Fig. 1. A neighbor-joining phylogenetic tree based on 16S rRNA gene sequences showing the relationships between the strains isolated in this study and their closest relatives in the phylum *Pseudomonadota*. Filled circles indicate that the corresponding nodes were recovered by all treeing methods. Open circles indicate that the corresponding nodes were recovered by any two out of three. Bootstrap values over 70% are shown. Bar, 0.05 substitutions per nucleotide position.

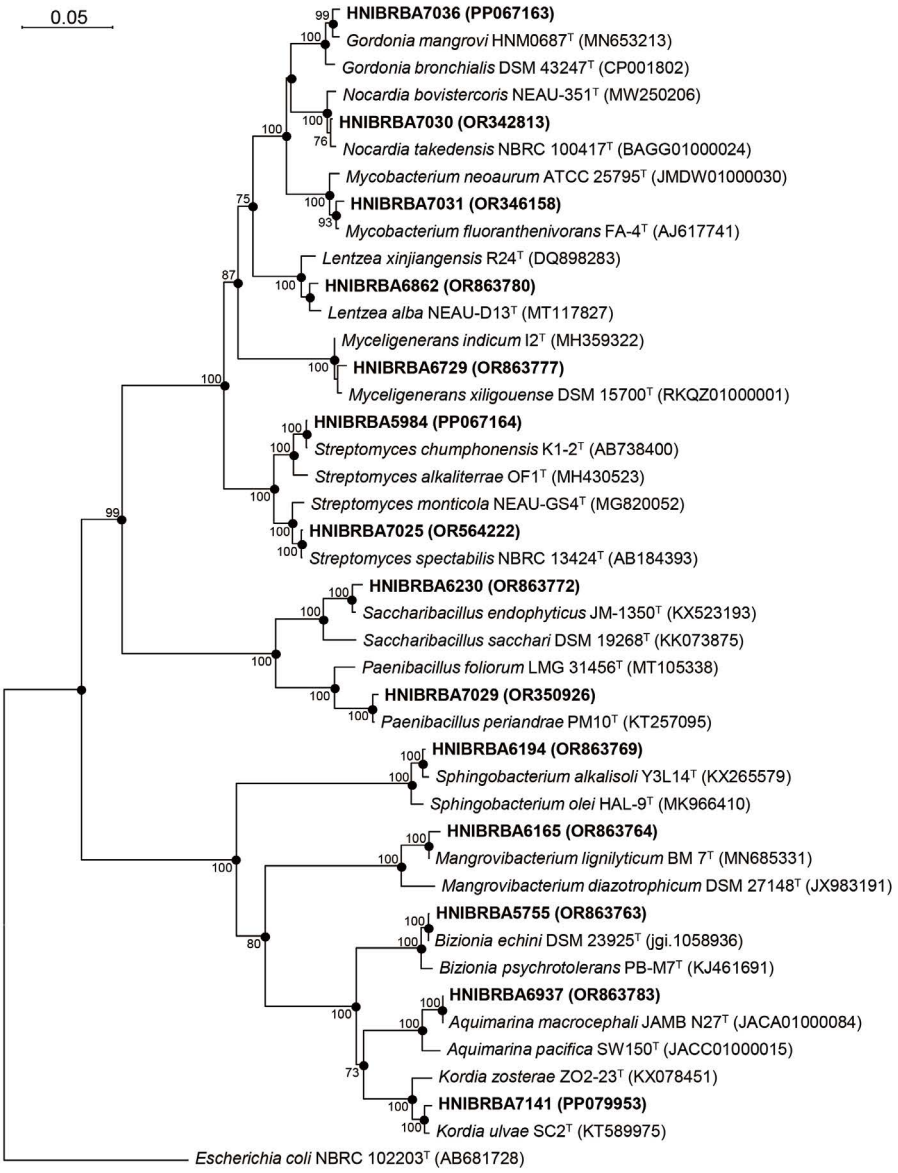

Fig. 2. Neighbor-joining phylogenetic tree, based on 16S rRNA gene sequences, showing the relationship between the strains isolated in this study and their relatives in the phylum *Actinomycedota*, *Bacillota* and *Bacteroidota*. Filled circles indicate that the corresponding nodes were recovered by all treeing methods. Open circles indicate that the corresponding nodes were recovered by any two out of three. Bootstrap values over 70% are shown. Bar, 0.05 substitutions per nucleotide position.

Description of *Bizionia echini* M23HP44

The cells are Gram-stain-negative, non-flagellated, and rod-shaped. The colonies are circular, convex, entire, and orange-colored after incubating for 7 days on MA at 20°C. They are positive for gelatin hydrolysis and cytochrome oxidase; but negative for nitrate reduction, indole production, 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 M23HP44 (= HNIBRBA5755) was isolated from a halophyte sample from Dallido Island (34°46′55.4″N, 126°19′40.8″E), Jeollanam-do, Korea. The GenBank accession number of the 16S rRNA gene sequence is OR863763.

Description of *Salipiger marinus* M23SW15

The cells are Gram-stain-negative, non-flagellated, and rod-shaped. The colonies are circular, convex, entire, and yellow-colored after incubating for 7 days on MA

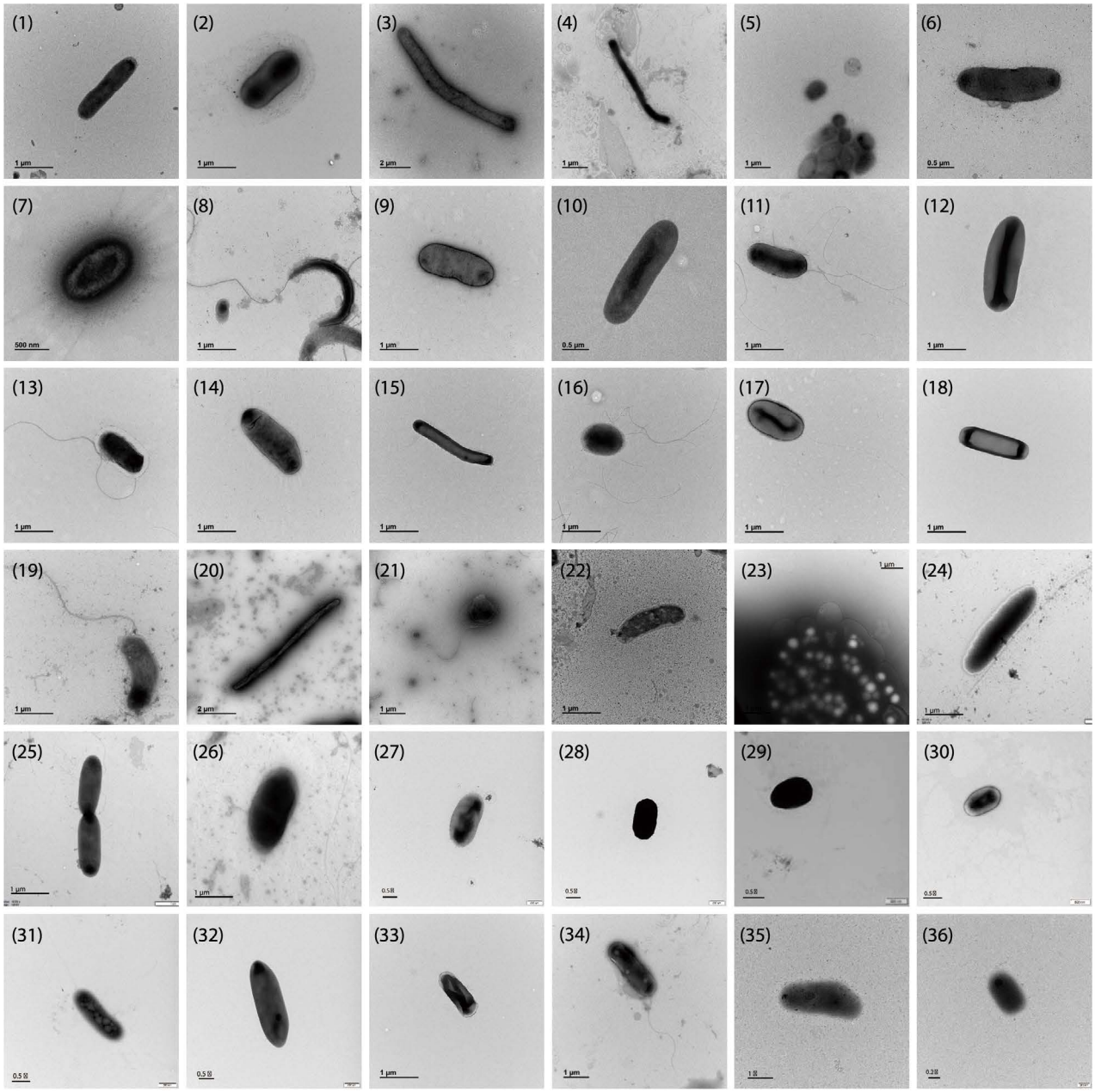

Fig. 3. Transmission electron micrographs of cells of the strains isolated in this study. Strains: 1, HNIBRBA5755; 2, HNIBRBA5793; 3, HNIBRBA5984; 4, HNIBRBA6165; 5, HNIBRBA6169; 6, HNIBRBA6170; 7, HNIBRBA6184; 8, HNIBRBA6189; 9, HNIBRBA6194; 10, HNIBRBA6208; 11, HNIBRBA6209; 12, HNIBRBA6230; 13, HNIBRBA6248; 14, HNIBRBA6333; 15, HNIBRBA6729; 16, HNIBRBA6820; 17, HNIBRBA6822; 18, HNIBRBA6862; 19, HNIBRBA6905; 20, HNIBRBA6937; 21, HNIBRBA6938; 22, HNIBRBA6943; 23, HNIBRBA6947; 24, HNIBRBA7025; 25, HNIBRBA7026; 26, HNIBRBA7027; 27, HNIBRBA7028; 28, HNIBRBA7029; 29, HNIBRBA7030; 30, HNIBRBA7031; 31, HNIBRBA7032; 32, HNIBRBA7033; 33, HNIBRBA7036; 34, HNIBRBA7039; 35, HNIBRBA7140; 36, HNIBRBA7141. Scale bars are indicated in parenthesis after strain ID.

at 20°C. They are positive for urease, esculin hydrolysis and cytochrome oxidase; but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, gelatin hydrolysis and β-galactosidase in API 20NE. D-glucose, L-arabinose, D-mannose, D-mannitol, D-maltose, potassium gluconate adipic acid, malic acid, trisodium citrate and phenylacetic acid are utilized as sole carbon sources; but *N*-acetyl-glucosamine and capric acid are not. Strain M23SW15 (= HNIBRBA5793) was isolated from a sea water sample from Amtaedo Island (34°48′5.74″N, 126°7′11.63″E), Jeollanam-do, Korea. The GenBank accession number of the

16S rRNA gene sequence is OR863775.

Description of *Streptomyces chumphonensis* R23HP9

The cells are Gram-stain-positive, non-flagellated, and rod-shaped. The colonies are circular, umbonate, entire, and white-colored after incubating for 7 days on R2A at 20°C. They are 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 is utilized as a sole carbon source; but 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. Strain R23HP9 (= HNIBRBA5984) was isolated from a halophyte samplefrom Amtaedo Island (34°51′7.58″N, 126°6′4.47″E), Jeollanam-do, Korea. The GenBank accession number of the 16S rRNA gene sequence is PP067164.

Description of *Mangrovibacterium lignilyticum* M23HP108

The cells are Gram-stain-negative, non-flagellated, and rod-shaped. The colonies are circular, convex, entire, and orange-red colored after incubating for 7 days on MA at 20°C. They are 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 M23HP108 (= HNIBRBA6165) was isolated from a halophyte sample from Gadeokdo Island (35°03′30.4″N, 128°50′44.9″E), Busan, Korea. The GenBank accession number of the 16S rRNA gene sequence is OR863764.

Description of *Pseudosulfitobacter pseudonitzschiae* M23HP116

The cells are Gram-stain-negative, non-flagellated, and rod-shaped. The colonies are circular, convex, entire, and beige-colored after incubating for 7 days on MA at 20°C. They are positive for glucose fermentation, arginine dihydrolase, urease, and cytochrome oxidase; but negative for nitrate reduction, indole production, esculin hydrolysis, gelatin hydrolysis, and β-galactosidase in API 20NE. D-glucose, L-arabinose, D-mannitol, potassium gluconate, adipic acid, and malic acid are utilized as sole carbon sources; but D-mannose, *N*-acetyl-glucosamine, D-maltose, capric acid, trisodium citrate, and phenylacetic acid are not. Strain M23HP116 (= HNIBRBA6169) was isolated from a halophyte sample from Gadeokdo Island (34°48′5.74″N, 126°7′11.63″E), Busan, Korea. The GenBank accession number of the 16S rRNA gene sequence is OR863765.

Description of *Qipengyuania aestuarii* M23HP119

The cells are Gram-stain-negative, non-flagellated, and rod-shaped. The colonies are circular, convex, entire, and beige-colored after incubating for 7 days on MA at 20°C. They are positive for glucose fermentation, arginine dihydrolase, urease, and cytochrome oxidase; but negative for nitrate reduction, indole production, esculin hydrolysis, gelatin hydrolysis, and β-galactosidase in API 20NE. D-glucose, L-arabinose, D-mannitol, potassium gluconate, adipic acid, and malic acid are utilized as sole carbon sources; but D-mannose, *N*-acetyl-glucosamine, D-maltose, capric acid, trisodium citrate, and phenylacetic acid are not. Strain M23HP119 (= HNIBRBA6170) was isolated from a halophyte sample from Gadeokdo Island (34°48′5.74″N, 126°7′11.63″E), Busan, Korea. The GenBank accession number of the 16S rRNA gene sequence is OR863766.

Description of *Aurantiacibacter xanthus* M23HP134

The cells are Gram-stain-negative, non-flagellated, and rod-shaped. The colonies are circular, convex, entire, and yellow-colored after incubating for 7 days on MA at 20°C. They are positive for urease, esculin hydrolysis, β-galactosidase and cytochrome oxidase; but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, and gelatin hydrolysis in API 20NE. D-glucose, and L-arabinose are utilized as sole carbon sources; but D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid are not. Strain M23HP134 (= HNIBRBA6184) was isolated from a halophyte sample from Gadeokdo Island (34°48′5.74″N, 126°7′11.63″E), Busan, Korea. The GenBank accession number of the 16S rRNA gene sequence is OR863767.

Description of *Saccharospirillum correiae* M23HP139

The cells are Gram-stain-negative, flagellated, and rod-shaped. The colonies are circular, convex, entire, and white-colored after incubating for 7 days on MA at 20°C. They are 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, D-mannose and D-maltose are utilized as sole carbon sources; but L-arabinose, D-manni-

tol, *N*-acetyl-glucosamine, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid are not. Strain M23HP139 (= HNIBRBA6189) was isolated from a halophyte sample from Gadeokdo Island (34°48′5.74″N, 126°7′11.63″E), Busan, Korea. The GenBank accession number of the 16S rRNA gene sequence is OR863768.

Description of *Sphingobacterium alkalisoli* M23HP145

The cells are Gram-stain-negative, flagellated, and rod-shaped. The colonies are circular, convex, entire, and white-colored after incubating for 7 days on MA at 20 °C. They are 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, D-mannose, *N*-acetyl-glucosamine, and D-maltose are utilized as sole carbon sources; but L-arabinose, D-mannitol, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid are not. Strain M23HP145 (= HNIBRBA6194) was isolated from a halophyte sample from Aphaedo Island (34°51′32.7″N, 126°13′54″E), Jeollanam-do, Korea. The GenBank accession number of the 16S rRNA gene sequence is OR863769.

Description of *Hydrogenophaga carboriunda* M23HP170

The cells are Gram-stain-negative, flagellated, and rod-shaped. The colonies are circular, convex, entire, and yellow-colored after incubating for 7 days on MA at 20°C. They are 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, potassium gluconate, adipic acid, malic acid, trisodium citrate, and phenylacetic acid are utilized as sole carbon sources; but *N*-acetyl-glucosamine, D-maltose, and capric acid are not. Strain M23HP170 (= HNIBRBA6208) was isolated from a halophyte sample, Aphaedo Island (34°51′32.7″N, 126°13′54″E) from Jeollanam-do, Korea. The GenBank accession number of the 16S rRNA gene sequence is OR863770.

Description of *Rhizobium sphaerophysae* M23HP171

The cells are Gram-stain-negative, flagellated, and rod-shaped. The colonies are circular, convex, entire, and beige-colored after incubating for 7 days on MA at 20°C. They are positive for nitrate reduction, glucose fermentation, urease, esculin hydrolysis, β-galactosidase, and cytochrome oxidase; but negative for indole production, arginine dihydrolase, and gelatin hydrolysis in API 20NE. D-glucose, L-arabinose, D-mannose, D-mannitol, potassium gluconate, adipic acid, malic acid, trisodium citrate, and phenylacetic acid are utilized as sole carbon sources; but *N*-acetyl-glucosamine, D-maltose and capric acid are not. Strain M23HP139 (= HNIBRBA6209) was isolated from a halophyte sample from Aphaedo Island (34°51′32.7″N, 126°13′54″E), Jeollanam-do, Korea. The GenBank accession number of the 16S rRNA gene sequence is OR863771.

Description of *Saccharibacillus endophyticus* M23HP199

The cells are Gram-stain-positive, non-flagellated, and rod-shaped. The colonies are circular, convex, entire, and white-colored after incubating for 7 days on MA at 20°C. They are positive for nitrate reduction, esculin hydrolysis, β-galactosidase, and cytochrome oxidase; but negative for indole production, glucose fermentation, arginine dihydrolase, urease, and gelatin hydrolysis in API 20NE. L-arabinose, D-mannose, D-mannitol, D-maltose, and potassium gluconate are utilized as sole carbon sources; but *N*-acetyl-glucosamine, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid are not. Strain M23HP199 (= HNIBRBA6230) was isolated from a halophyte sample from Aphaedo Island (34°51′32.7″N, 126°13′54″E), Jeollanam-do, Korea. The GenBank accession number of the 16S rRNA gene sequence is OR863772.

Description of *Roseibium litorale* M23HP230

The cells are Gram-stain-negative, flagellated, and rod-shaped. The colonies are circular, convex, entire, and yellow-colored after incubating for 7 days on MA at 20°C. They are positive for glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis and β-galactosidase; but negative for nitrate reduction, indole production, gelatin hydrolysis, and cytochrome oxidase in API 20NE. D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, adipic acid, malic acid, and trisodium citrate are utilized as sole carbon sources; but potassium gluconate, capric acid and phenylacetic acid are not. Strain M23HP230 (= HNIBRBA6248) was isolated from a halophyte sample from Ganghwado Island (37°35′41.5″N, 126°26′34.04″E), Incheon, Korea. The GenBank accession number of the 16S rRNA gene sequence is OR863773.

Description of *Pararhodobacter aggregans* M23HP266

The cells are Gram-stain-negative, non-flagellated,

and rod-shaped. The colonies are circular, convex, entire, and yellow-colored after incubating for 7 days on MA at 20°C. They are positive for nitrate reduction, esculin hydrolysis, β-galactosidase, and cytochrome oxidase; but negative for indole production, glucose fermentation, arginine dihydrolase, urease, and gelatin hydrolysis in API 20NE. D-glucose, L-arabinose, D-mannitol, malic acid, trisodium citrate, phenylacetic acid are utilized as sole carbon sources; but D-mannose, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, and adipic acid are not. Strain M23HP266 (= HNIBRBA6333) was isolated from a halophyte sample from Geumhodo Island (34°41′52.0″N, 126°21′59.0″E), Jeollanam-do, Korea. The GenBank accession number of the 16S rRNA gene sequence is OR863774.

Description of *Myceligenerans indicum* R23HP188

The cells are Gram-stain-positive, non-flagellated, and rod-shaped. The colonies are circular, convex, entire, and white-colored after incubating for 7 days on R2A at 20°C. They are 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, and D-maltose are utilized as sole carbon sources; but D-mannitol, *N*-acetyl-glucosamine, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid are not. Strain R23HP188 (= HNIBRBA6729) was isolated from a halophyte sample from Muuido Island (34°48′5.74″N, 126°7′11.63″E), Incheon, Korea. The GenBank accession number of the 16S rRNA gene sequence is OR863777.

Description of *Halomonas malpeensis* M23HP354

The cells are Gram-stain-negative, flagellated, and rod-shaped. The colonies are circular, convex, entire, and white-colored after incubating for 7 days on MA at 20°C. They are positive for nitrate reduction, arginine dihydrolase and urease; but negative for indole production, glucose fermentation, esculin hydrolysis, gelatin hydrolysis, β-galactosidase, and cytochrome oxidase in API 20NE. D-glucose, potassium gluconate, malic acid, and trisodium citrate are utilized as sole carbon sources; but L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, capric acid, adipic acid, and phenylacetic acid are not. Strain M23HP354 (= HNIBRBA6820) was isolated from a halophyte sample from Gageodo Island (34°2′57.3″N, 125°8′1.1″E), Jeollanam-do, Korea. The GenBank accession number of the 16S rRNA gene sequence is OR863778.

Description of *Salinicola socius* M23HP356

The cells are Gram-stain-negative, flagellated, and rod-shaped. The colonies are circular, convex, entire, and yellow-colored after incubating for 7 days on MA at 20°C. They are positive for glucose fermentation, arginine dihydrolase, and urease; but negative for nitrate reduction, indole production, esculin hydrolysis, gelatin hydrolysis, β-galactosidase, and cytochrome oxidase in API 20NE. D-glucose, L-arabinose, D-mannose, D-mannitol, potassium gluconate, malic acid, and trisodium citrate are utilized as sole carbon sources; but *N*-acetyl-glucosamine, D-maltose, capric acid, adipic acid, and phenylacetic acid are not. Strain M23HP356 (= HNIBRBA6822) was isolated from a halophyte sample from Gageodo Island (34°2′57.3″N, 125°8′1.1″E), Jeollanam-do, Korea. The GenBank accession number of the 16S rRNA gene sequence is OR863779.

Description of *Lentzea alba* R23HP317

The cells are Gram-stain-positive, non-flagellated, and rod-shaped. The colonies are circular, convex, entire, and white-colored after incubating for 7 days on MA at 20°C. They are 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 and malic acid are utilized as sole carbon sources; but potassium gluconate, capric acid, adipic acid, trisodium citrate, and phenylacetic acid are not. Strain R23HP317 (= HNIBRBA6862) was isolated from a halophyte sample from Gageodo Island (34°2′57.3″N, 125°8′1.1″E), Jeollanam-do, Korea. The GenBank accession number of the 16S rRNA gene sequence is OR863780.

Description of *Vibrio amylolyticus* M23SO83

The cells are Gram-stain-negative, flagellated, and rod-shaped. The colonies are circular, convex, entire, and yellow-colored after incubating for 7 days on MA at 20°C. They are positive for nitrate reduction, glucose fermentation, arginine dihydrolase, esculin hydrolysis, β-galactosidase and cytochrome oxidase; but negative for indole production, urease, and gelatin hydrolysis in API 20NE. D-glucose, D-mannitol, and malic acid are utilized as sole carbon sources; but L-arabinose, D-mannose, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, trisodium citrate, and phenylacetic acid are not. Strain M23SO83 (= HNIBRBA6905) was isolated from a tidal flat sample from Gageodo Island (34°4′7″N, 125°6′6″E), Jeollanam-do, Korea. The GenBank accession number of the 16S

rRNA gene sequence is OR863781.

Description of *Aquimarina macrocephali* M23SW434

The cells are Gram-stain-negative, non-flagellated, and rod-shaped. The colonies are circular, convex, entire, and orange-colored after incubating for 7 days on MA at 20°C. They are positive for nitrate reduction, esculin hydrolysis, gelatin hydrolysis, and cytochrome oxidase; but negative for indole production, 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 M23SW434 (= HNIBRBA6937) was isolated from a sea water sample from Gageodo Island (34°4′7″N, 125°6′6″E), Jeollanam-do, Korea. The GenBank accession number of the 16S rRNA gene sequence is OR863783.

Description of *Vibrio gallaecicus* M23SW435

The cells are Gram-stain-negative, flagellated, and rod-shaped. The colonies are circular, convex, entire, and yellow-colored after incubating for 7 days on MA at 20°C. They are positive for nitrate 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, potassium gluconate, and malic acid are utilized as sole carbon sources; but L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, capric acid, adipic acid, trisodium citrate, and phenylacetic acid are not. Strain M23SW435 (= HNIBRBA6938) was isolated from a sea water sample from Gageodo Island (34°48′5.74″N, 126°7′11.63″E), Jeollanam-do, Korea. The GenBank accession number of the 16S rRNA gene sequence is OR863784.

Description of *Shewanella woodyi* M23SW444

The cells are Gram-stain-negative, non-flagellated, and rod-shaped. The colonies are circular, convex, entire, and beige-colored after incubating for 7 days on MA at 20°C. They are positive for nitrate reduction, glucose fermentation, arginine dihydrolase, esculin hydrolysis, gelatin hydrolysis, and cytochrome oxidase; but negative for indole production, urease and β-galactosidase in API 20NE. D-glucose, *N*-acetyl-glucosamine, D-maltose, malic acid, and phenylacetic acid are utilized as sole carbon sources; but L-arabinose, D-mannose, D-mannitol, potassium gluconate, capric acid, adipic acid, and trisodium citrate are not. Strain M23SW444 (= HNIBRBA6943) was isolated from a sea water sample from Gageodo Island (34°48′5.74″N, 126°7′11.63″E), Jeollanam-do, Korea. The GenBank accession number of the 16S rRNA gene sequence is OR863785.

Description of *Paraphotobacterium marinum* M23SW448

The cells are Gram-stain-negative, non-flagellated, and rod-shaped. The colonies are circular, convex, entire, and beige-colored after incubating for 7 days on MA at 20°C. They are 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 M23SW448 (= HNIBRBA6947) was isolated from a sea water sample from Gageodo Island (34°48′5.74″N, 126°7′11.63″E), Jeollanam-do, Korea. The GenBank accession number of the 16S rRNA gene sequence is OR863786.

Description of *Streptomyces spectabilis* UCR7

The cells are Gram-stain-positive, non-flagellated, and rod-shaped. The colonies are circular, entire, and red-colored after incubating for 7 days on MA at 28°C. They are positive for urease, esculin hydrolysis, gelatin hydrolysis, β-galactosidase, and cytochrome oxidase; but negative for nitrate reduction, indole production, glucose dihydrolase, and arginine dihydrolase in API 20NE. D-glucose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, potassium gluconate, and malic acid are utilized as sole carbon sources; but L-arabinose, D-maltose, capric acid, adipic acid, trisodium citrate, and phenylacetic acid are not. Strain UCR7 (= HNIBRBA7025) was isolated from an agricultural soil sample from Seogwipo-si (33°22′28.4″N, 126°41′53″E), Jeju-do, Korea. The GenBank accession number of the 16S rRNA gene sequence is OR564222.

Description of *Atopomonas hussainii* WA2

The cells are Gram-stain-negative, flagellated, and rod-shaped. The colonies are circular, convex, entire, and cream-colored after incubating for 7 days on MA at 28°C. They are 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, D-maltose, capric acid and malic acid are utilized as sole carbon sources; but L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, potassium gluconate, adipic acid, trisodium citrate, and phenylacetic acid are not. Strain WA2 (= HNIBRBA7026)

was isolated from a tidal flat sample from Ganghwado Island (37°39′7.1″N, 126°19′53.2″E), Incheon, Korea. The GenBank accession number of the 16S rRNA gene sequence is OR492599.

Description of *Ruegeria alba* WD6

The cells are Gram-stain-negative, flagellated, and rod-shaped. The colonies are circular, convex, entire, and white-colored after incubating for 7 days on MA at 28°C. They are positive for esculin hydrolysis, gelatin hydrolysis and cytochrome oxidase; but negative for nitrate reduction, indole production, 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 WD6 (= HNIBRBA7027) was isolated from a tidal flat sample from Ganghwado Island (37°41′36.5″N, 126°21′36″E), Incheon, Korea. The GenBank accession number of the 16S rRNA gene sequence is OR535062.

Description of *Caballeronia arvi* DG2UV-4-2

The cells are Gram-stain-negative, non-flagellated, and rod-shaped. The colonies are circular, slightly convex, glistening, and cream-colored after incubating for 7 days on R2A at 25°C. They are positive for nitrate reduction, indole production, esculin hydrolysis, gelatin hydrolysis, β-galactosidase, and cytochrome oxidase; but negative for glucose fermentation, arginine dihydrolase, and urease in API 20NE. D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, potassium gluconate, adipic acid, malic acid, trisodium citrate, and phenylacetic acid are utilized as sole carbon sources but D-maltose and capric acid are not. Strain DG2UV-4-2 (= HNIBRBA7028) was isolated from a soil sample from Yeongheungdo Island (37°16′51.2″N, 126°28′28.51″E), Incheon, Korea. The GenBank accession number of the 16S rRNA gene sequence is OR342744.

Description of *Paenibacillus periandrae* BT773

The cells are Gram-stain-positive, flagellated, and rod-shaped. The colonies are circular, slightly convex, glistening, and cream-colored after incubating for 7 days on R2A at 25°C. They are positive for glucose fermentation, urease, esculin hydrolysis, gelatin hydrolysis, β-galactosidase, and cytochrome oxidase; but negative for nitrate reduction, indole production, and arginine dihydrolase in API 20NE. D-glucose, D-mannose, *N*-acetyl-glucosamine, and D-maltose are utilized as sole carbon sources; but L-arabinose, D-mannitol, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid are not. Strain BT773 (= HNIBRBA7029) was isolated from a soil sample from Ungdo Island (36°55′23.4″N, 126°22′19.2″E), Seosan-si, Korea. The GenBank accession number of the 16S rRNA gene sequence is OR350926.

Description of *Nocardia takedensis* KR3-23

The cells are Gram-stain-positive, flagellated, and rod-shaped. The colonies are circular, slightly convex, glistening, and white-yellow colored after incubating for 7 days on R2A at 25°C. They are positive for indole production, esculin hydrolysis, and gelatin hydrolysis; but negative for nitrate reduction, glucose fermentation, arginine dihydrolase, urease, 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 KR3-23 (= HNIBRBA7030) was isolated from a soil sample from Jawoldo Island (37°15′15.6″N, 126°18′1.8″E), Incheon, Korea. The GenBank accession number of the 16S rRNA gene sequence is OR342813.

Description of *Mycolicibacterium fluoranthenivorans* KR3-11

The cells are Gram-stain-positive, flagellated, and rod-shaped. The colonies are circular, convex, entire, and white-colored after incubating for 7 days on MA at 20°C. They are positive for esculin hydrolysis and gelatin hydrolysis; but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, 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 KR3-11 (= HNIBRBA7031) was isolated from a soil sample from Jawoldo Island (37°15′15.6″N, 126°18′1.8″E), Incheon, Korea. The GenBank accession number of the 16S rRNA gene sequence is OR346158.

Description of *Phyllobacterium trifolii* BU6-25

The cells are Gram-stain-negative, flagellated, and rod-shaped. The colonies are circular, slightly convex, mucoid, and cream-colored after incubating for 7 days on R2A at 25°C. They are 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 BU6-25 (= HNIBRBA7032) was isolated from a soil sample from Ungdo Island (36°55′23.4″N, 126°22′19.2″E), Seosan-si, Korea. The GenBank accession number of the 16S rRNA gene sequence is PP709217.

Description of *Sphingomonas psychrotolerans* DG1-23

The cells are Gram-stain-negative, non-flagellated, and rod-shaped. The colonies are circular, slightly convex, glistening, and yellow-colored after incubating for 7 days on R2A at 25°C. They are positive for nitrate reduction, indole production, esculin hydrolysis, gelatin hydrolysis, β-galactosidase, and cytochrome oxidase; but negative for glucose fermentation, arginine dihydrolase, and urease in API 20NE. D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, potassium gluconate, adipic acid, malic acid, trisodium citrate, and phenylacetic acid are utilized as sole carbon sources; but D-maltose and capric acid are not. Strain DG1-23 (= HNIBRBA7033) was isolated from a soil sample from Yeongheungdo Island (37°16′51.2″N, 126°28′28.51″E), Incheon, Korea. The GenBank accession number of the 16S rRNA gene sequence is OR342727.

Description of *Gordonia mangrovi* 22HPR-12

The cells are Gram-stain-positive, non-flagellated, and rod-shaped. The colonies are circular, convex, entire, and pink-colored after incubating for 7 days on R2A at 20°C. They are positive for urease; but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, esculin hydrolysis, gelatin hydrolysis, β-galactosidase, and cytochrome oxidase in API 20NE. D-glucose, D-mannose, D-mannitol, trisodium citrate, and phenylacetic acid are utilized as sole carbon sources; but L-arabinose, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, and malic acid are not. Strain 22HPR-12 (= HNI BRBA7036) was isolated from a halophyte sample from Chujado Island (34°48′5.74″N, 126°7′11.63″E), Jeju, Korea. The GenBank accession number of the 16S rRNA gene sequence is PP067163.

Description of *Rhizobium rhizolycopersici* R23HP227

The cells are Gram-stain-negative, flagellated, and rod-shaped. The colonies are circular, convex, entire, and beige-colored after incubating for 7 days on R2A at 20°C. They are positive for urease, esculin hydrolase, β-galactosidase, and cytochrome oxidase; but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, and gelatin hydrolysis in API 20NE. D-glucose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, malic acid, trisodium citrate, and phenylacetic acid are utilized as sole carbon sources; but L-arabinose, D-mannose, potassium gluconate, capric acid, and adipic acid are not. Strain R23HP227 (= HNIBRBA7039) was isolated from a halophyte sample from Geumhodo Island (34°41′52″N, 126°21′59″E), Jeollanam-do, Korea. The GenBank accession number of the 16S rRNA gene sequence is OR889344.

Description of *Erythrobacter aurantius* R31

The cells are Gram-stain-negative, non-flagellated, and rod-shaped. The colonies are circular, convex, entire, and yellow-colored after incubating for 7 days on MA at 30°C. They are positive for esculin hydrolysis, gelatin hydrolysis, and cytochrome oxidase; but negative for nitrate reduction, indole production, 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 R31 (= HNIBRBA7140) was isolated from a sea water sample from Seonjaedo Island (37°14′12.1″N, 126°31′24.6″E), Incheon, Korea. The GenBank accession number of the 16S rRNA gene sequence is PP079952.

Description of *Kordia ulvae* DB13

The cells are Gram-stain-negative, non-flagellated, and rod-shaped. The colonies are circular, convex, entire, and orange-colored after incubating for 7 days on MA at 30°C. They are 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 DB13 (= HNIBRBA7141) was isolated from a sea water sample from Daebudo Island (37°15′5.4″N, 126°33′45.7″E), Gyeonggi, Korea. The GenBank accession number of the 16S rRNA gene sequence is PP079953.

Conflicts of Interest

The author of this paper has no affiliation with any interests and is solely responsible for the paper.

Acknowledgements

This study was supported by the "Survey of Indigenous Species in Korean Islands" research grant (HNIBR202101111; HNIBR202301108) awarded by the Honam National Institute of Biological Resources at the Ministry of Environment in Korea.

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Submitted: February 28, 2024
Revised: April 8, 2024
Accepted: July 23, 2024