Journal of Species Research 14(4):374-385, 2025
https://doi.org/10.12651/JSR.2025.14.4.374

Open Access

Unrecorded bacterial species from halophilic and contaminated environments in Korea: Descriptions of 33 species isolated in 2021 and 2022

Jung-Hun Jo[1], Se-Yoon Chun[1], Eun-Young Lee[2], Ki-Eun Lee[2] and Wan-Taek Im[1,*]

[1]*Department of Biotechnology, Hankyong National University, Anseong 17579, Republic of Korea*
[2]*Microorganism Resources Division, National Institute of Biological Resources, Incheon 22689, Republic of Korea*

**Correspondent: wandra@hknu.ac.kr*

This study describes 33 previously unrecorded bacterial species strains isolated from specialized halophilic and contaminated environments in Korea. The bacterial strains were isolated from unique ecological niches, including solar saltern, mudflats, and contaminated soils from highly polluted sites such as landfills and parking lots. These habitats harbor diverse microbial communities, offering insights into bacterial adaptation and distribution. The findings contribute to the understanding of microbial diversity in extreme and anthropogenically impacted environments. Based on high 16S rRNA gene sequence similarity (>98.7%) and the formation of a robust phylogenetic clade with the closest species, each strain was determined to belong to a predefined bacterial species. There is no official report that these 33 species belonged to 4 phyla, 7 classes, 17 orders, 19 families, and 27 genera, which were assigned to *Muricauda*, *Kaistella*, *Hymenobacter* and *Flavobacterium* of the phylum *Bacteroidota*; *Streptomyces*, *Rhodococcus*, *Rathayibacter*, *Nocardioides*, *Cryobacterium*, *Arthrobacter* and *Aeromicrobium* of the phylum *Actinomycetota*; *Thioclava*, *Sulfitobacter*, *Spiribacter*, *Simplicispira*, *Shewanella*, *Roseovarius*, *Qipengyuania*, *Pseudomonas*, *Maritalea*, *Marinobacter*, *Halomonas*, *Devosia*, *Chromohalobacter* and *Brevundimonas* of the phylum *Pseudomonadota*; *Virgibacillus* and *Alkalihalobacillus* of the phylum *Bacillota*. Gram-staining results, colony and cell morphologies, basic biochemical characteristics, isolation sources, and strain IDs are also described in the species description section.

Keywords: 16S rRNA gene, culture-dependent isolation, environmental microbiota, phylogenetic profiling, taxonomic characterization

All content in the Journal of Species Research (JSR), published by the National Institute of Biological Resources (NIBR), is Open Access, meaning it is freely accessible online to everyone without fees or the need for authors' permission. Open Access articles are automatically archived in the Korea Institute of Science and Technology Information (KISTI)'s Open Access repository, AccessON. All JSR content is published and distributed under the terms of the Creative Commons Attribution-NonCommercial-NoDerivatives 4.0 International License (CC BY-NC-ND 4.0). This license permits non-commercial use, distribution, and reproduction in any medium, provided the original author and source are properly credited. However, no modifications or derivative works are allowed.

Introduction

Environmental microorganisms play crucial roles in maintaining ecosystem stability, particularly in extreme habitats where selective pressures shape unique microbial communities. Contaminated soils, subjected to prolonged exposure to pollutants such as heavy metals and hydrocarbons, develop complex microbial ecosystems. These environments drive microbial adaptation and diversification, often leading to the emergence of specialized taxa capable of surviving under nutrient-limited and chemically fluctuating conditions. Notably, landfill and parking lot soils, frequently exposed to petroleum derivatives, heavy metal leachates, and industrial runoff, serve as reservoirs for metabolically versatile bacterial communities. Studies have identified members of the genera *Sphingomonas* and *Flavobacterium* in these environments, with certain species exhibiting hydrocarbon degradation capabilities

©2025 National Institute of Biological Resources.
This article was authored by [Jung-Hun Jo, Se-Yoon Chun, Eun-Young Lee, Ki-Eun Lee and Wan-Taek Im] and is published by the National Institute of Biological Resources under the terms of the Creative Commons Attribution-NonCommercial-NoDerivatives 4.0 International License (CC BY-NC-ND 4.0). Non-commercial use, distribution, and reproduction in any medium are permitted, provided the original authors are properly credited and the work is not modified in any way.

and heavy metal resistance, thereby contributing to biogeochemical cycling and pollutant detoxification (Raghad, 2019). Similarly, halophilic environments, characterized by high salinity levels, impose distinct selective pressures that shape microbial diversity. Halophilic microorganisms, including extreme halophiles, have evolved specialized metabolic pathways and enzymatic systems that allow them to survive and function in high-salinity conditions. For instance, species of the genus *Halobacterium* have been isolated from such environments, demonstrating unique metabolic adaptations that not only enable survival in hypersaline conditions but also hold biotechnological potential. These halophilic bacteria are of particular interest for applications such as the bioremediation of saline industrial wastewater and the enzymatic treatment of salt-rich pollutants (Martínez-Espinosa, 2024). As part of a broader effort to explore microbial diversity in specialized environments, we conducted a large-scale investigation of bacterial communities in both contaminated and halophilic habitats across Korea during 2021 and 2022. Supported by the National Institute of Biological Resources (NIBR), this study identified bacterial species spanning seven classes—*Actinomycetes*, *Alphaproteobacteria*, *Betaproteobacteria*, *Gammaproteobacteria*, *Bacilli*, *Cytophagia*, and *Flavobacteriia*—distributed across 17 different orders. Here, we present an overview of 33 previously unreported bacterial species discovered during this research program, contributing to a deeper understanding of microbial adaptations in specialized and extreme environments.

Materials and Methods

A total of 33 bacterial strains affiliated to the *Actinomycetes*, *Alphaproteobacteria*, *Betaproteobacteria*, *Gammaproteobacteria*, *Bacilli*, *Cytophagia* and *Flavobacteriia* were isolated from unique ecological niches, including salt evaporation ponds, mudflats, and contaminated soil samples. Mud, seawater and soil samples were processed separately, spread onto diverse culture media including R2A and marine agar 2216 (+5% NaCl), and incubated at 25 and 30°C for 5−10 days (Table 1). The designated strain IDs, sources, culture media, and incubation conditions are summarized in Table 1. All strains were purified as single colonies and stored as 20−25% (w/v) glycerol suspension −80°C as well as lyophilized ampoules.

The morphology was studied on agar plates for 2−5 days under their optimum temperature. Cell size and shape were examined using scanning electron microscopy. Gram staining was performed using a Gram-staining kit of the standard procedures. Using API 20NE (bioMérieux) the biochemical characteristics were performed according to the manufacturer's instructions.

Bacterial DNA extraction, PCR amplification, and 16S rRNA gene sequencing followed the standard procedures outlined by Lane (1991). The 16S rRNA gene sequences from the 47 bacterial strains were compared to sequences in GenBank using BLASTN and also analyzed through the EzBioCloud database (Yoon *et al*., 2017). For phylogenetic analysis, sequence alignments were performed with the Clustal_X program (Thompson *et al*., 1997), and any gaps were manually edited using BioEdit (Hall, 1999). Evolutionary distances were computed using the Kimura two-parameter model (Kimura, 1983). Phylogenetic trees were constructed via the neighbor-joining method (Saitou and Nei, 1987) in the MEGA X software (Kumar *et al*., 2018), with bootstrap values calculated from 1,000 replications (Felsenstein, 1985).

Results and Discussion

The 33 strains were distributed in 7 classes of the *Actinomycetes*, *Alphaproteobacteria*, *Betaproteobacteria*, *Gammaproteobacteria*, *Bacilli*, *Cytophagia* and *Flavobacteriia*; 2 strains for the class *Bacilli*, 7 strains for the *Actinomycetes*, 9 strains for the *Alphaproteobacteria*, 1 strain for the *Betaproteobacteria*, 9 strains for the *Gammaproteobacteria*, 1 strain for the *Cytophagia* and 4 strains for the *Flavobacteriia* (Table 1). These strains were Gram-staining-negative or positive, chemoheterotrophic, rod, short-rod, or coccoid shaped showing in Fig. 1.

The strains in the phylum *Actinomycetota* (Fig. 2) were found to belong to 1 classes 7 separate genera: *Streptomyces* (1 species), *Rhodococcus* (1 species), *Rathayibacter* (1 species), *Nocardioides* (1 species), *Cryobacterium* (1 species), *Arthrobacter* (1 species), and *Aeromicrobium* (1 species).

Fig. 3 shows phylogenetic assignment of 19 strains of the phylum *Pseudomonadota* belong to 3 classes 14 separate genera: *Thioclave* (1 species), *Sulfitobacter* (1 species), *Roseovarius* (2 species), *Qipengyuania* (1 species), *Maritalea* (1 species), *Devosia* (2 species), *Brevundimonas* (1 species), *Simplicispira* (1 species), *Spiribacter* (2 species), *Shewanella* (1 species), *Pseudomonas* (1 species), *Marinobacter* (2 species), *Halomonas* (2 species), and *Chromohalobacter* (1 species).

Fig. 4 shows phylogenetic assignment of 7 strains of the phyla *Bacillota* and *Bacteroidota* belong to 3 classes 6 separate genera: *Virgibacillus* (1 species), *Alkalihalobacillus* (1 species), *Hymenobacter* (1 species), *Muricauda* (2 species), *Kaistella* (1 species), and *Flavobacterium* (1 species).

Here we report 33 unrecorded bacterial species in Korea belonging to 7 classes of 4 phyla.

Table 1. The taxonomic affiliations of isolated strains belonging to the classes *Actinomycetes*, *Alphaproteobacteria*, *Betaproteobacteria*, *Gammaproteobacteria*, *Bacilli*, *Cytophagia* and *Flavobacteriia*.

Class	Order	Family	Genus	Strain ID	NIBR ID	Most closely related species	Similarity (%)	Isolation source	Isolation site	Medium	Incubation conditions (°C, days)
Actinomycetes	*Microbacteriales*	*Microbacteriaceae*	*Rathayibacter*	Du119	NIBRBAC000509522	*Rathayibacter rubneri*	100.00	Contaminated soil	Anseong-si	R2A	25°C
Actinomycetes	*Micrococcales*	*Micrococcaceae*	*Arthrobacter*	Du194	NIBRBAC000509525	*Arthrobacter glacialis*	99.18	Contaminated soil	Anseong-si	R2A	25°C
Actinomycetes	*Streptomycetales*	*Streptomycetaceae*	*Streptomyces*	P23	NIBRBAC000509526	*Streptomyces lateritius*	100.00	Contaminated soil	Anseong-si	R2A	25°C
Actinomycetes	*Mycobacteriales*	*Nocardiaceae*	*Rhodococcus*	P101	NIBRBAC000509528	*Prescottella defluvii*	100.00	Contaminated soil	Anseong-si	R2A	25°C
Actinomycetes	*Microbacteriales*	*Microbacteriaceae*	*Cryobacterium*	P108	NIBRBAC000509529	*Cryobacterium soli*	99.78	Contaminated soil	Anseong-si	R2A	25°C
Actinomycetes	*Propionibacteriales*	*Nocardioidaceae*	*Nocardioides*	Du230	NIBRBAC000509530	*Nocardioides pacificus*	99.44	Contaminated soil	Anseong-si	R2A	25°C
Actinomycetes	*Propionibacteriales*	*Nocardioidaceae*	*Aeromicrobium*	Du262	NIBRBAC000509532	*Aeromicrobium phoceense*	100.00	Contaminated soil	Anseong-si	R2A	25°C
Alphaproteobacteria	*Rhodobacterales*	*Rhodobacteraceae*	*Roseovarius*	T3	NIBRBAC000508810	*Roseovarius tibetensis*	99.93	Salt evaporation pond	Taean-gun	MA + 5% NaCl	30°C
Alphaproteobacteria	*Rhodobacterales*	*Rhodobacteraceae*	*Roseovarius*	T12	NIBRBAC000508811	*Roseovarius tolerans*	100	Salt evaporation pond	Taean-gun	MA + 5% NaCl	30°C
Alphaproteobacteria	*Sphingomonadales*	*Erythrobacteraceae*	*Qipengyuania*	SC77	NIBRBAC000508816	*Qipengyuania vesicularis*	99.36	Mudflats	Hwaseong-si	MA + 5% NaCl	25°C
Alphaproteobacteria	*Rhizobiales*	*Hyphomicrobiaceae*	*Maritalea*	SC80	NIBRBAC000508817	*Maritalea mobilis*	99.93	Mudflats	Hwaseong-si	MA + 5% NaCl	25°C
Alphaproteobacteria	*Rhodobacterales*	*Rhodobacteraceae*	*Thioclava*	SC162	NIBRBAC000508820	*Thioclava nitratireducens*	100	Mudflats	Hwaseong-si	MA + 5% NaCl	28°C
Alphaproteobacteria	*Rhodobacterales*	*Rhodobacteraceae*	*Sulfitobacter*	SC164	NIBRBAC000508821	*Sulfitobacter faviae*	99.86	Mudflats	Hwaseong-si	MA + 5% NaCl	25°C
Alphaproteobacteria	*Caulobacterales*	*Caulobacteraceae*	*Brevundimonas*	Du49	NIBRBAC000509520	*Brevundimonas mediterranea*	99.71	Contaminated soil	Anseong-si	R2A	25°C
Alphaproteobacteria	*Rhizobiales*	*Devosiaceae*	*Devosia*	Du137	NIBRBAC000509523	*Devosia epidermidihirudinis*	98.72	Contaminated soil	Anseong-si	R2A	25°C
Alphaproteobacteria	*Rhizobiales*	*Devosiaceae*	*Devosia*	Du184	NIBRBAC000509524	*Devosia limi*	99.43	Contaminated soil	Anseong-si	R2A	25°C
Bacilli	*Bacillales*	*Bacillaceae*	*Virgibacillus*	GP109	NIBRBAC000508814	*Virgibacillus flavescens*	99.33	Mudflats	Hwaseong-si	MA + 5% NaCl	25°C
Bacilli	*Bacillales*	*Bacillaceae*	*Alkalihalobacillus*	SC171	NIBRBAC000508822	*Alkalihalobacillus pseudofirmus*	99.93	Mudflats	Hwaseong-si	MA + 5% NaCl	30°C
Betaproteobacteria	*Burkholderiales*	*Comamonadaceae*	*Simplicispira*	Du248	NIBRBAC000509531	*Simplicispira psychrophila*	99.31	Contaminated soil	Anseong-si	R2A	25°C
Cytophagia	*Cytophagales*	*Hymenobacteraceae*	*Hymenobacter*	Du96	NIBRBAC000509521	*Hymenobacter actinosclerus*	99.44	Contaminated soil	Anseong-si	R2A	25°C
Flavobacteriia	*Flavobacteriales*	*Flavobacteriaceae*	*Muricauda*	SC11	NIBRBAC000508815	*Muricauda ruestringensis*	99.52	Mudflats	Hwaseong-si	MA + 5% NaCl	25°C
Flavobacteriia	*Flavobacteriales*	*Flavobacteriaceae*	*Muricauda*	SC140	NIBRBAC000508818	*Muricauda chongwuensis*	99.24	Mudflats	Hwaseong-si	MA + 5% NaCl	25°C
Flavobacteriia	*Flavobacteriales*	*Flavobacteriaceae*	*Flavobacterium*	Du4	NIBRBAC000509519	*Flavobacterium chryseum*	99.34	Contaminated soil	Anseong-si	R2A	25°C
Flavobacteriia	*Flavobacteriales*	*Flavobacteriaceae*	*Kaistella*	P84	NIBRBAC000509527	*Kaistella daneshvariae*	100.00	Contaminated soil	Anseong-si	R2A	25°C
Gammaproteobacteria	*Oceanospirillales*	*Halomonadaceae*	*Halomonas*	A8	NIBRBAC000508805	*Halomonas azerica*	99.11	Salt evaporation pond	Taean-gun	MA + 5% NaCl	30°C
Gammaproteobacteria	*Alteromonadales*	*Alteromonadaceae*	*Marinobacter*	B9	NIBRBAC000508806	*Marinobacter aquaticus*	99.37	Salt evaporation pond	Taean-gun	MA + 5% NaCl	37°C
Gammaproteobacteria	*Alteromonadales*	*Alteromonadaceae*	*Marinobacter*	B20	NIBRBAC000508807	*Marinobacter vulgaris*	99.73	Salt evaporation pond	Taean-gun	MA + 5% NaCl	37°C
Gammaproteobacteria	*Oceanospirillales*	*Halomonadaceae*	*Halomonas*	D12	NIBRBAC000508808	*Halomonas saccharevitans*	99.72	Salt evaporation pond	Taean-gun	MA + 5% NaCl	30°C
Gammaproteobacteria	*Oceanospirillales*	*Halomonadaceae*	*Chromohalobacter*	D37	NIBRBAC000508809	*Chromohalobacter salexigens*	99.93	Salt evaporation pond	Taean-gun	MA + 5% NaCl	37°C
Gammaproteobacteria	*Chromatiales*	*Ectothiorhodospiraceae*	*Spiribacter*	T18	NIBRBAC000508812	*Spiribacter roseus*	99.79	Salt evaporation pond	Taean-gun	MA + 5% NaCl	37°C
Gammaproteobacteria	*Chromatiales*	*Ectothiorhodospiraceae*	*Spiribacter*	T26	NIBRBAC000508813	*Spiribacter salinus*	99.11	Salt evaporation pond	Taean-gun	MA + 5% NaCl	37°C
Gammaproteobacteria	*Alteromonadales*	*Shewanellaceae*	*Shewanella*	SC153	NIBRBAC000508819	*Shewanella carassii*	99.79	Mudflats	Hwaseong-si	MA + 5% NaCl	35°C
Gammaproteobacteria	*Pseudomonadales*	*Pseudomonadaceae*	*Pseudomonas*	Du18	NIBRBAC000509533	*Pseudomonas sivasensis*	100	Contaminated soil	Anseong-si	R2A	25°C

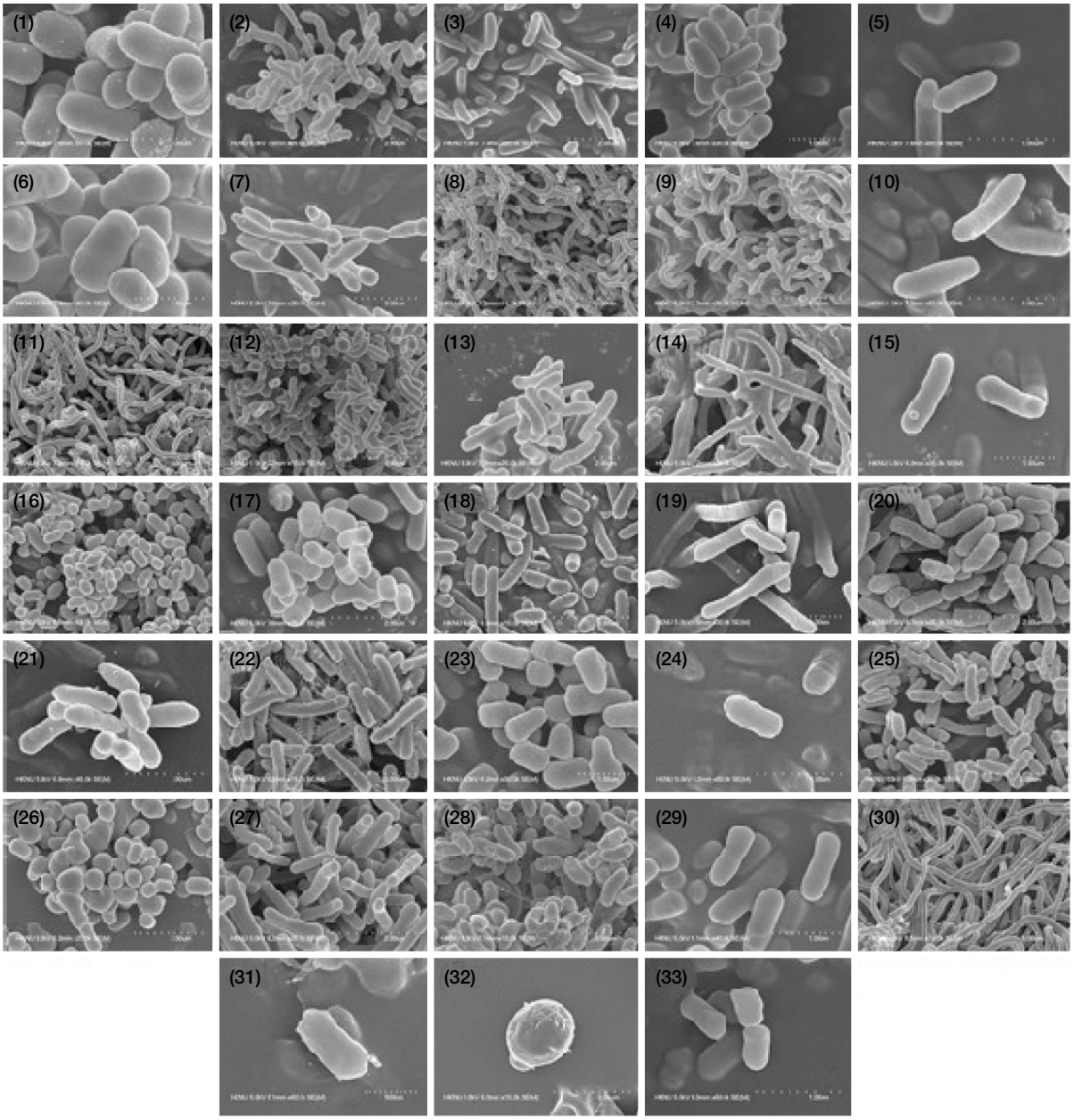

Fig. 1. Scanning electron micrograph of cells of the strains isolated in this study. Strains: 1, A8; 2, B9; 3, B20; 4, D12; 5, D37; 6, T3; 7, T12; 8, T18; 9, T26; 10, GP109; 11, SC11; 12, SC77; 13, SC80; 14, SC140; 15, SC153; 16, SC162; 17, SC164; 18, SC171; 19, Du4; 20, Du18; 21, Du49; 22, Du96; 23, Du119; 24, Du137; 25, Du184; 26, Du194; 27, Du230; 28, Du248; 29, Du262; 30, P23; 31, P84; 32, P101; 33, P108.

Description of *Halomonas azerica* A8

Cells are Gram-staining-negative, non-flagellated and rod shaped. Colonies are circular, entire, convex and pale brown-colored after 3 days incubation on marine agar with 5% sodium chloride at 30°C. In the API 20NE system, positive for glucose acidification, utilization of D-glucose, D-mannitol, D-maltose, potassium gluconate, malic acid and trisodium citrate, but negative for nitrate reduction, indole production, arginine dihydrolase, urease activity, esculin hydrolysis, gelatin hydrolysis, β-galactosidase activity, oxidase activity, utilization of L-arabinose, D-mannose, *N*-acetyl-D-glucosamine, capric acid, adipic acid and phenylacetic acid. Strain A8 (=NIBRBAC000508805) was isolated from salt evaporation pond in Nam-myeon, Taean-gun, Chungcheongnam-do, Republic of Korea (36° 36′27.0″N 126°18′17.1″E).

Description of *Marinobacter aquaticus* B9

Cells are Gram-staining-negative, non-flagellated and rod shaped. Colonies are circular, convex and ivory-

colored after 3 days incubation on marine agar with 5% sodium chloride at 37°C. In the API 20NE system, positive for oxidase activity, but negative for nitrate reduction, indole production, glucose acidification, arginine dihydrolase, urease activity, esculin hydrolysis, gelatin hydrolysis, β-galactosidase activity, utilization of D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. Strain B9 (=NIBRBAC000508806) was isolated from salt evaporation pond in Nam-myeon, Taean-gun, Chungcheongnam-do, Republic of Korea (36°36′27.0″N 126°18′17.1″E).

Description of *Marinobacter vulgaris* B20

Cells are Gram-staining-negative, non-flagellated and rod shaped. Colonies are circular, convex and cream-colored after 3 days incubation on marine agar with 5% sodium chloride at 37°C. In the API 20NE system, positive for nitrate reduction, urease activity, utilization of D-glucose, L-arabinose, *N*-acetyl-D-glucosamine, D-maltose, potassium gluconate, adipic acid and malic acid, but negative for indole production, glucose acidification, arginine dihydrolase, esculin hydrolysis, gelatin hydrolysis, β-galactosidase activity, oxidase activity, utilization of D-mannose, D-mannitol, capric acid, trisodium citrate and phenylacetic acid. Strain B20 (=NIBRBAC000508807) was isolated from salt evaporation pond in Nam-myeon, Taean-gun, Chungcheongnam-do, Republic of Korea (36°36′27.0″N 126°18′17.1″E).

Description of *Halomonas saccharevitans* D12

Cells are Gram-staining-negative, non-flagellated and rod shaped. Colonies are circular, entire, convex and ivory-colored after 3 days incubation on marine agar with 5% sodium chloride at 30°C. In the API 20NE system, positive for nitrate reduction and oxidase activity, but negative for indole production, glucose acidification, arginine dihydrolase, urease activity, esculin hydrolysis, gelatin hydrolysis, β-galactosidase activity, utilization of D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. Strain D12 (=NIBRBAC000508808) was isolated from salt evaporation pond in Nam-myeon, Taean-gun, Chungcheongnam-do, Republic of Korea (36°36′27.0″N 126°18′17.1″E).

Description of *Chromohalobacter salexigens* D37

Cells are Gram-staining-negative, non-flagellated and rod shaped. Colonies are circular, convex, smooth and ivory-colored after 3 days incubation on marine agar with 5% sodium chloride at 37°C. In the API 20NE system, positive for nitrate reduction, β-galactosidase activity, oxidase activity, utilization of D-glucose, L-arabinose, D-mannose, D-mannitol, D-maltose, malic acid and trisodium citrate, but negative for indole production, glucose acidification, arginine dihydrolase, urease activity, esculin hydrolysis, gelatin hydrolysis, utilization of *N*-acetyl-D-glucosamine, potassium gluconate, capric acid, adipic acid and phenylacetic acid. Strain D37 (=NIBRBAC000508809) was isolated from salt evaporation pond in Nam-myeon, Taean-gun, Chungcheongnam-do, Republic of Korea (36°36′27.0″N 126°18′17.1″E).

Description of *Roseovarius tibetensis* T3

Cells are Gram-staining-negative, non-flagellated and rod shaped. Colonies are circular, convex, smooth and ivory-colored after 3 days incubation on marine agar with 5% sodium chloride at 30°C. In the API 20NE system, positive for nitrate reduction, gelatin hydrolysis, β-galactosidase activity, oxidase activity, utilization of D-glucose, D-mannitol and *N*-acetyl-D-glucosamine, but negative for indole production, glucose acidification, arginine dihydrolase, urease activity, esculin hydrolysis, utilization of L-arabinose, D-mannose, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. Strain T3 (=NIBRBAC000508810) was isolated from salt evaporation pond in Nam-myeon, Taean-gun, Chungcheongnam-do, Republic of Korea (36°36′27.0″N 126°18′17.1″E).

Description of *Roseovarius tolerans* T12

Cells are Gram-staining-negative, non-flagellated and rod shaped. Colonies are circular, convex, smooth and ivory-colored after 3 days incubation on marine agar with 5% sodium chloride at 30°C. In the API 20NE system, positive for nitrate reduction, oxidase activity and utilization of *N*-acetyl-D-glucosamine, but negative for indole production, glucose acidification, arginine dihydrolase, urease activity, esculin hydrolysis, gelatin hydrolysis, β-galactosidase activity, utilization of D-glucose, L-arabinose, D-mannose, D-mannitol, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. Strain T12 (=NIBRBAC 000508811) was isolated from salt evaporation pond in Nam-myeon, Taean-gun, Chungcheongnam-do, Republic of Korea (36°36′27.0″N 126°18′17.1″E).

Description of *Spiribacter roseus* T18

Cells are Gram-staining-negative, non-flagellated and Curved-rod-shaped. Colonies are circular, convex and pink-colored after 7 days incubation on marine agar with 5% sodium chloride at 37°C. In the API 20NE system, positive for urease activity and oxidase activity, but negative for nitrate reduction, indole production, glucose acidification, arginine dihydrolase, esculin hydrolysis, gelatin hydrolysis and β-galactosidase activity, utilization of D-

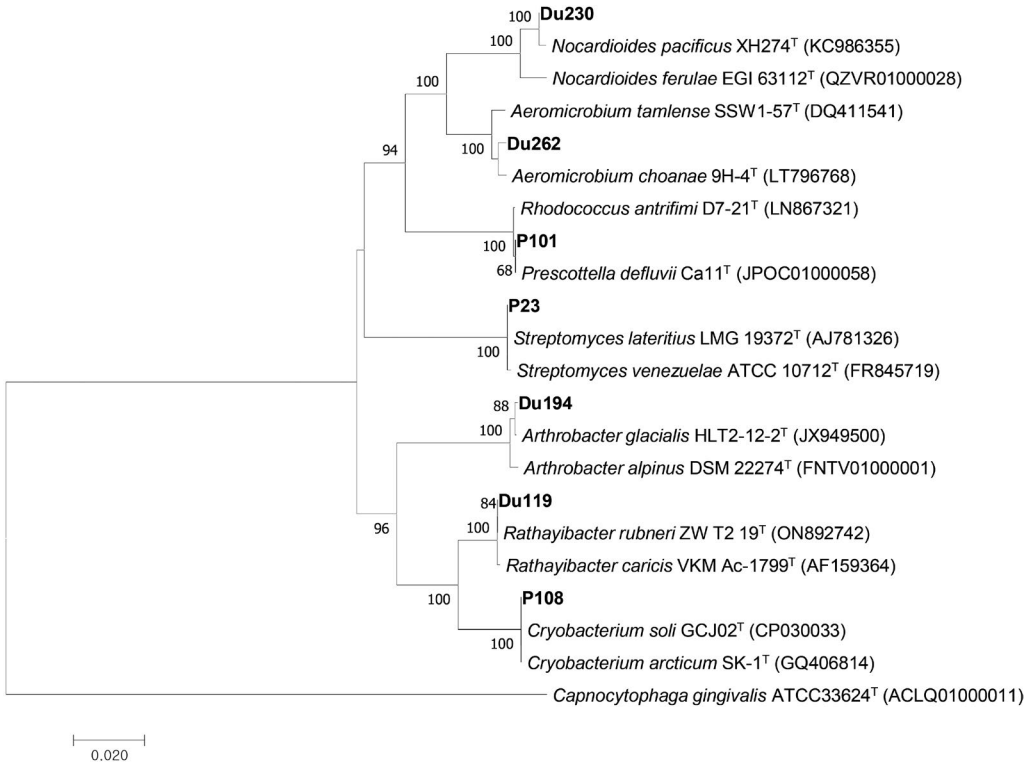

Fig. 2. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences, showing the relationship between the strains in the phylum *Actinomycetota*. Bootstrap values (>60%) based on 1,000 replications are shown on the branches. The tree was constructed using the neighbor-joining method. Bar, 0.02 substitutions per nucleotide position.

glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. Strain T18 (=NIBRBAC000508812) was isolated from salt evaporation pond in Nam-myeon, Taean-gun, Chungcheongnam-do, Republic of Korea (36°36′27.0″N 126°18′17.1″E).

Description of *Spiribacter salinus* T26

Cells are Gram-staining-negative, non-flagellated and Curved-rod-shaped. Colonies are circular, convex and pink-colored after 7 days incubation on marine agar with 5% sodium chloride at 37°C. In the API 20NE system, positive for oxidase activity, but negative for nitrate reduction, indole production, glucose acidification, arginine dihydrolase, urease activity, esculin hydrolysis, gelatin hydrolysis, β-galactosidase activity, utilization of D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. Strain T26 (=NIBRBAC000508813) was isolated from salt evaporation pond in Nam-myeon, Taean-gun, Chungcheongnam-do, Republic of Korea (36°36′27.0″N 126°18′17.1″E).

Description of *Virgibacillus flavescens* GP109

Cells are Gram-staining-positive, non-flagellated and rod shaped. Colonies are circular, convex and pale orange-colored after 3 days incubation on marine agar with 5% sodium chloride at 25°C. In the API 20NE system, positive for gelatin hydrolysis and oxidase activity, but negative for nitrate reduction, indole production, glucose acidification, arginine dihydrolase, urease activity, esculin hydrolysis, β-galactosidase activity, utilization of D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. Strain GP109 (=NIBRBAC000508814) was isolated from mudflats in Seosin-myeon, Hwaseong-si, Gyeonggi-do, Republic of Korea (37°07′15.2″N 126°41′06.0″E).

Description of *Muricauda ruestringensis* SC11

Cells are Gram-staining-negative, non-flagellated and rod shaped. Colonies are circular, convex and yellow-colored after 3 days incubation on marine agar with 5% sodium chloride at 25°C. In the API 20NE system, positive for esculin hydrolysis, gelatin hydrolysis, oxidase activity, utilization of D-mannose and *N*-acetyl-D-glucosamine, but negative for nitrate reduction, indole production, glucose

acidification, arginine dihydrolase, urease activity, β-galactosidase activity, utilization of D-glucose, L-arabinose, D-mannitol, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. Strain SC11 (=NIBRBAC000508815) was isolated from mudflats in Ujeong-eup, Hwaseong-si, Gyeonggi-do, Republic of Korea (37°01′49.2″N 126°45′60.0″E).

Description of *Qipengyuania vesicularis* SC77

Cells are Gram-staining-negative, non-flagellated and rod shaped. Colonies are circular, convex and red-colored after 3 days incubation on marine agar with 5% sodium chloride at 25°C. In the API 20NE system, positive for oxidase activity, but negative for nitrate reduction, indole production, glucose acidification, arginine dihydrolase, urease activity, esculin hydrolysis, gelatin hydrolysis, β-galactosidase activity, utilization of D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. Strain SC77 (=NIBRBAC000508816) was isolated from mudflats in Ujeong-eup, Hwaseong-si, Gyeonggi-do, Republic of Korea (37°01′49.2″N 126°45′60.0″E).

Description of *Maritalea mobilis* SC80

Cells are Gram-staining-negative, non-flagellated and rod shaped. Colonies are circular, convex and ivory-colored after 3 days incubation on marine agar with 5% sodium chloride at 25°C. In the API 20NE system, positive for nitrate reduction, glucose acidification, β-galactosidase activity, oxidase activity, utilization of D-glucose, D-mannose, *N*-acetyl-D-glucosamine and D-maltose, but negative for indole production, arginine dihydrolase, urease activity, esculin hydrolysis, gelatin hydrolysis, utilization of L-arabinose, D-mannitol, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. Strain SC80 (=NIBRBAC000508817) was isolated from mudflats in Ujeong-eup, Hwaseong-si, Gyeonggi-do, Republic of Korea (37°01′49.2″N 126°45′60.0″E).

Description of *Muricauda chongwuensis* SC140

Cells are Gram-staining-negative, non-flagellated and rod shaped. Colonies are circular, convex and yellow-colored after 3 days incubation on marine agar with 5% sodium chloride at 25°C. In the API 20NE system, positive for esculin hydrolysis, oxidase activity, utilization of D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, potassium gluconate, capric acid, adipic acid, malic acid and trisodium citrate, but negative for nitrate reduction, indole production, glucose acidification, arginine dihydrolase, urease activity, gelatin hydrolysis, β-galactosidase activity, utilization of D-maltose and phenylacetic acid. Strain SC140 (=NIBRBAC000508818) was isolated from mudflats in Ujeong-eup, Hwaseong-si, Gyeonggi-do, Republic of Korea (37°01′49.2″N 126°45′60.0″E).

Description of *Shewanella carassii* SC153

Cells are Gram-staining-negative, non-flagellated and rod shaped. Colonies are circular, convex and pale orange-colored after 3 days incubation on marine agar with 5% sodium chloride at 35°C. In the API 20NE system, positive for gelatin hydrolysis, oxidase activity, utilization of D-glucose, L-arabinose, *N*-acetyl-D-glucosamine, capric acid and malic acid, but negative for nitrate reduction, indole production, glucose acidification, arginine dihydrolase, urease activity, esculin hydrolysis, β-galactosidase activity, utilization of D-mannose, D-mannitol, D-maltose, potassium gluconate, adipic acid, trisodium citrate and phenylacetic acid. Strain SC153 (=NIBRBAC000508819) was isolated from mudflats in Ujeong-eup, Hwaseong-si, Gyeonggi-do, Republic of Korea (37°01′49.2″N 126°45′60.0″E).

Description of *Thioclava nitratireducens* SC162

Cells are Gram-staining-negative, non-flagellated and rod shaped. Colonies are circular, convex and ivory-colored after 3 days incubation on marine agar with 5% sodium chloride at 28°C. In the API 20NE system, positive for nitrate reduction, esculin hydrolysis, β-galactosidase activity, oxidase activity, utilization of D-glucose, L-arabinose, D-mannitol and D-maltose, but negative for indole production, glucose acidification, arginine dihydrolase, urease activity, gelatin hydrolysis, utilization of D-mannose, *N*-acetyl-D-glucosamine, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. Strain SC162 (=NIBRBAC000508820) was isolated from mudflats in Ujeong-eup, Hwaseong-si, Gyeonggi-do, Republic of Korea (37°01′49.2″N 126°45′60.0″E).

Description of *Sulfitobacter faviae* SC164

Cells are Gram-staining-negative, non-flagellated and rod shaped. Colonies are circular, convex and white-colored after 3 days incubation on marine agar with 5% sodium chloride at 25°C. In the API 20NE system, positive for oxidase activity and utilization of D-glucose, but negative for nitrate reduction, indole production, glucose acidification, arginine dihydrolase, urease activity, esculin hydrolysis, gelatin hydrolysis, β-galactosidase activity, utilization of L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. Strain SC164 (=NIBRBAC000508821) was isolated from mudflats in Ujeong-eup, Hwaseong-si, Gyeonggi-do, Republic of Korea (37°01′49.2″N 126°45′60.0″E).

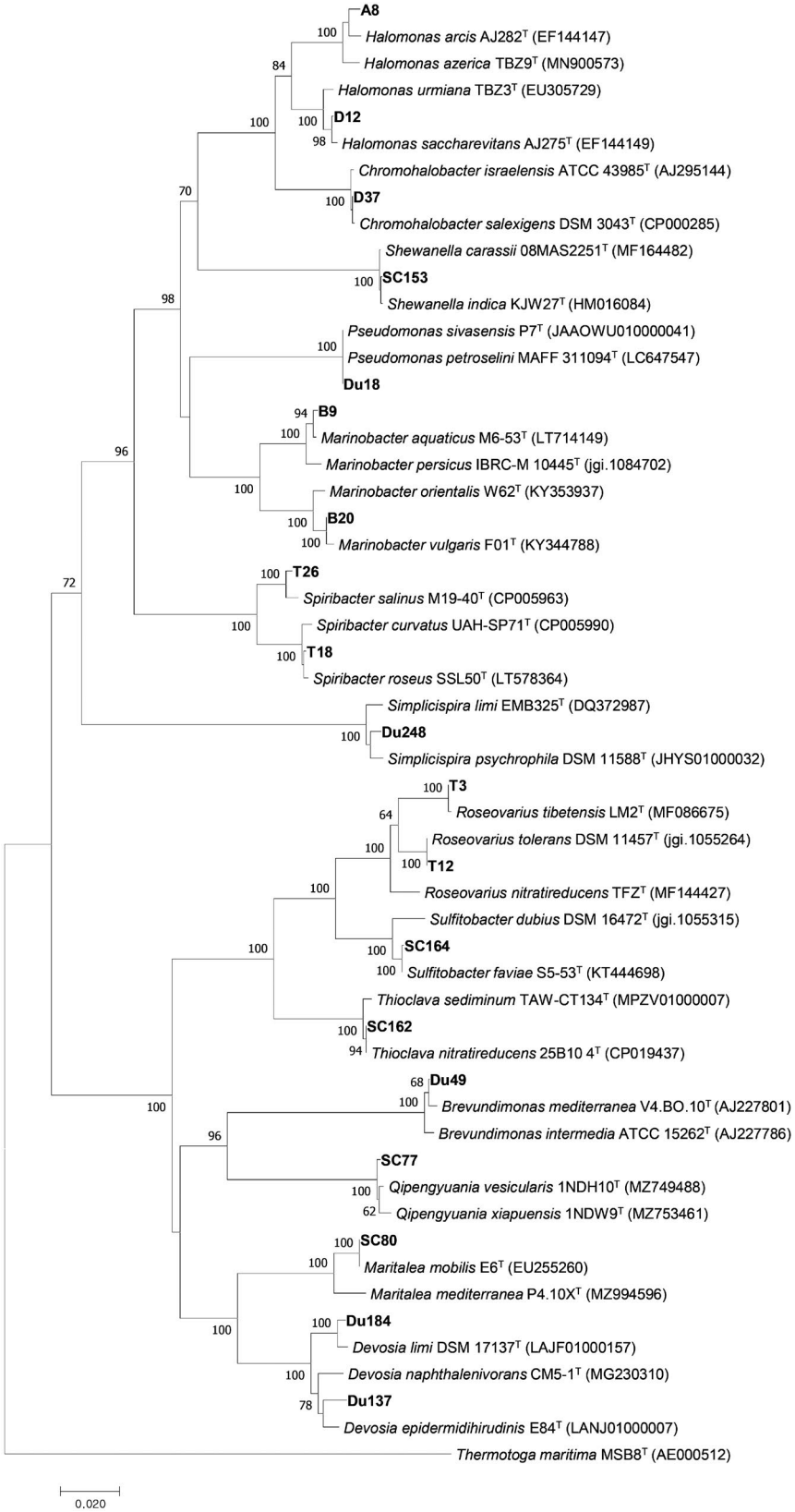

Fig. 3. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences, showing the relationship between the strains in the phylum *Pseudomonadota*. Bootstrap values (>60%) based on 1,000 replications are shown on the branches. The tree was constructed using the neighbor-joining method. Bar, 0.02 substitutions per nucleotide position.

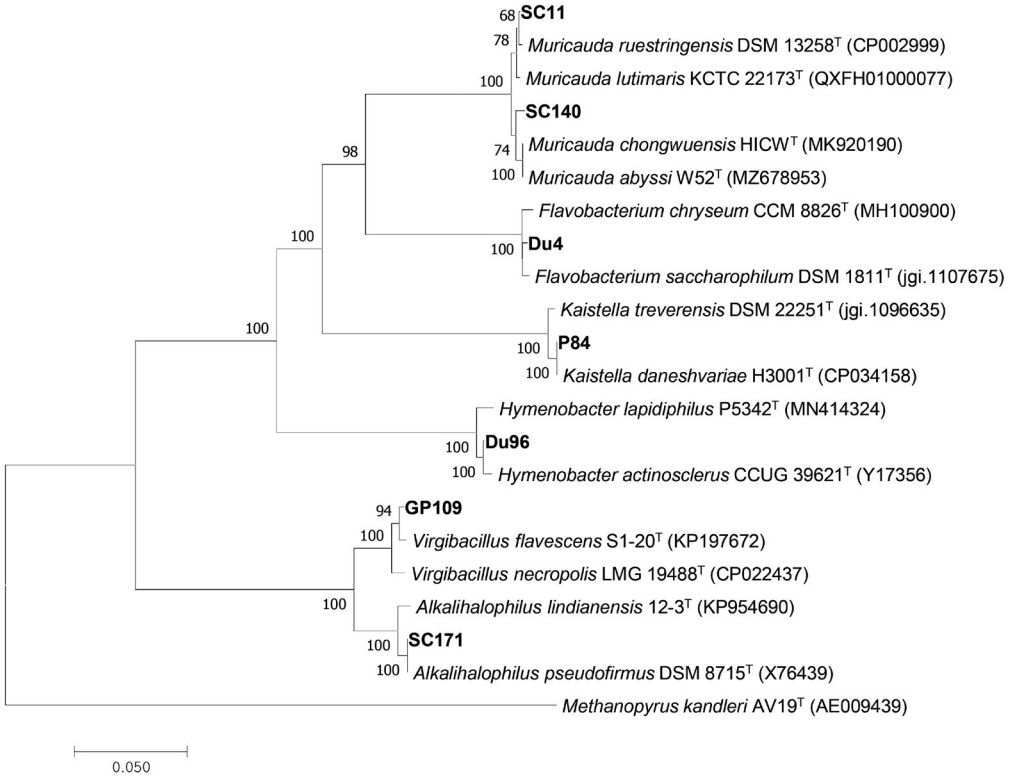

Fig. 4. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences, showing the relationship between the strains in the phylum *Bacillota* and *Bacteroidota*. Bootstrap values (>60%) based on 1,000 replications are shown on the branches. The tree was constructed using the neighbor-joining method. Bar, 0.05 substitutions per nucleotide position.

Description of *Alkalihalobacillus pseudofirmus* SC171

Cells are Gram-staining-positive, non-flagellated and rod shaped. Colonies are circular, convex and pale yellow-colored after 3 days incubation on marine agar with 5% sodium chloride at 30°C. In the API 20NE system, positive for nitrate reduction, oxidase activity, utilization of *N*-acetyl-D-glucosamine, malic acid and trisodium citrate, but negative for indole production, glucose acidification, arginine dihydrolase, urease activity, esculin hydrolysis, gelatin hydrolysis, β-galactosidase activity, utilization of D-glucose, L-arabinose, D-mannose, D-mannitol, D-maltose, potassium gluconate, capric acid, adipic acid and phenylacetic acid. Strain SC171 (=NIBRBAC000508822) was isolated from mudflats in Ujeong-eup, Hwaseong-si, Gyeonggi-do, Republic of Korea (37°01′49.2″N 126°45′60.0″E).

Description of *Flavobacterium chryseum* Du4

Cells are Gram-staining-negative, non-flagellated and rod shaped. Colonies are circular, entire, convex and yellow-colored after 3 days incubation on R2A at 25°C. In the API 20NE system, positive for glucose acidification, arginine dihydrolase, esculin hydrolysis, β-galactosidase activity, oxidase activity, utilization of D-glucose, L-arabinose, D-mannose, *N*-acetyl-D-glucosamine and D-maltose, but negative for nitrate reduction, indole production, urease activity, gelatin hydrolysis, utilization of D-mannitol, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. Strain Du4 (=NIBRBAC000509519) was isolated from contaminated soil in Seokjeong-dong, Anseong-si, Gyeonggi-do, Republic of Korea (37°00′25.3″N 127°15′39.4″E).

Description of *Pseudomonas sivasensis* Du18

Cells are Gram-staining-negative, non-flagellated and rod shaped. Colonies are circular, entire, convex and cream-colored after 3 days incubation on R2A at 25°C. In the API 20NE system, positive for arginine dihydrolase, gelatin hydrolysis, oxidase activity, utilization of D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, potassium gluconate, capric acid, malic acid and trisodium citrate, but negative for nitrate reduction, indole production, glucose acidification, urease activity, esculin hydrolysis, β-galactosidase activity, utilization of D-maltose, adipic acid and phenylacetic acid. Strain Du18 (=NIBR BAC000509533) was isolated from contaminated soil in Seokjeong-dong, Anseong-si, Gyeonggi-do, Republic of Korea (37°00′25.3″N 127°15′39.4″E).

Description of *Brevundimonas mediterranea* Du49

Cells are Gram-staining-negative, non-flagellated and rod shaped. Colonies are circular, entire, convex and pale orange-colored after 3 days incubation on R2A at 25°C. In the API 20NE system, positive for esculin hydrolysis, oxidase activity, utilization of D-glucose, D-maltose and malic acid, but negative for nitrate reduction, indole production, glucose acidification, arginine dihydrolase, urease activity, gelatin hydrolysis, β-galactosidase activity, utilization of L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, potassium gluconate, capric acid, adipic acid, trisodium citrate and phenylacetic acid. Strain Du49 (=NIBRBAC000509520) was isolated from contaminated soil in Seokjeong-dong, Anseong-si, Gyeonggi-do, Republic of Korea (37°00′25.3″N 127°15′39.4″E).

Description of *Hymenobacter actinosclerus* Du96

Cells are Gram-staining-negative, non-flagellated and rod shaped. Colonies are circular, entire, convex and red-colored after 3 days incubation on R2A at 25°C. In the API 20NE system, positive for oxidase activity, utilization of D-glucose, *N*-acetyl-D-glucosamine, D-maltose and malic acid, but negative for nitrate reduction, indole production, glucose acidification, arginine dihydrolase, urease activity, esculin hydrolysis, gelatin hydrolysis, β-galactosidase activity, utilization of L-arabinose, D-mannose, D-mannitol, potassium gluconate, capric acid, adipic acid, trisodium citrate and phenylacetic acid. Strain Du96 (=NIBR BAC000509521) was isolated from contaminated soil in Seokjeong-dong, Anseong-si, Gyeonggi-do, Republic of Korea (37°00′25.3″N 127°15′39.4″E).

Description of *Rathayibacter rubneri* Du119

Cells are Gram-staining-positive, non-flagellated and rod shaped. Colonies are circular, entire, convex and cream-colored after 3 days incubation on R2A at 25°C. In the API 20NE system, positive for urease activity, esculin hydrolysis, β-galactosidase activity, oxidase activity, utilization of D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, potassium gluconate, adipic acid, malic acid, trisodium citrate and phenylacetic acid, but negative for nitrate reduction, indole production, glucose acidification, arginine dihydrolase, gelatin hydrolysis and utilization of capric acid. Strain Du119 (=NIBR BAC000509522) was isolated from contaminated soil in Seokjeong-dong, Anseong-si, Gyeonggi-do, Republic of Korea (37°00′25.3″N 127°15′39.4″E).

Description of *Devosia epidermidihirudinis* Du137

Cells are Gram-staining-negative, non-flagellated and rod shaped. Colonies are circular, entire, raised and orange-colored after 3 days incubation on R2A at 25°C. In the API 20NE system, positive for urease activity, esculin hydrolysis, β-galactosidase activity, oxidase activity, utilization of D-glucose, D-maltose, potassium gluconate and phenylacetic acid, but negative for nitrate reduction, indole production, glucose acidification, arginine dihydrolase, gelatin hydrolysis, utilization of L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, capric acid, adipic acid, malic acid and trisodium citrate. Strain Du137 (=NIBR BAC000509523) was isolated from contaminated soil in Seokjeong-dong, Anseong-si, Gyeonggi-do, Republic of Korea (37°00′25.3″N 127°15′39.4″E).

Description of *Devosia limi* Du184

Cells are Gram-staining-negative, non-flagellated and rod shaped. Colonies are circular, entire, convex and white-colored after 3 days incubation on R2A at 25°C. In the API 20NE system, positive for urease activity, esculin hydrolysis, β-galactosidase activity, oxidase activity, utilization of D-mannose and phenylacetic acid, but negative for nitrate reduction, indole production, glucose acidification, arginine dihydrolase, gelatin hydrolysis, utilization of D-glucose, L-arabinose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid and trisodium citrate. Strain Du184 (=NIBR BAC000509524) was isolated from contaminated soil in Seokjeong-dong, Anseong-si, Gyeonggi-do, Republic of Korea (37°00′25.3″N 127°15′39.4″E).

Description of *Arthrobacter glacialis* Du194

Cells are Gram-staining-positive, non-flagellated and rod shaped. Colonies are circular, entire, convex and pale yellow-colored after 3 days incubation on R2A at 25°C. In the API 20NE system, positive for nitrate reduction, urease activity, esculin hydrolysis, β-galactosidase activity, utilization of D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, potassium gluconate and malic acid, but negative for indole production, glucose acidification, arginine dihydrolase, gelatin hydrolysis, oxidase activity, utilization of capric acid, adipic acid, trisodium citrate and phenylacetic acid. Strain Du194 (=NIBRBAC000509525) was isolated from contaminated soil in Seokjeong-dong, Anseong-si, Gyeonggi-do, Republic of Korea (37°00′25.3″N 127°15′39.4″E).

Description of *Streptomyces lateritius* P23

Cells are Gram-staining-positive, non-flagellated and filamentous shaped. Colonies are filamentous, umborate and white-colored after 3 days incubation on R2A at 25°C. In the API 20NE system, positive for nitrate reduction, esculin hydrolysis, β-galactosidase activity, utilization of D-glucose, D-mannose, *N*-acetyl-D-glucosamine, potassium gluconate and malic acid, but negative for indole pro-

duction, glucose acidification, arginine dihydrolase, urease activity, gelatin hydrolysis, oxidase activity, utilization of L-arabinose, D-mannitol, D-maltose, capric acid, adipic acid, trisodium citrate and phenylacetic acid. Strain P23 (=NIBRBAC000509526) was isolated from contaminated soil in Seokjeong-dong, Anseong-si, Gyeonggi-do, Republic of Korea (37°00′25.3″N 127°15′39.4″E).

Description of *Kaistella daneshvariae* P84

Cells are Gram-staining-negative, non-flagellated and rod shaped. Colonies are circular, entire, convex and cream-colored after 3 days incubation on R2A at 25°C. In the API 20NE system, positive for arginine dihydrolase, urease activity, esculin hydrolysis, β-galactosidase activity, oxidase activity, utilization of D-glucose, D-maltose and potassium gluconate, but negative for nitrate reduction, indole production, glucose acidification, gelatin hydrolysis, utilization of L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. Strain P84 (=NIBRBAC000509527) was isolated from contaminated soil in Seokjeong-dong, Anseong-si, Gyeonggi-do, Republic of Korea (37°00′25.3″N 127°15′39.4″E).

Description of *Prescottella defluvii* P101

Cells are Gram-staining-positive, non-flagellated and coccoid shaped. Colonies are circular, entire, raised and white-colored after 3 days incubation on R2A at 25°C. In the API 20NE system, positive for glucose acidification, esculin hydrolysis, oxidase activity, utilization of D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine and potassium gluconate, but negative for nitrate reduction, indole production, arginine dihydrolase, urease activity, gelatin hydrolysis, β-galactosidase activity, utilization of D-maltose, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. Strain P101 (=NIBRBAC000509528) was isolated from contaminated soil in Seokjeong-dong, Anseong-si, Gyeonggi-do, Republic of Korea (37°00′25.3″N 127°15′39.4″E).

Description of *Cryobacterium soli* P108

Cells are Gram-staining-positive, non-flagellated and rod shaped. Colonies are circular, entire, convex and yellow-colored after 3 days incubation on R2A at 25°C. In the API 20NE system, positive for esculin hydrolysis, β-galactosidase activity, oxidase activity, utilization of D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose and potassium gluconate, but negative for nitrate reduction, indole production, glucose acidification, arginine dihydrolase, urease activity, gelatin hydrolysis, utilization of capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. Strain P108 (=NIBRBAC000509529) was isolated from contaminated soil in Seokjeong-dong, Anseong-si, Gyeonggi-do, Republic of Korea (37°00′25.3″N 127°15′39.4″E).

Description of *Nocardioides pacificus* Du230

Cells are Gram-staining-positive, non-flagellated and rod shaped. Colonies are circular, entire, raised and pale yellow-colored after 3 days incubation on R2A at 25°C. In the API 20NE system, positive for nitrate reduction, esculin hydrolysis, gelatin hydrolysis, β-galactosidase activity, utilization of D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, potassium gluconate, adipic acid and malic acid, but negative for indole production, glucose acidification, arginine dihydrolase, urease activity, oxidase activity, utilization of capric acid, trisodium citrate and phenylacetic acid. Strain Du230 (=NIBRBAC000509530) was isolated from contaminated soil in Seokjeong-dong, Anseong-si, Gyeonggi-do, Republic of Korea (37°00′25.3″N 127°15′39.4″E).

Description of *Simplicispira psychrophila* Du248

Cells are Gram-staining-negative, non-flagellated and rod shaped. Colonies are circular, entire, raised and cream-colored after 3 days incubation on R2A at 25°C. In the API 20NE system, positive for oxidase activity and utilization of malic acid, but negative for nitrate reduction, indole production, glucose acidification, arginine dihydrolase, urease activity, esculin hydrolysis, gelatin hydrolysis, β-galactosidase activity, utilization of D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, trisodium citrate and phenylacetic acid. Strain Du248 (=NIBRBAC 000509531) was isolated from contaminated soil in Seokjeong-dong, Anseong-si, Gyeonggi-do, Republic of Korea (37°00′25.3″N 127°15′39.4″E).

Description of *Aeromicrobium phoceense* Du262

Cells are Gram-staining-positive, non-flagellated and rod shaped. Colonies are circular, entire, raised and yellow-colored after 3 days incubation on R2A at 25°C. In the API 20NE system, positive for nitrate reduction, esculin hydrolysis, β-galactosidase activity, utilization of D-glucose, D-maltose, potassium gluconate and adipic acid, but negative for indole production, glucose acidification, arginine dihydrolase, urease activity, gelatin hydrolysis, oxidase activity, utilization of L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, capric acid, malic acid, trisodium citrate and phenylacetic acid. Strain Du262 (=NIBR BAC000509532) was isolated from contaminated soil in Seokjeong-dong, Anseong-si, Gyeonggi-do, Republic of Korea (37°00′25.3″N 127°15′39.4″E).

Conflicts of Interest

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

Acknowledgements

This research was supported by grants from the research program of the National Institute of Biological Resources, funded by the Ministry of Environment of the Republic of Korea in 2021 and 2022 (No. NIBR202102109 and NIBR 202203112).

References

Felsenstein, J. 1985. Confidence limit on phylogenies: an approach using the bootstrap. Evolution 39:783-791.

Hall, T.A. 1999. BioEdit: a user-friendly biological sequence alignment editor and analysis program for Windows 95/98/NT. Nucleic Acids Symp. Ser. 41:95-98.

Kimura, M. 1983. The Neutral Theory of Molecular Evolution. Cambridge: Cambridge University Press, Cambridge, New York.

Kumar, S., G. Stecher, M. Li, C. Knyaz and K. Tamura. 2018. MEGA X: molecular evolutionary genetics analysis across computing platforms. Mol. Biol. Evol. 35:1547-1549.

Lane, D.J. 1991. 16S/23S rRNA sequencing. In: Stackebrandt, E. and Goodfellow, M. (eds.), Nucleic acid techniques in bacterial systematics. Wiley, New York, USA.

Martínez-Espinosa, R.M. 2024. Halophilic archaea as tools for bioremediation technologies. Appl. Microbiol. Biotechnol. 108(1):401

Raghad, J. 2019. The potential role of *Sphingomonas paucimobilis* in bioremediation of soils contaminated with hydrocarbon and heavy metal. Malaysian Journal of Science 38(3):48-58.

Saitou, N. and M. Nei. 1987. The neighbor-joining method: a new method for reconstructing phylogenetic trees. Mol. Biol. Evol. 4(4):406-425.

Thompson, J.D., T.J. Gibson, F. Plewniak, F. Jeanmougin and D.G. Higgins. 1997. The CLUSTAL_X windows interface: flexible strategies for multiple sequence alignment aided by quality analysis tools. Nucleic Acids Res. 25:4876-4882.

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 and whole genome assemblies. Int. J. Syst. Evol. Microbiol. 67:1613-1617.

Submitted: February 16, 2025
Revised: March 13, 2025
Accepted: April 10, 2025