Journal of Species Research 13(3):310-317, 2024

A report of 20 unrecorded bacterial species isolated from island and coastal ecosystems in 2023

Da Som Kim[1], Seung Yeol Shin[2], Heeyoung Kang[2], Jae Ho Song[2] and Song-Ih Han[1,*]

[1]*Department of Microbial Biotechnology of Science & Technology, Mokwon University, Daejeon 35349, Republic of Korea*
[2]*Division of Microbiology, Honam National Institute of Biological Resources, Mokpo 58762, Republic of Korea*

**Correspondent: h1882@mokwon.ac.kr*

Various samples from island and coastal ecosystems in South Korea were investigated to discover unrecorded bacterial species. Soils from these areas, along with seawater samples, were plated on marine agar and R2A agar (containing 3% sea salt). From these samples, approximately 1,070 bacterial strains were isolated as single colonies and identified using 16S rRNA gene sequences. A total of 20 strains, which exhibited at least 98.7% similarity in their 16S rRNA gene sequences to those of validly published bacterial species not yet reported in Korea, were identified as unrecorded bacterial species. These strains belonged to three phyla, six classes, 10 orders, 14 families, and 16 genera. These were assigned as follows: *Thioclava*, *Breoghania*, *Acidovorax*, *Erythrobacter*, *Paracoccus*, *Jiella*, *Aurantimonas*, and *Qipengyuania* within the class *Alphaproteobacteria*; *Pseudomonas*, *Cobetia*, and *Rheinheimera* within the class *Gammaproteobacteria*; *Aequorivita*, *Leeuwenhoekiella*, and *Polaribacter* within the class *Flavobacteriia*; *Algoriphagus* within the class *Cytophagia*; and *Microbacterium* within the class *Actinobacteria*. The unreported species underwent further taxonomic characterization, which included assessments of Gram reaction, colony and cell morphology, biochemical and phylogenetic characteristics.

Keywords: 16S rRNA gene, coastal area, halophyte, soil, unrecorded bacterial species

DOI:10.12651/JSR.2024.13.3.310

INTRODUCTION

Island and coastal ecosystems, directly influenced by freshwater inputs, exhibit an exceptional diversity compared to oceanic habitats. These environments are known for supporting higher bacterial productivity within the complex microbial realm, as highlighted by Aguiló-Ferretjans *et al.* (2008) and He *et al.* (2024). Such habitats are rich in novel microorganisms that possess unique adaptations, yet many key microbial taxa remain uncultivated (Newton *et al.*, 2011). Consequently, most surveys targeting unrecorded and new species have focused on island coasts (Kim *et al.*, 2020). Despite the evident significance of these environments, studies dedicated to describing the unrecorded and new species within island coastal habitats are notably limited (Aguiló-Ferretjans *et al.*, 2008). In response, the Korean government has initiated a research program aimed at identifying unrecorded bacterial species across the country, marking a significant step in its research endeavors (Baek and Yi, 2018). In 2023, a comprehensive collection of soil, rhizosphere soil, and seawater samples from island coastal environments was undertaken, leading to the isolation of both unrecorded bacterial species and new species within Korea. In this study, 16S rRNA gene sequencing analyses, 20 bacterial strains assigned to the classes *Flavobacteriia*, *Alphaproteobacteria*, *Gammaproteobacteria*, *Betaproteobacteria*, *Cytophagia*, and *Actinomycetes* were identified as unrecorded bacterial species in Korea. Herein we report the phylogenetic information and taxonomic characteristics of the unrecorded bacterial species.

MATERIALS AND METHODS

Various soil, rhizosphere soil, and seawater samples were collected from coastal areas. The details of the samples are presented in Table 1. Each sample of soil, rhizosphere soil, and seawater was suspended in distilled water and serially diluted. Using a spread plating technique on agar media, an aliquot of 100 μL from each of the soil, rhizosphere soil, and seawater samples was spread onto

Table 1. Information of sampling site for sample collected.

NO.	Sample name (scientific name)	Sampling site	Strain ID	Latitude and longitude
1	Soil of saltern	Seocheon-gun	2HN01	36°00′32.5″N 126°45′19.9″E
2	Rhizosphere soils of halophyte (*Phragmites australis*)	Seocheon-gun	2HN02	36°00′32.5″N 126°45′19.9″E
3	Seawater	Seocheon-gun	2HN03	36°00′32.5″N 126°45′19.9″E
4	Epilithic (mineral surface) biofilm	Seocheon-gun	2HN04	36°00′32.5″N 126°45′19.9″E
5	Soils of saltern	Seocheon-gun	2HN05	36°02′02.3″N 126°39′57.7″E
6	Rhizosphere soils of halophyte (*Phragmites australis*)	Seocheon-gun	2HN06	36°08′02.3″N 126°39′57.7″E
7	Soil of saltern	Tong-Yeong	2HN07	34°47′18.4″N 128°28′03.5″E
8	Rhizosphere soils of halophyte (*Suaeda maritima*)	Tong-Yeong	2HN08	34°47′15.3″N 128°28′03.7″E
9	Seawater	Haenam-gun	2HN09	34°25′26.1″N 126°39′11.5″E
10	Seawater	Wando-gun	2HN10	34°20′52.0″N 126°44′15.4″E
11	Seawater	Yeongkwang-gun	2HN11	35°21′50.12″N 126°25′19.98″E
12	Seawater	Wando-gun	2HN12	34°22′42.69″N 126°38′24.96″E
13	Seawater	Jindo-gun	2HN13	34°26′15.99″N 126°21′23.45″E
14	Seawater	Muan-gun	2HN14	35°4′26.31″N 126°27′27.08″E
15	Soil of saltern	Shinan-gun	2HN24	34°50′11.57″N 126°21′55.05″E
16	Rhizosphere soils of halophyte (*Suaeda maritima*)	Shinan-gun	2HN25	34°50′11.57″N 126°21′55.05″E
17	Rhizosphere soils of halophyte (*Limonium tetragonum*)	Shinan-gun	2HN26	34°50′11.57″N 126°21′55.05″E

R2A agar (containing 3% sea salt) and Marine Agar. Subsequently, these were incubated at 25°C for 14 days. Bacterial strains were purified by subculturing single colonies on Marine Agar and R2A medium (containing 3% sea salt). Pure cultures were preserved at −80°C in a 20% (v/v) glycerol suspension and in lyophilized ampoules. Details about the strains, culture medium, and incubation conditions are presented in Table 2. For the determination of colony morphology, cells were cultivated to their stationary phase, and bacterial strains were observed on agar plates. Cellular morphology, the presence of flagella, and cell size were examined using a transmission electron microscope (CM200; Philips) after staining with 2% (w/v) uranyl acetate, and a scanning electron microscope (S-4800; Hitachi). Biochemical characteristics were determined using the API 20E system (bioMérieux) according to the manufacturer's instructions. For the identification of bacterial strains isolated in this study, bacterial DNA extraction, PCR amplification, and 16S rRNA gene sequencing were performed using standard procedures, as previously described by Yang and Cho (2008). For the determination of 16S rRNA gene sequences, universal primers 518F and 805R were utilized. The 16S rRNA gene sequences were compared with those of other bacterial strains using the EZBioCloud server (Yoon *et al*., 2017) and NCBI Basic Local Alignment Search Tool (BLAST). A cutoff value of 98.7% sequence similarity was applied for the demarcation of bacterial species (Chun *et al*., 2018). Consequently, bacterial strains exhibiting 98.7% or higher sequence similarities with published species, yet not previously reported in Korea, were identified as unreported bacterial species. For phylogenetic analyses, multiple sequence alignments of the 16S rRNA gene sequences between isolated strains and reference type strains were conducted using ClustalW, as implemented in MEGA X (Kumar *et al*., 2018). The robustness of the inferred phylogenetic trees was assessed by bootstrap analyses based on 1,000 random re-samplings (Felsenstein, 1985).

Results and Discussion

After analyzing the 16S rRNA gene sequences of approximately 1,070 bacterial strains, many strains belonging to novel and previously unreported bacterial species were isolated. A total of 20 strains were identified. Information on these strains, including identification, taxonomic assignment, and accession numbers for HNIBR and GenBank, is listed in Table 2. The delineation of the strains to established bacterial species, based on 16S rRNA gene sequence similarity, was confirmed by phylogenetic trees, as shown in Fig. 1. The 20 unrecorded bacterial species were phylogenetically diverse, belonging to three phyla, six classes, 10 orders, 14 families, and 16 genera. The unrecorded species were assigned to three species of the class *Flavobacteriia*, seven species of the class *Alphaproteobacteria*, eight species of the class *Gammaproteobacteria*, one species of the class *Betaproteobacteria*, one species of the class *Cytophagia*, one species of the class *Actinomycetes* (Table 2).

At the generic level, these unreported species belong to the genera *Thioclava*, *Breoghania*, *Acidovorax*, *Erythro-*

Table 2. Summary of strains isolated from soils coastal areas and rhizosphere and their taxonomic affiliation.

Class	Order	Family	Strain ID	HNIBR ID	Accession number	Closest species	Medium	Incubation conditions
Alphaproteobacteria	*Rhodobacterales*	*Paracoccaceae*	2HN02-17	HNIBRBA6958	OR726107	*Thioclava dalianensis*	MA	25°C 3 d
	Hyphomicrobiales	*Breoghaniaceae*	2HN05-60	HNIBRBA6959	OR726109	*Breoghania corrubedonensis*	R2A (3% sea salt)	25°C 3 d
	Sphingomonadales	*Erythrobacteraceae*	2HN08-47	HNIBRBA6967	OR726117	*Erythrobacter nanhaiensis*	R2A (3% sea salt)	25°C 3 d
	Rhodobacterales	*Paracoccaceae*	2HN08-43	HNIBRBA6970	OR726120	*Paracoccus indicus*	R2A (3% sea salt)	25°C 3 d
	Hyphomicrobiales	*Aurantimonadaceae*	2HN25-4	HNIBRBA6972	OR726122	*Jiella mangrovi*	MA	25°C 3 d
	Hyphomicrobiales	*Aurantimonadaceae*	2HN26-43	HNIBRBA6974	OR726124	*Aurantimonas coralicida*	R2A (3% sea salt)	25°C 3 d
	Sphingomonadales	*Erythrobacteraceae*	2HN26-58	HNIBRBA6975	OR726125	*Qipengyuania huizhouensis*	R2A (3% sea salt)	25°C 3 d
Betaproteobacteria	*Burkholderiales*	*Comamonadaceae*	2HN12-41	HNIBRBA6963	OR726113	*Acidovorax facilis*	R2A (3% sea salt)	25°C 3 d
Gammaproteobacteria	*Pseudomonadales*	*Pseudomonadaceae*	2HN13-47	HNIBRBA6960	OR726110	*Pseudomonas piscium* (*piscicola*)	R2A (3% sea salt)	25°C 3 d
	Oceanospirillales	*Halomonadaceae*	2HN07-54	HNIBRBA6961	OR726111	*Cobetia marina*	R2A (3% sea salt)	25°C 3 d
	Chromatiales	*Chromatiaceae*	2HN12-39	HNIBRBA6962	OR726112	*Rheinheimera chironomi*	R2A (3% sea salt)	25°C 3 d
	Pseudomonadales	*Pseudomonadaceae*	2HN13-30	HNIBRBA6964	OR726114	*Pseudomonas psychrophila*	MA	25°C 3 d
	Pseudomonadales	*Pseudomonadaceae*	2HN11-29	HNIBRBA6965	OR726115	*Pseudomonas laoshanensis*	R2A (3% sea salt)	25°C 3 d
	Pseudomonadales	*Pseudomonadaceae*	2HN14-44	HNIBRBA6968	OR726118	*Pseudomonas leptonychotis*	R2A (3% sea salt)	25°C 3 d
	Pseudomonadales	*Pseudomonadaceae*	2HN14-72	HNIBRBA6969	OR726119	*Pseudomonas atacamensis*	R2A (3% sea salt)	25°C 3 d
	Pseudomonadales	*Pseudomonadaceae*	2HN26-16	HNIBRBA6973	OR726123	*Pseudomonas kurunegalensis*	MA	25°C 3 d
Flavobacteriia	*Flavobacteriales*	*Flavobacteriaceae*	2HN02-4	HNIBRBA6957	OR726106	*Aequorivita aquimaris*	MA	25°C 3 d
	Flavobacteriales	*Flavobacteriaceae*	2HN05-56	HNIBRBA6976	OR726108	*Leeuwenhoekiella parthenopeia*	R2A (3% sea salt)	25°C 3 d
Cytophagia	*Cytophagales*	*Cyclobacteriaceae*	2HN11-44	HNIBRBA6966	OR726116	*Algoriphagus litoralis*	R2A (3% sea salt)	25°C 3 d
Actinomycetes	*Micrococcales*	*Microbacteriaceae*	2HN24-40	HNIBRBA6971	OR726121	*Microbacterium awajiense*	R2A (3% sea salt)	25°C 3 d

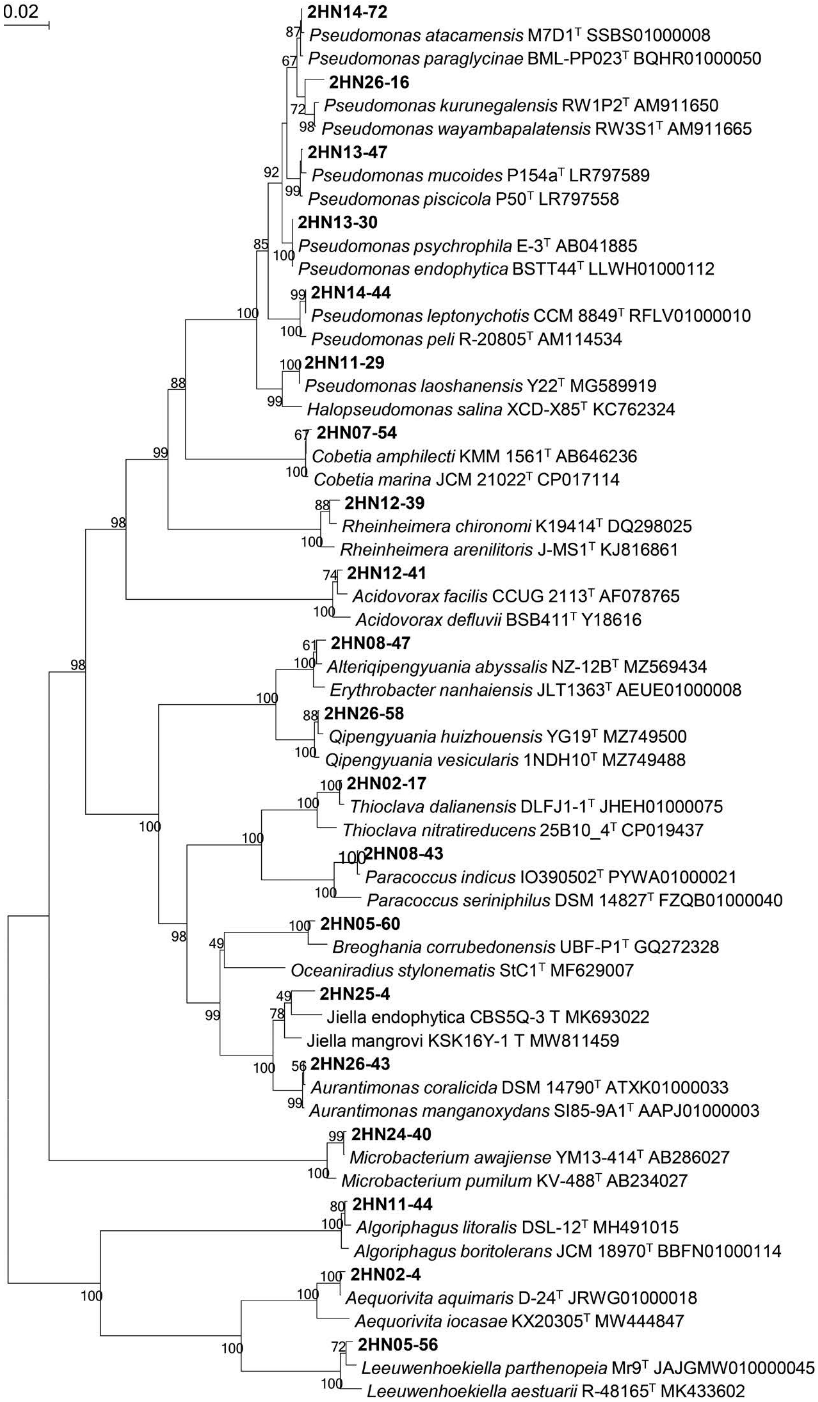

Fig. 1. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences showing the relationship between the strains isolated in this study and their closest bacterial species. Bootstrap values over 70% are shown at nodes for neighbor-joining, maximum parsimony, maximum likelihood, respectively. Scale bar = 0.02 substitutions per nucleotide position.

bacter, *Paracoccus*, *Jiella*, *Aurantimonas*, and *Qipengyuania* within the class *Alphaproteobacteria*; *Pseudomonas*, *Cobetia*, and *Rheinheimera* within the class *Gammaproteobacteria*; *Aequorivita*, *Leeuwenhoekiella*, and *Polaribacter* within the class *Flavobacteriia*; *Algoriphagus* within the class *Cytophagia*; and *Microbacterium* within the class *Actinomycetes*. Detailed morphological and physiological characteristics of the 20 unrecorded bacterial species are provided in the strain descriptions that follow.

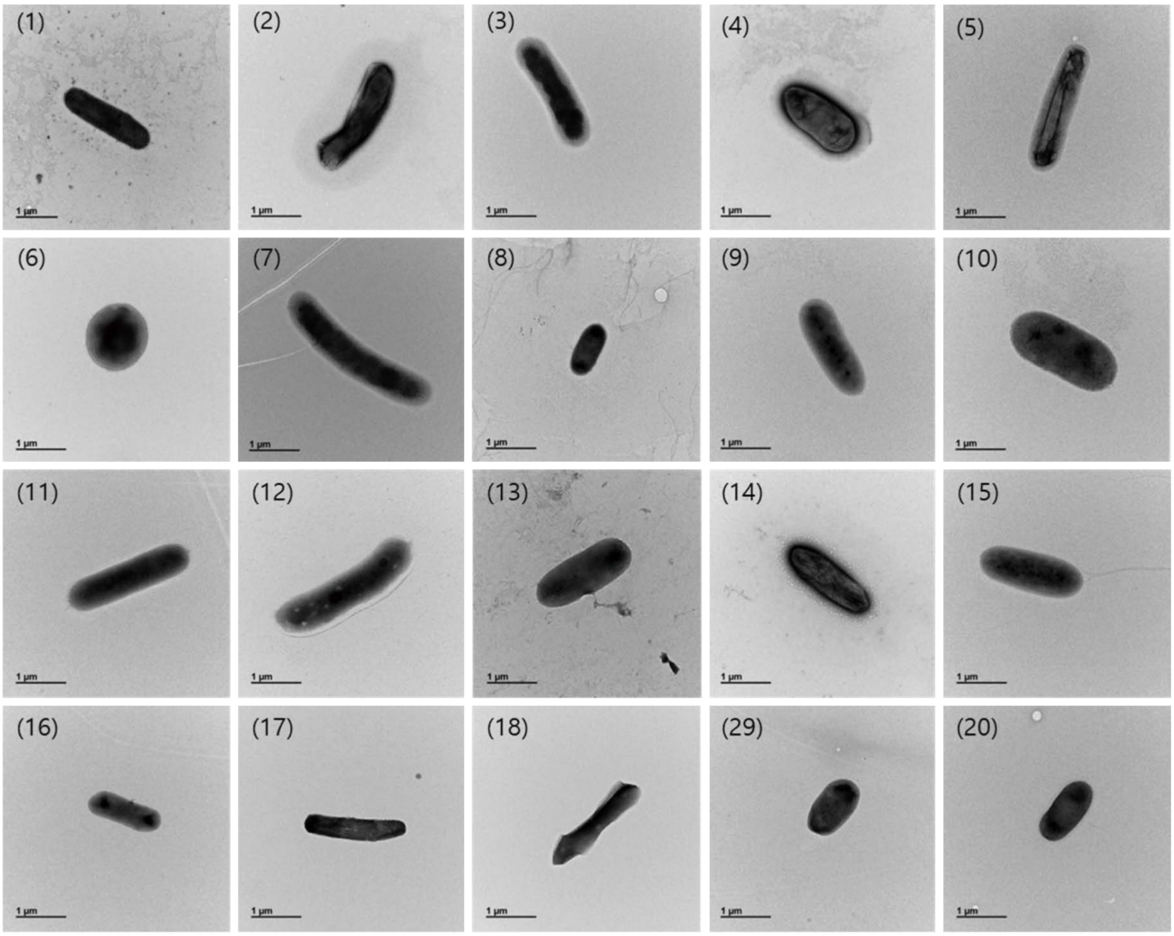

Fig. 2. Transmission electron micrographs of cells of the strains isolated in this study. Strains: 1, 2HN02-4; 2, 2HN02-17; 3, 2HN05-56; 4, 2HN05-60; 5, 2HN07-54; 6, 2HN08-43; 7, 2HN08-47; 8, 2HN11-29; 9, 2HN11-44; 10, 2HN12-39; 11, 2HN12-41; 12, 2HN13-30; 13, 2HN13-47; 14, 2HN14-44; 15, 2HN14-72; 16, 2HN24-40; 17, 2HN25-4; 18, 2Hn26-16; 19, 2HN26-43; 20, 2HN26-58.

Description of *Aequorivita aquimaris* 2HN02-4

Cells are Gram-stain-negative, aerobic, non-flagellated, and bacilli-shaped. Colonies are circular, convex, entire, and orange after incubating for 3 days on Marine Agar at 25°C. The strain is positive for β-galactosidase, arginine dihydrolase, acetoin production, and gelatinase; but negative for lysine decarboxylase, ornithine decarboxylase, citrate utilization, H2S production, urease, tryptophan deaminase, and indole production according to API 20E tests. Strain 2HN02-4 was isolated from rhizosphere soils of a halophyte collected from the Keumgang Estuary (36° 00′32.5″N 126°45′19.9″E), Gunsan, Jeollabuk-do, Korea. The GenBank accession number for the 16S rRNA gene sequence is OR726106.

Description of *Thioclava dalianensis* 2HN02-17

Cells are Gram-stain-negative, aerobic, non-flagellated, and rod-shaped. Colonies are circular, convex, entire, and white after incubation for 3 days on Marine Agar at 25°C. The strain is positive for β-galactosidase, arginine dihydrolase, lysine decarboxylase, ornithine decarboxylase, urease, and acetoin production; but negative for citrate utilization, H2S production, tryptophan deaminase, indole production, and gelatinase as determined by API 20E testing. Strain 2HN02-17 was isolated from the rhizosphere soils of a halophyte collected from Keumgang Estuary (36°00′32.5″N 126°45′19.9″E), Gunsan, Jeollabuk-do, Korea. The GenBank accession number for the 16S rRNA gene sequence is OR726107.

Description of *Breoghania corrubedonensis* 2HN05-60

Cells are Gram-stain-negative, aerobic, flagellated, and rod-shaped. Colonies are circular, convex, entire, and white after incubation for 3 days on R2A Agar (containing 3% sea salt) at 25°C. The strain is positive for arginine dihydrolase, tryptophan deaminase, and acetoin production; but negative for β-galactosidase, lysine decarboxylase, ornithine decarboxylase, citrate utilization, H2S production, urease, indole production, and gelatinase as determined by API 20E testing. Strain 2HN05-60 was isolated from the soils of coastal areas collected from Oknam-ri (36°02′02.3″N 126°39′57.7″E), Seocheon-gun, Chungcheongnam-do, Korea. The GenBank accession number for the 16S rRNA gene sequence is OR726109.

Description of *Pseudomonas piscicola* 2HN13-47

Cells are Gram-stain-negative, aerobic, flagellated, and rod-shaped. Colonies are irregular, flat, undulate, and white after incubation for 3 days on R2A Agar (3% sea salt) at 25°C. The strain is positive for arginine dihydrolase, ornithine decarboxylase, citrate utilization, and acetoin production; but negative for β-galactosidase, lysine decarboxylase, H2S production, urease, tryptophan deaminase, indole production, and gelatinase as determined by API 20E testing. Strain 2HN13-47 was isolated from seawater collected from Gagye Beach (34°26′15.99″N 126°21′23.45″E), Jindo-gun, Jeollanam-do, Korea. The GenBank accession number for the 16S rRNA gene sequence is OR726110.

Description of *Cobetia marina* 2HN07-54

Cells are Gram-stain-negative, aerobic, flagellated, and rod-shaped. Colonies are circular, raised, entire, and white after incubation for 3 days on R2A Agar (3% sea salt) at 25°C. The strain is positive for β-galactosidase, arginine dihydrolase, tryptophan deaminase, and acetoin production; but negative for lysine decarboxylase, ornithine decarboxylase, citrate utilization, H2S production, urease, indole production, and gelatinase as determined by API 20E testing. Strain 2HN07-54 was isolated from the soils of coastal areas collected from Hansan-do Island (34°47′18.4″N 128°28′03.5″E), Tongyeong-si, Gyeongsangnam-do, Korea. The GenBank accession number for the 16S rRNA gene sequence is OR726111.

Description of *Rheinheimera chironomi* 2HN12-39

Cells are Gram-stain-negative, aerobic, non-flagellated, and rod-shaped. Colonies are irregular, flat, undulate, and white after incubation for 3 days on R2A Agar (3% sea salt) at 25°C. The strain is positive for β-galactosidase, tryptophan deaminase, acetoin production, and gelatinase; but negative for arginine dihydrolase, lysine decarboxylase, ornithine decarboxylase, citrate utilization, H2S production, urease, and indole production as determined by API 20E testing. Strain 2HN12-39 was isolated from seawater collected from Shinheung-ri (34°22′42.69″N 126°38′24.96″E), Wando-gun, Jeollanam-do, Korea. The Gen Bank accession number for the 16S rRNA gene sequence is OR726112.

Description of *Acidovorax facilis* 2HN12-41

Cells are Gram-stain-negative, aerobic, flagellated, and rod-shaped. Colonies are irregular, flat, undulate, and yellow after incubation for 3 days on R2A Agar (3% sea salt) at 25°C. The strain is positive for urease, tryptophan deaminase, and acetoin production; but negative for β-galactosidase, arginine dihydrolase, lysine decarboxylase, ornithine decarboxylase, citrate utilization, H2S production, gelatinase, and indole production as determined by API 20E testing. Strain 2HN12-41 was isolated from seawater collected from Shinheung-ri (34°22′42.69″N 126°38′24.96″E), Wando-gun, Jeollanam-do, Korea. The Gen Bank accession number for the 16S rRNA gene sequence is OR726113.

Description of *Pseudomonas psychrophila* 2HN13-30

Cells are Gram-stain-negative, aerobic, flagellated, and rod-shaped. Colonies are irregular, flat, undulate, and white after incubation for 3 days on Marine Agar at 25°C. The strain is positive for arginine dihydrolase, citrate utilization, urease, tryptophan deaminase, and acetoin production; but negative for β-galactosidase, lysine decarboxylase, ornithine decarboxylase, H2S production, indole production, and gelatinase as determined by API 20E testing. Strain 2HN13-30 was isolated from seawater collected from Gagye Beach (34°26′15.99″N 126°21′23.45″E), Jindo-gun, Jeollanam-do, Korea. The GenBank accession number for the 16S rRNA gene sequence is OR726114.

Description of *Pseudomonas laoshanensis* 2HN11-29

Cells are Gram-stain-negative, aerobic, flagellated, and rod-shaped. Colonies are irregular, flat, undulate, and white after incubation for 3 days on R2A Agar (3% sea salt) at 25°C. The strain is positive for urease, tryptophan deaminase, and acetoin production; but negative for β-galactosidase, arginine dihydrolase, lysine decarboxylase, ornithine decarboxylase, citrate utilization, H2S production, gelatinase, and indole production as determined by API 20E testing. Strain 2HN11-29 was isolated from seawater collected from the Gusuri coastal area (35°21′50.12″N 126°25′19.98″E), Yeonggwang-gun, Jeollanam-do, Korea. The GenBank accession number for the 16S rRNA gene sequence is OR726115.

Description of *Algoriphagus litoralis* 2HN11-44

Cells are Gram-stain-negative, aerobic, non-flagellated, and rod-shaped. Colonies are circular, raised, entire, and orange after incubation for 3 days on R2A Agar (3% sea salt) at 25°C. The strain is positive for β-galactosidase, tryptophan deaminase, and acetoin production; but negative for arginine dihydrolase, lysine decarboxylase, ornithine decarboxylase, citrate utilization, H2S production, urease, gelatinase, and indole production as determined by API 20E testing. Strain 2HN11-44 was isolated from seawater collected from the Gusuri coastal area (35°

21′50.12″N 126°25′19.98″E), Yeonggwang-gun, Jeollanam-do, Korea. The GenBank accession number for the 16S rRNA gene sequence is OR726116.

Description of *Erythrobacter nanhaiensis* 2HN08-47

Cells are Gram-stain-negative, aerobic, flagellated, and rod-shaped. Colonies are irregular, flat, undulate, and orange after incubation for 3 days on R2A Agar (3% sea salt) at 25°C. The strain is positive for β-galactosidase, tryptophan deaminase, and acetoin production; but negative for arginine dihydrolase, lysine decarboxylase, ornithine decarboxylase, citrate utilization, H2S production, urease, gelatinase, and indole production as determined by API 20E testing. Strain 2HN08-47 was isolated from the rhizosphere soils of a halophyte collected from Hansando Island (34°47′18.4″N 128°28′03.5″E), Tongyeong-si, Gyeongsangnam-do, Korea. The GenBank accession number for the 16S rRNA gene sequence is OR726117.

Description of *Pseudomonas leptonychotis* 2HN14-44

Cells are Gram-stain-negative, aerobic, flagellated, and rod-shaped. Colonies appear irregular, flat, undulate, and white after incubation for 3 days on R2A Agar (3% sea salt) at 25°C. The strain is positive for arginine dihydrolase, urease, tryptophane deaminase, and acetoin production; but negative for β-galactosidase, lysine decarboxylase, ornithine decarboxylase, citrate utilization, H2S production, indole production, and gelatinase as determined by API 20E testing. Strain 2HN14-44 was isolated from seawater collected from Haeunri (35°4′26.31″N 126°27′27.08″E), Muan-gun, Jeollanam-do, Korea. The GenBank accession number of the 16S rRNA gene sequence is OR726118.

Description of *Pseudomonas atacamensis* 2HN14-72

Cells are Gram-stain-negative, aerobic, flagellated, and rod-shaped. Colonies appear irregular, flat, undulate, and white after incubation for 3 days on R2A Agar (3% sea salt) at 25°C. The strain is positive for arginine dihydrolase, citrate utilization, tryptophane deaminase, and acetoin production; but negative for β-galactosidase, lysine decarboxylase, ornithine decarboxylase, H2S production, urease, indole production, and gelatinase as determined by API 20E testing. Strain 2HN14-72 was isolated from seawater collected from Haeunri (35°4′26.31″N 126° 27′27.08″E), Muan-gun, Jeollanam-do, Korea. The Gen Bank accession number of the 16S rRNA gene sequence is OR726119.

Description of *Paracoccus indicus* 2HN08-43

Cells are Gram-stain-negative, aerobic, non-flagellated, and cocci-shaped. Colonies appear irregular, flat, undulate, and white after incubation for 3 days on R2A Agar (3% sea salt) at 25°C. The strain is positive for arginine dihydrolase, β-galactosidase, citrate utilization, urease, tryptophane deaminase, and acetoin production; but negative for lysine decarboxylase, ornithine decarboxylase, H2S production, gelatinase, and indole production as determined by API 20E testing. Strain 2HN08-43 was isolated from rhizosphere soils of a halophyte collected from Hansando Island (34°47′18.4″N 128°28′03.5″E), Tongyeong-si, Gyeongsangnam-do, Korea. The GenBank accession number of the 16S rRNA gene sequence is OR726120.

Description of *Microbacterium awajiense* 2HN24-40

Cells are Gram-stain-positive, aerobic, non-flagellated, and rod-shaped. Colonies are circular, raised, entire, and yellow after incubation for 3 days on R2A Agar (3% sea salt) at 25°C. The strain is positive for β-galactosidase and gelatinase; but negative for arginine dihydrolase, lysine decarboxylase, ornithine decarboxylase, citrate utilization, H2S production, urease, tryptophane deaminase, indole production, and acetoin production as determined by API 20E testing. Strain 2HN24-40 was isolated from soils of coastal areas collected from Shinjangri (34°50′11.57″N 126°21′55.05″E), Shinan-gun, Jeollanam-do, Korea. The GenBank accession number of the 16S rRNA gene sequence is OR726121.

Description of *Jiella mangrove* 2HN25-4

Cells are Gram-stain-negative, aerobic, non-flagellated, and rod-shaped. Colonies are irregular, flat, undulate, and yellow after incubation for 3 days on Marine Agar at 25°C. The strain is positive for urease and acetoin production; but negative for β-galactosidase, arginine dihydrolase, lysine decarboxylase, ornithine decarboxylase, citrate utilization, H2S production, tryptophan deaminase, indole production, and gelatinase as determined by API 20E testing. Strain 2HN25-4 was isolated from the rhizosphere soils of a halophyte collected from Shinjangri (34°50′11.57″N 126° 21′55.05″E), Shinan-gun, Jeollanam-do, Korea. The Gen Bank accession number for the 16S rRNA gene sequence is OR726122.

Description of *Pseudomonas kurunegalensis* 2HN26-16

Cells are Gram-stain-negative, aerobic, flagellated, and rod-shaped. Colonies are irregular, flat, undulate, and white after incubation for 3 days on Marine Agar at 25°C. The strain is positive for arginine dihydrolase, citrate utilization, and acetoin production; but negative for β-galactosidase, lysine decarboxylase, ornithine decarboxylase, H2S production, urease, tryptophan deaminase, indole production, and gelatinase as determined by API 20E testing. Strain 2HN26-16 was isolated from the rhizosphere soils of a halophyte collected from Shinjangri (34°50′11.57″N 126°21′55.05″E), Shinan-gun, Jeollanam-do, Korea. The GenBank accession number for the 16S rRNA gene sequence is OR726123.

Description of *Aurantimonas coralicida* 2HN26-43

Cells are Gram-stain-negative, aerobic, flagellated, and rod-shaped. Colonies are circular, raised, entire, and yellow after incubation for 3 days on Marine Agar at 25°C. The strain is positive for arginine dihydrolase, urease, and acetoin production; but negative for β-galactosidase, lysine decarboxylase, ornithine decarboxylase, citrate utilization, H2S production, tryptophan deaminase, indole production, and gelatinase as determined by API 20E testing. Strain 2HN26-43 was isolated from the rhizosphere soils of a halophyte collected from Shinjangri (34°50′11.57″N 126°21′55.05″E), Shinan-gun, Jeollanam-do, Korea. The Gen Bank accession number for the 16S rRNA gene sequence is OR726124.

Description of *Qipengyuania huizhouensis* 2HN26-58

Cells are Gram-stain-negative, aerobic, flagellated, and rod-shaped. Colonies are circular, raised, entire, and orange after incubation for 3 days on R2A agar (3% sea salt) at 25°C. The strain is positive for tryptophan deaminase and acetoin production; but negative for β-galactosidase, arginine dihydrolase, lysine decarboxylase, ornithine decarboxylase, citrate utilization, H2S production, urease, indole production, and gelatinase as determined by API 20E testing. Strain 2HN26-58 was isolated from the rhizosphere soils of a halophyte collected from Shinjangri (34°50′11.57″N 126°21′55.05″E), Shinan-gun, Jeollanam-do, Korea. The GenBank accession number for the 16S rRNA gene sequence is OR726125.

Description of *Leeuwenhoekiella parthenopeia* 2HN05-56

Cells are Gram-stain-negative, aerobic, flagellated, and rod-shaped. Colonies are circular, convex, entire, and yellow after incubation for 3 days on R2A agar (3% sea salt) at 25°C. The strain is positive for β-galactosidase, tryptophan deaminase, and acetoin production; but negative for arginine dihydrolase, lysine decarboxylase, ornithine decarboxylase, citrate utilization, H2S production, urease, indole production, and gelatinase as determined by API 20E testing. Strain 2HN05-56 was isolated from the soils of coastal areas collected from Oknam-ri (36°02′02.3″N 126°39′57.7″E), Seocheon-gun, Chungcheongnam-do, Korea. The GenBank accession number for the 16S rRNA gene sequence is OR726108.

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 research grant "Survey of island-coastal indigenous organisms (Prokaryotes)" (HNIBR202301211) from Honam National Institute of Biological Resources (HNIBR) in Korea.

REFERENCES

Aguiló-Ferretjans, M.M., R. Bosch, C. Martín-Cardona, J. Lalucat and B. Nogales. 2008. Phylogenetic analysis of the composition of bacterial communities in human-exploited coastal environments from Mallorca Island (Spain). Systematic and Applied Microbiology 31:231-240.

Baek, C. and H. Yi. 2018. A report of 22 unrecorded bacterial species in Korea, isolated from Namhangang. Journal of Species Research 7:114-122.

Chun, J., A. Oren, A. Ventosa, H. Christensen, D.R. Arahal, M.S. da Costa, A.P. Rooney, H. Yi, X.-W. Xu, S. De Meyer and M.E. Trujillo. 2018. Proposed minimal standards for the use of genome data for the taxonomy of prokaryotes. Int. J. Syst. Evol. Microbiol. 68:461-466.

Felsenstein, J. 1985. Confidence Limits on Phylogenies: An Approach Using the Bootstrap. Evolution 39:783-791.

He, Y., B. Sen and G. Wang. 2024. Diversity and Dynamics of Microbial Communities in Marine Ecosystems. Water 16:1-31.

Kim, M., K.E. Lee, I.T. Cha, B.H. Lee and S.J. Park. 2020. Eight unrecorded bacterial species isolated from soil and marine sediment in Korea. J. Species Res. 9:339-345.

Kumar, S., G. Stecher, M. Li, C. Knyaz and K. Tamura. 2018. MEGA X: molecular evolutionary genetics analysis across computing platforms. Molecular Biology and Evolution 35(6):1547-1549.

Newton, R.J., S.E. Jones, A. Eiler, K.D. McMahon and S. Bertilsson. 2011. A Guide to the Natural History of Freshwater Lake Bacteria. Microbiology and Molecular Biology Reviews 75(1):14-49.

Yang, S.J. and B.C. Cho. 2008. Comparison of DNA extraction protocols for marine microorganisms. Journal of Microbiological Methods 72(2):124-132.

Yoon, S.H., S.M. Ha, S. Kwon, J. Lim, Y. Kim, H. Seo and J. Chun. 2017. Introducing EzBioCloud: a taxonomically united database of 16S rRNA gene sequences and wholegenome assemblies. Int. J. Syst. Evol. Microbiol. 67:1613-1617.

Submitted: March 15, 2024
Accepted: April 15, 2024