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Report on 49 unrecorded bacterial species in Korea from the phyla *Actinomycetota*, *Bacillota*, *Bacteroidota*, *Fusobacteriota*, and *Pseudomonadota*, isolated from wetlands in 2024

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A total of 49 unrecorded bacterial species were isolated from freshwater and soil samples collected in 2024 from wetlands in Korea. The isolated strains were classified into 5 phyla, 11 classes, 22 orders, 30 families, and 37 genera. Among the isolates, 3 species belong to the phylum *Actinomycetota*, 11 species belong to the phylum *Bacillota*, 8 species belong to the phylum *Bacteroidota*, 27 species belong to the phylum *Pseudomonadota*. Phylogenetic analyses based on 16S rRNA gene sequences revealed that each strain clustered with its closest reported strain, showing higher than 98.7%. Detailed information on the 49 species, including isolation sources, phylogenetic positions, Gram-staining results, colony and cell morphology, biochemical characteristics, and strain names, are provided in the species descriptions.

Keywords: 16S rRNA gene, freshwater, soil, unrecorded species, wetland

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Introduction

Wetlands are integral to ecosystems, supporting biodiversity by providing habitats for diverse microorganisms, including aerobic and anaerobic species (Bodelier and Dedysh, 2013; Alikhani *et al*., 2021). Microorganisms in wetlands contribute to biogeochemical cycles by decomposing organic matter and driving biosynthetic processes essential to ecosystem functions, indicating their critical role in maintaining ecosystem resilience (Macarena and Jeannette, 2021; Li *et al*., 2024). A recent study also reported the isolation of methanotrophic bacteria capable of oxidizing methane from wetlands in Korea, which can reduce major greenhouse gas methane (Gwak *et al*., 2022). These findings suggest that wetland ecosystems harbor significant biological resources with the potential to address future challenges, including carbon neutrality and environmental pollution.

According to the Biodiversity Statistics of Korea published by the Ministry of Environment, Korea hosts 55 wetland protection areas spanning 1,640.77 km^2 and 24 Ramsar-designated sites covering 202.67 km^2 (National Biodiversity Center, 2024), indicating the ecological significance of wetlands and their potential as reservoirs of valuable microbial resources for practical applications. Although numerous studies have analyzed microbial communities and isolated microbes from wetlands in Korea, a significant proportion of microorganisms remains unisolated and unreported (Kim *et al*., 2021; Kim *et al*., 2024). Therefore, in this study, we isolated aerobic and anaerobic

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bacterial species from freshwater and soil samples collected from various wetland environments in Korea and analyzed their phylogenetic characteristics using 16S rRNA gene sequences, along with their morphological and physicochemical properties. These results will provide valuable insights into the microbial diversity of wetland ecosystems in Korea and contribute to the understanding of their ecological roles, as well as their potential applications in biotechnology and environmental management.

Materials and Methods

A total of 49 unrecorded bacterial strains were isolated aerobically and anaerobically from freshwater and soil samples collected from various wetlands in Korea. For aerobic bacterial strain isolation, freshwater samples were directly diluted in phosphate-buffered saline (PBS), while soil samples were homogenized by mixing 1 g of soil with 1 mL of PBS prior to dilution. These solutions were spread onto diverse culture media, including ammonium mineral salts agar (AMS; MB Cell, Korea), Luria Bertani agar (LB; BD, USA), Methylosinus medium 2 agar (MM2; Dedysh and Dunfield, 2014), de Man, Rogosa and Sharpe agar (MRS; BD, USA), nutrient agar (NA; BD, USA), nitrate mineral salts agar (NMS; Whittenbury *et al*., 1970), Reasoner's 2A agar (R2A; BD, USA), 0.5×R2A agar, 2×R2A agar, tryptic soy agar (TSA; BD, USA) supplemented with 0.03% (w/v) sodium pyruvate (Kawasaki and Kamagata, 2017) and incubated at temperatures between 20 and 37°C for durations ranging from 1 to 7 day. All strains were purified as single colonies and stored at −80°C in 15% glycerol suspension and 10% skim milk as well as lyophilized ampoules. The anaerobic bacterial strains were isolated using a modified version of the aerobic protocol. Briefly, all procedures were conducted in an anaerobic chamber (COY Laboratory Products) filled with 90% N_2, 5% CO_2, and 5% H_2, and all reagents and media used in the experiments were placed in the anaerobic chamber for more than a day to remove any residual oxygen before use. Freshwater samples were directly diluted in PBS, spread onto yeast extract peptone dextrose agar (YPD; MB Cell, Korea), R2A, and brain heart infusion agar (BHI; MB Cell, Korea) supplemented with 0.03% (w/v) sodium pyruvate, and incubated at 30°C for 5 days. Soil samples were inoculated into YPD, R2A, and BHI broths supplemented with 0.03% (w/v) sodium pyruvate, incubated at 30°C for 7 days, and then diluted in PBS. The diluted samples were subsequently spread onto YPD, R2A, and BHI agar plates corresponding to their respective broths, followed by incubation at 30°C for 5 days. All strains were purified as single colonies and stored at −80°C in 15% glycerol suspension, 10% skim milk, or lyophilized ampoules.

Colony morphology was observed on agar plates after bacterial colonies reached the stationary phase, and cell morphology and size were examined by transmission electron microscope (TEM; H-7650, Hitachi, Japan) after staining with 5% (w/v) uranyl acetate, or a scanning electron microscope (SEM; JSM6700F, JEOL, Japan) following pre-fixation with 5% paraformaldehyde and 5% glutaraldehyde, and post-fixation with 1% osmium tetroxide. Gram-staining was performed according to the classic procedure described by Doetsch (1981). Biochemical characteristics were assessed using the API 20NE (bioMérieux) for aerobic bacteria and the API 20A (bioMérieux) for strictly anaerobic bacteria. The API 20A assessment was conducted in anaerobic chamber.

For phylogenetic analyses, the 16S rRNA genes were PCR-amplified using the bacterial universal primers 27F and 1492R (Weisburg *et al*., 1991) and sequenced using 337F, 785F, and 800R primers (Lane, 1991) at Macrogen (Korea). The 16S rRNA gene sequences were compared with those of published bacterial species using the EzBio Cloud database (Yoon *et al*., 2017). The 16S rRNA gene sequences with $\geq$98.7% similarity to published species but not previously reported in Korea were classified as unrecorded bacterial species in this study. The 16S rRNA gene sequences of 49 bacterial strains were aligned with their closest phylogenetic taxa using ClustalW (Thompson *et al*., 1994). Phylogenetic trees were then reconstructed in MEGA11 (Tamura *et al*., 2021) with Neighbor-Joining (NJ; Saitou and Nei, 1987), Maximum Likelihood (ML; Felsenstein, 1981), and Maximum Parsimony (MP; Fitch, 1971) algorithms. The reliability of the inferred phylogenetic trees was assessed through bootstrap analyses using 1,000 replicates (Felsenstein, 1985).

Results and Discussion

A total of 49 unrecorded bacterial species, classified into 5 phyla, 11 classes, 22 orders, 30 families, and 37 genera, were identified based on 16S rRNA gene sequence analysis (Table 1). The three species were classified into the phylum *Actinomycetota*, assigned to the orders *Micrococcales* and *Mycobacteriales* of the class *Actinomycetia*. The 11 species were classified into the phylum *Bacillota*, assigned to the orders *Bacillales* and *Lactobacillales* of the class *Bacilli*; *Eubacteriales* and *Lachnospirales* of the class *Clostridia*. The 7 species were classified into the phylum *Bacteroidota*, assigned to the order *Bacteroidales* of the class *Bacteroidia*; *Chitinophagales* of the class *Chitinophagia*; the order *Cytophagales* of the class *Cytophagia*. The one species was classified into the phylum *Fusobacteriota*, assigned to the order *Fusobacteriales* of the class *Fusobacteriia*. The 27 species were classified into the phylum *Pseudomonadota*, assigned to the orders *Hyp-*

Table 1. The taxonomic affiliation of isolated strains belonging to the phyla *Actinomycetota*, *Bacillota*, *Bacteroidota*, *Pseudomonadota* and *Fusobacteriota*.

Phylum	Class	Order	Family	Genus	Strain No.	NIBR ID	Closest species	Similarity (%)	Isolation source	Incubation medium	Incubation condition
Actinomycetota	*Actinomycetia*	*Micrococcales*	*Cellulomonadaceae*	*Cellulomonas*	ODMA_43	NNIBR202411BA2526	*Cellulomonas marina*	99.45	Freshwater	LB	30°C, 2 days
			Intrasporangiaceae	*Terrabacter*	24KSAY-1	NNIBR202411BA2556	*Terrabacter terrae*	100	Soil	AMS	30°C, 4 days
		Mycobacteriales	*Corynebacteriaceae*	*Corynebacterium*	LMHU_19	NNIBR202411BA2523	*Corynebacterium terpenotabidum*	100	Freshwater	LB	30°C, 2 days
Bacillota	*Bacilli*	*Bacillales*	*Bacillaceae*	*Bacillus*	24KSB-2	NNIBR202411BA2579	*Bacillus safensis*	99.59	Soil	NMS	30°C, 4 days
			Staphylococcaceae	*Staphylococcus*	OPL_17	NNIBR202411BA2528	*Staphylococcus cohnii*	100	Freshwater	0.5×R2A	30°C, 2 days
		Lactobacillales	*Lactobacillaceae*	*Paucilactobacillus*	PWIIM2	NNIBR202411BA2546	*Paucilactobacillus oligofermentans*	99.60	Freshwater	MRS	20°C, 3 days
	Clostridia	*Eubacteriales*	*Clostridiaceae*	*Clostridium*	GSS2	NNIBR202411BA2538	*Clostridium aciditolerans*	99.64	Soil	R2A	30°C, 3 days
					MS2-5	NNIBR202411BA2543	*Clostridium carboxidivorans*	99.58	Soil	R2A	30°C, 3 days
					GSS3	NNIBR202411BA2539	*Clostridium magnum*	99.01	Soil	R2A	30°C, 3 days
					CS1-3	NNIBR202411BA2540	*Clostridium nigeriense*	98.82	Soil	R2A	30°C, 3 days
					GSS8	NNIBR202411BA2537	*Clostridium rhizosphaerae*	99.86	Soil	R2A	30°C, 3 days
					BSBE4	NNIBR202411BA2536	*Clostridium weizhouense*	99.65	Soil	BHI	30°C, 3 days
					LS5	NNIBR202411BA2548	*Clostridium zeae*	99.93	Soil	R2A	30°C, 3 days
		Lachnospirales	*Lachnospiraceae*	*Lachnotalea*	NWD3	NNIBR202411BA2552	*Lachnotalea glycerini*	100	Freshwater	YPD	30°C, 3 days
Bacteroidota	*Bacteroidia*	*Bacteroidales*	*Bacteroidaceae*	*Bacteroides*	24KS-9-1	NNIBR202411BA2570	*Bacteroides pyogenes*	99.10	Soil	NMS	37°C, 5 days
			Prevotellaceae	*Prevotella*	NWA5	NNIBR202411BA2551	*Prevotella herbatica*	98.97	Freshwater	YPD	30°C, 3 days
	Chitinophagia	*Chitinophagales*	*Chitinophagaceae*	*Hydrotalea*	24KSMF-4	NNIBR202411BA2568	*Hydrotalea sandarakina*	99.59	Soil	MM2	30°C, 4 days
	Cytophagia	*Cytophagales*	*Spirosomaceae*	*Dyadobacter*	OGLA_24	NNIBR202411BA2527	*Dyadobacter fermentans*	99.09	Freshwater	0.5×R2A	30°C, 2 days
	Flavobacteriia	*Flavobacteriales*	*Flavobacteriaceae*	*Flavobacterium*	LYRR_9	NNIBR202411BA2532	*Flavobacterium tistrianum*	99.02	Freshwater	LB	30°C, 2 days
			Weeksellaceae	*Chryseobacterium*	LPL_15	NNIBR202411BA2524	*Chryseobacterium artocarpi*	98.96	Freshwater	LB	30°C, 2 days
					XSHD_25	NNIBR202411BA2610	*Chryseobacterium lecithinasegens*	99.03	Freshwater	2×R2A	30°C, 2 days
Fusobacteriota	*Fusobacteriia*	*Fusobacteriales*	*Fusobacteriaceae*	*Fusobacterium*	24KS-13-1	NNIBR202411BA2571	*Fusobacterium varium*	99.44	Freshwater	NMS	37°C, 5 days

Table 1. Continued

Phylum	Class	Order	Family	Genus	Strain No.	NIBR ID	Closest species	Similarity (%)	Isolation source	Incubation medium	Incubation condition
Pseudomonadota	*Alphaproteobacteria*	*Hyphomicrobiales*	*Pleomorphomonadaceae*	*Oharaeibacter*	24KSNC-7	NNIBR202411BA2561	*Oharaeibacter diazotrophicus*	99.86	Soil	NMS	30°C, 4 days
		Rhizobiales	*Hyphomicrobiaceae*	*Hyphomicrobium*	24KSA-51	NNIBR202411BA2567	*Hyphomicrobium facile*	99.14	Soil	AMS	30°C, 4 days
			Nitrobacteraceae	*Bradyrhizobium*	24KSME-3	NNIBR202411BA2622	*Bradyrhizobium uaiense*	99.76	Soil	MM2	30°C, 7 days
			Phyllobacteriaceae	*Mesorhizobium*	24KSAZ-13	NNIBR202411BA2563	*Mesorhizobium shonense*	99.72	Soil	AMS	30°C, 4 days
			Rhizobiaceae	*Ciceribacter*	23KSNF-4	NNIBR202411BA2569	*Ciceribacter selenitireducens*	99.72	Soil	NMS	30°C, 4 days
		Rhodospirillales	*Azospirillaceae*	*Nitrospirillum*	23KSAJ-10	NNIBR202411BA2562	*Nitrospirillum iridis*	99.58	Soil	AMS	30°C, 4 days
		Sphingomonadales	*Sphingomonadaceae*	*Novosphingobium*	24KSNB-7	NNIBR202411BA2578	*Novosphingobium lentum*	98.72	Soil	NMS	30°C, 4 days
					XDMA_21	NNIBR202411BA2574	*Novosphingobium taihuense*	99.63	Soil	2×R2A	30°C, 4 days
				Sphingomonas	LYRR_8	NNIBR202411BA2533	*Sphingomonas citri*	99.93	Freshwater	LB	30°C, 2 days
					MWIIL1	NNIBR202411BA2541	*Sphingomonas paucimobilis*	99.93	Freshwater	LB	20°C, 3 days
					24KSMF-10	NNIBR202411BA2557	*Sphingomonas pruni*	100	Soil	MM2	30°C, 4 days
	Betaproteobacteria	*Burkholderiales*	*Burkholderiaceae*	*Burkholderia*	24KSMA-17	NNIBR202411BA2576	*Burkholderia vietnamiensis*	99.70	Soil	MM2	30°C, 4 days
				Pandoraea	24KSMA-16	NNIBR202411BA2560	*Pandoraea cepalis*	100	Soil	MM2	30°C, 4 days
				Thiomonas	24KSAY-16	NNIBR202411BA2555	*Thiomonas arsenitoxydans*	99.86	Soil	AMS	30°C, 5 days
				Trinickia	24KSA-46	NNIBR202411BA2623	*Trinickia dinghuensis*	98.96	Soil	NMS	30°C, 4 days
				Paraburkholderia	24KSAB-1	NNIBR202411BA2559	*Paraburkholderia kururiensis*	99.79	Soil	AMS	30°C, 4 days
		Neisseriales	*Chromobacteriaceae*	*Aquitalea*	MWIIR11	NNIBR202411BA2542	*Aquitalea pelogenes*	99.93	Freshwater	R2A	20°C, 3 days
	Gammaproteobacteria	*Alteromonadales*	*Shewanellaceae*	*Shewanella*	LSDB_2	NNIBR202411BA2525	*Shewanella azerbaijanica*	99.32	Freshwater	LB	30°C, 2 days
		Enterobacterales	*Enterobacteriaceae*	*Citrobacter*	RSDB_9	NNIBR202411BA2531	*Citrobacter meridianamericanus*	99.73	Freshwater	R2A	30°C, 2 days
				Klebsiella	23KSNG-3	NNIBR202411BA2566	*Klebsiella pneumoniae*	99.86	Soil	NMS	30°C, 4 days
				Klebsiella	BW1-7	NNIBR202411BA2535	*Klebsiella quasipneumoniae*	99.72	Freshwater	2×R2A	20°C, 3 days
		Lysobacterales	*Rhodanobacteraceae*	*Luteibacter*	24KSMB-6	NNIBR202411BA2565	*Luteibacter flocculans*	99.58	Soil	MM2	30°C, 4 days
		Pseudomonadales	*Pseudomonadaceae*	*Pseudomonas*	RGLA_46	NNIBR202411BA2529	*Pseudomonas citri*	100	Freshwater	R2A	30°C, 2 days
					HW1-6	NNIBR202411BA2516	*Pseudomonas lalkuanensis*	99.37	Freshwater	2×R2A	20°C, 3 days
					24KSN-25	NNIBR202411BA2572	*Pseudomonas petroselini*	99.93	Soil	NMS	30°C, 4 days
		Xanthomonadales	*Xanthomonadaceae*	*Pseudoxanthomonas*	23KSNF-10	NNIBR202411BA2558	*Pseudoxanthomonas helianthi*	99.66	Soil	NMS	30°C, 4 days
				Thermomonas	TSM_13	NNIBR202411BA2534	*Thermomonas mangrovi*	99.05	Freshwater	TSA	30°C, 2 days

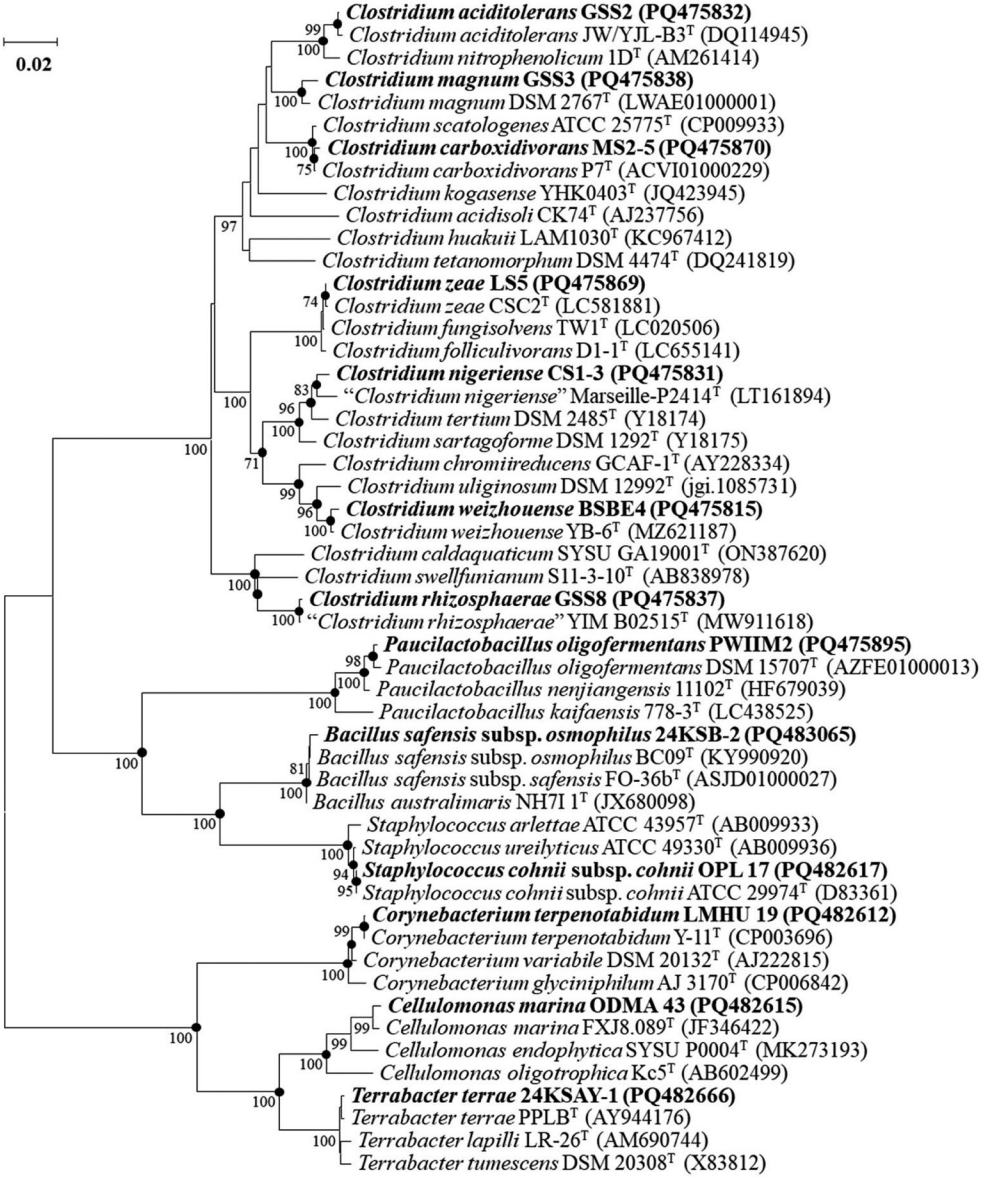


Fig. 1. Neighbor-joining (NJ) phylogenetic tree based on 16S rRNA gene sequences, showing the relationships between bacterial strains isolated in this study and their relatives in the phylum *Actinomycetota*, *Bacillota*. Bootstrap values (>70%) based on 1,000 replications are shown at branch points. Filled circles indicate nodes recovered in both the maximum likelihood (ML) and maximum parsimony (MP) algorithms. The scale bar represents 0.02 nucleotide substitutions per site.

homicrobiales, *Rhizobiales*, *Rhodospirillales*, and *Sphingomonadales* of the class *Alphaproteobacteria*; *Burkholderiales* and *Neisseriales* of the class *Betaproteobacteria*; *Alteromonadales*, the orders *Enterobacterales*, *Lysobacterales*, *Pseudomonadales*, and *Xanthomonadales* of the class *Gammaproteobacteria*. The phylogenetic relationships of the bacterial species isolated based on the 16S rRNA gene sequence were confirmed by phylogenetic trees (Figs. 1, 2, 3, and 4). Transmission or scanning electron microscopy images of strains are shown in Fig. 5. Among 49 unrecorded bacterial species, 13 species are Gram-stain-positive and 36 species are Gram-stain-negative. Strains OPL_17 and 23KSNG-3 are coccus-shaped while the other strains are rod-shaped. Detailed physicochemical, morphological and biochemical characteristics of the unrecorded species are described in the following strain description.

Description of *Cellulomonas marina* ODMA_43

Cells are Gram-stain-positive, flagellated (Zhang *et al*., 2013), facultatively anaerobic, and rod-shaped. The cell

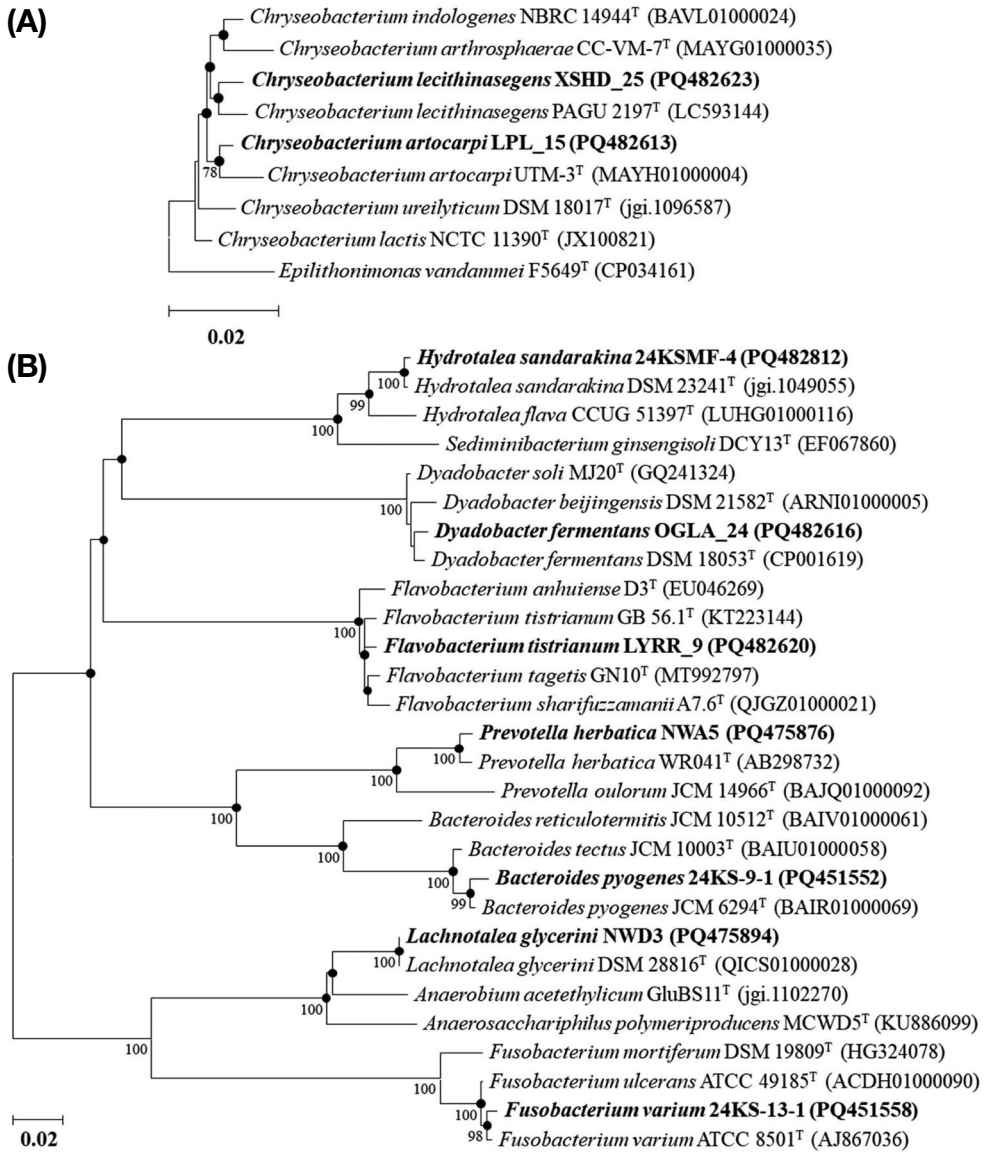


Fig. 2. Neighbor-joining (NJ) phylogenetic trees based on 16S rRNA gene sequences, showing the relationships between bacterial strains isolated in this study and their relatives in the genus *Chryseobacterium* (A) and the phyla *Bacteroidota* and *Fusobacteriota* (B). Bootstrap values (>70%) based on 1,000 replications are shown at branch points. Filled circles indicate nodes recovered in both the maximum likelihood (ML) and maximum parsimony (MP) algorithms. The scale bar represents 0.02 nucleotide substitutions per site.

size measures 0.90 μm in length and 0.45 μm in width. Colonies are smooth, raised, circular, and cream-colored after incubation for 2 days on LB agar at 30°C. In API 20NE, positive for esculin hydrolysis, and β-galactosidase; but negative for nitrates reduction, indole production, glucose fermentation, arginine dihydrolase, urease, and gelatin hydrolysis. D-Glucose, L-arabinose, D-mannose, D-mannitol, D-maltose, and potassium gluconate are utilized as sole carbon sources; but *N*-acetyl-glucosamine, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid are not. Strain ODMA_43 (=NNIBR 202411BA2526) was isolated from freshwater from Wonsinheung-dong (36°20′13.7″N 127°20′10.5″E), Yuseong-gu, Daejeon, Korea. The GenBank accession number for the 16S rRNA gene sequence of strain ODMA_43 is PQ 482615.

Description of *Terrabacter terrae* 24KSAY-1

Cells are Gram-stain-positive, flagellated, aerobic, and rod-shaped. The cell size measures 3.90 μm in length and 0.9 μm in width. Colonies are circular, and yellow-colored after incubation for 4 days on AMS agar at 30°C. In API 20NE, positive for nitrates reduction, esculin hydrolysis, gelatin hydrolysis, and β-galactosidase; but negative for indole production, glucose fermentation, arginine dihydro-

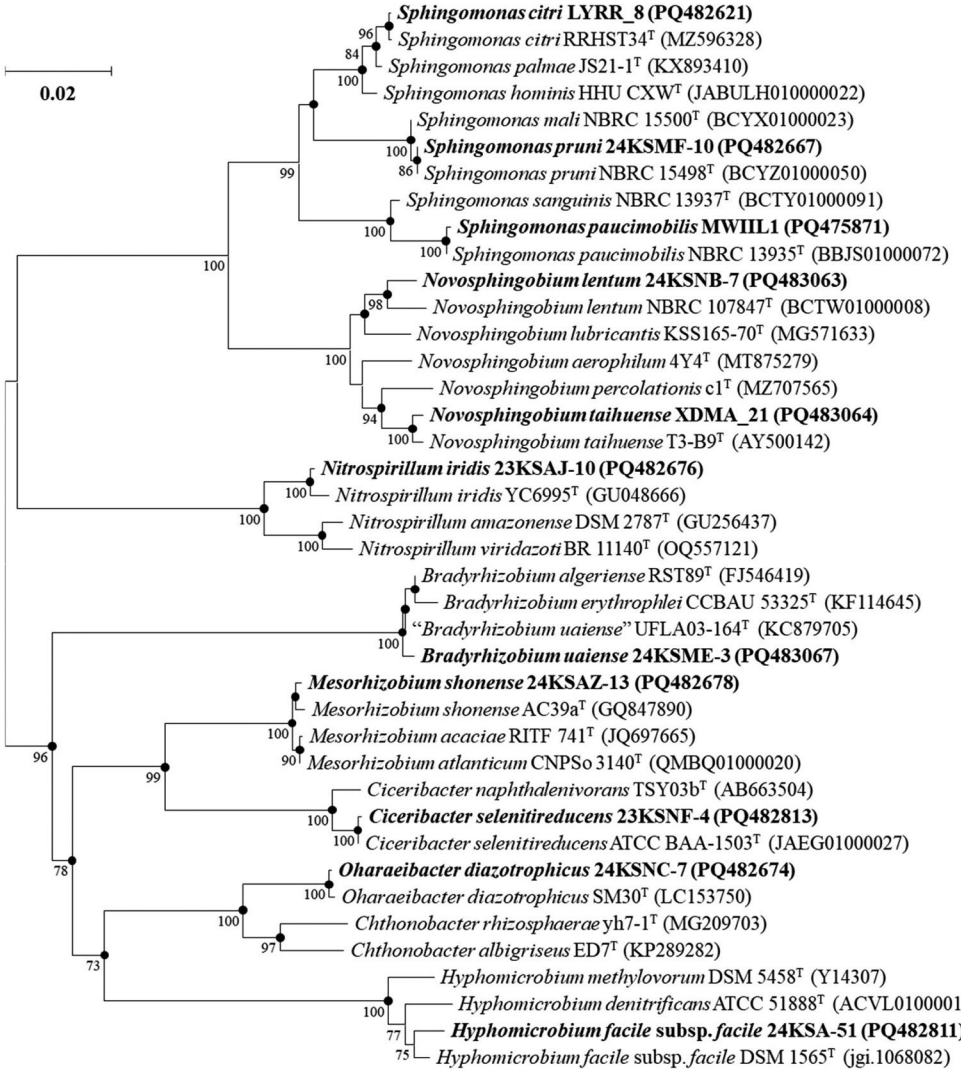


Fig. 3. Neighbor-joining (NJ) phylogenetic tree based on 16S rRNA gene sequences, showing the relationships between bacterial strains isolated in this study and their relatives in the class *Alphaproteobacteria*. Bootstrap values (>70%) based on 1,000 replications are shown at branch points. Filled circles indicate nodes recovered in both the maximum likelihood (ML) and maximum parsimony (MP) algorithms. The scale bar represents 0.02 nucleotide substitutions per site.

lase, and urease. D-Glucose, D-mannose, D-mannitol, D-maltose, potassium gluconate, and malic acid are utilized as sole carbon sources; but L-arabinose, *N*-acetyl-glucosamine, capric acid, adipic acid, trisodium citrate, and phenylacetic acid are not. Strain 24KSAY-1 (=NNIBR2024 11BA2556) was isolated from soil from Ugok-ri (36°41′ 50.6″N 128°13′26.3″E), Sanbuk-myeon, Mungyeong, Gyeongsangbuk-do, Korea. The GenBank accession number for the 16S rRNA gene sequence of strain 24KSAY-1 is PQ482666.

Description of *Corynebacterium terpenotabidum* LMHU_19

Cells are Gram-stain-positive, non-flagellated, aerobic, and rod-shaped. The cell size measures 1.05 μm in length and 0.52 μm in width. Colonies are dry, raised, circular, and cream-colored after incubation for 2 days on LB agar at 30°C. In API 20NE, positive for arginine dihydrolase, urease, and esculin hydrolysis; but negative for nitrates reduction, indole production, glucose fermentation, gelatin hydrolysis, β-galactosidase. D-Glucose, D-mannose, potassium gluconate, and adipic acid are utilized as sole carbon sources; but L-arabinose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, capric acid, malic acid, trisodium citrate, phenylacetic acid are not. Strain LMHU_19 (=NNIBR 202411BA2523) was isolated from freshwater from Doryong-dong (36°22′25.0″N 127°23′02.4″E), Yuseong-gu, Daejeon, Korea. The GenBank accession number for the

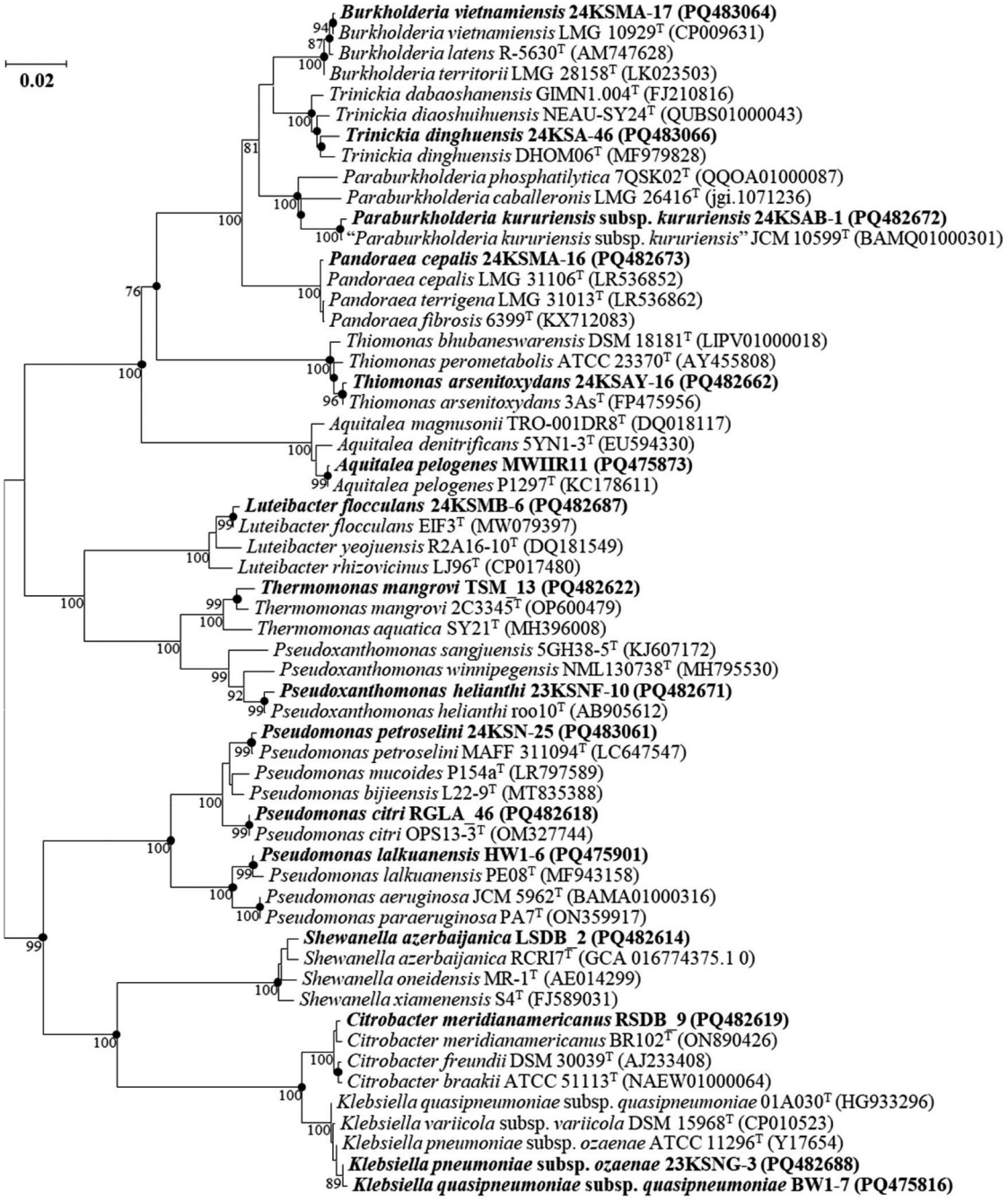


Fig. 4. Neighbor-joining (NJ) phylogenetic tree based on 16S rRNA gene sequences, showing the relationships between bacterial strains isolated in this study and their relatives in the class *Betaproteobacteria* and *Gammaproteobacteria*. Bootstrap values (>70%) based on 1,000 replications are shown at branch points. Filled circles indicate nodes recovered in both the maximum likelihood (ML) and maximum parsimony (MP) algorithms. The scale bar represents 0.02 nucleotide substitutions per site.

16S rRNA gene sequence of strain LMHU_19 is PQ482612.

Description of *Bacillus safensis* subsp. *osmophilus* 24KSB-2

Cells are Gram-stain-positive, flagellated, aerobic, and rod-shaped. The cell size measures 1.20 μm in length and 0.80 μm in width. Colonies are circular, and beige-colored after incubation for 4 days on NMS agar at 30°C. In API 20NE, positive for nitrates reduction; but negative for indole production, glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis, gelatin hydrolysis, and

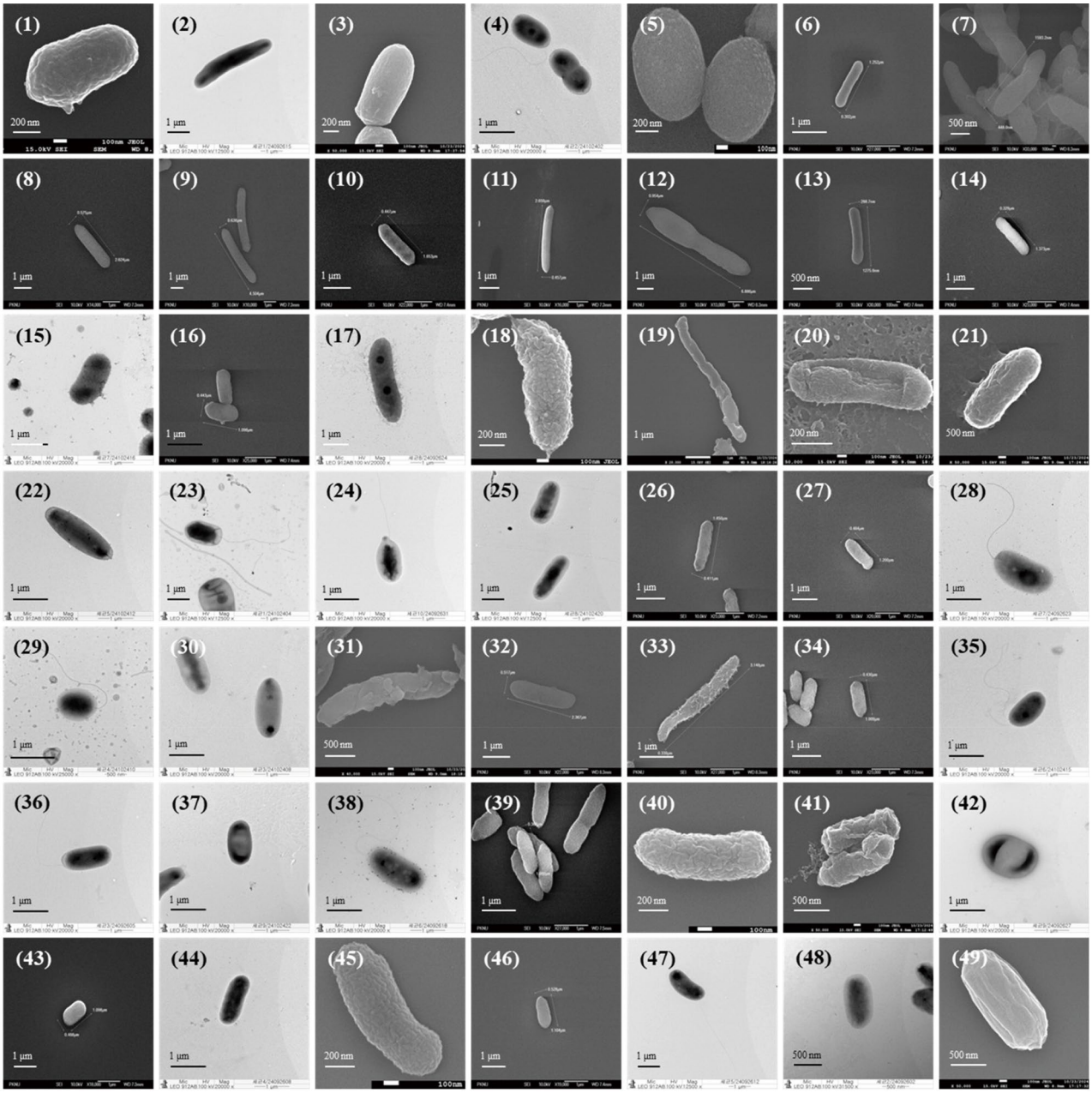


Fig. 5. Transmission electron or scanning electron micrographs of cells of the strains isolated in this study. Strains: 1, ODMA_43; 2, 24KSAY-1; 3, LMHU_19; 4, 24KSB-2; 5, OPL_17; 6, PWIIM2; 7, GSS2; 8, MS2-5; 9, GSS3; 10, CS1-3; 11, GSS8; 12, BSBE4; 13, LS5; 14, NWD3; 15, 24KS-9-1; 16, NWA5; 17, 24KSMF-4; 18, OGLA_24; 19, LYRR_9; 20, LPL_15; 21, XSHD_25; 22, 24KS-13-1; 23, 24KSNC-7; 24, 24KSA-51; 25, 24KSME-3; 26, 24KSAZ-13; 27, 23KSNF-4; 28, 23KSAJ-10; 29, 24KSNB-7; 30, XDMA_21; 31, LYRR_8; 32, MWIIL1; 33, 24KSMF-10; 34, 24KSMA-17; 35, 24KSMA-16; 36, 24KSAY-16; 37, 24KSA-46; 38, 24KSAB-1; 39, MWIIR11; 40, LSDB_2; 41, RSDB_9; 42, 23KSNG-3; 43, BW1-7; 44, 24KSMB-6; 45, RGLA_46; 46, HW1-6; 47, 24KS*N*-25; 48, 23KSNF-10; 49, TSM_13.

β-galactosidase. D-Glucose, adipic acid, malic acid, trisodium citrate, and phenylacetic acid are utilized as sole carbon sources; but L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, and capric acid are not. Strain 24KSB-2 (= NNIBR202411 BA2579) was isolated from soil from Wacho-ri (36°02′18.6″ N 126°47′48.1″E), Hwayang-myeon, Seocheon, Chungcheongnam-do, Korea. The GenBank accession number for the 16S rRNA gene sequence of strain 24KSB-2 is PQ483065.

Description of *Staphylococcus cohnii* subsp. *cohnii* OPL_17

Cells are Gram-stain-positive, non-flagellated, faculta-

tively anaerobic, and coccus-shaped. The cell size measures 0.96 μm in length and 0.58 μm in width. Colonies are dry, raised, circular, and cream-colored after incubation for 2 days on 0.5 × R2A agar at 30°C. In API 20NE, positive for nitrates reduction, arginine dihydrolase, urease, esculin hydrolysis; but negative for indole production, glucose fermentation, gelatin hydrolysis, and β-galactosidase. D-Glucose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, malic acid, and trisodium citrate are utilized as sole carbon sources; but L-arabinose, capric acid, adipic acid, and phenylacetic acid are not. Strain OPL_17 (=NNIBR202411BA2528) was isolated from freshwater from Gwanpyeong-dong (36°25′00.6″N 127°22′45.2″E), Yuseong-gu, Daejeon, Korea. The GenBank accession number for the 16S rRNA gene sequence of strain OPL_17 is PQ482617.

Description of *Paucilactobacillus oligofermentans* PWIIM2

Cells are Gram-stain-positive, non-flagellated, microaerophilic, and rod-shaped. The cell size measures 1.25 μm in length and 0.30 μm in width. Colonies are flat, circular, and white-colored after incubation for 3 days on MRS agar at 20°C. In API 20NE, negative for nitrates reduction, indole production, glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis, gelatin hydrolysis, and β-galactosidase. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid are not utilized as sole carbon sources. Strain PWIIM2 (=NNIBR202411BA2546) was isolated from freshwater from Gucheon-ri (35°31′38.5″N 128°58′04.5″E), Danjang-myeon, Miryang, Gyeongsangnam-do, Korea. The GenBank accession number for the 16S rRNA gene sequence of strain PWIIM2 is PQ475895.

Description of *Clostridium aciditolerans* GSS2

Cells are Gram-stain-positive, flagellated, strictly anaerobic, and rod-shaped. The cell size measures 1.59 μm in length and 0.45 μm in width. Colonies are flat, irregular, and transparent after incubation for 3 days on R2A agar at 30°C. In API 20A, positive for indole production, esculin hydrolysis and acid production from D-glucose, D-mannitol, D-maltose, salicin, D-xylose, L-arabinose, glycerol, D-cellobiose, D-mannose, D-raffinose, D-sorbitol, D-rhamnose and D-trehalose; but negative for urease activity, gelatin hydrolysis, catalase activity and acid production from D-lactose, sucrose and D-melezitose. Strain GSS2 (=NNIBR202411BA2538) was isolated from soil from Gucheon-ri (35°32′11.6″N 128°59′16.7″E), Danjang-myeon, Miryang, Gyeongsangnam-do, Korea. The GenBank accession number for the 16S rRNA gene sequence of strain GSS2 is PQ475832.

Description of *Clostridium carboxidivorans* MS2-5

Cells are Gram-stain-positive, flagellated (Liou *et al*., 2005), strictly anaerobic, and rod-shaped. The cell size measures 2.62 μm in length and 0.58 μm in width. Colonies are flat, irregular, and beige-colored after incubation for 3 days on R2A agar at 30°C. In API 20A, positive for acid production from D-glucose, L-arabinose, D-mannose and D-rhamnose; but negative for indole production, urease activity, gelatin hydrolysis, esculin hydrolysis, catalase activity and acid production from D-mannitol, D-lactose, sucrose, D-maltose, salicin, D-xylose, glycerol, D-cellobiose, D-melezitose, D-raffinose, D-sorbitol and D-trehalose. Strain MS2-5 (=NNIBR202411BA2543) was isolated from soil from Joil-ri (35°27′54.2″N 129°08′37.4″E), Samdong-myeon, Ulju-gun, Ulsan, Korea. The GenBank accession number for the 16S rRNA gene sequence of strain MS2-5 is PQ475870.

Description of *Clostridium magnum* GSS3

Cells are Gram-stain-positive, flagellated (Schink, 1984), strictly anaerobic, and rod-shaped. The cell size measures 4.50 μm in length and 0.64 μm in width. Colonies are flat, irregular, and beige-colored after incubation for 3 days on R2A agar at 30°C. In API 20A, positive for indole production, urease activity, gelatin hydrolysis, esculin hydrolysis and acid production from D-glucose, D-maltose, D-xylose, D-cellobiose and D-trehalose; but negative for catalase activity and acid production from D-mannitol, D-lactose, sucrose, salicin, L-arabinose, glycerol, D-mannose, D-melezitose, D-raffinose, D-sorbitol and D-rhamnose. Strain GSS3 (=NNIBR202411BA2539) was isolated from soil from Gucheon-ri (35°32′11.6″N 128°59′16.7″E), Danjang-myeon, Miryang, Gyeongsangnam-do, Korea. The Gen Bank accession number for the 16S rRNA gene sequence of strain GSS3 is PQ475838.

Description of *Clostridium nigeriense* CS1-3

Cells are Gram-stain-positive, non-flagellated (Alou *et al*., 2018), strictly anaerobic, and rod-shaped. The cell size measures 1.65 μm in length and 0.45 μm in width. Colonies are flat, circular, opaque, and white-colored after incubation for 3 days on R2A agar at 30°C. In API 20A, positive for indole production, urease activity, gelatin hydrolysis, catalase activity and acid production from D-glucose, D-lactose, sucrose, D-maltose, salicin, D-cellobiose, D-mannose and D-trehalose; but negative for esculin hydrolysis and acid production from D-mannitol, D-xylose, L-arabinose, glycerol, D-melezitose, D-raffinose, D-sorbitol and D-rhamnose. Strain CS1-3 (=NNIBR202411BA2540) was isolated from soil from Gucheon-ri (35°32′11.6″N 128°59′16.7″E), Danjang-myeon, Miryang, Gyeongsangnam-do, Korea. The GenBank accession number for the 16S rRNA gene sequence of strain CS1-3 is PQ475831.

Description of *Clostridium rhizosphaerae* GSS8

Cells are Gram-stain-positive, flagellated (Li *et al*., 2023), strictly anaerobic, and rod-shaped. The cell size measures 2.66 μm in length and 0.46 μm in width. Colonies are raised, irregular, and white-colored after incubation for 3 days on R2A agar at 30°C. In API 20A, positive for indole production, urease activity, gelatin hydrolysis, catalase activity and acid production from D-glucose, D-lactose, D-maltose, salicin, D-cellobiose and D-mannose; but negative for esculin hydrolysis and acid production from D-mannitol, sucrose, D-xylose, L-arabinose, glycerol, D-melezitose, D-raffinose, D-sorbitol, D-rhamnose and D-trehalose. Strain GSS8 (=NNIBR202411BA2537) was isolated from soil from Gucheon-ri (35°32′11.6″N 128°59′16.7″E), Danjang-myeon, Miryang, Gyeongsangnam-do, Korea. The GenBank accession number for the 16S rRNA gene sequence of strain GSS8 is PQ475837.

Description of *Clostridium weizhouense* BSBE4

Cells are Gram-stain-positive, flagellated (Li *et al*., 2022), strictly anaerobic, and rod-shaped. The cell size measures 6.88 μm in length and 0.95 μm in width. Colonies are flat, irregular, and white-colored after incubation for 3 days on BHI agar at 30°C. In API 20A, positive for indole production, urease activity, gelatin hydrolysis and acid production from D-glucose, D-mannitol, D-maltose, salicin, D-mannose, D-sorbitol and D-trehalose; but negative for esculin hydrolysis, catalase activity and acid production from D-lactose, sucrose, D-xylose, L-arabinose, glycerol, D-cellobiose, D-melezitose, D-raffinose and D-rhamnose. Strain BSBE4 (=NNIBR202411BA2536) was isolated from soil from Samnak-dong (35°09′15.2″N 128°57′55.4″E), Sasang-gu, Busan, Korea. The GenBank accession number for the 16S rRNA gene sequence of strain BSBE4 is PQ475815.

Description of *Clostridium zeae* LS5

Cells are Gram-stain-positive, non-flagellated, strictly anaerobic, and rod-shaped. The cell size measures 1.28 μm in length and 0.29 μm in width. Colonies are flat, circular, and yellow-colored after incubation for 3 days on R2A agar at 30°C. In API 20A, positive for indole production, urease activity, gelatin hydrolysis, catalase activity and acid production from D-glucose, D-mannitol, D-lactose, D-maltose, salicin, D-xylose, L-arabinose, D-cellobiose, D-mannose, D-rhamnose and D-trehalose; but negative for esculin hydrolysis and acid production from sucrose, glycerol, D-melezitose, D-raffinose and D-sorbitol. Strain LS5 (=NNIBR202411BA2548) was isolated from soil from Gucheon-ri (35°32′04.0″N 128°59′10.0″E), Danjang-myeon, Miryang, Gyeongsangnam-do, Korea. The Gen Bank accession number for the 16S rRNA gene sequence of strain LS5 is PQ475869.

Description of *Lachnotalea glycerini* NWD3

Cells are Gram-stain-negative, non-flagellated, strictly anaerobic, and rod-shaped. The cell size measures 1.37 μm in length and 0.33 μm in width. Colonies are mucoid, raised, and beige-colored after incubation for 3 days on PYG agar at 30°C. In API 20A, positive for indole production, urease activity, gelatin hydrolysis and acid production from D-glucose, D-mannitol, D-lactose, sucrose, D-maltose, salicin, D-xylose, L-arabinose, glycerol, D-cellobiose, D-mannose, D-melezitose, D-raffinose, D-sorbitol, D-rhamnose and D-trehalose; but negative for esculin hydrolysis, catalase activity. Strain NWD3 (=NNIBR202411 BA2552) was isolated from soil from Sandaewol-ri (37°49′10.0″N 128°53′08.5″E), Sacheon-myeon, Gangneung, Gangwon-do, Korea. The GenBank accession number for the 16S rRNA gene sequence of strain NWD3 is PQ475894.

Description of *Bacteroides pyogenes* 24KS-9-1

Cells are Gram-stain-negative, non-flagellated, strictly anaerobic, and rod-shaped. The cell size measures 1.60 μm in length and 0.80 μm in width. Colonies are circular, and beige-colored after incubation for 5 days on NMS agar at 37°C. In API 20A, positive for indole production, gelatin hydrolysis, esculin hydrolysis and acid production from D-glucose, D-lactose, sucrose, D-maltose, glycerol, D-mannose and D-sorbitol; but negative for urease activity, catalase activity and acid production from D-mannitol, salicin, D-xylose, L-arabinose, D-cellobiose, D-melezitose, D-raffinose, D-rhamnose and D-trehalose. Strain 24KS-9-1 (=NNIBR202411BA2570) was isolated from soil from Sangcho-ri (36°41′50.6″N 128°13′26.3″E), Mungyeong-eup, Mungyeong, Gyeongsangbuk-do, Korea. The Gen Bank accession number for the 16S rRNA gene sequence of strain 24KS-9-1 is PQ451552.

Description of *Prevotella herbatica* NWA5

Cells are Gram-stain-negative, non-flagellated, strictly anaerobic, and rod-shaped. The cell size measures 1.1 μm in length and 0.44 μm in width. Colonies are flat, circular, and beige-colored after incubation for 3 days on PYG agar at 30°C. In API 20A, positive for indole production, urease activity, gelatin hydrolysis, catalase activity and acid production from D-glucose, D-lactose, D-maltose, salicin, D-xylose, L-arabinose, D-cellobiose, D-mannose, D-sorbitol, D-rhamnose and D-trehalose; but negative for esculin hydrolysis and acid production from D-mannitol, sucrose, glycerol, D-melezitose and D-raffinose. Strain NWA5 (=NNIBR 202411BA2551) was isolated from soil from Sandaewol-ri (37°49′12.4″N 128°53′16.3″E), Sacheon-myeon, Gangneung, Gangwon-do, Korea. The GenBank accession number for the 16S rRNA gene sequence of strain NWA5 is PQ475876.

Description of *Hydrotalea sandarakina* 24KSMF-4

Cells are Gram-stain-negative, non-flagellated, aerobic, and rod-shaped. The cell size measures 2.20 μm in length and 0.70 μm in width. Colonies are circular, and pink-colored after incubation for 4 days on MM2 agar at 30°C. In API 20NE, positive for esculin hydrolysis, and β-galactosidase; but negative for nitrates reduction, indole production, glucose fermentation, arginine dihydrolase, urease, and gelatin hydrolysis. D-Glucose, *N*-acetyl-glucosamine, D-maltose, and potassium gluconate are utilized as sole carbon sources; but L-arabinose, D-mannose, D-mannitol, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid are not. Strain 24KSMF-4 (=NNIBR2024 11BA2568) was isolated from soil from Gadae-ri (37°02′41.0″N 128°24′11.4″E), Gagok-myeon, Danyang-gun, Chungcheongbuk-do, Korea. The GenBank accession number for the 16S rRNA gene sequence of strain 24KSMF-4 is PQ482812.

Description of *Dyadobacter fermentans* OGLA_24

Cells are Gram-stain-negative, non-flagellated, aerobic, and rod-shaped. The cell size measures 1.17 μm in length and 0.40 μm in width. Colonies are smooth, raised, circular, and white-colored after incubation for 2 days on 0.5× R2A agar at 30°C. In API 20NE, positive for arginine dihydrolase, and urease; but negative for nitrates reduction, indole production, glucose fermentation, esculin hydrolysis, gelatin hydrolysis, and β-galactosidase. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, malic acid, trisodium citrate, and phenylacetic acid are utilized as sole carbon sources; but adipic acid is not. Strain OGLA_24 (=NNIBR202411BA2527) was isolated from freshwater from Bongmyeong-dong (36°21′24.5″N 127°21′16.6″E), Yuseong-gu, Daejeon, Korea. The GenBank accession number for the 16S rRNA gene sequence of strain OGLA_24 is PQ482616.

Description of *Flavobacterium tistrianum* LYRR_9

Cells are Gram-stain-negative, non-flagellated, aerobic, and rod-shaped. The cell size measures 3.25 μm in length and 0.50 μm in width. Colonies are smooth, raised, circular, and orange-colored after incubation for 2 days on LB agar at 30°C. In API 20NE, positive for arginine dihydrolase, urease, esculin hydrolysis, and β-galactosidase; but negative for nitrates reduction, indole production, glucose fermentation, and gelatin hydrolysis. D-Glucose, L-arabinose, D-mannose, *N*-acetyl-glucosamine, D-maltose, potassium, and malic acid are utilized as sole carbon sources; but D-mannitol, gluconate, capric acid, adipic acid, trisodium citrate, and phenylacetic acid are not. Strain LYRR_9 (=NNIBR202411BA2532) was isolated from freshwater from Eoeun-dong (36°21′40.9″N 127°21′26.9″E), Yuseong-gu, Daejeon, Korea. The GenBank accession number for the 16S rRNA gene sequence of strain LYRR_9 is PQ482 620.

Description of *Chryseobacterium artocarpi* LPL_15

Cells are Gram-stain-negative, non-flagellated, aerobic, and rod-shaped. The cell size measures 1.55 μm in length and 0.45 μm in width. Colonies are mucoid, raised, circular, and yellow-colored after incubation for 2 days on LB agar at 30°C. In API 20NE, positive for indole production, arginine dihydrolase, urease, esculin hydrolysis, and gelatin hydrolysis; but negative for nitrates reduction, glucose fermentation, and β-galactosidase. D-Glucose, L-arabinose, D-mannose, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid are utilized as sole carbon sources; but D-mannitol is not. Strain LPL_15 (=NNIBR 202411BA2524) was isolated from freshwater from Gwan-pyeong-dong (36°25′00.6″N 127°22′45.2″E), Yuseong-gu, Daejeon, Korea. The GenBank accession number for the 16S rRNA gene sequence of strain LPL_15 is PQ482613.

Description of *Chryseobacterium lecithinasegens* XSHD_25

Cells are Gram-stain-negative, non-flagellated, aerobic, and rod-shaped. The cell size measures 1.24 μm in length and 0.50 μm in width. Colonies are smooth, raised, circular, and yellow-colored after incubation for 2 days on 2× R2A agar at 30°C. In API 20NE, positive for indole production, arginine dihydrolase, urease, esculin hydrolysis, and gelatin hydrolysis; but negative for nitrates reduction, glucose fermentation, and β-galactosidase. D-Glucose, D-mannose, D-maltose, potassium gluconate, adipic acid, malic acid, trisodium citrate, and phenylacetic acid are utilized as sole carbon sources; but L-arabinose, D-mannitol, *N*-acetyl-glucosamine, and capric acid are not. Strain XSHD_25 (=NNIBR202411BA2610) was isolated from freshwater from Jung-dong (36°25′00.6″N 127°22′45.2″ E), Dong-gu, Daejeon, Korea. The GenBank accession number for the 16S rRNA gene sequence of strain XSHD_ 25 is PQ482623.

Description of *Fusobacterium varium* 24KS-13-1

Cells are Gram-stain-negative, non-flagellated, strictly anaerobic, and rod-shaped. The cell size measures 2.30 μm in length and 0.80 μm in width. Colonies are circular, and beige-colored after incubation for 5 days on NMS agar at 37°C. In API 20A, positive for esculin hydrolysis and acid production from D-glucose and D-mannose; but negative for indole production, urease activity, gelatin hydrolysis, catalase activity and acid production from D-mannitol,

D-lactose, sucrose, D-maltose, salicin, D-xylose, L-arabinose, glycerol, D-cellobiose, D-melezitose, D-raffinose, D-sorbitol, D-rhamnose and D-trehalose. Strain 24KS-13-1 (=NNIBR202411BA2571) was isolated from freshwater from Ugok-ri (36°41′50.6″N 128°13′26.3″E), Sanbuk-myeon, Mungyeong, Gyeongsangbuk-do, Korea. The Gen Bank accession number for the 16S rRNA gene sequence of strain 24KS-13-1 is PQ451558.

Description of *Oharaeibacter diazotrophicus* 24KSNC-7

Cells are Gram-stain-negative, flagellated, aerobic, and rod-shaped. The cell size measures 1.80 μm in length and 1.00 μm in width. Colonies are circular, and beige-colored after incubation for 4 days on NMS agar at 30°C. In API 20NE, positive for gelatin hydrolysis; but negative for nitrates reduction, indole production, glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis, and β-galactosidase. D-Glucose, L-arabinose, D-mannitol, D-maltose, and malic acid are utilized as sole carbon sources; but D-mannose, *N*-acetyl-glucosamine, potassium gluconate, capric acid, adipic acid, trisodium citrate, and phenylacetic acid are not. Strain 24KSNC-7 (=NNIBR202411BA2561) was isolated from soil from Hyeonnae-ri (37°36′48.7″N 129°02′23.4″E), Okgye-myeon, Gangneung, Gangwon-do, Korea. The GenBank accession number for the 16S rRNA gene sequence of strain 24KSNC-7 is PQ482674.

Description of *Hyphomicrobium facile* subsp. *facile* 24KSA-51

Cells are Gram-stain-negative, flagellated, aerobic, and rod-shaped. The cell size measures 1.30 μm in length and 0.60 μm in width. Colonies are circular, and beige-colored after incubation for 4 days on AMS agar at 30°C. In API 20NE, negative for nitrates reduction, indole production, glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis, gelatin hydrolysis, and β-galactosidase. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid are not utilized as sole carbon sources. Strain 24KSA-51 (=NNIBR202411BA2567) was isolated from soil from Bongmyeong-ri (36°02′48.4″N 126°46′10.9″E), Hwayang-myeon, Seocheon, Chungcheongnam-do, Korea. The Gen Bank accession number for the 16S rRNA gene sequence of strain 24KSA-51 is PQ482811.

Description of *Bradyrhizobium uaiense* 24KSME-3

Cells are Gram-stain-negative, non-flagellated, aerobic, and rod-shaped. The cell size measures 1.50 μm in length and 0.90 μm in width. Colonies are circular, and beige-colored after incubation for 7 days on MM2 agar at 30°C. In API 20NE, negative for nitrates reduction, indole production, glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis, gelatin hydrolysis, and β-galactosidase. Adipic acid is utilized as sole carbon sources; but D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, malic acid, trisodium citrate, and phenylacetic acid are not. Strain 24KSME-3 (=NNIBR202411BA2622) was isolated from soil from Gadae-ri (37°02′41.0″N 128°24′11.4″E), Gagok-myeon, Danyang-gun, Chungcheongbuk-do, Korea. The GenBank accession number for the 16S rRNA gene sequence of strain 24KSME-3 is PQ483067.

Description of *Mesorhizobium shonense* 24KSAZ-13

Cells are Gram-stain-negative, flagellated, aerobic, and rod-shaped. The cell size measures 1.45 μm in length and 0.41 μm in width. Colonies are circular, and beige-colored after incubation for 4 days on AMS agar at 30°C. In API 20NE, positive for esculin hydrolysis; but negative for nitrates reduction, indole production, glucose fermentation, arginine dihydrolase, urease, gelatin hydrolysis, and β-galactosidase. D-Mannose is utilized as sole carbon sources; but D-glucose, L-arabinose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid are not. Strain 24KSAZ-13 (=NNIBR202411BA2563) was isolated from soil from Ugok-ri (36°41′50.6″N 128°13′26.3″E), Sanbuk-myeon, Mungyeong, Gyeongsangbuk-do, Korea. The GenBank accession number for the 16S rRNA gene sequence of strain 24KSAZ-13 is PQ482678.

Description of *Ciceribacter selenitireducens* 23KSNF-4

Cells are Gram-stain-negative, non-flagellated, aerobic, and rod-shaped. The cell size measures 1.20 μm in length and 0.48 μm in width. Colonies are circular, and beige-colored after incubation for 4 days on NMS agar at 30°C. In API 20NE, positive for esculin hydrolysis, and β-galactosidase; but negative for nitrates reduction, indole production, glucose fermentation, arginine dihydrolase, urease, and gelatin hydrolysis. *N*-Acetyl-glucosamine, capric acid, adipic acid, malic acid, and trisodium citrate are utilized as sole carbon sources; but D-glucose, L-arabinose, D-mannose, D-mannitol, D-maltose, potassium gluconate, and phenylacetic acid are not. Strain 23KSNF-4 (=NNIBR202411BA2569) was isolated from soil from Gadae-ri (37°02′41.0″N 128°24′11.4″E), Gagok-myeon, Danyang-gun, Chungcheongbuk-do, Korea. The GenBank accession number for the 16S rRNA gene sequence of strain 23KSNF-4 is PQ482813.

Description of *Nitrospirillum iridis* 23KSAJ-10

Cells are Gram-stain-negative, flagellated, facultatively anaerobic, and rod-shaped. The cell size measures 1.80 μm in length and 0.90 μm in width. Colonies are circular, and beige-colored after incubation for 4 days on AMS agar at 30°C. In API 20NE, positive for nitrates reduction, esculin hydrolysis, and β-galactosidase; but negative for indole production, glucose fermentation, arginine dihydrolase, urease, and gelatin hydrolysis. D-Glucose, L-arabinose, D-mannose, D-maltose, and potassium gluconate are utilized as sole carbon sources; but D-mannitol, *N*-acetyl-glucosamine, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid are not. Strain 23KSAJ-10 (=NNIBR 202411BA2562) was isolated from soil from Sangcho-ri (36°45′43.8″N 128°04′28.8″E), Mungyeong-eup, Mungyeong, Gyeongsangbuk-do, Korea. The GenBank accession number for the 16S rRNA gene sequence of strain 23KSAJ-10 is PQ482676.

Description of *Novosphingobium lentum* 24KSNB-7

Cells are Gram-stain-negative, flagellated (Tiirola *et al*., 2005), aerobic, and rod-shaped. The cell size measures 0.90 μm in length and 0.70 μm in width. Colonies are circular, and yellow-colored after incubation for 4 days on NMS agar at 30°C. In API 20NE, positive for esculin hydrolysis; but negative for nitrates reduction, indole production, glucose fermentation, arginine dihydrolase, urease, gelatin hydrolysis, and β-galactosidase. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid are not utilized as sole carbon sources. Strain 24KSNB-7 (=NNIBR202411BA2578) was isolated from soil from Wichon-ri (37°45′58.3″N 128°50′37.9″E), Seongsan-myeon, Gangneung, Gangwon-do, Korea. The GenBank accession number for the 16S rRNA gene sequence of strain 24KSNB-7 is PQ483063.

Description of *Novosphingobium taihuense* XDMA_21

Cells are Gram-stain-negative, non-flagellated, aerobic, and rod-shaped. The cell size measures 1.70 μm in length and 0.80 μm in width. Colonies are circular, and yellow-colored after incubation for 4 days on 2×R2A agar at 30°C. In API 20NE, positive for esculin hydrolysis, and β-galactosidase; but negative for nitrates reduction, indole production, glucose fermentation, arginine dihydrolase, urease, and gelatin hydrolysis. D-Glucose, D-mannose, D-maltose, potassium gluconate, adipic acid, and malic acid are utilized as sole carbon sources; but L-arabinose, D-mannitol, *N*-acetyl-glucosamine, capric acid, trisodium citrate, and phenylacetic acid are not. Strain XDMA_21 (=NNIBR202411BA2574) was isolated from soil from Sangcho-ri (36°45′43.8″N 128°04′28.8″E), Mungyeong-eup, Mungyeong, Gyeongsangbuk-do, Korea. The Gen Bank accession number for the 16S rRNA gene sequence of strain XDMA_21 is PQ483064.

Description of *Sphingomonas citri* LYRR_8

Cells are Gram-stain-negative, non-flagellated, aerobic, and rod-shaped. The cell size measures 2.35 μm in length and 0.55 μm in width. Colonies are smooth, raised, circular, and orange-colored after incubation for 2 days on LB agar at 30°C. In API 20NE, positive for arginine dihydrolase, urease, and esculin hydrolysis; but negative for nitrates reduction, indole production, glucose fermentation, gelatin hydrolysis, and β-galactosidase. D-Glucose, D-mannose, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, adipic acid, malic acid, and trisodium citrate are utilized as sole carbon sources; but L-arabinose, D-mannitol, capric acid, and phenylacetic acid are not. Strain LYRR_8 (=NNIBR202411BA2533) was isolated from freshwater from Eoeun-dong (36°21′40.9″N 127°21′26.9″E), Yuseong-gu, Daejeon, Korea. The GenBank accession number for the 16S rRNA gene sequence of strain LYRR_8 is PQ 482621.

Description of *Sphingomonas paucimobilis* MWIIL1

Cells are Gram-stain-negative, flagellated (Toh *et al*., 2011), aerobic, and rod-shaped. The cell size measures 2.37 μm in length and 0.52 μm in width. Colonies are flat, circular, and yellow-colored after incubation for 3 days on LB agar at 20°C. In API 20NE, positive for esculin hydrolysis, and β-galactosidase; but negative for nitrates reduction, indole production, glucose fermentation, arginine dihydrolase, urease, and gelatin hydrolysis. D-Glucose, L-arabinose, D-mannose, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, adipic acid, malic acid, and trisodium citrate are utilized as sole carbon sources; but D-mannitol, capric acid, and phenylacetic acid are not. Strain MWIIL1 (=NNIBR202411BA2541) was isolated from freshwater from Joil-ri (35°27′54.2″N 129°08′37.4″E), Samdong-myeon, Ulju-gun, Ulsan, Korea. The GenBank accession number for the 16S rRNA gene sequence of strain MWIIL1 is PQ475871.

Description of *Sphingomonas pruni* 24KSMF-10

Cells are Gram-stain-negative, flagellated, aerobic, and rod-shaped. The cell size measures 3.15 μm in length and 0.34 μm in width. Colonies are circular, and yellow-colored after incubation for 4 days on MM2 agar at 30°C. In API 20NE, positive for esculin hydrolysis, gelatin hydrolysis, and β-galactosidase; but negative for nitrates reduction, indole production, glucose fermentation, arginine dihydro-

lase, and urease. D-Glucose, L-arabinose, D-mannose, *N*-acetyl-glucosamine, D-maltose, and adipic acid are utilized as sole carbon sources; but D-mannitol, potassium gluconate, capric acid, malic acid, trisodium citrate, and phenylacetic acid are not. Strain 24KSMF-10 (=NNIBR2024 11BA2557) was isolated from soil from Gadae-ri (37°02′41.0″N 128°24′11.4″E), Gagok-myeon, Danyang-gun, Chungcheongbuk-do, Korea. The GenBank accession number for the 16S rRNA gene sequence of strain 24KSMF-10 is PQ482667.

Description of *Burkholderia vietnamiensis* 24KSMA-17

Cells are Gram-stain-negative, flagellated (Gillis *et al*., 1995), facultatively anaerobic, and rod-shaped. The cell size measures 1.01 μm in length and 0.43 μm in width. Colonies are circular, and beige-colored after incubation for 4 days on MM2 agar at 30°C. In API 20NE, positive for nitrates reduction, and β-galactosidase; but negative for indole production, glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis, and gelatin hydrolysis. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, potassium gluconate, capric acid, malic acid, trisodium citrate, and phenylacetic acid are utilized as sole carbon sources; but D-maltose, and adipic acid are not. Strain 24KSMA-17 (=NNIBR202411BA2576) was isolated from soil from Ugok-ri (36°41′50.6″N 128°13′26.3″E), Sanbuk-myeon, Mungyeong, Gyeongsangbuk-do, Korea. The GenBank accession number for the 16S rRNA gene sequence of strain 24KSMA-17 is PQ483064.

Description of *Pandoraea cepalis* 24KSMA-16

Cells are Gram-stain-negative, flagellated, aerobic, and rod-shaped. The cell size measures 1.20 μm in length and 0.70 μm in width. Colonies are circular, and beige-colored after incubation for 4 days on MM2 agar at 30°C. In API 20NE, positive for nitrates reduction; but negative for indole production, glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis, gelatin hydrolysis, and β-galactosidase. Potassium gluconate, capric acid, malic acid, trisodium citrate, and phenylacetic acid are utilized as sole carbon sources; but D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, and adipic acid are not. Strain 24KSMA-16 (=NNIBR202411BA 2560) was isolated from soil from Ugok-ri (36°41′50.6″N 128°13′26.3″E), Sanbuk-myeon, Mungyeong, Gyeongsangbuk-do, Korea. The GenBank accession number for the 16S rRNA gene sequence of strain 24KSMA-16 is PQ482673.

Description of *Thiomonas arsenitoxydans* 24KSAY-16

Cells are Gram-stain-negative, flagellated, facultatively anaerobic, and rod-shaped. The cell size measures 1.40 μm in length and 0.60 μm in width. Colonies are circular, and beige-colored after incubation for 5 days on AMS agar at 30°C. In API 20NE, positive for nitrates reduction; but negative for indole production, glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis, gelatin hydrolysis, and β-galactosidase. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid are not utilized as sole carbon sources. Strain 24KSAY-16 (=NNIBR202411 BA2555) was isolated from soil from Ugok-ri (36°41′50.6″ N 128°13′26.3″E), Sanbuk-myeon, Mungyeong, Gyeongsangbuk-do, Korea. The GenBank accession number for the 16S rRNA gene sequence of strain 24KSAY-16 is PQ482662.

Description of *Trinickia dinghuensis* 24KSA-46

Cells are Gram-stain-negative, non-flagellated, aerobic, and rod-shaped. The cell size measures 1.40 μm in length and 0.70 μm in width. Colonies are circular, and beige-colored after incubation for 4 days on NMS agar at 30°C. In API 20NE, positive for β-galactosidase; but negative for nitrates reduction, indole production, glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis, and gelatin hydrolysis. D-Glucose, L-arabinose, D-mannitol, D-maltose, potassium gluconate, malic acid, and phenylacetic acid are utilized as sole carbon sources; but D-Mannose, *N*-acetyl-glucosamine, capric acid, adipic acid, and trisodium citrate are not. Strain 24KSA-46 (=NNIBR202411BA2623) was isolated from soil from Sinya-ri (36°27′09.9″N 126°21′28.1″E), Anmyeon-eup, Taean-gun, Chungcheongnam-do, Korea. The GenBank accession number for the 16S rRNA gene sequence of strain 24KSA-46 is PQ483066.

Description of *Paraburkholderia kururiensis* subsp. *kururiensis* 24KSAB-1

Cells are Gram-stain-negative, flagellated, aerobic, and rod-shaped. The cell size measures 1.90 μm in length and 0.90 μm in width. Colonies are circular, and beige-colored after incubation for 4 days on AMS agar at 30°C. In API 20NE, positive for nitrates reduction, urease, and β-galactosidase; but negative for indole production, glucose fermentation, arginine dihydrolase, esculin hydrolysis, and gelatin hydrolysis. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, adipic acid, malic acid, trisodium citrate, and phenylacetic acid are utilized as sole carbon sources; but capric acid is not. Strain 24KSAB-1 (=NNIBR202411BA 2559) was isolated from soil from Wichon-ri (37°45′ 58.3″N 128°50′37.9″E), Seongsan-myeon, Gangneung, Gangwon-do, Korea. The GenBank accession number for the 16S rRNA gene sequence of strain 24KSAB-1 is PQ482672.

Description of *Aquitalea pelogenes* MWIIR11

Cells are Gram-stain-negative, non-flagellated, facultatively anaerobic, and rod-shaped. The cell size measures 1.06 μm in length and 0.37 μm in width. Colonies are flat, circular, and white-colored after incubation for 3 days on R2A agar at 20°C. In API 20NE, positive for nitrates reduction, indole production, and arginine dihydrolase; but negative for glucose fermentation, urease, esculin hydrolysis, gelatin hydrolysis, and β-galactosidase. D-Glucose, *N*-acetyl-glucosamine, potassium gluconate, capric acid, malic acid, and phenylacetic acid are utilized as sole carbon sources; but L-arabinose, D-mannose, D-mannitol, D-maltose, adipic acid, and trisodium citrate are not. Strain MWIIR11 (=NNIBR202411BA2542) was isolated from freshwater from Joil-ri (35°27′54.2″N 129°08′37.4″E), Samdong-myeon, Ulju-gun, Ulsan, Korea. The GenBank accession number for the 16S rRNA gene sequence of strain MWIIR11 is PQ475873.

Description of *Shewanella azerbaijanica* LSDB_2

Cells are Gram-stain-negative, non-flagellated, facultatively anaerobic, and rod-shaped. The cell size measures 0.90 μm in length and 0.33 μm in width. Colonies are mucoid, raised, circular, and yellow-colored after incubation for 2 days on LB agar at 30°C In API 20NE, positive for nitrates reduction, arginine dihydrolase, urease, esculin hydrolysis, and gelatin hydrolysis; but negative for indole production, glucose fermentation, and β-galactosidase. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, adipic acid, malic acid, trisodium citrate, and phenylacetic acid are utilized as sole carbon sources; but capric acid is not. Strain LSDB_2 (=NNIBR202411BA2525) was isolated from freshwater from Wonsinheung-dong (36°20′00.4″N 127° 19′57.4″E), Yuseong-gu, Daejeon, Korea. The GenBank accession number for the 16S rRNA gene sequence of strain LSDB_2 is PQ482614.

Description of *Citrobacter meridianamericanus* RSDB_9

Cells are Gram-stain-negative, non-flagellated, facultatively anaerobic, and rod-shaped. The cell size measures 1.19 μm in length and 0.44 μm in width. Colonies are smooth, raised, circular, and white-colored after incubation for 2 days on R2A agar at 30°C. In API 20NE, positive for nitrates reduction, indole production, glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis, and β-galactosidase; but negative for gelatin hydrolysis. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, malic acid, and trisodium citrate are utilized as sole carbon sources; but adipic acid, and phenylacetic acid are not. Strain RSDB_9 (=NNIBR202411BA2531) was isolated from freshwater from Wonsinheung-dong (36°20′00.4″N 127°19′57.4″E), Yuseong-gu, Daejeon, Korea. The GenBank accession number for the 16S rRNA gene sequence of strain RSDB_9 is PQ482619.

Description of *Klebsiella pneumoniae* subsp. *ozaenae* 23KSNG-3

Cells are Gram-stain-negative, non-flagellated, facultatively anaerobic, and coccus-shaped. The cell size measures 1.60 μm in length and 1.20 μm in width. Colonies are circular, and beige-colored after incubation for 4 days on NMS agar at 30°C. In API 20NE, positive for nitrates reduction, glucose fermentation, urease, esculin hydrolysis, and β-galactosidase; but negative for indole production, arginine dihydrolase, and gelatin hydrolysis. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid are utilized as sole carbon sources. Strain 23KSNG-3 (=NNIBR202411BA2566) was isolated from soil from Ugok-ri (36°41′50.6″N 128°13′26.3″E), Sanbuk-myeon, Mungyeong, Gyeongsangbuk-do, Korea. The GenBank accession number for the 16S rRNA gene sequence of strain 23KSNG-3 is PQ482688.

Description of *Klebsiella quasipneumoniae* BW1-7

Cells are Gram-stain-negative, non-flagellated, aerobic, and rod-shaped. The cell size measures 1.10 μm in length and 0.49 μm in width. Colonies are flat, circular, and white-colored after incubation for 3 days on 2×R2A agar at 20°C. In API 20NE, positive for urease; but negative for nitrates reduction, indole production, glucose fermentation, arginine dihydrolase, esculin hydrolysis, gelatin hydrolysis, and β-galactosidase. D-Glucose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid are utilized as sole carbon sources; but L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, and D-maltose are not. Strain BW1-7 (=NNIBR 202411BA2535) was isolated from freshwater from Samnak-dong (35°09′15.2″N 128°57′55.4″E), Sasang-gu, Busan, Korea. The GenBank accession number for the 16S rRNA gene sequence of strain BW1-7 is PQ475816.

Description of *Luteibacter flocculans* 24KSMB-6

Cells are Gram-stain-negative, flagellated (Friedrich *et al*., 2023), aerobic, and rod-shaped. The cell size measures 1.40 μm in length and 0.60 μm in width. Colonies are circular, and yellow-colored after incubation for 4 days on MM2 agar at 30°C. In API 20NE, positive for esculin hydrolysis, gelatin hydrolysis, and β-galactosidase; but negative for nitrates reduction, indole production, glucose

fermentation, arginine dihydrolase, urease. D-Glucose, D-mannose, *N*-acetyl-glucosamine, D-maltose, and malic acid are utilized as sole carbon sources; but L-arabinose, D-mannitol, potassium gluconate, capric acid, adipic acid, trisodium citrate, and phenylacetic acid are not. Strain 24KSMB-6 (=NNIBR202411BA2565) was isolated from soil from Wichon-ri (37°45′58.3″N 128°50′37.9″E), Seongsan-myeon, Gangneung, Gangwon-do, Korea. The Gen Bank accession number for the 16S rRNA gene sequence of strain 24KSMB-6 is PQ482687.

Description of *Pseudomonas citri* RGLA_46

Cells are Gram-stain-negative, flagellated (Gao *et al*., 2023), aerobic, and rod-shaped. The cell size measures 1.00 μm in length and 0.35 μm in width. Colonies are smooth, raised, circular, scalloped, and white-colored after incubation for 2 days on R2A agar at 30°C. In API 20NE, positive for nitrates reduction, arginine dihydrolase, and urease; but negative for indole production, glucose fermentation, esculin hydrolysis, gelatin hydrolysis, and β-galactosidase. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, and trisodium citrate are utilized as sole carbon sources; but phenylacetic acid is not. Strain RGLA_46 (=NNIBR2024 11BA2529) was isolated from freshwater from Bongmyeong-dong (36°21′24.5″N 127°21′16.6″E), Yuseong-gu, Daejeon, Korea. The GenBank accession number for the 16S rRNA gene sequence of strain RGLA_46 is PQ 482618.

Description of *Pseudomonas lalkuanensis* HW1-6

Cells are Gram-stain-negative, non-flagellated, aerobic, and rod-shaped. The cell size measures 1.10 μm in length and 0.53 μm in width. Colonies are flat, inrregular, and white-colored after incubation for 3 days on 2×R2A agar at 20°C. In API 20NE, positive for nitrates reduction, arginine dihydrolase, and esculin hydrolysis; but negative for indole production, glucose fermentation, urease, gelatin hydrolysis, and β-galactosidase. D-Glucose, capric acid, malic acid, trisodium citrate, and phenylacetic acid are utilized as sole carbon sources; but L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, and adipic acid are not. Strain HW1-6 (=NNIBR 202411BA2516) was isolated from freshwater from Toerae-ri (35°18′45.0″N 128°47′47.9″E), Hallim-myeon, Gimhae, Gyeongsangnam-do, Korea. The GenBank accession number for the 16S rRNA gene sequence of strain HW1-6 is PQ475901.

Description of *Pseudomonas petroselini* 24KSN-25

Cells are Gram-stain-negative, flagellated, aerobic, and rod-shaped. The cell size measures 1.80 μm in length and 0.80 μm in width. Colonies are circular, and beige-colored after incubation for 4 days on NMS agar at 30°C. In API 20NE, positive for nitrates reduction, arginine dihydrolase, and gelatin hydrolysis; but negative for indole production, glucose fermentation, urease, esculin hydrolysis, and β-galactosidase. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, malic acid, and trisodium citrate are utilized as sole carbon sources; but adipic acid, and phenylacetic acid are not. Strain 24KS*N*-25 (=NNIBR 202411BA2572) was isolated from soil from Gangdang-ri (36°39′06.2″N 126°25′26.0″E), Buseok-myeon, Sosan, Chungcheongnam-do, Korea.The GenBank accession number for the 16S rRNA gene sequence of strain 24KSN-25 is PQ483061.

Description of *Pseudoxanthomonas helianthi* 23KSNF-10

Cells are Gram-stain-negative, non-flagellated, aerobic, and rod-shaped. The cell size measures 1.00 μm in length and 0.50 μm in width. Colonies are circular, and beige-colored after incubation for 4 days on NMS agar at 30°C. In API 20NE, positive for esculin hydrolysis, and β-galactosidase; but negative for nitrates reduction, indole production, glucose fermentation, arginine dihydrolase, urease, and gelatin hydrolysis. D-Glucose, L-arabinose, D-mannose, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, and malic acid are utilized as sole carbon sources; but D-mannitol, capric acid, adipic acid, trisodium citrate, and phenylacetic acid are not. Strain 23KSNF-10 (=NNIBR202411BA2558) was isolated from soil from Gadae-ri (37°02′41.0″N 128°24′11.4″E), Gagok-myeon, Danyang-gun, Chungcheongbuk-do, Korea. The GenBank accession number for the 16S rRNA gene sequence of strain 23KSNF-10 is PQ482671.

Description of *Thermomonas mangrovi* TSM_13

Cells are Gram-stain-negative, non-flagellated, aerobic, and rod-shaped. The cell size measures 1.50 μm in length and 0.67 μm in width. Colonies are viscid, convex, irregular, lobate, and white-colored after incubation for 2 days on TSA agar at 30°C. In API 20NE, positive for arginine dihydrolase, urease, esculin hydrolysis, and gelatin hydrolysis; but negative for nitrates reduction, indole production, glucose fermentation, and β-galactosidase. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, malic acid, and trisodium citrate are utilized as sole carbon sources; but capric acid, adipic acid, and phenylacetic acid are not. Strain TSM_13 (=NNIBR202411BA2534) was isolated from freshwater from Nosan-ri (36°27′12.6″N 127°26′27.1″E), Hyeondo-myeon, Seowon-gu, Cheongju-si, Chungcheong-

buk-do, Korea. The GenBank accession number for the 16S rRNA gene sequence of strain TSM_13 is PQ482622.

Conflicts of Interest

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

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