Korean Journal of Environmental Biology

Note

https://doi.org/10.11626/KJEB.2024.42.2.143

Korean J. Environ. Biol.
42(2) : 143-157 (2024)
ISSN 1226-9999 (print)
ISSN 2287-7851 (online)

A report on 29 unrecorded bacterial species isolated from the Nakdonggang River, Republic of Korea

Ahyoung Choi*, Ja Young Cho, Soo-Yeong Lee, Ji Young Jung, Kiwoon Baek, Seoni Hwang, Eui-Jin Kim and Jaeduk Goh

Biological Resources Research Department, Nakdonggang National Institute of Biological Resources (NNIBR), Sangju 37242, Republic of Korea

Contribution to Environmental Biology

- This study aims to offer a taxonomic perspective on species that have been reported abroad but have not yet been reported in Korea.
- To ensure that future researchers can access and preserve these biological resources, they have been deposited at FBCC (Freshwater Bioresources Culture Collection).
- This initiative will increase the availability of these resources for the scientific community, allowing for further research and exploration.

***Corresponding author**
Ahyoung Choi
Tel. 054-530-0841
E-mail. aychoi@nnibr.re.kr

Received: 1 February 2024
Revised: 15 April 2024
Revision accepted: 14 June 2024

Abstract: As part of the research program "Freshwater Prokaryotic Organisms Research and Discovery," freshwater samples were collected from the Nakdonggang River. After plating the samples on several culture media and incubating aerobically, approximately 900 bacterial strains were isolated and identified using 16S rRNA gene sequences. Among the bacterial isolates showing higher than 98.7% 16S rRNA gene sequence similarity with those of already confirmed bacterial species previously unreported in Korea, 29 strains were selected. These strains were phylogenetically diverse and belonged to 3 phyla, 6 classes, 13 orders, and 21 genera. At the genus level, these previously unreported species were found to be affiliated with *Novosphingobium*, *Sphingomonas*, *Polymorphobacter*, *Croceibacterium*, *Devosia*, *Endobacterium*, *Agaricicola*, *Bradyrhizobium*, *Paracoccus*, and *Pseudotabrizicola* of the class *Alphaproteobacteria*; *Undibacterium*, *Azonexus*, and *Dechloromonas* of the class *Betaproteobacteria*; *Acinetobacter* and *Budvicia* of the class *Gammaproteobacteria*; *Streptomyces*, *Nocardioides*, *Mycobacterium*, and *Cellulomonas* of the phylum *Actinomycetota*; *Flavobacterium* and *Pedobacter* of the phylum *Bacteroidota*. These species were further characterized by examining their Gram reaction, colony and cell morphologies, biochemical properties, and phylogenetic positions. Detailed descriptions of these 29 previously unreported species are provided.

Keywords: unrecorded bacterial species, freshwater, Nakdonggang River

1. INTRODUCTION

In pursuit of bolstering national biological sovereignty, the Ministry of Environment has set forth the ambitious goal of securing 100,000 species of native organisms by 2030. As of 2024, the cataloging of 60,010 national biological species has been completed, encompassing the discovery of 5,039 prokaryotes, including bacteria, with this number steadily on the rise (NIBR 2023). Nevertheless, the emphasis on uncovering bio-

logical resources remains primarily directed towards marine and terrestrial environments, highlighting the imperative for a comprehensive investigation into the prokaryotic inhabitants of domestic freshwater environments.

Freshwater environments, encompassing rivers, lakes, and groundwater, represent a mere 0.6% of Earth's total water, excluding glaciers. Despite their limited proportion, they play a vital role in sustaining human life (Wetzel 2023). However, these environments are highly vulnerable to environmental degradation, particularly due to industrialization and climate change. Alarming statistics reveal an 84% decline in freshwater species since 1970 (WHO 2008). The distribution of species in freshwater environments varies depending on factors such as river systems, streams, lake habitats, seasonal variations, and water layers. Advances in in-depth sequencing technology have rapidly enhanced our understanding of bacterial diversity and the fundamental processes of microbial ecology. This has led to a deeper comprehension of the intricate relationship between the functioning of aquatic ecosystems and the formation of bacterial communities (Edwards *et al.* 2006; Huse *et al.* 2008).

However, despite these technological advancements, the cultivation of predominant groups of microorganisms remains crucial for gaining a comprehensive understanding of bacteria and their ecological roles within freshwater environments. This cultivation-based approach provides valuable insights into the functional capabilities and interactions of these microbial communities in their natural habitats.

Pseudomonadota is a bacterial phylum that underwent renaming from '*Proteobacteria*' in 2021 (Oren and Garrity 2021). Presently, the phylum *Pseudomonadota* stands as the largest and most phenotypically diverse phylogenetic lineage. As of the time of this writing, taxonomic classification based on 16S rRNA gene sequences indicates that the phylum *Pseudomonadota* comprises six major phylogenetic classes: *Acidithiobacillia*, *Alphaproteobacteria*, *Betaproteobacteria*, *Gammaproteobacteria*, *Hydrogenophilalia*, and *Zetaproteobacteria*. Accounting for over 40% of all validly published prokaryotic genera, the *Pseudomonadota* encompass a significant portion of traditional Gram-negative bacteria (Stackebrandt *et al.* 1988). They exhibit remarkable metabolic diversity and hold substantial biological importance, encompassing the majority of known Gram-negative species of medical, veterinary, and industrial significance (Slonczewski *et al.* 2020).

Actinomycetota is a bacterial phylum that underwent renaming from '*Actinobacteria*' in 2021 (Oren and Garrity 2021). Representing a diverse phylum of Gram-positive bacteria, the *Actinomycetota* are characterized by their high G+C content (Gao and Gupta 2012). They inhabit both terrestrial and aquatic environments and play a crucial role in various ecosystems (Servin *et al.* 2008). As of the time of this writing, taxonomic classification based on 16S rRNA gene sequences indicates that the phylum *Actinomycetota* comprises six classes: *Acidimicrobiia*, *Actinomycetia*, *Coriobacteriia*, *Nitriliruptoria*, *Rubrobacteria*, and *Thermoleophilia*. The *Actinomycetota* stands out as one of the dominant bacterial phyla, boasting one of the largest bacterial genera, *Streptomyces*. *Streptomyces* and other *Actinomycetota* play crucial roles in soil health by contributing significantly to biological buffering (Donald *et al.* 2022).

Bacteroidota is a bacterial phylum that was renamed from '*Bacteroidetes*' in 2021 (Oren and Garrity 2021). Comprising three large classes of Gram-negative, non-sporeforming, anaerobic or aerobic, and rod-shaped bacteria, the phylum *Bacteroidota* is widely distributed in various environments, including soil, sediments, seawater, as well as in the gastrointestinal tract and on the skin of animals (Krieg *et al.* 2010). As of the time of writing, based on taxonomic classification using 16S rRNA gene sequences, there are six classes within the phylum *Bacteroidota*, including *Bacteroidia*, *Chitinophagia*, *Cytophagia*, *Flavobacteriia*, *Saprospiria*, and *Sphingobacteriia*.

In this project, we collect physicochemical information and samples from various freshwater habitats, including rivers, wetlands, and brackish water areas, with a primary focus on the Nakdonggang River water system. The objective is to discover 29 previously unrecorded species by isolating prokaryotes from both river water and soil samples. Genetic information exceeding 1,350 base pairs is confirmed through 16S rRNA gene sequence analysis. To ensure taxonomic evidence, we gather transmission electron microscope image data, culture information (such as medium, temperature, and culture period), and information for polyphasic classification characteristic analysis. This report presents the phylogenetic and phenotypic characterization of these bacterial species.

2. MATERIALS AND METHODS

A total of 29 bacterial strains were isolated from the Nakdonggang River using the standard dilution plating method on several culture media, including marine agar 2211 (MA), 1/10-diluted MA (1/10 MA), Reasoner's 2A (R2A), 1/10-diluted R2A (1/10 R2A), nutrient agar (NA), 1/10-diluted NA (1/10 NA), 1/10-diluted tryptic soy agar (1/10 TSA), or Inorganic Salts Starch (ISP) Agar 4. These isolates were subsequently incubated at 15−25°C for 14 days. Following serial dilution spreading, all strains were purified as single colonies, and the pure cultures were preserved as 20% glycerol suspensions at −80°C. The strain IDs, culture media, and incubation conditions are summarized in Table 1. Colony morphologies of the bacterial strains were observed on agar plates using a magnifying glass after the cells were cultivated until reaching the stationary phase. Cellular morphology and size were examined using transmission electron microscopy (Talos L120C; ThermoFisher Scientific, MA, USA). Gram staining was performed using a Gram-staining kit (BioMérieux, France), and biochemical characteristics were assessed using API 20NE galleries (BioMérieux, France) following the manufacturer's instructions.

For 16S rRNA sequence analysis, genomic DNA from the isolates was extracted using the DNeasy Blood & Tissue kit (Qiagen, Hilden, Germany) following the manufacturer's instructions. The 16S rRNA gene of the strains was amplified by PCR using universal bacterial primers 27F and 1492R and sequenced via Sanger sequencing (Weisburg *et al.* 1991). The resulting almost full-length 16S rRNA gene sequences were identified using the "16S-based ID" service in EzBioCloud (Yoon *et al.* 2017), with a sequence similarity cutoff value set at 98.7%. Bacterial strains exhibiting ≥98.7% sequence similarity with known bacterial species previously unreported in Korea were selected as unreported bacterial species.

For phylogenetic analyses, multiple sequence alignments between the 16S rRNA gene sequences of the isolates and those of reference-type strains were performed using the Clustal_W program and manually checked with EzEditor (Jeon *et al.* 2014). Based on the aligned sequences, phylogenetic trees were generated using the neighbor-joining method (Saitou and Nei 1987) with the Kimura 2-parameter model (Kimura 1980) implemented in MEGA 7.0 software (Kumar *et al.* 2016). The robustness of the inferred phylogenetic trees was evaluated through bootstrap analyses based on 1,000 random re-samplings (Felsenstein 1985).

3. RESULTS AND DISCUSSION

The 16S rRNA gene sequence analyses conducted on approximately 900 bacterial strains obtained in this study revealed that some strains belonged to novel species or species previously unreported in Korea. Among these, 29 strains exhibited ≥98.7% 16S rRNA gene sequence similarities with unrecorded bacterial species in Korea and belonged to 3 phyla, 6 classes, 13 orders, and 21 genera. The taxonomic composition and identification results of these species are summarized in Table 1. At the genus level, the unreported species were found to belong to various taxa, including *Novosphingobium*, *Sphingomonas*, *Polymorphobacter*, *Croceibacterium*, *Devosia*, *Endobacterium*, *Agaricicola*, *Bradyrhizobium*, *Paracoccus*, and *Pseudotabrizicola* within the class *Alphaproteobacteria*; *Undibacterium*, *Azonexus*, and *Dechloromonas* within the class *Betaproteobacteria*; *Acinetobacter* and *Budvicia* within the class *Gammaproteobacteria*; *Streptomyces*, *Nocardioides*, *Mycobacterium*, and *Cellulomonas* within the phylum *Actinomycetota*; *Flavobacterium* and *Pedobacter* within the phylum *Bacteroidota*. The phylogenetic tree of the bacterial strains assigned to the phylum *Pseudomonadato* is shown in Figure 1 and Figure 2, and the two phyla *Actinomycetota* and *Bacteroidota* are shown in Figure 3, respectively. These figures depict the phylogenetic relationships between the isolates and closely related species. Transmission electron microscopic images of the isolates are provided in Figure 4.

In summary, this study identified 29 bacterial species previously unreported in Korean freshwater ecosystems, and the characteristics of these unreported bacterial species are presented and described herein.

3.1. Description of *Novosphingobium bradum* 23ND15S-033

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies grown on R2A are circular, convex, and pale yellow after incubation for 7 days at 25°C. Positive for nitrate reduction, esculin hydrolysis, gelatinase, and β-galactosidase in API 20NE, but negative

Table 1. Summary of unrecorded freshwater bacterial strains isolated from the Nakdonggang River and their taxonomic affiliations

Phylum	Class	Order	Family	Strain ID	NNIBR ID	Most closely related species	Similarity (%)	Isolation source	Medium	Incubation conditions
Pseudomonadota	*Alpha-proteobacteria*	*Sphingomonadales*	*Sphingomonadaceae*	23ND15S-033	NNIBR2023641BA2573	*Novosphingobium bradum*	99.1	Riverside sediment	R2A	25°C, 7 d
				23ND23W-034	NNIBR2023641BA456	*Novosphingobium silvae*	99.9	Surface water	MA	20°C, 3 d
				23ND49W-23	NNIBR2023641BA2569	*Novosphingobium lubricantis*	100.0	Surface water	R2A	25°C, 7 d
				23ND16S-022	NNIBR2023641BA2574	*Sphingomonas aracearum*	99.9	Submerged sediment	R2A	25°C, 7 d
				23ND19S-017	NNIBR2023641BA2575	*Sphingomonas glacialis*	99.2	Submerged sediment	R2A	25°C, 7 d
				23ND30S-6	NNIBR2023641BA491	*Polymorphobacter multimanifer*	98.9	Riverside sediment	NA	25°C, 3 d
				23ND04W-109	NNIBR2023641BA216	*Polymorphobacter fuscus*	99.2	Surface water	R2A	25°C, 3 d
			Erythrobacteraceae	23ND33W-6	NNIBR2023641BA2585	*Croceibacterium mercuriale*	99.8	Surface water	MA	25°C, 7 d
		Rhizobiales	*Devosiaceae*	23ND54W-032	NNIBR2023641BA2580	*Devosia beringensis*	99.4	Surface water	MA	25°C, 7 d
				23ND17S-33	NNIBR2023641BA2567	*Devosia crocina*	98.9	Riverside sediment	1/10 NA	25°C, 7 d
			Rhizobiaceae	23ND19W-039	NNIBR2023641BA2576	*Endobacterium cereale*	99.2	Surface water	R2A	25°C, 7 d
			Methylopila	JR11	NNIBR2017301BA4	*Agaricicola taiwanensis*	99.2	Hyporheic water	R2A	25°C, 3 d
			Nitrobacteraceae	JR13	NNIBR2017301BA5	*Bradyrhizobium ingae*	99.1	Hyporheic water	R2A	25°C, 3 d
		Rhodobacterales	*Rhodobacteraceae*	23ND53W-035	NNIBR2023641BA2579	*Paracoccus everestensis*	99.6	Surface water	ISP4	25°C, 7 d
				23ND29W-22	NNIBR2023641BA1307	*Pseudotabrizicola sediminis*	99.1	Surface water	MA	25°C, 3 d
	Beta-proteobacteria	*Burkholderiales*	*Oxalobacteraceae*	23ND53W-014	NNIBR2023641BA2577	*Undibacterium nitidum*	99.2	Surface water	1/10 MA	25°C, 7 d
				23ND29W-88	NNIBR2023641BA1326	*Undibacterium umbellatum*	99.6	Surface water	R2A	25°C, 3 d
		Rhodocyclales	*Azonexaceae*	23ND53W-029	NNIBR2023641BA2578	*Azonexus fungiphilus*	99.8	Surface water	R2A	25°C, 7 d
				23ND17S-76	NNIBR2023641BA2586	*Dechloromonas denitrificans*	99.9	Riverside sediment	1/10 MA	25°C, 7 d
	Gamma-proteobacteria	*Moraxellales*	*Moraxellaceae*	22ND44W-048	NNIBR2023641BA2571	*Acinetobacter tandoii*	99.3	Surface water	1/10 TSA	25°C, 7 d
		Enterobacterales	*Budviciaceae*	23ND30W-38	NNIBR2023641BA470	*Budvicia aquatica*	99.3	Surface water	MA	20°C, 3 d
Actinomycetota	*Actinomycetes*	*Streptomycetales*	*Streptomycetaceae*	23ND22S-017	NNIBR2023641BA329	*Streptomyces glauciniger*	99.4	Riverside sediment	1/10 MA	20°C, 3 d
				23ND29S-75	NNIBR2023641BA2005	*Streptomyces ossamyceticus*	99.9	Riverside sediment	R2A	25°C, 3 d
		Propionibacteriales	*Nocardioidaceae*	23ND42S-12	NNIBR2023641BA2568	*Nocardioides intraradicalis*	99.5	Riverside sediment	1/10 MA	25°C, 7 d
		Mycobacteriales	*Mycobacteriaceae*	23ND08W-19	NNIBR2023641BA2584	*Mycobacterium komossense*	99.0	Surface water	1/10 MA	25°C, 7 d
		Cellulomonadales	*Cellulomonadaceae*	23ND29S-16	NNIBR2023641BA1366	*Cellulomonas carbonis*	99.2	Riverside sediment	MA	25°C, 3 d
Bacteroidota	*Flavobacteriia*	*Flavobacteriales*	*Flavobacteriaceae*	23ND04S-005	NNIBR2023641BA184	*Flavobacterium restrictum*	99.5	Riverside sediment	1/10 R2A	15°C, 3 d
	Flavobacteriia	*Flavobacteriales*	*Flavobacteriaceae*	23ND49W-22	NNIBR2023641BA2570	*Flavobacterium ammoniigenes*	99.1	Surface water	1/10 MA	25°C, 7 d
	Sphingobacteriia	*Sphingobacteriales*	*Sphingobacteriaceae*	JR29	NNIBR2017301BA6	*Pedobacter cryoconitis*	99.3	Hyporheic water	NA	25°C, 3 d

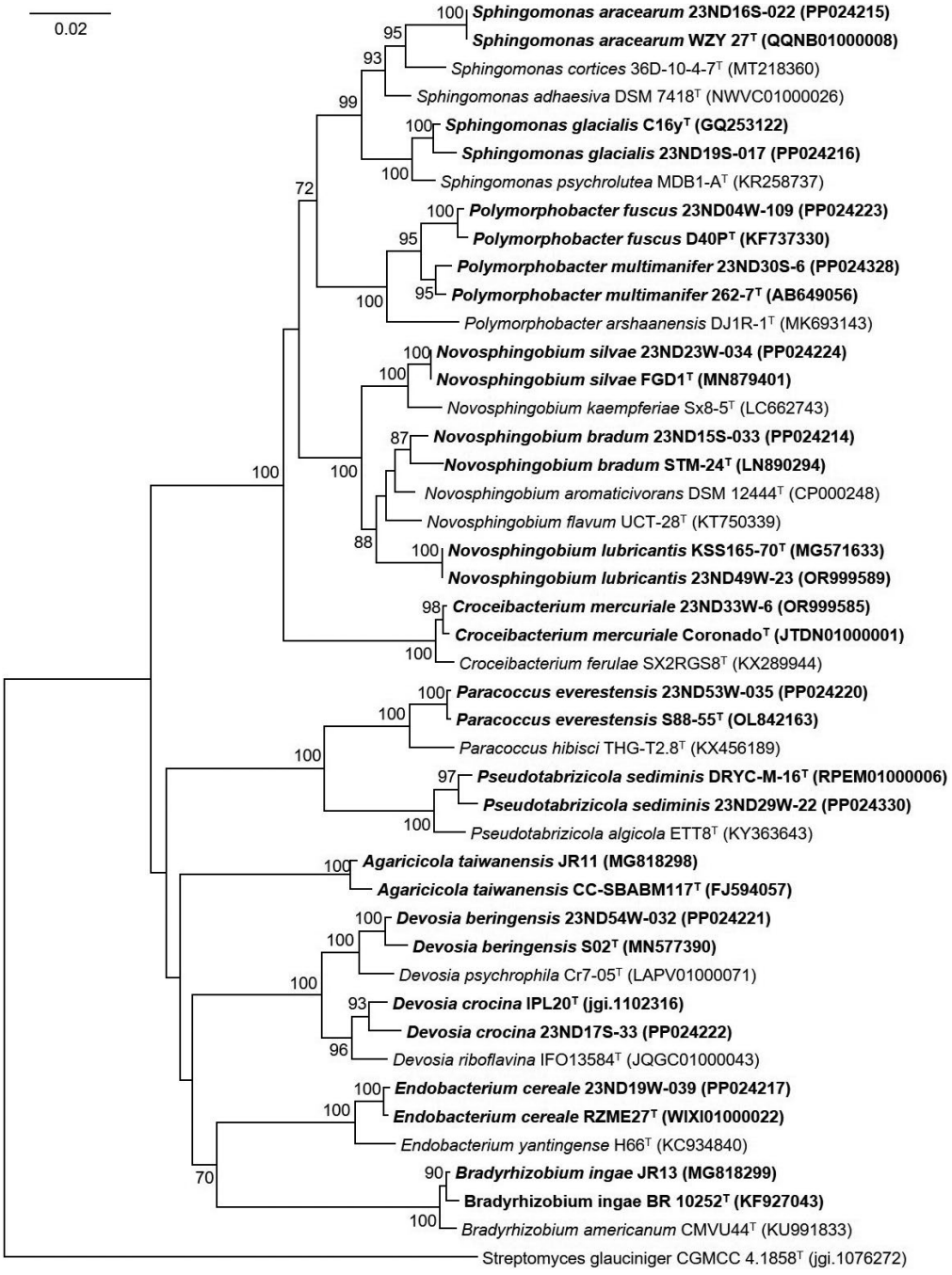

Fig. 1. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences showing the relationship between the strains isolated in this study and their relatives in the class *Alphaproteobacteria*. Bootstrap values (>70%) are shown at nodes. Bar, 0.02 substitutions per nucleotide position.

for indole production, glucose fermentation, arginine dihydrolase, and urease. D-glucose and D-mannose are utilized. Does not utilize L-arabinose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain 23ND15S-033 displays the highest 16S rRNA gene sequence similarity with *Novosphingobium bradum* STM-24^{T} (99.1%).

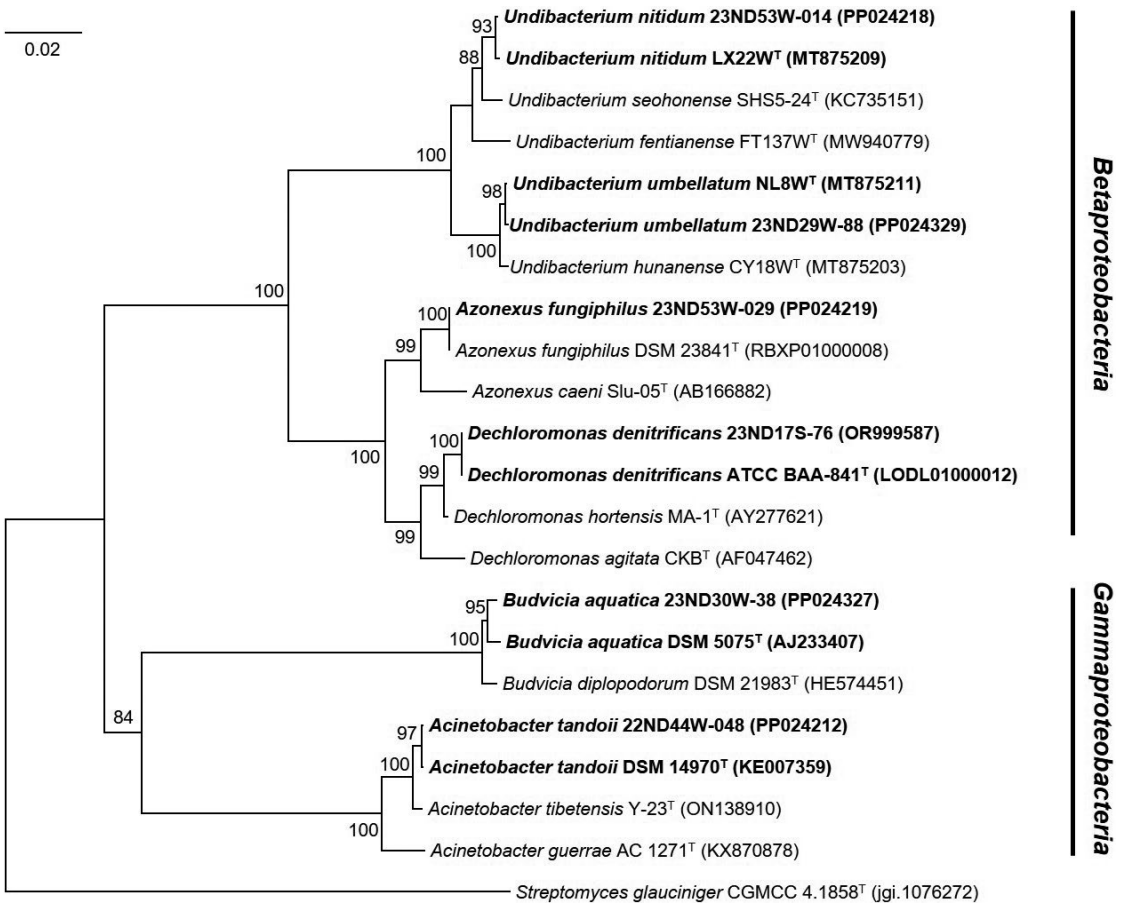

Fig. 2. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences showing the relationship between the strains isolated in this study and their relatives in the classes *Betaproteobacteria* and *Gammaproteobacteria*. Bootstrap values (>70%) are shown at nodes. Bar, 0.02 substitutions per nucleotide position.

Strain 23ND15S-033 (=NNIBR2023641BA2573=FBCC-B15827) was isolated from riverside sediment collected in Ulju-gun, Ulsan, Korea (35°4′13″N 128°8′2.9″E). The GenBank accession number of the 16S rRNA gene sequence is PP024214.

3.2. Description of *Novosphingobium silvae* 23ND23W-034

Cells are Gram-stain-negative, flagellated, and rod-shaped. Colonies grown on MA are circular, convex, and ivory after incubation for 3 days at 20°C. Positive for esculin hydrolysis, and β-galactosidase in API 20NE, but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, and gelatinase. D-maltose, adipic acid, and malic acid are utilized. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, potassium gluconate, capric acid, trisodium citrate, and phenylacetic acid. Strain 23ND23W-034 displays the highest 16S rRNA gene sequence similarity with *Novosphingobium silvae* FGD1^T (99.9%). Strain 23ND23W-034 (=NNIBR2023641BA456=FBCC-B13527) was isolated from surface water collected in Bonghwa-gun, Gyeongsangbuk-do (37°4′0.7″N 128°59′0.9″E). The GenBank accession number of the 16S rRNA gene sequence is PP024224.

3.3. Description of *Novosphingobium lubricantis* 23ND49W-23

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies grown on 0.1 MA are circular, and pale yellow after incubation for 7 days at 25°C. Negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, esculin

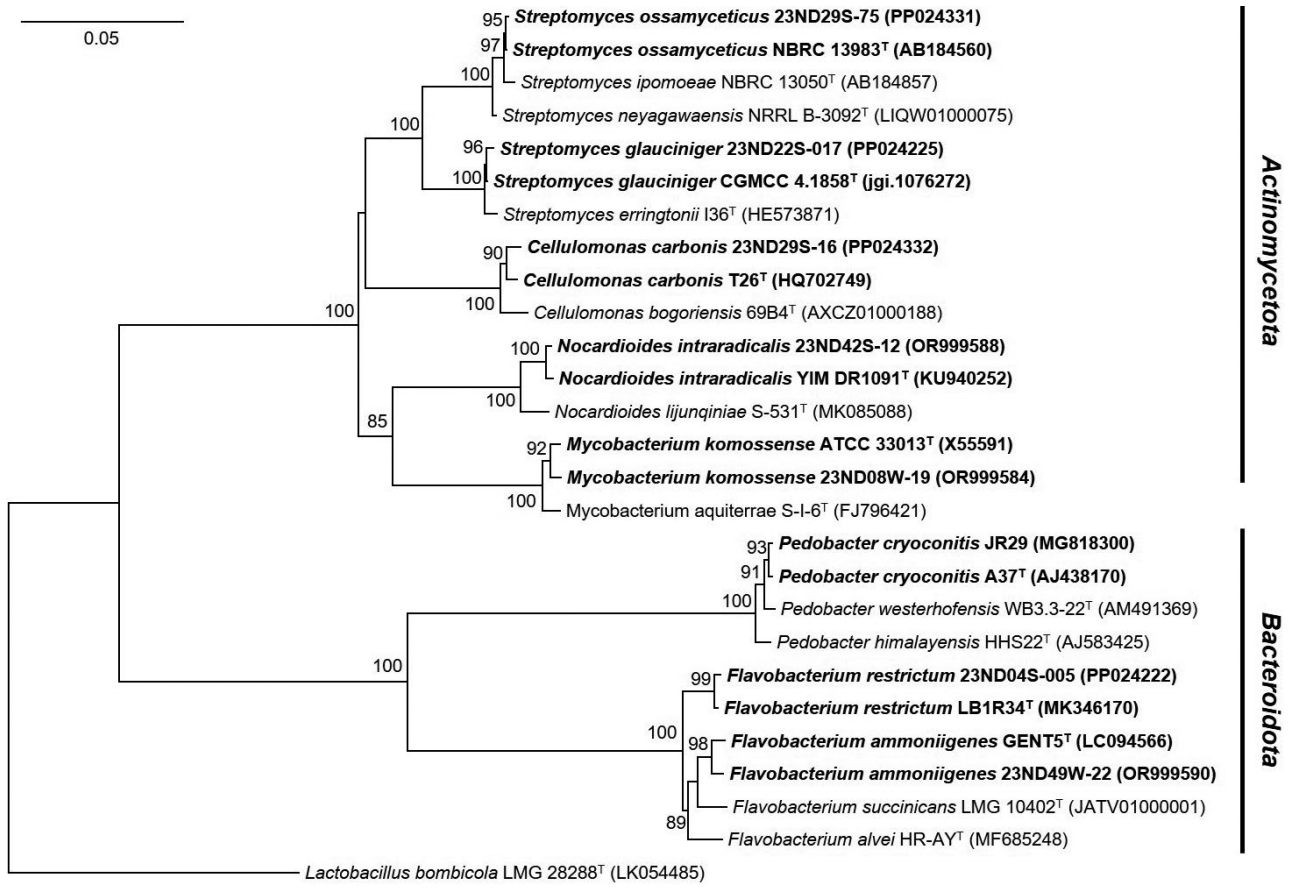

Fig. 3. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences showing the relationship between the strains isolated in this study and their relatives in the phylum *Actinomycetota* and *Bacteroidota*. Bootstrap values (>70%) are shown at nodes. Bar, 0.05 substitutions per nucleotide position.

hydrolysis, gelatinase, and β-galactosidase in API 20NE. Does not utilize 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. Strain 23ND49W-23 displays the highest 16S rRNA gene sequence similarity with *Novosphingobium lubricantis* KSS 165-70^T (100.0%). Strain 23ND49W-23 (=NNIBR2023 641BA2569=FBCC-B15831) was isolated from surface water collected in Uljin-gun, Gyeongsangbuk-do, Korea (37°4′24.57″N 129°23′57.8″E). The GenBank accession number of the 16S rRNA gene sequence is OR999589.

3.4. Description of *Sphingomonas aracearum* 23ND16S-022

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies grown on R2A are circular, convex, and yellow after incubation for 7 days at 25°C. Positive for esculin hydrolysis, gelatinase, and β-galactosidase in API 20NE, but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, and urease. Does not utilize 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. Strain 23ND16S-022 displays the highest 16S rRNA gene sequence similarity with *Sphingomonas aracearum* WZY 27^T (99.9%). Strain 23ND16S-022 (=NNIBR2023641BA2574=FBCC-B15826) was isolated from submerged sediment collected in Goseong-gun, Gyeongsangnam-do, Korea (34°58′53.3″N 128°13′18.4″E). The GenBank accession number of the 16S rRNA gene sequence is PP024215.

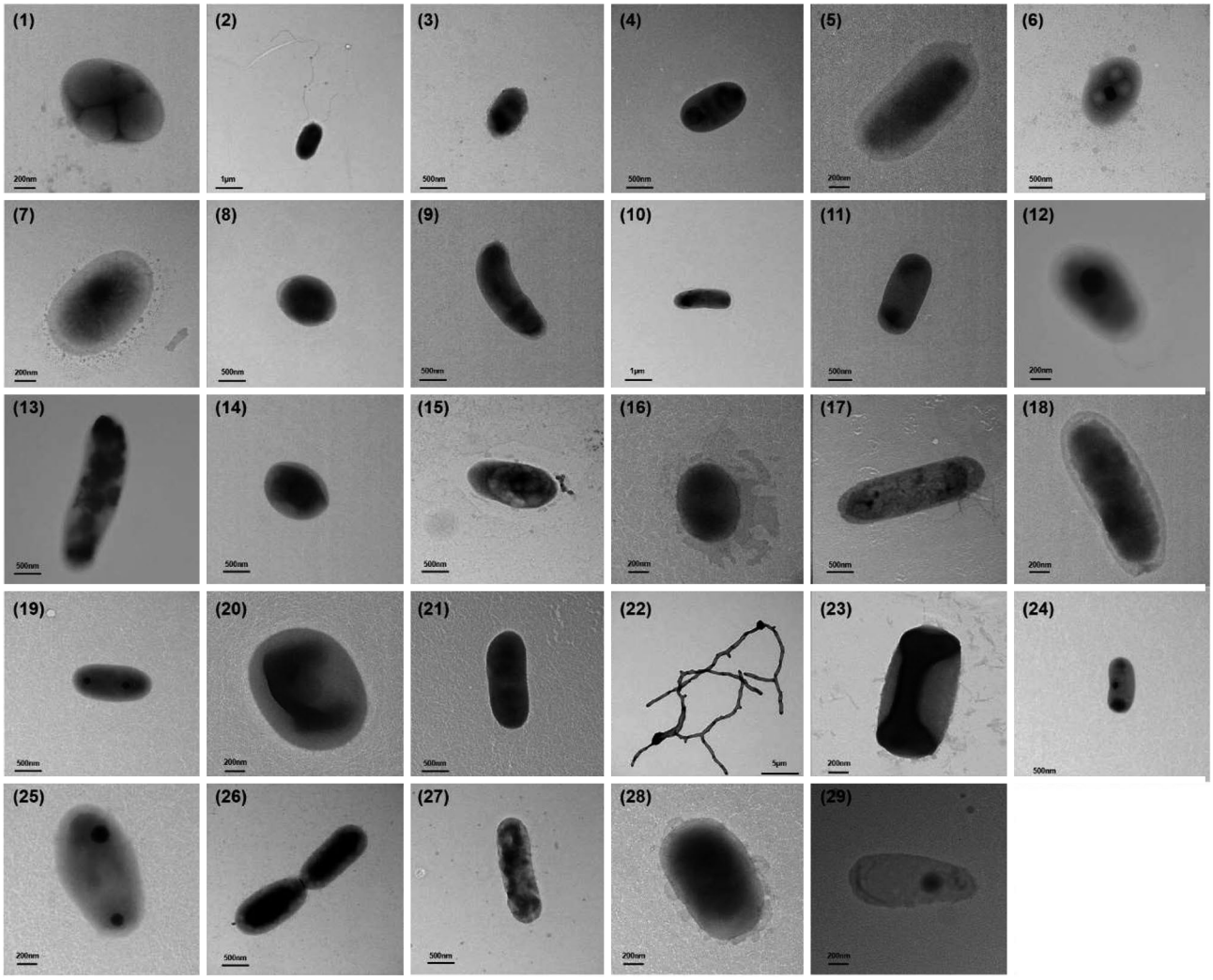

Fig. 4. Transmission electron micrographs of cells of the strains isolated in this study. Strains: 1, 23ND15S-033; 2, 23ND23W-034; 3, 23ND49W-23; 4, 23ND16S-022; 5, 23ND19S-017; 6, 23ND30S-6; 7, 23ND04W-109; 8, 23ND33W-6; 9, 23ND54W-032; 10, 23ND17S-33; 11, 23ND19W-039; 12, JR11; 13, JR13; 14, 23ND53W-035; 15, 23ND29W-22; 16, 23ND53W-014; 17, 23ND29W-88; 18, 23ND53W-029; 19, 23ND17S-76; 20, 22ND44W-048; 21, 23ND30W-38; 22, 23ND22S-017; 23, 23ND29S-75; 24, 23ND42S-12; 25, 23ND08W-19; 26, 23ND29S-16; 27, 23ND04S-005; 28, 23ND49W-22; 29, JR29.

3.5. Description of *Sphingomonas glacialis* 23ND19S-017

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies grown on R2A are circular, convex, and yellow after incubation for 7 days at 25°C. Positive for esculin hydrolysis, and β-galactosidase in API 20NE, but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, and gelatinase. Does not utilize 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. Strain 23ND19S-017 displays the highest 16S rRNA gene sequence similarity with *Sphingomonas glacialis* C16y^{T} (99.2%). Strain 23ND19S-017 (=NNIBR 2023641BA2575=FBCC-B15825) was isolated from submerged sediment collected in Bonghwa-gun, Gyeongsangbuk-do, Korea (37°0′58.19″N 128°43′53.62″E). The GenBank accession number of the 16S rRNA gene sequence is PP024216.

3.6. Description of *Polymorphobacter multimanifer* 23ND30S-6

Cells are Gram-stain-negative, non-flagellated, and short rod-shaped. Colonies grown on NA are circular, convex, smooth, and brownish after incubation for 3 days at 25°C. Negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis, gelatinase, and β-galactosidase in API 20NE. Does not utilize 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. Strain 23ND30S-6 displays the highest 16S rRNA gene sequence similarity with *Polymorphobacter multimanifer* 262-7^T (98.9%). Strain 23ND30S-6 (=NNIBR 2023641BA491=FBCC-B13563) was isolated from riverside sediment collected in Seongju-gun, Gyeongsangbuk-do, Korea (35°46′26.46″N 128°25′21.37″E). The GenBank accession number of the 16S rRNA gene sequence is PP024328.

3.7. Description of *Polymorphobacter fuscus* 23ND04W-109

Cells are Gram-stain-negative, non-flagellated, and short rod-shaped. Colonies grown on R2A are circular, convex, and orange-brown after incubation for 3 days at 25°C. Positive for esculin hydrolysis, gelatinase, and β-galactosidase in API 20NE, but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, and urease. Does not utilize 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. Strain 23ND04W-109 displays the highest 16S rRNA gene sequence similarity with *Polymorphobacter fuscus* D40P^T (99.2%). Strain 23ND04W-109 (=NNIBR2023641BA216=FBCC-B12939) was isolated from surface water collected in Andong-si, Gyeongsangbuk-do, Korea (35°37′31.32″N 127°44′20.35″E). The GenBank accession number of the 16S rRNA gene sequence is PP024223.

3.8. Description of *Croceibacterium mercurial* 23ND33W-6

Cells are Gram-stain-negative, non-flagellated, and short rod-shaped. Colonies grown on R2A are circular, convex, smooth, and yellow after incubation for 7 days at 25°C. Positive for esculin hydrolysis, gelatinase, and β-galactosidase in API 20NE, but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, and urease. D-glucose, L-arabinose, and D-mannose are utilized. Does not utilize D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain 23ND33W-6 displays the highest 16S rRNA gene sequence similarity with *Croceibacterium mercurial* Coronado^T (99.8%). Strain 23ND33W-6 (=NNIBR2023641BA2585=FBCC-B15850) was isolated from surface water collected in Geochang-gun, Gyeongsangnam-do, Korea (34°51′13.02″N 128°0′35.54″E). The GenBank accession number of the 16S rRNA gene sequence is OR999585.

3.9. Description of *Devosia beringensis* 23ND54W-032

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies grown on MA are circular, and light yellow after incubation for 7 days at 25°C. Positive for glucose fermentation, esculin hydrolysis, gelatinase, and β-galactosidase in API 20NE, but negative for nitrate reduction, indole production, arginine dihydrolase, and urease. D-mannitol and adipic acid are utilized. Does not utilize D-glucose, L-arabinose, D-mannose, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, malic acid, trisodium citrate, and phenylacetic acid. Strain 23ND54W-032 displays the highest 16S rRNA gene sequence similarity with *Devosia beringensis* S02^T (99.4%). Strain 23ND54W-032 (=NNIBR 2023641BA2580=FBCC-B15820) was isolated from surface water collected in Samcheok-si, Gangwon-do, Korea (37°8′59.4″N 129°18′36.5″E). The GenBank accession number of the 16S rRNA gene sequence is PP024221.

3.10. Description of *Devosia crocina* 23ND17S-33

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies grown on 0.1NA are circular, smooth, and white after incubation for 7 days at 25°C. Positive for nitrate reduction, urease, esculin hydrolysis, and β-galactosidase in API 20NE, but negative for indole production, glucose fermentation, arginine dihydrolase, and gelatinase. D-glucose, L-arabinose, and D-mannose, D-mannitol, *N*-acetyl-glucosamine,

and D-maltose are utilized. Does not utilize potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain 23ND17S-33 displays the highest 16S rRNA gene sequence similarity with *Devosia crocina* IPL20^T (98.9%). Strain 23ND 17S-33 (=NNIBR2023641BA2567=FBCC-B15833) was isolated from riverside sediment collected in Sacheon-si, Gyeongsangnam-do, Korea (35°0′49.1″N 123° 8′4.6″E). The GenBank accession number of the 16S rRNA gene sequence is OR999586.

3.11. Description of *Endobacterium cereale* 23ND19W-039

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies grown on R2A are circular, smooth, and pale ivory after incubation for 7 days at 25°C. Positive for glucose fermentation, urease, esculin hydrolysis, and *β*-galactosidase in API 20NE, but negative nitrate reduction, indole production, arginine dihydrolase, and gelatinase. L-arabinose and malic acid are utilized. Does not utilize D-glucose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, trisodium citrate, and phenylacetic acid. Strain 23ND19W-039 displays the highest 16S rRNA gene sequence similarity with *Endobacterium cereale* RZME27^T (99.2%). Strain 23ND19W-039 (=NNIBR2023641BA2576=FBCC-B15824) was isolated from surface water collected in Bonghwa-gun, Gyeongsangbuk-do, Korea (37°0′ 58.19″N 128°43′53.62″E). The GenBank accession number of the 16S rRNA gene sequence is PP024217.

3.12. Description of *Agaricicola taiwanensis* JR11

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies grown on R2A are circular, convex, and yellow after incubation for 3 days at 25°C. Positive for esculin hydrolysis in API 20NE, but negative nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, gelatinase, and *β*-galactosidase. Malic acid is utilized. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, trisodium citrate, and phenylacetic acid. Strain JR11 displays the highest 16S rRNA gene sequence similarity with *Agaricicola taiwanensis* CC-SBABM117^T (99.2%). Strain JR11 (=NNIBR 2017301BA4=FBCC-B3373) was isolated from hyporheic water collected in Yecheon-gun, Gyeongsangbuk-do, Korea (36°34′29.06″N 128°19′16.68″E). The GenBank accession number of the 16S rRNA gene sequence is MG818298.

3.13. Description of *Bradyrhizobium ingae* JR13

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies grown on R2A are circular, convex, and white after incubation for 3 days at 25°C. Positive for nitrate reduction, indole production, urease, and esculin hydrolysis in API 20NE, but negative glucose fermentation, arginine dihydrolase, gelatinase, and *β*-galactosidase. Does not utilize 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. Strain JR13 displays the highest 16S rRNA gene sequence similarity with *Bradyrhizobium ingae* 51778^T (99.1%). Strain JR11 (=NNIBR2017301BA5=FBCC-B3374) was isolated from hyporheic water collected in Yecheon-gun, Gyeongsangbuk-do, Korea (36°34′ 29.06″N 128°19′16.68″E). The GenBank accession number of the 16S rRNA gene sequence is MG818299.

3.14. Description of *Paracoccus everestensis* 23ND53W-035

Cells are Gram-stain-negative, non-flagellated, and cocci-shaped. Colonies grown on ISP4 are circular, convex, and orange after incubation for 7 days at 25°C. Positive for glucose fermentation, esculin hydrolysis, gelatinase, and *β*-galactosidase in API 20NE, but negative nitrate reduction, indole production, arginine dihydrolase, and urease. D-mannitol and adipic acid are utilized. Does not utilize D-glucose, L-arabinose, D-mannose, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, malic acid, trisodium citrate, and phenylacetic acid. Strain 23ND53W-035 displays the highest 16S rRNA gene sequence similarity with *Paracoccus everestensis* S8-55^T (99.6%). Strain 23ND53W-035 (=NNIBR2023641BA2579=FBCC-B15821) was isolated from surface water collected in Changwon-si, Gyeongsangnam-do, Korea (37°10′52.7″N 129°19′ 40.7″E). The GenBank accession number of the 16S rRNA gene sequence is PP024220.

3.15. Description of *Pseudotabrizicola sediminis* 23ND29W-22

Cells are Gram-stain-negative, non-flagellated, and cocci-shaped. Colonies grown on ISP4 are circular, convex, and orange after incubation for 7 days at 25°C. Positive for nitrate reduction, esculin hydrolysis, and β-galactosidase in API 20NE, but negative indole production, glucose fermentation, arginine dihydrolase, urease, and gelatinase. Does not utilize 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. Strain 23ND29W-22 displays the highest 16S rRNA gene sequence similarity with *Pseudotabrizicola sediminis* DRYC-M-16^T (99.1%). Strain 23ND 29W-22 (=NNIBR2023641BA1307=FBCC-B14353) was isolated from surface water collected in Changnyeong-gun, Gyeongsangnam-do, Korea (35°35′35.41″ N 128°21′38.02″E). The GenBank accession number of the 16S rRNA gene sequence is PP024330.

3.16. Description of *Undibacterium nitidum* 23ND53W-014

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies grown on 0.1 MA are circular, convex, and pale white after incubation for 7 days at 25°C. Positive for nitrate reduction and esculin hydrolysis in API 20NE, but negative indole production, glucose fermentation, arginine dihydrolase, urease, gelatinase, and β-galactosidase. Does not utilize 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. Strain 23ND53W-014 displays the highest 16S rRNA gene sequence similarity with *Undibacterium nitidum* LX22W^T (99.2%). Strain 23ND53W-014 (=NNIBR2023641BA2577=FBCC-B15823) was isolated from surface water collected in Changwon-si, Gyeongsangnam-do, Korea (37°10′52.7″N 129°19′40.7″ E). The GenBank accession number of the 16S rRNA gene sequence is PP024218.

3.17. Description of *Undibacterium umbellatum* 23ND29W-88

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies grown on R2A are circular, convex, smooth, and white after incubation for 3 days at 25°C. Positive for nitrate reduction and esculin hydrolysis in API 20NE, but negative indole production, glucose fermentation, arginine dihydrolase, urease, gelatinase, and β-galactosidase. D-mannose, *N*-acetyl-glucosamine, D-maltose, adipic acid, and trisodium citrate are utilized. Does not utilize D-glucose, L-arabinose, D-mannitol, potassium gluconate, capric acid, malic acid, and phenylacetic acid. Strain 23ND29W-88 displays the highest 16S rRNA gene sequence similarity with *Undibacterium umbellatum* KW1^T (99.6%). Strain 23ND29W-88 (=NNIBR2023641BA1326=FBCC-B14 372) was isolated from surface water collected in Changnyeong-gun, Gyeongsangnam-do, Korea (35°35′35.41″ N 128°21′38.02″E). The GenBank accession number of the 16S rRNA gene sequence is PP024329.

3.18. Description of *Azonexus fungiphilus* 23ND53W-029

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies grown on R2A are circular, convex, and light ivory after incubation for 7 days at 25°C. Positive for esculin hydrolysis in API 20NE, but negative nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, gelatinase, and β-galactosidase. Potassium gluconate and malic acid are utilized. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, capric acid, adipic acid, trisodium citrate, and phenylacetic acid. Strain 23ND53W-029 displays the highest 16S rRNA gene sequence similarity with *Azonexus fungiphilus* DSM 23841^T (99.8%). Strain 23ND 53W-029 (=NNIBR2023641BA2578=FBCC-B15822) was isolated from surface water collected in Changwon-si, Gyeongsangnam-do, Korea (37°10′52.7″N 129°19′ 40.7″E). The GenBank accession number of the 16S rRNA gene sequence is PP024219.

3.19. Description of *Dechloromonas denitrificans* 23ND17S-76

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies grown on 0.1 MA are small, circular, and white after incubation for 7 days at 25°C. Positive for nitrate reduction in API 20NE, but negative indole production, glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis, gelatinase, and β-galactosidase. Does not utilize 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. Strain 23ND17S-76 displays the highest 16S rRNA gene sequence similarity with *Dechloromonas denitrificans* ATCC BAA-841^T (99.9%). Strain 23ND17S-76 (=NNIBR2023641BA2586=FBCC-B15851) was isolated from riverside sediment collected in Sacheon-si, Gyeongsangnam-do, Korea (35°0′49.1″N 128°8′4.6″E). The GenBank accession number of the 16S rRNA gene sequence is OR999587.

3.20. Description of *Acinetobacter tandoii* 22ND44W-048

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies grown on 0.1 TSA are convex, circular, and pale white after incubation for 7 days at 25°C. Positive for esculin hydrolysis in API 20NE, but negative nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, gelatinase, and *β*-galactosidase. Capric acid, malic acid, trisodium citrate, and phenylacetic acid are utilized. Does not utilize utilize D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, and adipic acid. Strain 22ND44W-048 displays the highest 16S rRNA gene sequence similarity with *Acinetobacter tandoii* DSM 14970^T (99.3%). Strain 22ND44W-048 (=NNIBR2023641BA2571=FBCC-B15829) was isolated from surface water collected in Sacheon-si, Gyeongsangnam-do, Korea (35°03′33.3″N 128°0′49.8″E). The GenBank accession number of the 16S rRNA gene sequence is PP024212.

3.21. Description of *Budvicia aquatica* 23ND30W-38

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies grown on MA are circular, convex, smooth, and beige after incubation for 3 days at 20°C. Positive for nitrate reduction and glucose fermentation in API 20NE, but negative indole production, arginine dihydrolase, urease, esculin hydrolysis, gelatinase, and *β*-galactosidase. D-glucose, L-arabinose, D-mannitol, *N*-acetyl-glucosamine, potassium gluconate, and malic acid are utilized. Does not utilize D-mannosel, D-maltose, capric acid, adipic acid, trisodium citrate, and phenylacetic acid. Strain 23ND30W-38 displays the highest 16S rRNA gene sequence similarity with *Budvicia aquatica* DSM 5075^T (99.3%). Strain 23ND30W-38 (=NNIBR2023641BA470=FBCC-B13542) was isolated from surface water collected in Seongju-gun, Gyeongsangbuk-do, Korea (35°46′26.46″N 128°25′21.37″E). The GenBank accession number of the 16S rRNA gene sequence is PP024327.

3.22. Description of *Streptomyces glauciniger* 23ND22S-017

Cells are Gram-stain-negative, non-flagellated, and filamentous-shaped. Colonies grown on 0.1 MA are circular, convex, and grey after incubation for 3 days at 20°C. Positive for esculin hydrolysis and gelatinase in API 20NE, but negative nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, and *β*-galactosidase. D-glucose, L-arabinose, D-mannosel, D-mannosel, D-maltose, potassium gluconate, adipic acid, and malic acid are utilized. Does not *N*-acetyl-glucosamine, capric acid, trisodium citrate, and phenylacetic acid. Strain 23ND22S-017 displays the highest 16S rRNA gene sequence similarity with *Streptomyces glauciniger* CGMCC 4.1858^T (99.4%). Strain 23ND22S-017 (=NNIBR2023641BA329=FBCC-B13400) was isolated from riverside sediment collected in Uiseong-gun, Gyeongsangbuk-do, Korea (36°31′8.08″N 128°40′28.01″E). The GenBank accession number of the 16S rRNA gene sequence is PP024225.

3.23. Description of *Streptomyces ossamyceticus* 23ND29S-75

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies grown on R2A are irregular, rough, undulate, and beige after incubation for 3 days at 25°C. Positive for nitrate reduction, esculin hydrolysis, and *β*-galactosidase in API 20NE, but negative indole production, glucose fermentation, arginine dihydrolase, urease, and gelatinase. Does not utilize 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. Strain 23ND29S-75 displays the highest 16S rRNA gene sequence similarity with *Streptomyces ossamyceticus* NBRC 13983^T (99.9%). Strain 23ND29S-75 (=NNIBR2023641BA2005=FBCC-B15035) was isolated from riverside sediment collected in Changnyeong-

gun, Gyeongsangnam-do, Korea (35°35′35.41″N 128° 21′38.02″E). The GenBank accession number of the 16S rRNA gene sequence is PP024331.

3.24. Description of *Nocardioides intraradicalis* 23ND42S-12

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies grown on 0.1 MA are circular and pale yellow after incubation for 7 days at 25°C. Positive for nitrate reduction and β-galactosidase in API 20NE, but negative for indole production, glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis, and gelatinase. Does not utilize 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. Strain 23ND42S-12 displays the highest 16S rRNA gene sequence similarity with *Nocardioides intraradicalis* YIM DR1091^T (99.5%). Strain 23ND42S-12 (=NNIBR2023641BA2568=FBCC-B15830) was isolated from riverside sediment collected in Ulju-gun, Ulsan, Korea (35°3′26″N 128°53′1″E). The GenBank accession number of the 16S rRNA gene sequence is OR999588.

3.25. Description of *Mycobacterium komossense* 23ND08W-19

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies grown on 0.1 MA are circular and pale yellow after incubation for 7 days at 25°C. Positive for nitrate reduction, esculin hydrolysis, and β-galactosidase in API 20NE, but negative for indole production, glucose fermentation, arginine dihydrolase, urease, and gelatinase. Does not utilize 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. Strain 23ND08W-19 displays the highest 16S rRNA gene sequence similarity with *Mycobacterium komossense* ATCC 33013^T (99.0%). Strain 23ND 08W-19 (=NNIBR2023641BA2584=FBCC-B15849) was isolated from surface water collected in Sancheong-gun, Gyeongsangnam-do, Korea (35°20′28.42″N 127° 49′47.61″E). The GenBank accession number of the 16S rRNA gene sequence is OR999584.

3.26. Description of *Cellulomonas carbonis* 23ND29S-16

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies grown on MA are circular, convex, smooth, and yellowish after incubation for 3 days at 25°C. Positive for esculin hydrolysis and β-galactosidase in API 20NE, but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, and gelatinase. D-glucose and potassium gluconate are utilized. Does not utilize L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain 23ND29S-16 displays the highest 16S rRNA gene sequence similarity with *Cellulomonas carbonis* T26^T (99.2%). Strain 23ND29S-16 (=NNIBR2023641BA1366=FBCC-B14 377) was isolated from riverside sediment collected in Changnyeong-gun, Gyeongsangnam-do, Korea (35° 35′35.41″N 128°21′38.02″E). The GenBank accession number of the 16S rRNA gene sequence is PP024332.

3.27. Description of *Flavobacterium restrictum* 23ND04S-005

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies grown on 0.1 R2A are convex and yellow after incubation for 3 days at 15°C. Positive for esculin hydrolysis and β-galactosidase in API 20NE, but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, and gelatinase. Does not utilize 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. Strain 23ND04S-005 displays the highest 16S rRNA gene sequence similarity with *Flavobacterium restrictum* LB1R34^T (99.5%). Strain 23ND04S-005 (=NNIBR2023641BA184=FBCC-B12907) was isolated from riverside sediment collected in Andong-si, Gyeongsangbuk-do, Korea (35°37′31.32″N 127°44′ 20.35″E). The GenBank accession number of the 16S rRNA gene sequence is PP024222.

3.28. Description of *Flavobacterium ammoniigenes* 23ND49W-22

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies grown on 0.1 MA are small, cir-

cular, and yellow after incubation for 7 days at 25°C. Positive for nitrate reduction, esculin hydrolysis, and *β*-galactosidase in API 20NE, but negative for indole production, glucose fermentation, arginine dihydrolase, urease, and gelatinase. Does not utilize 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. Strain 23ND49W-22 displays the highest 16S rRNA gene sequence similarity with *Flavobacterium ammoniigenes* GENT5^{T} (99.1%). Strain 23ND49W-22 (=NNIBR2023641BA2570=FBCC-B15832) was isolated from surface water collected in Uljin-gun, Gyeongsangbuk-do, Korea (37°4′24.57″N 129°23′57.8″E). The GenBank accession number of the 16S rRNA gene sequence is OR999590.

3.29. Description of *Pedobacter cryoconitis* JR29

Cells are Gram-stain-negative, non-flagellated, and rod-shaped. Colonies grown on NA are circular, convex, mucoid, and cream after incubation for 3 days at 25°C. Positive for indole production, esculin hydrolysis, gelatinase, and *β*-galactosidase in API 20NE, but negative for nitrate reduction, glucose fermentation, arginine dihydrolase, and urease. D-glucose, L-arabinose, D-mannose, and D-maltose are utilized. Does not utilize D-mannitol, *N*-acetyl-glucosamine, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain JR29 displays the highest 16S rRNA gene sequence similarity with *Pedobacter cryoconitis* PAMC 27485^{T} (99.3%). Strain JR29 (=NNIBR2017301BA6=FBCC-B3383) was isolated from hyporheic water collected in Yecheon-gun, Gyeongsangbuk-do, Korea (36°34′29.06″N 128°19′16.68″E). The GenBank accession number of the 16S rRNA gene sequence is OR999590.

CRediT authorship contribution statement

A Choi: Project administration, Conceptualization, Writing-Original draft, Funding acquisition, Writing-Reviewing and editing. **JY Cho:** Investigation, Data curation. **SY Lee:** Investigation, Data curation. **JY Jung:** Investigation, Data curation. **K Baek:** Investigation, Data curation. **S Hwang:** Investigation, Data curation. **EJ Kim:** Investigation, Data curation. **J Goh:** Supervision.

Declaration of Competing Interest

The authors declare no conflict of interest.

ACKNOWLEDGEMENTS

This study was supported by a grant from the Nakdonggang National Institute of Biological Resources (NNIBR), funded by the Ministry of Environment (MOE) of the Republic of Korea (NNIBR20241103).

REFERENCES

Donald L, A Pipite, R Subramani, J Owen, RA Keyzers and T Taufa. 2022. *Streptomyces*: still the biggest producer of new natural secondary metabolites, a current perspective. Microbiol. Res. 13:418–465. https://doi.org/10.3390/microbiolres13030031

Edwards RA, B Rodriguez-Brito, L Wegley, M Haynes, M Breitbart, DM Peterson, MO Saar, S Alexander, EC Alexander Jr. and F Rohwer. 2006. Using pyrosequencing to shed light on deep mine microbial ecology. BMC Genomics 7:57. https://doi.org/10.1186/1471-2164-7-57

Felsenstein J. 1985. Confidence limits on phylogenies: An approach using the bootstrap. Evolution 39:783–791. https://doi.org/10.2307/2408678

Gao B and RS Gupta. 2012. Phylogenetic framework and molecular signatures for the main clades of the phylum *Actinobacteria*. Microbiol. Mol. Biol. Rev. 76:66–112. https://doi.org/10.1128/mmbr.05011-11

Huse SM, L Dethlefsen, JA Huber, DM Welch, DA Relman and ML Sogin. 2008. Exploring microbial diversity and taxonomy using SSU rRNA hypervariable tag sequencing. PLoS Genet. 4:e1000255. https://doi.org/10.1371/annotation/3d8a6578-ce56-45aa-bc71-05078355b851

Jeon YS, K Lee, SC Park, BS Kim, YJ Cho, SM Ha and J Chun. 2014. EzEditor: A versatile sequence alignment editor for both rRNA-and protein-coding genes. Int. J. Syst. Evol. Microbiol. 64:689–691. https://doi.org/10.1099/ijs.0.059360-0

Kimura M. 1980. A simple method for estimating evolutionary rates of base substitutions through comparative studies of nucleotide sequences. J. Mol. Evol. 16:111–120. https://doi.org/10.1007/BF01731581

Krieg NR, W Ludwig, J Euzéby and WB Whitman. 2010. Phylum

XIV. *Bacteroidetes* phyl. nov. pp. 25–469. In: Bergey's Manual of Systematic Bacteriology. Volume 4: The *Bacteroidetes*, *Spirochaetes*, *Tenericutes* (*Mollicutes*), *Acidobacteria*, *Fibrobacteres*, *Fusobacteria*, *Dictyoglomi*, *Gemmatimonadetes*, *Lentisphaerae*, *Verrucomicrobia*, *Chlamydiae*, and *Planctomycetes* (Krieg NR, JT Staley, DR Brown, BP Hedlund, BJ Paster, NL Ward, W Ludwig and WB Whitman, eds.). 2nd Edition. Springer. New York. https://doi.org/10.1007/978-0-387-68572-4

Kumar S, G Stecher and K Tamura. 2016. MEGA7: Molecular evolutionary genetics analysis version 7.0 for bigger datasets. Mol. Biol. Evol. 33:1870–1874. https://doi.org/10.1093/molbev/msw054

NIBR. 2023. National List of Species of Korea. National Institute of Biological Resources. Incheon, Korea. https://www.kbr.go.kr/ Accessed January 29, 2024.

Oren A and GM Garrity. 2021. Valid publication of the names of forty-two phyla of prokaryotes. Int. J. Syst. Evol. Microbiol. 71:005056. https://doi.org/10.1099/ijsem.0.005056

Saitou N and M Nei. 1987. The neighbor-joining method: A new method for reconstructing phylogenetic trees. Mol. Biol. Evol. 4:406–425. https://doi.org/10.1093/oxfordjournals.molbev.a040454

Servin JA, CW Herbold, RG Skophammer and JA Lake. 2008. Evidence excluding the root of the tree of life from the actinobacteria. Mol. Biol. Evol. 25:1–4. https://doi.org/10.1093/molbev/msm249

Slonczewski JL, J Foster and E Zinser. 2020. Microbiology: An Evolving Science. 5th Edition. W.W. Norton and Company. New York.

Stackebrandt E, RGE Murray and HG Truper. 1998. *Proteobacteria* classis nov., a name for the phylogenetic taxon that includes the "purple bacteria and their relatives". Int. J. Syst. Bacteriol. 38:321–325. https://doi.org/10.1099/00207713-38-3-321

Weisburg WG, SM Barns, DA Pelletier and DJ Lane. 1991. 16S ribosomal DNA amplification for phylogenetic study. J. Bacteriol. 173:697–703. https://doi.org/10.1128/jb.173.2.697-703.1991

Wetzel RG. 2023. Limnology: Lake and River Ecosystems. 4th Edition. Academic Press. San Diego, California.

WHO. 2008. Safer Water, Better Health: Costs, Benefits and Sustainability of Interventions to Protect and Promote Health. World Health Organization. Geneva. Switzerland.

Yoon SH, SM 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 whole-genome assemblies. Int. J. Syst. Evol. Microbiol. 67:1613–1617. https://doi.org/10.1099/ijsem.0.001755