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Unrecorded bacterial species from freshwater environments in Korea: Descriptions of 47 species isolated in 2021 and 2023

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Here we describe indigenous prokaryotic species in Korea, a total of 47 bacterial strains were isolated from freshwater and soil from the Republic of Korea. From the high 16S rRNA gene sequence similarity (>98.7%) and formation of a robust phylogenetic clade with the closest species, it was determined that each strain belonged to predefined bacterial species. There is no official report that these 47 species belonged to 4 phyla, 8 classes, 20 orders, 27 families, and 38 genera, which were assigned to *Sediminibacterium* and *Flavobacterium* of the phylum *Bacteroidota*; *Streptomyces*, *Solirubrobacter*, *Nonomuraea*, *Nocardioides*, *Nocardia*, *Mycobacterium*, *Micromonospora*, *Micrococcus*, *Microbacterium*, *Catellatospora*, and *Arthrobacter* of the phylum *Actinomycetota*; *Vogesella*, *Tabrizicola*, *Stenotrophomonas*, *Sphingorhabdus*, *Sphingomonas*, *Sphingobium*, *Pseudomonas*, *Piscinibacter*, *Phenylobacterium*, *Novosphingobium*, *Noviherbaspirillum*, *Neotabrizicola*, *Microvirga*, *Mesorhizobium*, *Lysobacter*, *Ideonella*, *Hydrogenophaga*, *Enterobacter*, and *Chakrabartia* of the phylum *Pseudomonadota*; *Trichococcus*, *Paenibacillus*, *Neobacillus*, *Jeotgalibacillus*, *Chryseomicrobium*, and *Bacillus* of the phylum *Bacillota*. Gram-staining results, colony and cell morphologies, basic biochemical characteristics, isolation sources, and strain IDs are also described in the species description section.

Keywords: 16S rRNA, bacterial diversity, freshwater, indigenous prokaryotic species in Korea, soil, unrecorded species

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Introduction

Freshwater accounts for 2.5% of the aquatic environment, while seawater makes up 97.5%. Freshwater, with only about 3.5% salt content, differs significantly from seawater and includes various ecosystems, such as rivers and streams, where water flows according to gradients and altitude differences. It exists in forms like rivers, lakes, and groundwater, representing roughly 0.6% of the Earth's total water system, excluding glaciers. Despite its small proportion, freshwater remains a crucial resource for human survival (Wetzel, 2001). In freshwater environments, most dominant prokaryotes remain uncultured, except for a few groups. Microorganisms are generally more abundant in downstream waters compared to upstream areas. Upstream waters tend to harbor microorganisms that thrive in low-nutrient conditions, whereas downstream environments support microorganisms that flourish in nutrient-rich waters. While many bacterial groups form biofilms, fungi and algae are also commonly found in these habitats. Microorganisms in oligotrophic and eutrophic lakes differ, with photosynthetic bacteria like *Cyanobacteria* dominating eutrophic lakes in summer. To date, about 20 bacterial phyla have been identified in freshwater ecosystems, with *Actinomycetota*, *Bacteroidota*, *Pseudomonadota*, *Cyanobacteriota*, and *Verrucomicrobiota* being

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predominant (Newton *et al*., 2011). According to GOLD statistics, environmental bacteria make up about 10% of all genomic projects, with most ecological research focusing on the digestive tract, oceans, and soil, while freshwater studies account for only 9.2% (Mukherjee *et al*., 2022). Similar to marine and terrestrial environments, freshwater prokaryotes primarily act as decomposers, breaking down organic matter into inorganic substances through microfood networks and playing a key role in greenhouse gas cycling. Despite their significant impact on human life, research on microbial diversity in freshwater environments remains relatively underexplored. Further studies could enhance our understanding of freshwater-specific prokaryotes and support efforts to discover new microbial species domestically.

During 2021 and 2023, we conducted research in freshwater environments across Korea, leading to the discovery of numerous novel and previously unreported bacterial species. Supported by the Nakdonggang National Institute of Biological Resources (NNIBR), this study identified species across eight bacterial classes: *Actinomycetes*, *Alphaproteobacteria*, *Betaproteobacteria*, *Gammaproteobacteria*, *Bacilli*, *Chitinophagia*, *Thermoleophilia*, and *Flavobacteriia*, which are distributed among 20 different orders. Here, we present a concise overview of the 47 unreported bacterial species discovered during this research program.

Materials and Methods

A total of 47 bacterial strains affiliated to the classse *Actinomycetes*, *Alphaproteobacteria*, *Betaproteobacteria*, *Gammaproteobacteria*, *Bacilli*, *Chitinophagia*, *Thermoleophilia*, and *Flavobacteriia* were isolated from freshwater and soil samples. Freshwater and soil samples were processed separately, spread onto diverse culture media including BHI, R2A, five folds-diluted R2A, YPD, nutrient, and five folds-diluted nutrient, and incubated at 20, 25 and 30°C for 5−10 days (Table 1). The designated strain IDs, sources, culture media, and incubation conditions are summarized in Table 1. All strains were purified as single colonies and stored as 20−25% (w/v) glycerol suspension −80°C as well as lyophilized ampoules.

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

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

Results and Discussion

The 47 strains were distributed in 8 classes of the *Actinomycetes*, *Alphaproteobacteria*, *Betaproteobacteria*, *Gammaproteobacteria*, *Bacilli*, *Chitinophagia*, *Thermoleophilia*, and *Flavobacteriia*; 6 strains for the class *Bacilli*, 14 strains for the *Actinomycetes*, 13 strains for the *Alphaproteobacteria*, 5 strains for the *Betaproteobacteria*, 5 strains for the *Gammaproteobacteria*, 1 strain for the *Chitinophagia*, 1 strain for the *Thermoleophilia* and 2 strains for the *Flavobacteriia* (Table 1). These strains were Gram-staining-negative or positive, chemoheterotrophic, rod, short-rod and coccoid shaped showing in Fig. 1.

The strains in the phylum *Actinomycetota* (Fig. 2) were found to belong to 2 classes 11 separate genera: *Streptomyces* (5 species), *Solirubrobacter* (1 species), *Nonomuraea* (1 species), *Nocardioides* (1 species), *Nocardia* (1 species), *Mycobacterium* (1 species), *Micromonospora* (1 species), *Micrococcus* (1 species), *Microbacterium* (1 species), *Catellatospora* (1 species), and *Arthrobacter* (1 species).

Fig. 3 shows phylogenetic assignment of 23 strains of the phylum *Pseudomonadota* belong to 3 classes 19 separate genera: *Vogesella* (1 species), *Tabrizicola* (1 species), *Stenotrophomonas* (1 species), *Sphingorhabdus* (1 species), *Sphingomonas* (3 species), *Sphingobium* (1 species), *Pseudomonas* (2 species), *Piscinibacter* (1 species), *Phenylobacterium* (1 species), *Novosphingobium* (1 species), *Noviherbaspirillum* (1 species), *Neotabrizicola* (1 species), *Microvirga* (1 species), *Mesorhizobium* (2 species), *Lysobacter* (1 species), *Ideonella* (1 species), *Hydrogenophaga* (1 species), *Enterobacter* (1 species), and *Chakrabartia* (1 species).

Fig. 4 shows phylogenetic assignment of 9 strains of the phyla *Bacillota* and *Bacteroidota* belong to 3 classes 8 separate genera: *Trichococcus* (1 species), *Paenibacillus* (1 species), *Neobacillus* (1 species), *Jeotgalibacillus* (1 species), *Chryseomicrobium* (1 species), *Bacillus* (1 species), *Sediminibacterium* (1 species), and *Flavobacterium* (2 species).

Here we report 47 unrecorded bacterial species in Korea

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

Class	Order	Family	Genus	Strain ID	NNIBR ID	Most closely related species	Similarity (%)	Isolation source	Isolation site	Medium	Incubation conditions (°C, days)
Thermoleophilia	*Solirubrobacterales*	*Solirubrobacteraceae*	*Solirubrobacter*	HS040	NNIBR2023642BA27	*Solirubrobacter taibaiensis*	99.86	Fresh water and soil	Hoengseong-gun	R2A	25°C, 2 days
Gammaproteobacteria	*Lysobacterales*	*Lysobacteraceae*	*Stenotrophomonas*	HS009	NNIBR2023642BA25	*Stenotrophomonas cyclobalanopsidis*	99.72	Fresh water and soil	Hoengseong-gun	R2A	25°C, 2 days
Gammaproteobacteria	*Pseudomonadales*	*Pseudomonadaceae*	*Pseudomonas*	H395	NNIBR2023642BA13	*Pseudomonas farris*	100.00	Fresh water and soil	Hwaseong-si	R2A	25°C, 2 days
Gammaproteobacteria	*Pseudomonadales*	*Pseudomonadaceae*	*Pseudomonas*	ru14	NNIBR2023642BA59	*Pseudomonas solani*	99.03	Fresh water and soil	Anseong-si	R2A	25°C, 2 days
Gammaproteobacteria	*Lysobacterales*	*Lysobacteraceae*	*Lysobacter*	A092	NNIBR2023642BA18	*Lysobacter lycopersici*	98.77	Fresh water and soil	Anseong-si	R2A	25°C, 2 days
Gammaproteobacteria	*Enterobacterales*	*Enterobacteriaceae*	*Enterobacter*	BHI-u-3	NNIBR2023642BA55	*Enterobacter hormaechei* subsp. *oharae*	99.33	Fresh water and soil	Hoengseong-gun	BHI	25°C, 2 days
Flavobacteriia	*Flavobacteriales*	*Flavobacteriaceae*	*Flavobacterium*	HS027	NNIBR2023642BA26	*Flavobacterium stagni*	99.37	Fresh water and soil	Hoengseong-gun	R2A	25°C, 2 days
Flavobacteriia	*Flavobacteriales*	*Flavobacteriaceae*	*Flavobacterium*	K77	NNIBR2021642BA16	*Flavobacterium turcicum*	99.4	Fresh water and soil	Anseong-si	R2A	25°C, 2 days
Chitinophagia	*Chitinophagales*	*Chitinophagaceae*	*Sediminibacterium*	R2A-P31	NNIBR2023642BA54	*Sediminibacterium magnilacihabitans*	100	Fresh water and soil	Anseong-si	TSA	25°C, 2 days
Betaproteobacteria	*Neisseriales*	*Chromobacteriaceae*	*Vogesella*	ol5	NNIBR2023642BA58	*Vogesella urethralis*	99.63	Fresh water and soil	Hoengseong-gun	TSA	25°C, 2 days
Betaproteobacteria	*Burkholderiales*	*Sphaerotilaceae*	*Piscinibacter*	HS207	NNIBR2023642BA35	*Piscinibacter caeni*	98.75	Fresh water and soil	Hoengseong-gun	R2A	25°C, 2 days
Betaproteobacteria	*Burkholderiales*	*Oxalobacteraceae*	*Noviherbaspirillum*	H165	NNIBR2023642BA6	*Noviherbaspirillum psychrotolerans*	98.92	Fresh water and soil	Hwaseong-si	R2A	25°C, 2 days
Betaproteobacteria	*Burkholderiales*	*Sphaerotilaceae*	*Ideonella*	H428	NNIBR2023642BA15	*Ideonella alba*	98.85	Fresh water and soil	Hwaseong-si	R2A	25°C, 2 days
Betaproteobacteria	*Burkholderiales*	*Comamonadaceae*	*Hydrogenophaga*	W076	NNIBR2023642BA39	*Hydrogenophaga crocea*	99.72	Fresh water and soil	Wonju-si	R2A	25°C, 2 days
Bacilli	*Lactobacillales*	*Carnobacteriaceae*	*Trichococcus*	BHIDKJ23	NNIBR2023642BA56	*Trichococcus collinsii*	99.85	Fresh water and soil	Hoengseong-gun	BHI	25°C, 2 days
Bacilli	*Bacillales*	*Paenibacillaceae*	*Paenibacillus*	A257	NNIBR2023642BA23	*Paenibacillus oryzae*	99.58	Fresh water and soil	Anseong-si	R2A	25°C, 2 days
Bacilli	*Bacillales*	*Bacillaceae*	*Neobacillus*	NBDL15	NNIBR2023642BA52	*Neobacillus rhizosphaerae*	98.9	Fresh water and soil	Hwaseong-si	NA	25°C, 2 days
Bacilli	*Bacillales*	*Planococcaceae*	*Jeotgalibacillus*	H268	NNIBR2023642BA9	*Jeotgalibacillus proteolyticus*	99.86	Fresh water and soil	Hwaseong-si	R2A	25°C, 2 days
Bacilli	*Bacillales*	*Planococcaceae*	*Chryseomicrobium*	TBS-Won-1	NNIBR2023642BA53	*Chryseomicrobium excrementi*	99.26	Fresh water and soil	Hwaseong-si	TSA	25°C, 2 days
Bacilli	*Bacillales*	*Bacillaceae*	*Bacillus*	Dk1	NNIBR2023642BA51	*Bacillus arachidis*	99.69	Fresh water and soil	Hwaseong-si	YPD	25°C, 2 days
Alphaproteobacteria	*Rhodobacterales*	*Paracoccaceae*	*Tabrizicola*	H356	NNIBR2023642BA11	*Tabrizicola rongguiensis*	99.50	Fresh water and soil	Hwaseong-si	R2A	25°C, 2 days
Alphaproteobacteria	*Sphingomonadales*	*Sphingomonadaceae*	*Sphingorhabdus*	H171	NNIBR2023642BA7	*Sphingorhabdus contaminans*	99.86	Fresh water and soil	Hwaseong-si	R2A	25°C, 2 days
Alphaproteobacteria	*Sphingomonadales*	*Sphingomonadaceae*	*Sphingomonas*	HS051	NNIBR2023642BA28	*Sphingomonas floccifaciens*	98.93	Fresh water and soil	Hoengseong-gun	R2A	25°C, 2 days
Alphaproteobacteria	*Sphingomonadales*	*Sphingomonadaceae*	*Sphingomonas*	HS090	NNIBR2023642BA30	*Sphingomonas piscinae*	99.93	Fresh water and soil	Hoengseong-gun	R2A	25°C, 2 days
Alphaproteobacteria	*Sphingomonadales*	*Sphingomonadaceae*	*Sphingomonas*	HS136	NNIBR2023642BA32	*Sphingomonas arenae*	99.72	Fresh water and soil	Hoengseong-gun	R2A	25°C, 2 days
Alphaproteobacteria	*Sphingomonadales*	*Sphingomonadaceae*	*Sphingobium*	A250	NNIBR2023642BA22	*Sphingobium scionense*	100.00	Fresh water and soil	Anseong-si	R2A	25°C, 2 days
Alphaproteobacteria	*Caulobacterales*	*Caulobacteraceae*	*Phenylobacterium*	W016	NNIBR2023642BA36	*Phenylobacterium soli*	98.86	Fresh water and soil	Wonju-si	R2A	25°C, 2 days
Alphaproteobacteria	*Sphingomonadales*	*Sphingomonadaceae*	*Novosphingobium*	H324	NNIBR2023642BA10	*Novosphingobium fontis*	98.79	Fresh water and soil	Hwaseong-si	R2A	25°C, 2 days
Alphaproteobacteria	*Rhodobacterales*	*Paracoccaceae*	*Neotabrizicola*	H400	NNIBR2023642BA14	*Neotabrizicola shimadae*	99.64	Fresh water and soil	Hwaseong-si	R2A	25°C, 2 days
Alphaproteobacteria	*Hyphomicrobiales*	*Methylobacteriaceae*	*Microvirga*	HS093	NNIBR2023642BA31	*Microvirga solisilvae*	99.07	Fresh water and soil	Hoengseong-gun	R2A	25°C, 2 days
Alphaproteobacteria	*Hyphomicrobiales*	*Phyllobacteriaceae*	*Mesorhizobium*	A283	NNIBR2023642BA24	*Mesorhizobium norvegicum*	100.00	Fresh water and soil	Anseong-si	R2A	25°C, 2 days
Alphaproteobacteria	*Hyphomicrobiales*	*Phyllobacteriaceae*	*Mesorhizobium*	W074	NNIBR2023642BA38	*Mesorhizobium olivaresii*	98.83	Fresh water and soil	Wonju-si	R2A	25°C, 2 days
Alphaproteobacteria	*Sphingomonadales*	*Sphingomonadaceae*	*Chakrabartia*	W052	NNIBR2023642BA37	*Chakrabartia godavariana*	99.79	Fresh water and soil	Wonju-si	R2A	25°C, 2 days

Table 1. Continued.

Class	Order	Family	Genus	Strain ID	NNIBR ID	Most closely related species	Similarity (%)	Isolation source	Isolation site	Medium	Incubation conditions (°C, days)
Actinomycetes	*Kitasatosporales*	*Streptomycetaceae*	*Streptomyces*	H217	NNIBR2023642BA8	*Streptomyces parvulus*	99.86	Fresh water and soil	Hwaseong-si	R2A	25°C, 2 days
Actinomycetes	*Kitasatosporales*	*Streptomycetaceae*	*Streptomyces*	A239	NNIBR2023642BA21	*Streptomyces silvae*	99.93	Fresh water and soil	Anseong-si	R2A	25°C, 2 days
Actinomycetes	*Kitasatosporales*	*Streptomycetaceae*	*Streptomyces*	HS165	NNIBR2023642BA33	*Streptomyces cremeus*	99.31	Fresh water and soil	Hoengseong-gun	R2A	25°C, 2 days
Actinomycetes	*Kitasatosporales*	*Streptomycetaceae*	*Streptomyces*	W082	NNIBR2023642BA40	*Streptomyces coriariae*	99.24	Fresh water and soil	Wonju-si	R2A	25°C, 2 days
Actinomycetes	*Kitasatosporales*	*Streptomycetaceae*	*Streptomyces*	R2ASOYN6	NNIBR2023642BA60	*Streptomyces barringtoniae*	99.6	Fresh water and soil	Wonju-si	R2A	25°C, 2 days
Actinomycetes	*Streptosporangiales*	*Streptosporangiaceae*	*Nonomuraea*	A145	NNIBR2023642BA19	*Nonomuraea spiralis*	98.86	Fresh water and soil	Anseong-si	R2A	25°C, 2 days
Actinomycetes	*Propionibacteriales*	*Nocardioidaceae*	*Nocardioides*	H366	NNIBR2023642BA12	*Nocardioides lacusdianchii*	99.51	Fresh water and soil	Hwaseong-si	R2A	25°C, 2 days
Actinomycetes	*Mycobacteriales*	*Nocardiaceae*	*Nocardia*	BHIDK31	NNIBR2023642BA57	*Nocardia asteroides*	100	Fresh water and soil	Wonju-si	BHI	25°C, 2 days
Actinomycetes	*Mycobacteriales*	*Mycobacteriaceae*	*Mycobacterium*	HS083	NNIBR2023642BA29	*Mycobacterium austroafricanum*	99.16	Fresh water and soil	Hoengseong-gun	R2A	25°C, 2 days
Actinomycetes	*Micromonosporales*	*Micromonosporaceae*	*Micromonospora*	A011	NNIBR2023642BA16	*Micromonospora palomenae*	99.72	Fresh water and soil	Anseong-si	R2A	25°C, 2 days
Actinomycetes	*Micrococcales*	*Micrococcaceae*	*Micrococcus*	H142	NNIBR2023642BA5	*Micrococcus terreus*	100.00	Fresh water and soil	Hwaseong-si	R2A	25°C, 2 days
Actinomycetes	*Micrococcales*	*Microbacteriaceae*	*Microbacterium*	HS173	NNIBR2023642BA34	*Microbacterium gallinarum*	98.96	Fresh water and soil	Hoengseong-gun	R2A	25°C, 2 days
Actinomycetes	*Micromonosporales*	*Micromonosporaceae*	*Catellatospora*	A071	NNIBR2023642BA17	*Catellatospora vulcania*	99.51	Fresh water and soil	Anseong-si	R2A	25°C, 2 days
Actinomycetes	*Micrococcales*	*Micrococcaceae*	*Arthrobacter*	A208	NNIBR2023642BA20	*Arthrobacter wentiniae*	99.93	Fresh water and soil	Anseong-si	R2A	25°C, 2 days

belonging to 8 classes of 4 phyla.

Description of *Micrococcus terreus* H142

Cells are Gram-staining-positive, non-flagellated and coccoid-shaped. Colonies are circular, raised, entire and light yellow-colored after 2 days incubation on R2A at 25°C. In the API 20NE system, positive for gelatin hydrolysis, utilization of D-glucose, D-maltose, potassium gluconate, adipic acid, malic acid, trisodium citrate and phenylacetic acid, but negative for nitrate reduction, indole production, glucose acidification, arginine dihydrolase, urease activity, esculin hydrolysis, β-galactosidase activity, oxidase activity, utilization of L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine and capric acid. Strain H142 (=NNIBR2023642BA5) was isolated from wet soil in Hwaseong-si, Gyeonggi-do, Republic of Korea (37°05′52.2″N 126°55′08.9″E).

Description of *Noviherbaspirillum psychrotolerans* H165

Cells are Gram-staining-negative, non-flagellated and rod-shaped. Colonies are circular, raised, entire and orange-colored after 2 days incubation on R2A at 25°C. In the API 20NE system, positive for oxidase activity, utilization of D-glucose, D-maltose, potassium gluconate, adipic acid and malic acid, but negative for nitrate reduction, indole production, glucose acidification, arginine dihydrolase, urease activity, esculin hydrolysis, gelatin hydrolysis, β-galactosidase activity, utilization of L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, capric acid, trisodium citrate and phenylacetic acid. Strain H165 (=NNIBR2023642BA6) was isolated from wet soil in Hwaseong-si, Gyeonggi-do, Republic of Korea (37°05′52.2″N 126°55′08.9″E).

Description of *Sphingorhabdus contaminans* H171

Cells are Gram-staining-negative, flagellated and rod-shaped. Colonies are circular, raised, entire and yellow-colored after 2 days incubation on R2A at 25°C. In the API 20NE system, positive for β-galactosidase activity and oxidase activity, but negative for nitrate reduction, indole production, glucose acidification, arginine dihydrolase, urease activity, esculin hydrolysis, gelatin hydrolysis, utilization of D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. Strain H171 (=NNIBR2023642BA7) was isolated from wet soil in Hwaseong-si, Gyeonggi-do, Republic of Korea (37°09′38.5″N 126°50′01.3″E).

Description of *Streptomyces parvulus* H217

Cells are Gram-staining-positive, non-flagellated and fila-

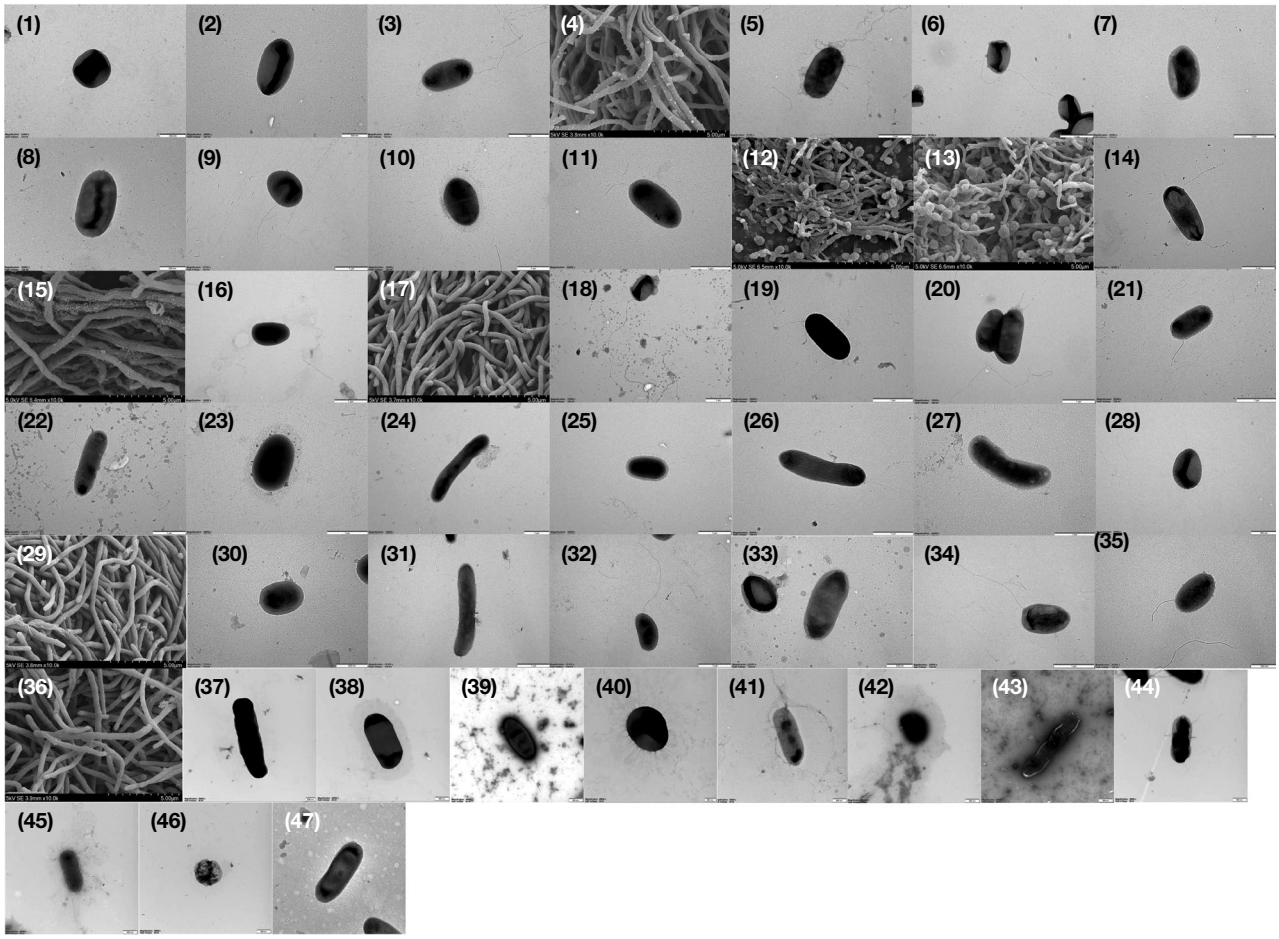


Fig. 1. Transmission and scanning electron micrographs of cells of the strains isolated in this study. Strains: 1, H142; 2, H165; 3, H171; 4, H217; 5, H268; 6, H324; 7, H356; 8, H366; 9, H395; 10, H400; 11, H428; 12, A011; 13, A071; 14, A092; 15, A145; 16, A208; 17, A239; 18, A250; 19, A257; 20, A283; 21, HS009; 22, HS027; 23, HS040; 24, HS051; 25, HS083; 26, HS090; 27, HS093; 28, HS136; 29, HS165; 30, HS173; 31, HS207; 32, W016; 33, W052; 34, W074; 35, W076; 36, W082; 37, K77; 38, Dk1; 39, NBDL15; 40, TBS-Won-1; 41, R2A-P31; 42, BHI-u-3; 43, BHIDKJ23; 44, BHIDK31; 45, ol5; 46, ru14; 47, R2ASOYN6.

mentous-shaped. Colonies are filamentous, umbonate and ivory-colored after 2 days incubation on R2A at 25°C. In the API 20NE system, positive for urease activity, esculin hydrolysis, β-galactosidase activity, utilization of D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, potassium gluconate, adipic acid, malic acid and trisodium citrate, but negative for nitrate reduction, indole production, glucose acidification, arginine dihydrolase, gelatin hydrolysis, oxidase activity, utilization of capric acid and phenylacetic acid. Strain H217 (=NNIBR2023642BA8) was isolated from wet soil in Hwaseong-si, Gyeonggi-do, Republic of Korea (37°08′ 51.0″N 126°51′56.2″E).

Description of *Jeotgalibacillus proteolyticus* H268

Cells are Gram-staining-positive, non-flagellated and rod-shaped. Colonies are circular, convex, entire and yellow-colored after 2 days incubation on TSA at 25°C. In the API 20NE system, positive for esculin hydrolysis, β-galactosidase activity, utilization of D-glucose, potassium gluconate, malic acid and trisodium citrate, but negative for nitrate reduction, indole production, glucose acidification, arginine dihydrolase, urease activity, gelatin hydrolysis, oxidase activity, utilization of L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, capric acid, adipic acid and phenylacetic acid. Strain H268 (=NNIBR2023642BA9) was isolated from wet soil in Hwaseong-si, Gyeonggi-do, Republic of Korea (37°08′ 51.0″N 126°51′56.2″E).

Description of *Novosphingobium fontis* H324

Cells are Gram-staining-negative, flagellated and oval-shaped. Colonies are circular, flat, entire and light yellow-colored after 2 days incubation on R2A at 25°C. In the

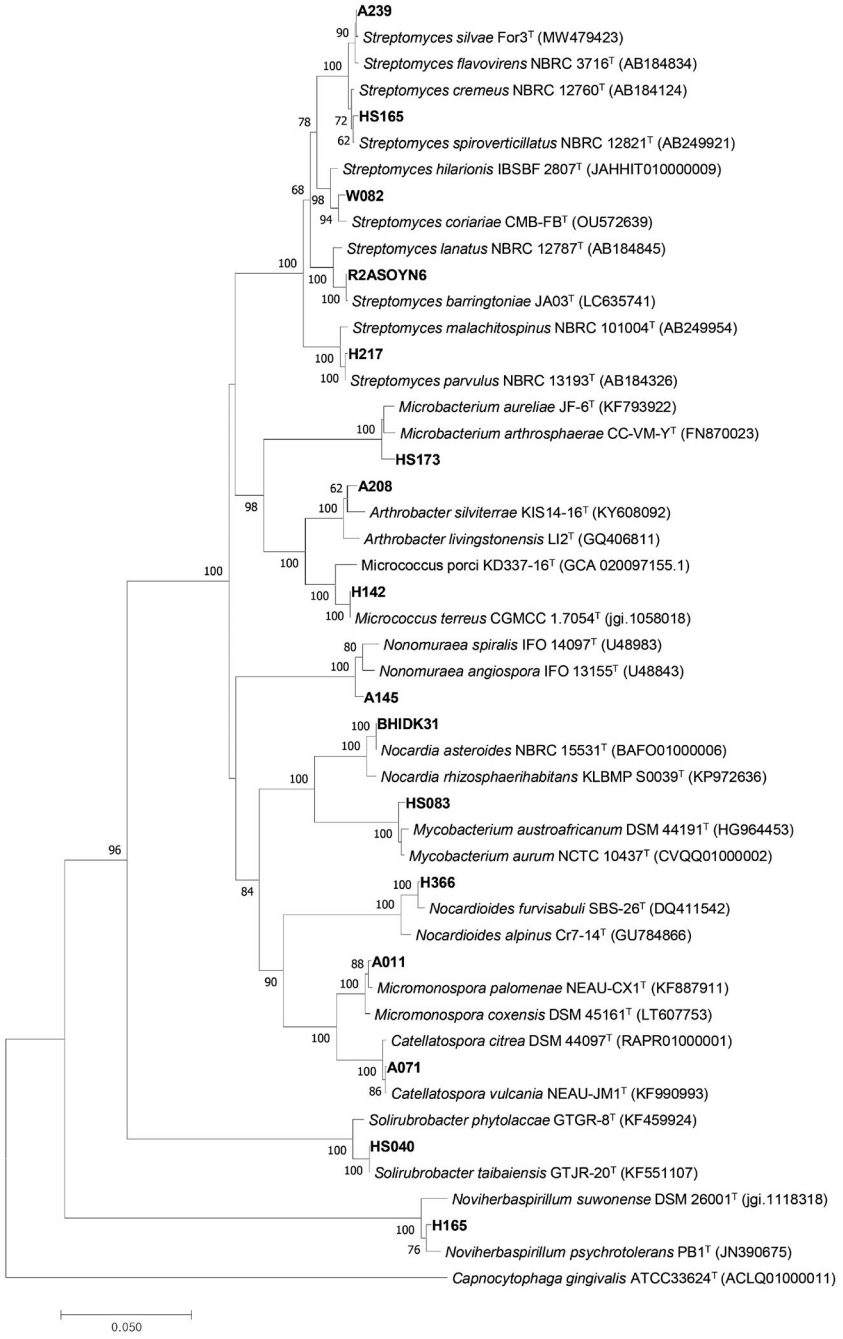


Fig. 2. Neighbor-joining phylogenetic tree, based on 16S rRNA gene sequences, showing the relationship between the strains in the phylum *Actinomycetota*. Bootstrap values (>60%) based on 1,000 replications are shown in the neighbor-joining method. Bar, 0.02 substitutions per nucleotide position.

API 20NE system, positive for nitrate reduction, esculin hydrolysis, β-galactosidase activity, oxidase activity, utilization of L-arabinose, D-mannitol, malic acid and trisodium citrate, but negative for indole production, glucose acidification, arginine dihydrolase, urease activity, gelatin hydrolysis, utilization of D-glucose, D-mannose, *N*-acetyl-D-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid and phenylacetic acid. Strain H324 (=NNIBR2023642BA10) was isolated from wet soil in Hwaseong-si, Gyeonggi-do, Republic of Korea (37°08′ 51.0″N 126°51′56.2″E).

Description of *Tabrizicola rongguiensis* H356

Cells are Gram-staining-negative, non-flagellated and

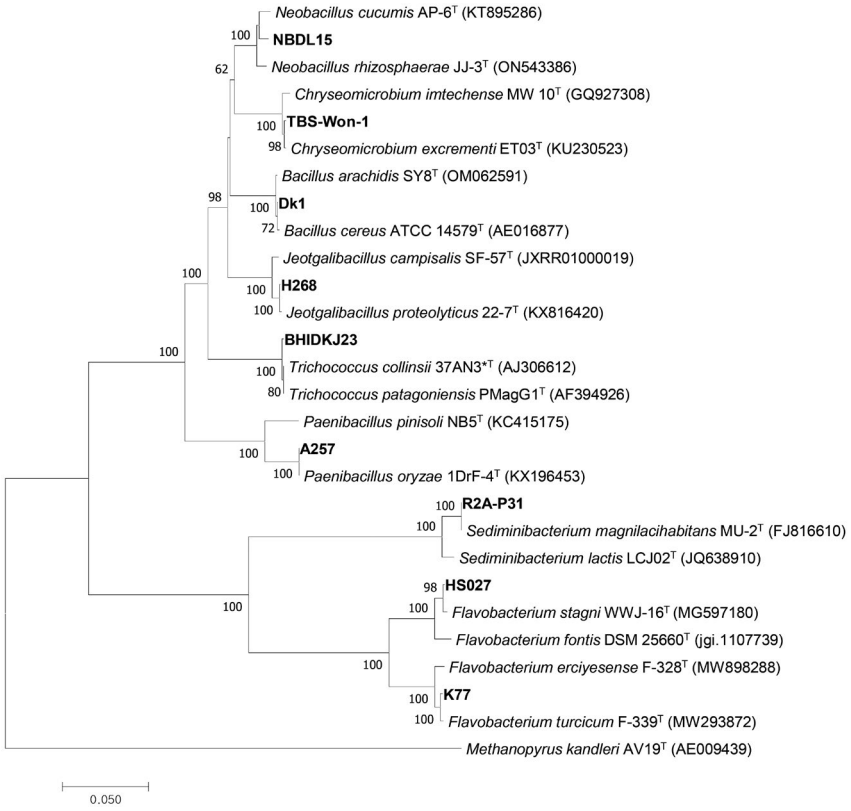


Fig. 3. Neighbor-joining phylogenetic tree, based on 16S rRNA gene sequences, showing the relationship between the strains in the phylum *Pseudomonadota*. Bootstrap values (>60%) based on 1,000 replications are shown in the neighbor-joining method. Bar, 0.02 substitutions per nucleotide position.

rod-shaped. Colonies are circular, convex, entire and ivory-colored after 2 days incubation on R2A at 25°C. In the API 20NE system, positive for nitrate reduction, esculin hydrolysis, β-galactosidase activity, oxidase activity, utilization of D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose and malic acid, but negative for indole production, glucose acidification, arginine dihydrolase, urease activity, gelatin hydrolysis, utilization of potassium gluconate, capric acid, adipic acid, trisodium citrate and phenylacetic acid. Strain H356 (=NNIBR2023642BA11) was isolated from wet soil in Hwaseong-si, Gyeonggi-do, Republic of Korea (37°10′27.8″N 126°52′09.8″E).

Description of *Nocardioides lacusdianchii* H366

Cells are Gram-staining-positive, non-flagellated and rod-shaped. Colonies are circular, flat, entire and ivory-colored after 2 days incubation on R2A at 25°C. In the API 20NE system, positive for esculin hydrolysis, β-galactosidase activity, utilization of D-glucose, L-arabinose, D-mannitol, D-maltose, potassium gluconate and malic acid, but negative for nitrate reduction, indole production, glucose acidification, arginine dihydrolase, urease activity, gelatin hydrolysis, oxidase activity, utilization of D-mannose, *N*-acetyl-D-glucosamine, capric acid, adipic acid, trisodium citrate and phenylacetic acid. Strain H366 (=NNIBR 2023642BA12) was isolated from wet soil in Hwaseong-si, Gyeonggi-do, Republic of Korea (37°10′27.8″N 126°52 09.8″E).

Description of *Pseudomonas farris* H395

Cells are Gram-staining-negative, flagellated and rod-shaped. Colonies are circular, convex, entire and cream-colored after 2 days incubation on R2A at 25°C. In the API 20NE system, positive for glucose acidification, arginine dihydrolase, oxidase activity, utilization of D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, potassium gluconate, capric acid, malic acid and trisodium citrate, but negative for nitrate reduction, indole production, urease activity, esculin hydrolysis, gelatin hydrolysis, β-galactosidase activity, utilization of D-maltose, adipic acid and phenylacetic acid. Strain H395 (=NNIBR 2023642BA13) was isolated from wet soil in Hwaseong-si, Gyeonggi-do, Republic of Korea (37°10′27.8″N 126°52′ 09.8″E).

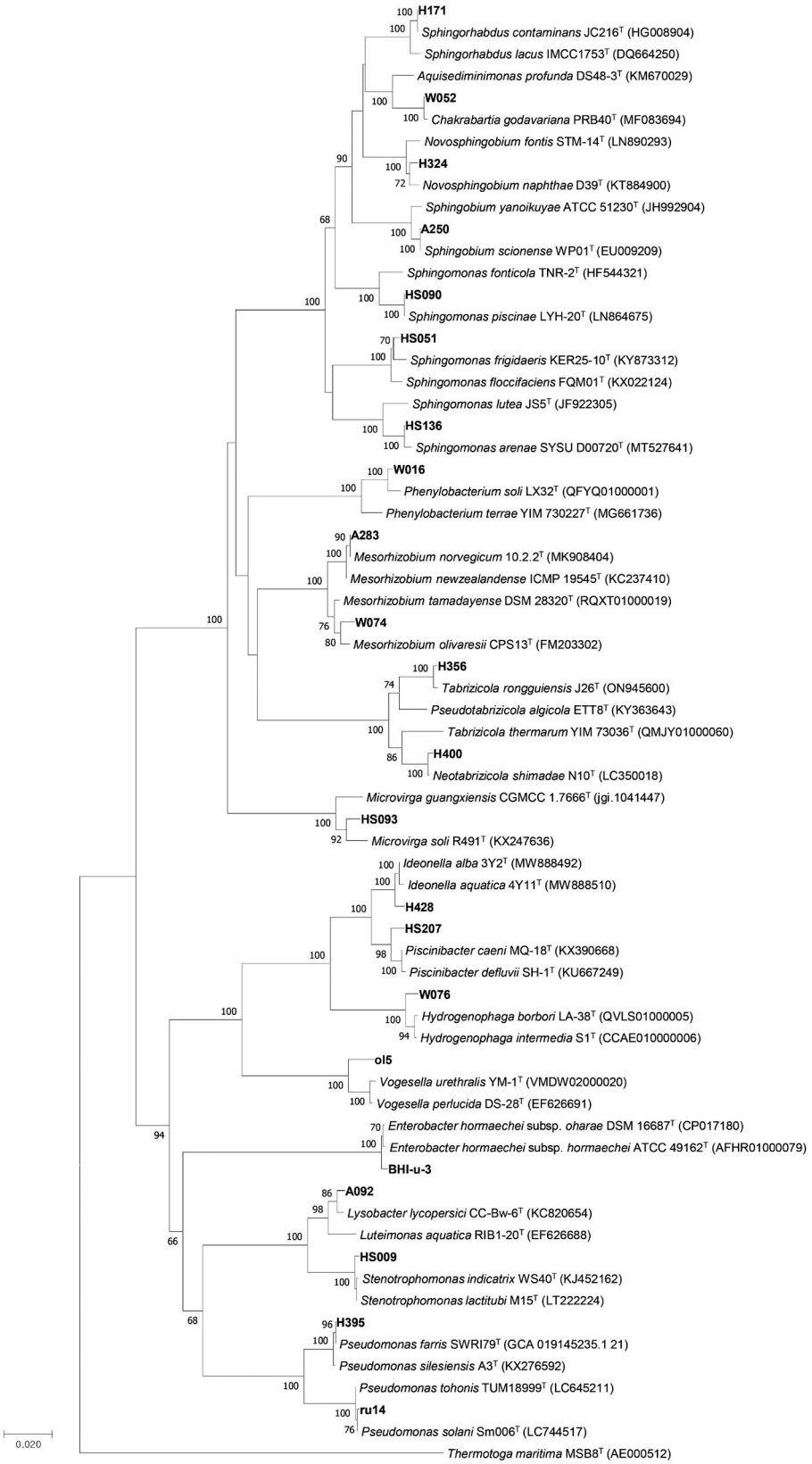


Fig. 4. Neighbor-joining phylogenetic tree, based on 16S rRNA gene sequences, showing the relationship between the strains in the phylum *Bacillota* and *Bacteroidota*. Bootstrap values (>60%) based on 1,000 replications are shown in the neighbor-joining method. Bar, 0.02 substitutions per nucleotide position.

Description of *Neotabrizicola shimadae* H400

Cells are Gram-staining-negative, non-flagellated and rod-shaped. Colonies are circular, raised, entire and ivory-colored after 2 days incubation on R2A at 25°C. In the API 20NE system, positive for esculin hydrolysis, β-galactosidase activity, oxidase activity, utilization of D-glucose, L-arabinose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose and potassium gluconate, but negative for nitrate reduction, indole production, glucose acidification, arginine dihydrolase, urease activity, gelatin hydrolysis, utilization of D-mannose, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. Strain H400 (=NNIBR 2023642BA14) was isolated from wet soil in Hwaseong-si, Gyeonggi-do, Republic of Korea (37°05′52.2″N 126° 55′08.9″E).

Description of *Ideonella alba* H428

Cells are Gram-staining-negative, flagellated and rod-shaped. Colonies are circular, raised, entire and ivory-colored after 2 days incubation on R2A at 25°C. In the API 20NE system, positive for esculin hydrolysis, oxidase activity and utilization of potassium gluconate, but negative for nitrate reduction, indole production, glucose acidification, arginine dihydrolase, urease activity, gelatin hydrolysis, β-galactosidase activity, utilization of D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. Strain H428 (=NNIBR2023642BA15) was isolated from wet soil in Hwaseong-si, Gyeonggi-do, Republic of Korea (37°09′ 38.5″N 126°50′01.3″E).

Description of *Micromonospora palomenae* A011

Cells are Gram-staining-positive, non-flagellated and Spherical to oval-shaped. Colonies are filamentous, umbonate and orange-colored after 2 days incubation on R2A at 25°C. In the API 20NE system, positive for nitrate reduction, esculin hydrolysis, β-galactosidase activity, utilization of D-glucose, D-mannose and D-maltose, but negative for indole production, glucose acidification, arginine dihydrolase, urease activity, gelatin hydrolysis, oxidase activity, utilization of L-arabinose, D-mannitol, *N*-acetyl-D-glucosamine, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. Strain A011 (=NNIBR2023642BA16) was isolated from wet soil in Anseong-si, Gyeonggi-do, Republic of Korea (37°03′40.7″N 127°08′43.5″E).

Description of *Catellatospora vulcania* A071

Cells are Gram-staining-positive, non-flagellated and Spherical to oval-shaped. Colonies are filamentous, umbonate and yellow-colored after 2 days incubation on R2A at 25°C. In the API 20NE system, positive for esculin hydrolysis, gelatin hydrolysis, β-galactosidase activity, utilization of D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, potassium gluconate and adipic acid, but negative for nitrate reduction, indole production, glucose acidification, arginine dihydrolase, urease activity, oxidase activity, utilization of capric acid, malic acid, trisodium citrate and phenylacetic acid. Strain A071 (=NNIBR2023642BA17) was isolated from wet soil in Anseong-si, Gyeonggi-do, Republic of Korea (37°03′40.7″N 127°08′43.5″E).

Description of *Lysobacter lycopersici* A092

Cells are Gram-staining-negative, flagellated and rod-shaped. Colonies are circular, flat, entire and light yellow-colored after 2 days incubation on R2A at 25°C. In the API 20NE system, positive for nitrate reduction and oxidase activity, but negative for indole production, glucose acidification, arginine dihydrolase, urease activity, esculin hydrolysis, gelatin hydrolysis, β-galactosidase activity, utilization of D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. Strain A092 (=NNIBR2023642BA18) was isolated from wet soil in Anseong-si, Gyeonggi-do, Republic of Korea (37°03′40.7″N 127°08′43.5″E).

Description of *Nonomuraea spiralis* A145

Cells are Gram-staining-positive, non-flagellated and filamentous-shaped. Colonies are filamentous, umbonate and light pink-colored after 2 days incubation on R2A at 25°C. In the API 20NE system, positive for esculin hydrolysis, β-galactosidase activity, utilization of D-glucose, L-arabinose, D-mannose, *N*-acetyl-D-glucosamine, D-maltose and malic acid, but negative for nitrate reduction, indole production, glucose acidification, arginine dihydrolase, urease activity, gelatin hydrolysis, oxidase activity, utilization of D-mannitol, potassium gluconate, capric acid, adipic acid, trisodium citrate and phenylacetic acid. Strain A145 (=NNIBR2023642BA19) was isolated from wet soil in Anseong-si, Gyeonggi-do, Republic of Korea (37°4′15.50″N 127°10′2.8″E).

Description of *Arthrobacter wenxiniae* A208

Cells are Gram-staining-positive, non-flagellated and rod-shaped. Colonies are circular, convex, entire and light green-colored after 2 days incubation on R2A at 25°C. In the API 20NE system, positive for nitrate reduction, urease activity, esculin hydrolysis, β-galactosidase activity, utilization of D-glucose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, potassium gluconate, malic acid, trisodium citrate and phenylacetic acid, but negative

for indole production, glucose acidification, arginine dihydrolase, gelatin hydrolysis, oxidase activity, utilization of L-arabinose, capric acid and adipic acid. Strain A208 (=NNIBR2023642BA20) was isolated from wet soil in Anseong-si, Gyeonggi-do, Republic of Korea (37°4′15.50″N 127°10′2.8″E).

Description of *Streptomyces silvae* A239

Cells are Gram-staining-positive, non-flagellated and filamentous-shaped. Colonies are filamentous, umbonate and light brown-colored after 2 days incubation on R2A at 25°C. In the API 20NE system, positive for nitrate reduction, esculin hydrolysis, gelatin hydrolysis, β-galactosidase activity, utilization of D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, potassium gluconate and adipic acid, but negative for indole production, glucose acidification, arginine dihydrolase, urease activity, oxidase activity, utilization of D-maltose, capric acid, malic acid, trisodium citrate and phenylacetic acid. Strain A239 (=NNIBR2023642BA21) was isolated from wet soil in Anseong-si, Gyeonggi-do, Republic of Korea (37°4′15.50″N 127°10′2.8″E).

Description of *Sphingobium scionense* A250

Cells are Gram-staining-negative, flagellated and rod-shaped. Colonies are circular, raised, entire and light yellow-colored after 2 days incubation on R2A at 25°C. In the API 20NE system, positive for nitrate reduction, esculin hydrolysis, β-galactosidase activity, utilization of D-glucose, L-arabinose, *N*-acetyl-D-glucosamine, D-maltose, potassium gluconate and malic acid, but negative for indole production, glucose acidification, arginine dihydrolase, urease activity, gelatin hydrolysis, oxidase activity, utilization of D-mannose, D-mannitol, capric acid, adipic acid, trisodium citrate and phenylacetic acid. Strain A250 (=NNIBR2023642BA22) was isolated from wet soil in Anseong-si, Gyeonggi-do, Republic of Korea (37°03′40.7″N 127°08′43.5″E).

Description of *Paenibacillus oryzae* A257

Cells are Gram-staining-positive, flagellated and rod-shaped. Colonies are circular, raised, entire and white-colored after 2 days incubation on R2A at 25°C. In the API 20NE system, positive for nitrate reduction, esculin hydrolysis, β-galactosidase activity, oxidase activity, utilization of L-arabinose, D-mannose and D-maltose, but negative for indole production, glucose acidification, arginine dihydrolase, urease activity, gelatin hydrolysis, utilization of D-glucose, D-mannitol, *N*-acetyl-D-glucosamine, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. Strain A257 (=NNIBR 2023642BA23) was isolated from wet soil in Anseong-si, Gyeonggi-do, Republic of Korea (37°03′40.7″N 127°08′43.5″E).

Description of *Mesorhizobium norvegicum* A283

Cells are Gram-staining-negative, non-flagellated and rod-shaped. Colonies are circular, convex, entire and cream-colored after 2 days incubation on R2A at 25°C. In the API 20NE system, positive for glucose acidification, urease activity, esculin hydrolysis, oxidase activity, utilization of D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, potassium gluconate and malic acid, but negative for nitrate reduction, indole production, arginine dihydrolase, gelatin hydrolysis, β-galactosidase activity, utilization of capric acid, adipic acid, trisodium citrate and phenylacetic acid. Strain A283 (=NNIBR2023642BA24) was isolated from wet soil in Anseong-si, Gyeonggi-do, Republic of Korea (37°02′46.5″N 127°09′05.0″E).

Description of *Stenotrophomonas cyclobalanopsidis* HS009

Cells are Gram-staining-positive, flagellated and rod-shaped. Colonies are circular, flat, entire and light yellow-green-colored after 2 days incubation on R2A at 25°C. In the API 20NE system, positive for esculin hydrolysis, gelatin hydrolysis, β-galactosidase activity, oxidase activity, utilization of D-glucose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, malic acid and trisodium citrate, but negative for nitrate reduction, indole production, glucose acidification, arginine dihydrolase, urease activity, utilization of L-arabinose, potassium gluconate, capric acid, adipic acid and phenylacetic acid. Strain HS009 (=NNIBR 2023642BA25) was isolated from wet soil in Hoengseong-gun, Gangwon-do, Republic of Korea (37°28′38.8″N 128°00′33.9″E).

Description of *Flavobacterium stagni* HS027

Cells are Gram-staining-negative, non-flagellated and rod-shaped. Colonies are circular, raised, entire and yellow-colored after 2 days incubation on R2A at 25°C. In the API 20NE system, positive for esculin hydrolysis, oxidase activity, utilization of D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid but negative for nitrate reduction, indole production, glucose acidification, arginine dihydrolase, urease activity, gelatin hydrolysis and β-galactosidase activity. Strain HS027 (=NNIBR 2023642BA26) was isolated from wet soil in Hoengseong-gun, Gangwon-do, Republic of Korea (37°28′38.8″N 128°00′33.9″E).

Description of *Solirubrobacter taibaiensis* HS040

Cells are Gram-staining-positive, non-flagellated and rod-shaped. Colonies are circular, raised, entire and white-colored after 2 days incubation on R2A at 25°C. In the API 20NE system, positive for arginine dihydrolase, urease activity, oxidase activity and utilization of trisodium citrate, but negative for nitrate reduction, indole production, glucose acidification, esculin hydrolysis, gelatin hydrolysis, β-galactosidase activity, utilization of D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid and phenylacetic acid. Strain HS040 (=NNIBR2023642BA27) was isolated from wet soil in Hoengseong-gun, Gangwon-do, Republic of Korea (37°29′26.9″N 127°59′48.0″E).

Description of *Sphingomonas floccifaciens* HS051

Cells are Gram-staining-negative, flagellated and rod-shaped. Colonies are circular, raised, entire and yellow-colored after 2 days incubation on R2A at 25°C. In the API 20NE system, positive for esculin hydrolysis, β-galactosidase activity, oxidase activity, utilization of D-mannose, *N*-acetyl-D-glucosamine, D-maltose and trisodium citrate, but negative for nitrate reduction, indole production, glucose acidification, arginine dihydrolase, urease activity, gelatin hydrolysis, utilization of D-glucose, L-arabinose, D-mannitol, potassium gluconate, capric acid, adipic acid, malic acid and phenylacetic acid. Strain HS051 (=NNIBR 2023642BA28) was isolated from wet soil in Hoengseong-gun, Gangwon-do, Republic of Korea (37°29′13.2″N 128°01′27.8″E).

Description of *Mycobacterium austroafricanum* HS083

Cells are Gram-staining-positive, non-flagellated and rod-shaped. Colonies are circular, raised, entire and light orange-colored after 2 days incubation on R2A at 25°C. In the API 20NE system, positive for nitrate reduction, glucose acidification, urease activity, utilization of D-glucose, D-mannitol, malic acid and trisodium citrate, but negative for indole production, arginine dihydrolase, esculin hydrolysis, gelatin hydrolysis, β-galactosidase activity, utilization of L-arabinose, D-mannose, *N*-acetyl-D-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid and phenylacetic acid. Strain HS083 (=NNIBR2023 642BA29) was isolated from wet soil in Hoengseong-gun, Gangwon-do, Republic of Korea (37°29′13.2″N 128°01′27.8″E).

Description of *Sphingomonas piscinae* HS090

Cells are Gram-staining-negative, flagellated and rod-shaped. Colonies are circular, raised, entire and yellow-colored after 2 days incubation on R2A at 25°C. In the API 20NE system, positive for esculin hydrolysis, β-galactosidase activity, oxidase activity, utilization of D-glucose, D-maltose and trisodium citrate, but negative for nitrate reduction, indole production, glucose acidification, arginine dihydrolase, urease activity, gelatin hydrolysis, utilization of L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, potassium gluconate, capric acid, adipic acid, malic acid and phenylacetic acid. Strain HS090 (=NNIBR2023642BA30) was isolated from wet soil in Hoengseong-gun, Gangwon-do, Republic of Korea (37°29′13.2″N 128°01′27.8″E).

Description of *Microvirga solisilvae* HS093

Cells are Gram-staining-negative, flagellated and rod-shaped. Colonies are circular, flat, entire and light pink-colored after 4 days incubation on R2A at 25°C. In the API 20NE system, positive for nitrate reduction, indole production, glucose acidification, arginine dihydrolase, urease activity, esculin hydrolysis, gelatin hydrolysis and β-galactosidase activity, but negative for oxidase activity, utilization of D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. Strain HS093 (=NNIBR2023642BA 31) was isolated from wet soil in Hoengseong-gun, Gangwon-do, Republic of Korea (37°29′13.2″N 128°01′27.8″E).

Description of *Sphingomonas arenae* HS136

Cells are Gram-staining-negative, non-flagellated and oval-shaped. Colonies are circular, raised, entire and orange-colored after 2 days incubation on R2A at 25°C. In the API 20NE system, positive for nitrate reduction, indole production, glucose acidification, arginine dihydrolase, urease activity, esculin hydrolysis, gelatin hydrolysis and β-galactosidase activity, but negative for oxidase activity, utilization of D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. Strain HS136 (=NNIBR 2023642BA32) was isolated from wet soil in Hoengseong-gun, Gangwon-do, Republic of Korea (37°29′41.4″N 128°01′34.1″E).

Description of *Streptomyces cremeus* HS165

Cells are Gram-staining-positive, non-flagellated and filamentous-shaped. Colonies are filamentous, umbonate and ivory-colored after 2 days incubation on R2A at 25°C. In the API 20NE system, positive for nitrate reduction, urease activity, esculin hydrolysis, β-galactosidase activity, oxidase activity, utilization of D-glucose, L-arabinose,

D-mannose, *N*-acetyl-D-glucosamine, D-maltose, potassium gluconate, adipic acid, malic acid and phenylacetic acid, but negative for indole production, glucose acidification, arginine dihydrolase, gelatin hydrolysis, utilization of D-mannitol, capric acid and trisodium citrate. Strain HS165 (=NNIBR2023642BA33) was isolated from wet soil in Hoengseong-gun, Gangwon-do, Republic of Korea (37°29′41.4″N 128°01′34.1″E).

Description of *Microbacterium gallinarum* HS173

Cells are Gram-staining-positive, non-flagellated and oval-shaped. Colonies are circular, raised, entire and yellow-colored after 2 days incubation on R2A at 25°C. In the API 20NE system, positive for esculin hydrolysis, β-galactosidase activity, utilization of D-glucose, D-mannose, D-mannitol, D-maltose, potassium gluconate and malic acid, but negative for nitrate reduction, indole production, glucose acidification, arginine dihydrolase, urease activity, gelatin hydrolysis, oxidase activity, utilization of L-arabinose, *N*-acetyl-D-glucosamine, capric acid, adipic acid, trisodium citrate and phenylacetic acid. Strain HS173 (=NNIBR2023642BA34) was isolated from wet soil in Hoengseong-gun, Gangwon-do, Republic of Korea (37°29′41.4″N 128°01′34.1″E).

Description of *Piscinibacter caeni* HS207

Cells are Gram-staining-negative, flagellated and rod-shaped. Colonies are circular, raised, entire and white-colored after 2 days incubation on R2A at 25°C. In the API 20NE system, positive for nitrate reduction, esculin hydrolysis, gelatin hydrolysis, β-galactosidase activity, oxidase activity, utilization of D-glucose, L-arabinose, D-mannose and D-mannitol, but negative for indole production, glucose acidification, arginine dihydrolase, urease activity, utilization of *N*-acetyl-D-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. Strain HS207 (=NNIBR 2023642BA35) was isolated from wet soil in Hoengseong-gun, Gangwon-do, Republic of Korea (37°29′41.4″N 128° 01′34.1″E).

Description of *Phenylobacterium soli* W016

Cells are Gram-staining-negative, flagellated and rod-shaped. Colonies are circular, flat, entire and white-colored after 2 days incubation on R2A at 25°C. In the API 20NE system, positive for nitrate reduction, urease activity, utilization of L-arabinose, *N*-acetyl-D-glucosamine, D-maltose, malic acid and phenylacetic acid, but negative for indole production, glucose acidification, arginine dihydrolase, esculin hydrolysis, gelatin hydrolysis, β-galactosidase activity, oxidase activity, utilization of D-glucose, D-mannose, D-mannitol, potassium gluconate, capric acid, adipic acid and trisodium citrate. Strain W016 (=NNIBR2023 642BA36) was isolated from wet soil in Wonju-si, Gangwon-do, Republic of Korea (37°24′49.0″N 127°58′20.5″E).

Description of *Chakrabartia godavariana* W052

Cells are Gram-staining-negative, flagellated and rod-shaped. Colonies are circular, raised, entire and yellow-colored after 2 days incubation on R2A at 25°C. In the API 20NE system, positive for oxidase activity and utilization of *N*-acetyl-D-glucosamine, but negative for nitrate reduction, indole production, glucose acidification, arginine dihydrolase, urease activity, esculin hydrolysis, gelatin hydrolysis, β-galactosidase activity, utilization of D-glucose, L-arabinose, D-mannose, D-mannitol, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. Strain W052 (=NNIBR2023642BA37) was isolated from wet soil in Wonju-si, Gangwon-do, Republic of Korea (37°24′49.0″N 127°58′20.5″E).

Description of *Mesorhizobium olivaresii* W074

Cells are Gram-staining-negative, flagellated and rod-shaped. Colonies are circular, raised, entire and white-colored after 2 days incubation on R2A at 25°C. In the API 20NE system, positive for urease activity, esculin hydrolysis, β-galactosidase activity, oxidase activity, utilization of D-glucose, L-arabinose, D-mannose, D-mannitol and D-maltose, but negative for nitrate reduction, indole production, glucose acidification, arginine dihydrolase, gelatin hydrolysis, utilization of *N*-acetyl-D-glucosamine, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. Strain W074 (=NNIBR 2023642BA38) was isolated from wet soil in Wonju-si, Gangwon-do, Republic of Korea (37°24′49.0″N 127°58′ 20.5″E).

Description of *Hydrogenophaga crocea* W076

Cells are Gram-staining-negative, flagellated and rod-shaped. Colonies are circular, raised, entire and cream-colored after 2 days incubation on R2A at 25°C. In the API 20NE system, positive for oxidase activity, utilization of D-glucose and potassium gluconate, but negative for nitrate reduction, indole production, glucose acidification, arginine dihydrolase, urease activity, esculin hydrolysis, gelatin hydrolysis, β-galactosidase activity, utilization of L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. Strain W076 (=NNIBR2023642BA39) was isolated from wet soil in Wonju-si, Gangwon-do, Republic of Korea (37°26′30.9″N 128°03′14.4″E).

Description of *Streptomyces coriariae* W082

Cells are Gram-staining-positive, non-flagellated and filamentous-shaped. Colonies are filamentous, umbonate and gray-colored after 2 days incubation on R2A at 25°C. In the API 20NE system, positive for esculin hydrolysis, β-galactosidase activity, utilization of D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, potassium gluconate, adipic acid, malic acid and trisodium citrate, but negative for nitrate reduction, indole production, glucose acidification, arginine dihydrolase, urease activity, gelatin hydrolysis, oxidase activity, utilization of capric acid and phenylacetic acid. Strain W082 (=NNIBR2023642BA40) was isolated from wet soil in Wonju-si, Gangwon-do, Republic of Korea (37°26′30.9″N 128°03′14.4″E).

Description of *Flavobacterium turcicum* K77

Cells are Gram-staining-negative, non-flagellated and rod-shaped. Colonies are circular, convex, entire and yellow-colored after 2 days incubation on R2A at 25°C. In the API 20NE system, positive for esculin hydrolysis, oxidase, utilization of D-glucose, D-mannose and D-maltose, but negative for nitrate reduction, indole production, glucose acidification, arginine dihydrolase, urease activity, gelatin hydrolysis, β-galactosidase activity, utilization of L-arabinose, D-mannitol, *N*-acetyl-D-glucosamine, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. Strain K77 (=NNIBR 2021642BA16) was isolated from fresh water in Anseong-si, Gyeonggi-do, Republic of Korea (36°59′09.0″N 127° 20′03.8″E).

Description of *Bacillus arachidis* Dk1

Cells are Gram-staining-positive, non-flagellated and rod-shaped. Colonies are circular, convex, entire and cream-colored after 2 days incubation on YPD at 25°C. In the API 20NE system, positive for nitrate reduction, gelatin hydrolysis, utilization of D-glucose, *N*-acetyl-D-glucosamine, D-maltose, potassium gluconate and malic acid, but negative for indole production, glucose acidification, arginine dihydrolase, urease activity, esculin hydrolysis, β-galactosidase activity, oxidase activity, utilization of L-arabinose, D-mannose, D-mannitol, capric acid, adipic acid, trisodium citrate and phenylacetic acid. Strain Dk1 (=NNIBR2023642BA51) was isolated from wet soil in Hwaseong-si, Gyeonggi-do, Republic of Korea (37°10′ 27.8″N 126°52′09.8″E).

Description of *Neobacillus rhizosphaerae* NBDL15

Cells are Gram-staining-positive, non-flagellated and rod-shaped. Colonies are circular, convex, entire and beige-colored after 2 days incubation on NA at 25°C. In the API 20NE system, positive for esculin hydrolysis, gelatin hydrolysis, β-galactosidase activity, oxidase activity, utilization of D-glucose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, potassium gluconate, malic acid and phenylacetic acid, but negative for nitrate reduction, indole production, glucose acidification, arginine dihydrolase, urease activity, utilization of L-arabinose, D-mannose, capric acid, adipic acid and trisodium citrate. Strain NBDL15 (=NNIBR2023642BA52) was isolated from wet soil in Hwaseong-si, Gyeonggi-do, Republic of Korea (37°09′38.5″N 126°50′01.3″E).

Description of *Chryseomicrobium excrementi* TBS-Won-1

Cells are Gram-staining-positive, non-flagellated and rod-shaped. Colonies are circular, raised, entire and yellow-colored after 2 days incubation on TSA at 25°C. In the API 20NE system, positive for gelatin hydrolysis, utilization of D-glucose, D-maltose and malic acid, but negative for nitrate reduction, indole production, glucose acidification, arginine dihydrolase, urease activity, esculin hydrolysis, β-galactosidase activity, oxidase activity, utilization of L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, potassium gluconate, capric acid, adipic acid, trisodium citrate and phenylacetic acid. Strain TBS-Won-1 (=NNIBR2023642BA53) was isolated from wet soil in Hwaseong-si, Gyeonggi-do, Republic of Korea (37°08′51.0″N 126°51′56.2″E).

Description of *Sediminibacterium magnilacihabitans* R2A-P31

Cells are Gram-staining-negative, non-flagellated and coccoid-shaped. Colonies are circular, raised, entire and beige-colored after 2 days incubation on TSA at 25°C. In the API 20NE system, positive for nitrate reduction, oxidase activity, but negative for indole production, glucose acidification, arginine dihydrolase, β-galactosidase activity, urease activity, esculin hydrolysis, gelatin hydrolysis utilization of D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. Strain R2A-P31 (=NNIBR 2023642BA54) was isolated from wet soil in Anseong-si, Gyeonggi-do, Republic of Korea (37°03′40.7″N 127° 08′43.5″E).

Description of *Enterobacter hormaechei* subsp. *oharae* BHI-u-3

Cells are Gram-staining-negative, flagellated and rod-shaped. Colonies are irregular, umbonate and light yellow-colored after 2 days incubation on BHI at 25°C. In the API 20NE system, positive for nitrate reduction, glucose acid-

ification, arginine dihydrolase, β-galactosidase activity, utilization of D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, potassium gluconate, malic acid, trisodium citrate and phenylacetic acid, but negative for indole production, urease activity, esculin hydrolysis, gelatin hydrolysis, oxidase activity, utilization of capric acid and adipic acid. Strain BHI-u-3 (=NNIBR 2023642BA55) was isolated from wet soil in Hoengseong-gun, Gangwon-do, Republic of Korea (37°28′38.8″N 128° 00′33.9″E).

Description of *Trichococcus collinsii* BHIDKJ23

Cells are Gram-staining-positive, non-flagellated and coccoid-shaped. Colonies are circular, raised, entire and light yellow-colored after 2 days incubation on BHI at 25°C. In the API 20NE system, positive for esculin hydrolysis, β-galactosidase activity, utilization of *N*-acetyl-D-glucosamine, adipic acid and malic acid, but negative for nitrate reduction, indole production, glucose acidification, arginine dihydrolase, urease activity, gelatin hydrolysis, oxidase activity, utilization of D-glucose, L-arabinose, D-mannose, D-mannitol, D-maltose, potassium gluconate, capric acid, trisodium citrate and phenylacetic acid. Strain BHIDKJ23 (=NNIBR2023642BA56) was isolated from wet soil in Hoengseong-gun, Gangwon-do, Republic of Korea (37°29′13.2″N 128°01′27.8″E).

Description of *Nocardia asteroides* BHIDK31

Cells are Gram-staining-positive, non-flagellated and rod-shaped. Colonies are filamentous, umbonate, lobate and yellow-colored after 2 days incubation on BHI at 25°C. In the API 20NE system, positive for nitrate reduction, utilization of D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, potassium gluconate, adipic acid, malic acid and trisodium citrate, but negative for indole production, glucose acidification, arginine dihydrolase, urease activity, esculin hydrolysis, gelatin hydrolysis, β-galactosidase activity, oxidase activity, utilization of capric acid and phenylacetic acid. Strain BHIDK31 (=NNIBR2023642BA57) was isolated from wet soil in Wonju-si, Gangwon-do, Republic of Korea (37°24′49.0″N 127°58′20.5″E).

Description of *Vogesella urethralis* ol5

Cells are Gram-staining-negative, flagellated and rod-shaped. Colonies are circular, raised, entire and light grey-colored after 2 days incubation on TSA at 25°C. In the API 20NE system, positive for nitrate reduction, indole production, gelatin hydrolysis, utilization of D-glucose, *N*-acetyl-D-glucosamine, D-maltose, potassium gluconate and malic acid, but negative for glucose acidification, arginine dihydrolase, urease activity, esculin hydrolysis, β-galactosidase activity, oxidase activity, utilization of L-arabinose, D-mannose, D-mannitol, capric acid, adipic acid, trisodium citrate and phenylacetic acid. Strain ol5 (=NNIBR2023642BA58) was isolated from wet soil in Hoengseong-gun, Gangwon-do, Republic of Korea (37°29′ 26.9″N 127°59′48.0″E).

Description of *Pseudomonas solani* ru14

Cells are Gram-staining-negative, non-flagellated and rod-shaped. Colonies are circular, raised, entire and cream-colored after 2 days incubation on R2A at 25°C. In the API 20NE system, positive for indole production, esculin hydrolysis, gelatin hydrolysis, utilization of D-glucose, L-arabinose, D-mannose, D-maltose and trisodium citrate, but negative for nitrate reduction, glucose acidification, arginine dihydrolase, urease activity, β-galactosidase activity, oxidase activity, utilization of D-mannitol, *N*-acetyl-D-glucosamine, potassium gluconate, capric acid, adipic acid, malic acid and phenylacetic acid. Strain ru14 (=NNIBR 2023642BA59) was isolated from wet soil in Anseong-si, Gyeonggi-do, Republic of Korea (37°02′46.5″N 127°09′ 05.0″E).

Description of *Streptomyces barringtoniae* R2ASOYN6

Cells are Gram-staining-positive, non-flagellated and coccoid-shaped. Colonies are filamentous, umbonate, curled and beige-colored after 2 days incubation on R2A at 25°C. In the API 20NE system, positive for arginine dihydrolase, but negative for nitrate reduction, indole production, glucose acidification, urease activity, esculin hydrolysis, gelatin hydrolysis, β-galactosidase activity, oxidase activity, utilization of D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. Strain R2ASOYN6 (=NNIBR2023642BA60) was isolated from wet soil in Wonju-si, Gangwon-do, Republic of Korea (37°26′30.9″N 128°03′14.4″E).

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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First record of the genus *Leptocotis* (Amphipoda, Hyperiidea, Oxycephalidae) from off Jeju Island, Korea, with description of newly recorded species, *Leptocotis tenuirostris*

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A newly recorded species, *Leptocotis tenuirostris* (Claus, 1871), belonging to the family Oxycephalidae Spence Bate, 1863, was collected during a pelagic zooplankton survey from off Jeju Island, Korea. This monotypic genus is characterized by a well-developed rostrum in both sexes and lanceolate rami of all uropods. *Leptocotis* is morphologically similar to other genera in the family, however, *Leptocotis* can be distinguished by the combined length of urosomites 2 and 3 and length of outer ramus on uropod 1. To date, only three genera of the family Oxycephalidae, *Oxycephalus* H. Milne Edwards, 1830, *Rhabdosoma* White, 1847, and *Streetsia* Stebbing, 1888, have been recorded in Korea, making this the first record of the genus *Leptocotis* in Korean waters. Additionally, a key to species of the family Oxycephalidae from Korean waters is provided.

Keywords: crustacean, hyperiid, Oxycephalid, plankton, taxonomy

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Introduction

The family Oxycephalidae Spence Bate, 1863, comprises holoplanktonic amphipods and common in the planktonic group especially in tropical and subtropical regions. Members of the Oxycephalidae can be distinguished from other families within the superfamily Platysceloidea by the presence of a well-developed rostrum in both sexes and lanceolate rami on all uropods (Zeidler, 2016). This family includes 19 species within eight genera (Horton *et al*., 2024). The genus *Leptocotis* Streets, 1877 is monotypic and was established by Streets in 1877 with *Leptocotis spinifera* Streets, 1877 as its type species. Currently, *Leptocotis spinifera* is considered a junior synonym of *Leptocotis tenuirostris* (Claus, 1871; Zeidler, 2016).

The history of the family Oxycephalidae began with the establishment of the genus *Oxycephalus* by H. Milne Edwards in 1830 with description of *Oxycephalus piscatoris* which is now referred to as *O. piscator*. Initially, Milne Edwards placed *O. piscatoris* in the family Hyperines, but Dana (1853) proposed a new classification of Crustaceans and placed Oxycephalidae as a subfamily named Oxycephalinae in the family Typhidae. Subsequently, Bate (1862) elevated the subfamily Oxycephalinae to family status as Oxycepahlidae.

Currently, three genera and three species of Oxycephalidae are recorded in Korean waters: *Oxycephalus clausi* Bovallius, 1887; *Rhabdosoma brevicaudatum* Stebbing, 1888; and *Streetsia porcella* (Claus, 1879) (Yoo, 1972; 1995; Shin and Lim, 2020). Although the genus *Leptocotis* Streets, 1877 had not previously been recorded in Korea, *Leptocotis tenuirostris* (Claus, 1871) was collected during a pelagic zooplankton survey from off Jejudo Island, Korea (Fig. 1). This paper represents the first record of the genus *Leptocotis* in Korea, adding a newly recorded species to the Korean hyperiid amphipod fauna. Further-

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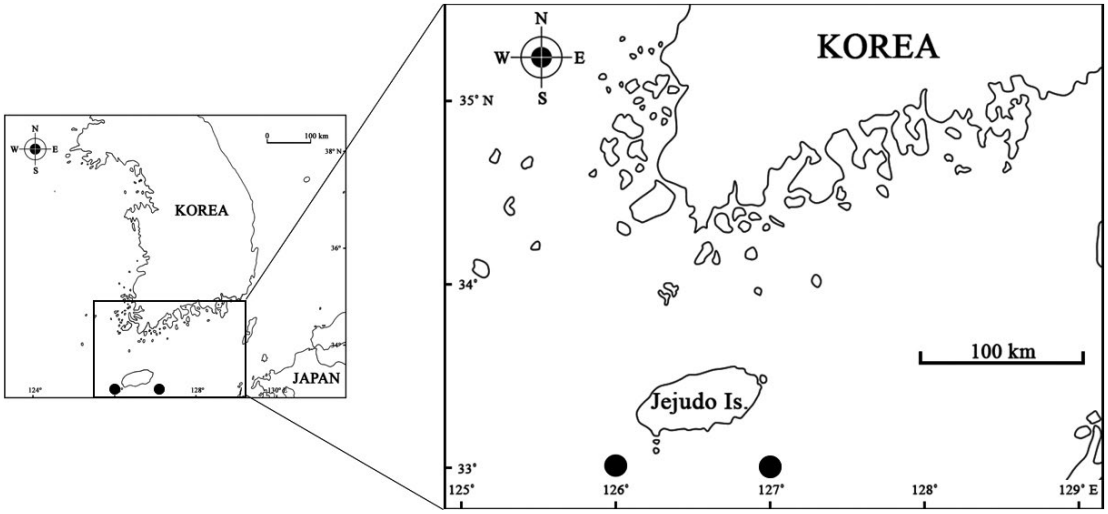


Fig. 1. Distribution of the *Leptocotis tenuirostris* (●: Jeju sea).

more, this study also provides a key for identifying species of the family Oxycephalidae found in Korean waters.

Materials and Methods

Specimens were collected with a MOCNESS net from subtidal waters of the South Sea, Korea (Fig. 1). The specimens were fixed in 95% ethanol and dissected in glycerol on Cobb's aluminum hole slides. The materials were examined under stereoscopic (Olympus SZX 10) and compound microscopes (Olympus BX 51), and drawings and measurements were made with the aid of a drawing tube. Line drawings were produced using the program Clip Studio Paint (Celsys, Japan). Body length was measured from the end of the rostrum to the end of the urosome, along the dorsal parabolic line of the body. The examined specimens are deposited at the National Institute of Biological Resources (NIBR) in Incheon, Korea and the Department of Biological Science, Dankook University (DKU) in Cheonan, Korea.

Systematic Accounts

Order Amphipoda Latreille, 1816
Suborder Hyperiidea H. Milne Edwards, 1830
Superfamily Platysceloidea Spence Bate, 1862
Family Oxycephalidae Dana, 1852
Genus *Leptocotis* Streets, 1877
긴꼬리뾰족머리옆새우속 (신칭)

***Leptocotis tenuirostris* (Claus, 1871) (Figs. 2, 3)**
긴꼬리뾰족머리옆새우 (신칭)
Oxycephalus tenuirostris Claus, 1871: 155.
Leptocotis tenuirostris Claus, 1887: 36; Bovallius, 1890: 117, pl. 5; Zeidler, 2016: 80, fig. 37.
Leptocotis spinifera Streets, 1877: 137; Streets, 1879: 283.
Leptocotis lindstromi Bovallius, 1887: 38.
Leptocotis ambobus Stebbing, 1888: 1594, fig. 204.
Leptocotis mindanaonis Stebbing, 1888: 1598, fig. 204.

Material examined. 1♂, dissected (appendages on one slide), NIBRIV0000927414, Jeju sea, 32°59′53″N, 125°59′43″E, 14 Jun 2019, by MOCNESS net, collected by SH Choo; 1♂, DKUAMP202411, Jeju sea, 33°01′12″N, 127°03′25″E, 8 Aug 2024, by MOCNESS net, collected by J Kim.

Description. Adult male (NIBRIV0000927414), body (Figs. 2, 3A) 10.2 mm long, elongate, narrow, dorsally smooth. Head elongate, strongly notched dorsally; rostrum elongate, narrow; eyes well developed, covering most of head except for rostrum, grouped in one field on each side of head. Pereonites 1–7 articulated with coxae. Pleonite 3, ventrodistal corner produced. Urosomite 2 fused with urosomite 3, length of urosomites 2–3 combined 3.49× width. Antenna 1 (Fig. 3B), peduncle 2-articulate, flagellum with large, expanded, crescent-shaped callynophore, with rows of aesthetascs on medial and posterior margins, with 3 small articles on anterodorsal corner. Antenna 2 (Fig. 3C) elongate, strongly zig-zagged, 5-articulate, with most articles fold back on each other.

Gnathopod 1 (Fig. 3D) subchelate; coxa expanded; ischium short, length 0.21× basis; merus, length 1.33× ischium, posterodistal corner with a seta; carpus subchelate, trapezoidal, length 2.62× merus, half of posterior margin serrated, posterodistal corner produced, knife-shaped, projection serrated; propodus ovate, length 0.74× carpus, anterior margin curved, with a seta, posterior margin serrated;



Fig. 2. *Leptocotis tenuirostris* (Claus, 1871), adult male, 10.2 mm, habitus. Scale bar = 1.0 mm.

dactylus falcate, relatively slender, length 0.52× propodus.

Gnathopod 2 (Fig. 3E) subchelate; coxa expanded, widening ventrally; basis slender, subrectangular, relatively long; ischium short, length 0.12× basis, posterior margin with a seta; merus trapezoidal, length 1.81× ischium, anterodistal corner with 2 setae, posterodistal corner with a seta; carpus subchelate, length 3.53× merus, anterior margin slightly convex, lateral margin with 8 setae, posterodistal produced, knife-shaped, projection serrated; propodus longish ovate, length 0.58× carpus, anterior margin slightly curved, posterior margin serrated; dactylus falcate, relatively slender, length 0.55× propodus.

Pereopod 3 (Fig. 3F) slender; coxa expanded; basis slender, elongate, slightly widening distally; ischium short, length 0.11× basis, anterior margin concave, posterior margin with a seta; merus 6.42× ischium, posterior margin with 4 setae; carpus subrectangular, length 0.81× merus; propodus slender, narrowing distally, length 1.11× carpus; dactylus falcate, narrow, elongate, length 0.51× propodus.

Pereopod 4 (Fig. 3G) similar to pereopod 3, but slightly elongated.

Pereopod 5 (Fig. 3H), coxa expanded; basis broad proximally, narrowing distally; ischium subquadrate, length 0.07× basis, anterodistal corner produced; merus subrectangular, length 8.91× ischium, anterior margin with 6 setules; carpus subrectangular, length 0.69× merus, anterior margin with 4 setules; propodus slender, length 1.45× carpus; dactylus narrow, falcate, length 0.36× propodus.

Pereopod 6 (Fig. 3I), coxa expanded; basis ovate, broad proximally, narrowing distally, posterodistal lobe produced; ischium subquadrate, very short, length 0.06× basis, anterodistal corner produced; merus subrectangular, elongate, length 8.56× ischium, anterior margin with serrulation, posterodistal corner slightly produced; carpus subrectangular, length 0.36× merus, anterior margin with serrulation; propodus slender, narrowing distally, length 0.48× carpus, anterior margin with serrulation; dactylus narrow, falcate, length 0.29× propodus.

Pereopod 7 (Fig. 3J) reduced in size, all articles present; coxa subrectangular, posterodistal lobe produced; basis large, expanded, slightly narrowing distally; ischium subquadrate, length 0.13× basis; merus 1.31× ischium; carpus subrectangular, length 1.17× merus; propodus subrectangular, narrowing distally, length 0.93× carpus; dactylus falcate, length 0.23× propodus.

Uropod 1 (Fig. 3K), peduncle subrectangular, narrowing distally, medial and lateral margin with serration; outer ramus characteristic in form, reduced in size, length 0.08× peduncle; inner ramus lanceolate, length 2.89× outer ramus, medial and lateral margin with serration.

Uropod 2 (Fig. 3K) shorter than uropod 1, peduncle subrectangular, medial and lateral margin with serration; outer ramus lanceolate, length 0.26× peduncle, medial and lateral margin with serration; inner ramus lanceolate, length 1.08× outer ramus, medial and lateral margin with serration.

Uropod 3 (Fig. 3K) shorter than uropods 1−2, peduncle subrectangular; outer ramus lanceolate, length 0.95× pe-

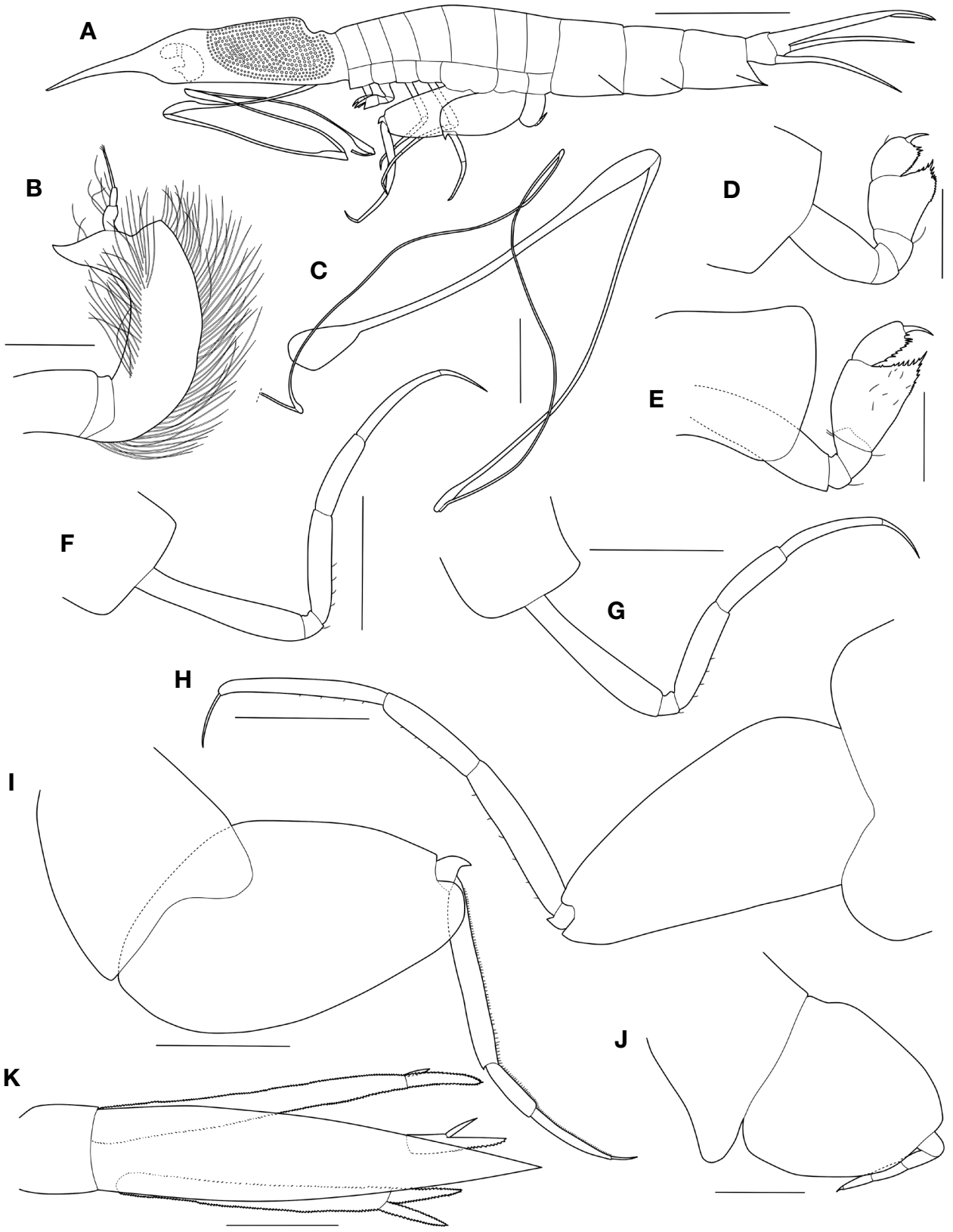


Fig. 3. *Leptocotis tenuirostris* (Claus, 1871), adult male, 10.2 mm. A, habitus; B, antenna 1; C, antenna 2; D, gnathopod 1; E, gnathopod 2; F, pereopod 3; G, pereopod 4; H, pereopod 5; I, pereopod 6; J, pereopod 7; K, uropods 1−3 and telson. Scale bars: A = 2.0 mm; C = 0.6 mm; K = 0.5 mm; F−I = 0.4 mm; B, D, E, J = 0.2 mm.

duncle, medial and lateral margins with serration; inner ramus lanceolate, length 1.54× outer ramus, fused with peduncle, lateral margin with serration.

Telson (Fig. 3K) fused with urosomite 3, elongate, isosceles triangle in shape, entire, unarmed.

Distribution. Worldwide.

Remarks. The genus *Leptocotis* Streets, 1877 resembles other genera within the family Oxycephalidae, such as *Cranocephalus* Bovallius, 1890; *Oxycephalus* H. Milne Edwards, 1830; *Streetsia* Stebbing, 1888; and *Tullbergella* Bovallius, 1887 by having rostrum that extends into a sharp point. However, *Leptocotis* can be distinguished from its congeners by the following features (different characteristics of *Cranocephalus*, *Oxycephalus*, *Streetsia*, and *Tullbergella* in brackets): 1) length of urosomites 2–3 combined more than 3× width (vs. less than 3× width in *Cranocephalus*, *Oxycephalus*, *Streetsia*, and *Tullbergella*); 2) gnathopod 1 subchelate (vs. chelate in *Oxycephalus*); 3) pereopod 7, coxa articulated with pereonites (vs. fused in *Cranocephalus*, *Streetsia*, and *Tullbergella*); 4) pereopod 7, all articles present (vs. articles reduced in *Tullbergella*); and 5) uropod 1 with very short outer ramus (vs. well-developed outer ramus in *Cranocephalus*, *Oxycephalus*, *Streetsia*, and *Tullbergella*). The specimens we observed align well with the original descriptions of *Leptocotis tenuirostris* provided by Claus (1871) and the later clarifications by Zeidler (2016).

Key to species of the family Oxycephalidae from Korean waters

1. Body extremely slender; rostrum long, needle-shaped ····· *Rhabdosoma brevicaudatum* Stebbing, 1888
– Body moderately slender; rostrum produced into sharp or blunt point ····· 2
2. Uropod 1, outer ramus very short ····· *Leptocotis tenuirostris* (Claus, 1871)
– Uropod 1, outer ramus well-developed ····· 3
3. Uropods 2–3, inner ramus fused with peduncle ····· *Oxycephalus clausi* Bovallius, 1887
– Uropods 2–3, inner ramus articulated with peduncle ····· *Streetsia porcella* (Claus, 1879)

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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Three unrecorded species of free-living marine nematodes of the order Enoplida Filipjev, 1929 (Nematoda) from Korea

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Three known species of the free-living nematodes were gathered from marine sediments of sublittoral zone in Korea and described and illustrated. *Belbolla zhangi* Guo & Warwick, 2001, which was originally described from the Bohai Sea, China, is recorded from the East Sea, Korea for the first time; only in the ratio *a* and *c′* (33−39 vs. 29−35, 3.5−4.5 vs. 2.9−3.7). Specimens of *Halalaimus gracilis* de Man, 1888 from East Sea, Korea largely agree with the original description of de Man (1888) of nematodes from North Sea and the redescription of Platt & Warwick (1983) of nematodes from the England, except for slightly longer body width (20−24 μm vs. 16−26 μm) and the body length (1,120−1,315 μm vs. 800−1,300 μm). *Oxystomina elongata* (Bütschli, 1874) Filipjev, 1921; apart from few minor morphological differences between the specimens from North Sea (Lorenzen, 1965) and from England (Warwick *et al*., 1998); in the value of "de Man ratio *b* which was higher in specimens from North Sea and England (*b* = 6.5−7.7 vs. 4.4−4.5) and slight difference in the body width (40−50 μm vs. 32−38 μm). The present study on unrecorded species improves the understanding of nematodes species diversity in Korean waters.

Keywords: *Belbolla*, free-living nematodes, *Halalaimus*, *Oxystomina*

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Introduction

We found about 80 species of free-living nematodes during a "Marine Biological Resources Survey Project" in the marine nematoda in Korea from 2022 to 2023, include three unrecorded species belonging to the genus *Belbolla*, *Halalaimus* and *Oxystomina* from Korea. The genus *Belbolla* Andrássy, 1973 is characterized by having a wide and narrow stoma divided into two parts, the presence of three teeth, with the largest tooth being the ventro-sublateral one, and the presence of a series of bulb-like muscular pharynx swellings in the posterior part of the pharynx (Platt and Warwick, 1983; Smol *et al*., 2014; Zhang, 2005). The genus *Halalaimus* was established by de Man in 1888 with the type species *H. gracilis* de Man, 1888 and 97 species of *Halalaimus* have been described so far (WoRMS Editorial Board, 2024; Nemys eds., 2024). The most important characteristic of the genus *Halalaimus* is both body ends being extremely attenuated, longitudinally greatly elongated amphids, a long conical-cylindrical tail and the presence of the caudal glands (Keppner, 1992; Smol *et al*., 2014). The genus *Oxystomina* Filipjev, 1918 is characterized by six inner labial papillae; six outer labial setae; four cephalic setae positioned slightly backward in cervical region; buccal cavity absent; oval-shaped amphidial fovea; prominent oval cells in the throughout body and the club-shaped tail (de Man, 1888; Warwick *et al*., 1998; Smol *et al*., 2014). *Oxystomina* was erected by Filipjev, 1918 with type spe-

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cies *O. elongata* (Bütschli, 1874) Filipjev, 1921 and 42 species of *Oxystomina* have been described to date (WoRMS Editorial Board, 2024; Nemys eds., 2024). This paper describes three known species belonging to the order Enoplida collected in the subtidal zone of Korean waters.

Materials and Methods

While conducting a survey of the meiofauna community along the Korean coastline from 2022 to 2023, *Belbolla* specimens were collected along the coast of Ilgwang-myeon, Gijang-gun, Busan (35°16′0.0″N, 129°16′50.0″E, at a depth of 16 m, in the clay sediment) on 30th April 2023, *Halalaimus* specimens were collected along the coast of Heunghae-eup, Buk-gu, Pohang (36°2′20.8″N, 129° 26′59.6″E, at a depth of 19 m, in the clay sediment) on 3rd May 2022 and *Oxystomina* specimens were collected along the coast of Mijo-myeon, Namhae-gun, Gyeongsangnam-do (34°40′55.0″N, 128°2′10.0″E, at a depth of 22 m, in the clay sediment) on 1st May 2023. Sediment samples were collected using a Smith-McIntyre grab with an area of 0.1 m^2, while meiofauna samples were obtained using a hand-held corer that has a surface area of 10 cm^2 and a depth of 5 cm. All samples were immediately preserved in 4% neutral buffered formalin at room temperature. Following the protocol by Burgess (2001), meiofauna were extracted in the laboratory, while nematodes were sorted using a grid-patterned Petri dish and observed with a stereoscopic microscope (S APO; Leica, Wetzlar, Germany). Sorted nematodes were subsequently placed in Seinhorst solution for dehydration and infiltration with glycerin, utilizing the glycerin-ethanol method (Seinhorst, 1959). Then nematode specimens were prepared on glass slides using anhydrous glycerin and glass beads (the size of the beads was chosen based on the diameter of the specimens) using a standard waxring technique (Hooper, 1986). For taxonomic studies, nematode specimens were observed using a 100× oil immersion objective combined with Nomarski Differential Interference Contrast (DIC) illumination. Drawings were created using an optical microscope with a camera lucida (BX-51; Olympus, Tokyo, Japan). All morphometric measurements were acquired from the figures utilizing a digital map-measurer and Leica Application Suite Version 4.12.0 (Leica, Wetzlar, Germany). Abbreviations used are as in the following: *a* - the ratio of body length to maximum body diameter; abd - anal body diameter (μm); AL - distance from anterior to anterior border of amphidial fovea (μm); amp - diameter of amphidial fovea (μm); amp cbd - corresponding body diameter at the level of amphidial fovea (μm); ampl - length of amphidial fovea (μm); ampw - width of amphidial fovea (μm); *b* - body length in relation to the pharynx length; BL - buccal cavity length (μm); bcd - buccal cavity diameter (μm); *c* - the ratio of body length to tail length; *c′* - the ratio of body length to anal body diameter; cbd - corresponding body diameter (μm); cs - length of cephalic setae (μm); cs-length of cervical setae (μm); dbs - distance between supplements (μm); dps - distance of the posterior pro-cloacal supplement from cloacal opening (μm); EPL - distance of ventral excretory pore from anterior end of body (μm); gub - length of gubernacular apophyses (μm); hd - diameter at the level of cephalic setae (μm); L - total body length (μm); mbd - maximum body diameter (μm); N cbd - corresponding body diameter at nerve ring (μm); NL - nerve ring from anterior end of body (μm); P cbd - corresponding body length at cardia (μm); s - spicule length as arc length divided by anal body diameter; spia - spicule length as arc (μm); spic - spicule length as chord (μm); TEL - length of teeth (μm); ter - length of terminal setae (μm); TL - tail length (μm); TLAS - total length of anterior supplement (μm); TLPS - total length of posterior supplement (μm); V% - vulva distance from anterior end as percentage of total body length.

Results and Discussion

Systematics

Class Enoplea Inglis, 1983
Subclass Enoplia Pearse, 1942
Order Enoplida Filipjev, 1929
Family Enchelidiidae Filipjev, 1918
Genus *Belbolla* Andrássy, 1973

***Belbolla zhangi* Guo & Warwick, 2001**

Original description (Guo & Warwick, 2001: 1581−1585, fig. 4a−e, the Bohai Sea, China)
Other descriptions (None)
Synonymised names (None)

Locality. The coast of Ilgwang-myeon, Gijang-gun, Busan: sub-tidal zone in Southern part of East Sea, Korea (35°16′ 0.0″N, 129°16′50.0″E), at a depth of 16 m, in the clay sediment.
Material. Three males (MABIK NA00158069, MABIK NA00158720, MABIK NA00158721) collected by Jung-Ho Hong at the coast of Gijang on 30th April 2023, from Research Vessel Haeyanghwnangkyung 3.
Measurements. All measurements data and morphometric ratios are given in Table 1.
Description. Males (Fig. 1, Table 1). The body is elongated and tube-shaped, narrowing at both ends, with a length ranging from 2,409−2,518 μm and a maximum body diameter 61−74 μm. The cuticle is smooth without lateral differentiation. The head is strongly narrowed, 10−13 μm in a diameter. Six outer labial sensilla are minute, with papillae form. Ten cephalic setae (5−8 μm) are loca-

Table 1. Morphometrics of *Belbolla zhangi* Guo & Warwick, 2001 from East Sea, Korea and *B. zhangi* Guo & Warwick, 2001 from Bohai Sea, China.

Characters	*B. zhangi* from East Sea, Korea		*B. zhangi* Guo & Warwick, 2001 from Bohai Sea[a]	
	♂; n = 3	♀; n = 0	♂; n = 4	♀; n = 2
L	2409–2518		2230–2750	2450–2780
mbd	61–74		68–78	64–84
hd	12–13		10–14	10–11
cs	5–10		8–10	8–9
cer	18–25		18–22	17–21
BL	11–18		12–18	12–13
bcd	6–8		6–9	5–7
amp	2–3		?	?
NL	209–274		240–290	230–275
N cbd	41–53		48–58	50–52
PL	482–624		540–580	490–590
P cbd	57–63		61–78	62–78
V%	n/a		n/a	44.1–44.6
abd	48–55		51–60	38–48
spic	54–71		56–74	n/a
gub	44–55		40–45	n/a
TL	180–218		170–210	152–160
TLPS	34–40		28–42	n/a
TLAS	40–45		36–47	n/a
dps	170–224		123–195	n/a
dbs	87–105		77–122	n/a
a	33–39		29–35	33–38
b	4.0–4.9		4.1–4.6	4.7–5.0
c	11.5–13.8		13.1–13.5	16.1–17.4
c′	3.5–4.5		2.9–3.7	3.3–4.0

All measurements in μm unless otherwise stated, except ratio *a*, *b*, *c*, *c′*, s. n/a: not applicable or unknown. Literature sources: [a]Guo & Warwick, 2001.

ted about 0.5 hd from anterior apex in one circle. The anterior region of the pharynx was covered with numerous cervical setae, which reached lengths of up to 18–25 μm. The diameter of the amphideal fovea is 2–3 μm, about 0.2 hd, located about 0.5 hd from anterior end. The buccal cavity features a robust wall, expansive and broad, and is separated into two sections by a cuticular ring (with no denticles): (i) a roomy anterior section, and (ii) a narrower and elongated posterior section. The total length of the buccal cavity is 11–18 μm, with a width of 6–8 μm. In the buccal cavity, there are three unequal teeth of which one right subventral tooth (about 8–12 μm long) is largest. Ocelli are not present. The pharynx measures 482–624 μm in length, expanding gradually and modified into eight pharyngeal bulbs. The nerve ring is located at 40–44% of the pharynx length. The cardia is minute, inconspicuous, surrounded by intestinal tissue. Diorchic, with the anterior testis positioned on the right side of the intestine, while the posterior testis was in the same position as the vas deferens. The spicules are uniform in length (85–99 μm) and have the same structure, featuring enlarged tips, 1.7–2.0 times as long as the cloacal body diameter. Gubernaculum is long, measuring 45–55 μm in length, 0.9–1.1 times the anal body diameter. Two wing-shaped precloacal supplements are strongly developed, an anterior precloacal supplement measuring 41–45 μm and a posterior precloacal supplement 33–35 μm in length. The anterior supplement is located 200–225 from the cloacal opening, the posterior supplement is positioned 104–137 from the cloacal opening. One precloacal setae (5–6 μm long) is located immediately anterior to cloaca. The tail is conico-cylindrical, tapering with the distal fifth being cylindrical. The tail length was 3.5–4.5 times the anal body diameter. The tip of the tail is slightly swollen and has a terminal spinneret, with terminal setae (about 5 μm long).

Remarks. To date, the genus *Belbolla* Andrássy, 1973 contains 21 valid species: *B. asupplementata* (Juario, 1974) Andrássy, 1973, *B. californica* (Allgén, 1951) Andrássy, 1973, *B. forkyspicula* Xiao & Guo, 2023, *B. gallanachmorae* (Inglis, 1961) Andrássy, 1973, *B. gracilis* Gagarin & Thanh, 2016, *B. heptabulba* (Timm, 1961) Andrássy, 1973, *B. huanghaiensis* Huang & Zhang, 2005, *B. insula* Belogurov, Fadeeva & Belogurova, 1983, *B. intarma* Belogurov & Belogurova, 1980, *B. longispiculata* Nasira, Shahina & Shamim, 2014, *B. mangrove* Zhu, Guo, Zhou, Shih, Li, Lee, Xu & Tam, 2023, *B. octobulba* Ban, Sun & Huang, 2023, *B. sinica* Wang, Guo & Wang, 2022, *B. stenocephalum* Huang & Zhang, 2005, *B. sundaensis* (Micoletzky, 1930) Andrássy, 1973, *B. teissieri* (Luc & De Coninck, 1959) Andrássy, 1973, *B. tenuidens* (Cobb, 1920) Andrássy, 1973, *B. vietnamica* Gagarin & Nguyen Dinh Tu, 2016, *B. warwicki* Huang & Zhang, 2005, *B. wonkimi* Rho, Lee, Lee & Min, 2020, *B. zhangi* Guo & Warwick, 2001 (Nemys eds., 2024; WoRMS Editorial Board, 2024). The East Sea, Korea specimens in general fit the original description of Guo & Warwick (2001), except in the ratio of tail length with the anal diameter (3.5–4.5 vs. 2.9–3.7) and slight difference in the body length ratio (33–39 vs. 29–35). We consider such differences as variations within one species.

Class Enoplea Inglis, 1983
Subclass Enoplia Pearse, 1942
Order Enoplida Filipjev, 1929
Family Oxystominidae Chitwood, 1935
Genus *Halalaimus* de Man, 1888

***Halalaimus gracilis* de Man, 1888**

Original description (de Man, 1888: 3, fig. 1a–b, North Sea)

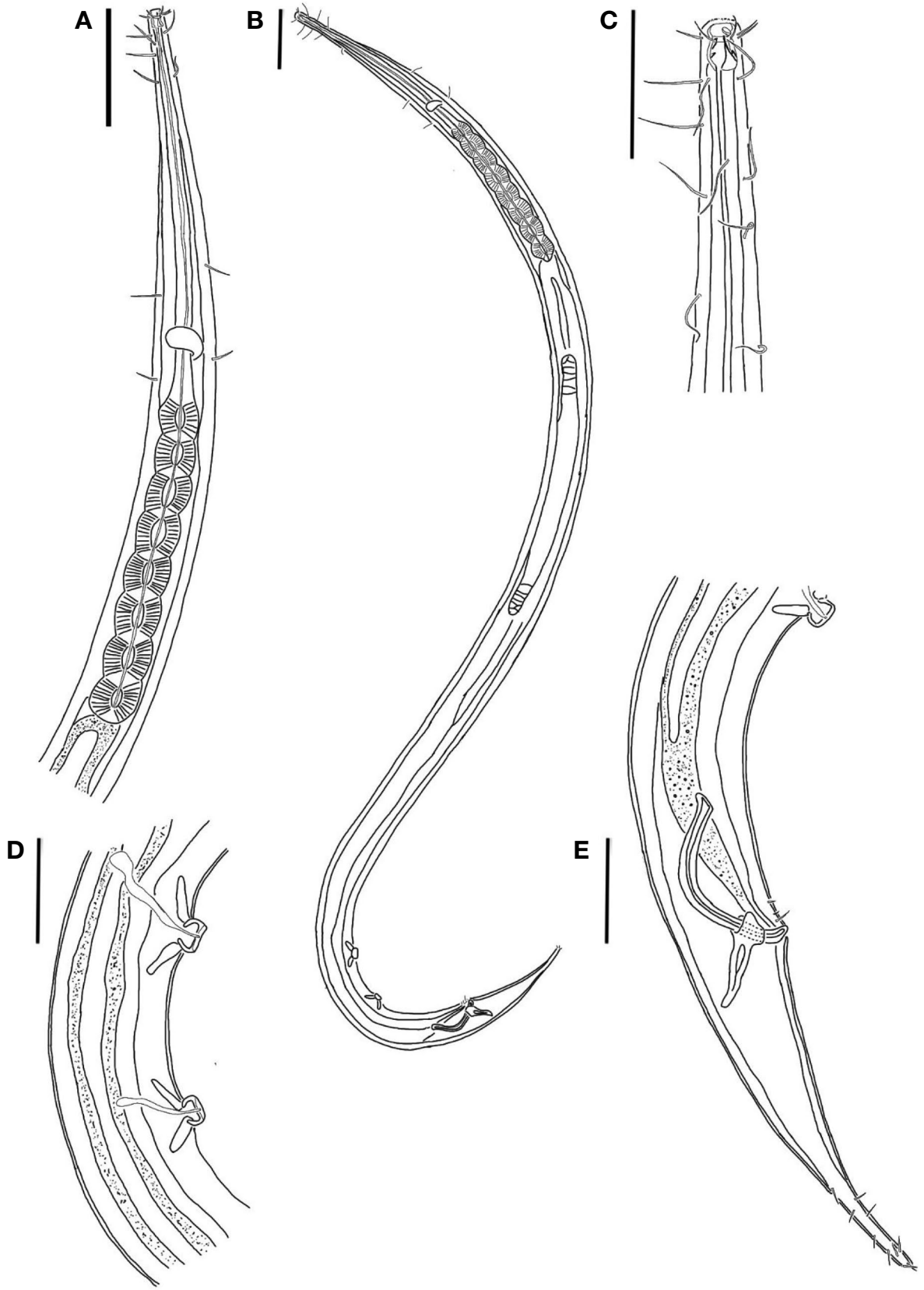


Fig. 1. *Belbolla zhangi* Guo & Warwick, 2001 from the East Sea, Korea: A, Male pharynx; B, Male habitus; C, Male head; D, Male precloacal suppelemants; E, Male tail. Scale bars: 100 μm (A, B) and 50 μm (C–E).

Other descriptions (de Man, 1922: 216–217, fig. 1, North Sea. Stekhoven, 1935: 21–22, fig. 88a–b, Baltic Sea. Bresslau and Stekhoven, 1940: 19, fig. 13a–b, Baltic Sea. Stekhoven, 1950: 38, fig. 9a–c, Baltic Sea. Allgén, 1951: 272–273, 321–322, 373, fig. 4a–b, Pacific Ocean. Timm, 1952: 78, fig. 3, Chesapeake Bay, USA. Gerlach, 1967: 21–22, fig. 3a–d, Red Sea. Platt and Warwick, 1983: 190–191 fig. 85a–e, England.)
Synonymised names (None)

Locality. The coast of Heunghae-eup, Buk-gu, Pohang: sub-tidal zone in Southern part of East Sea, Korea (36°2′ 20.8″N, 129°26′59.6″E), at a depth of 19 m, in the clay sediment.
Material. Three males (MABIK NA00157796, MABIK NA00158711, MABIK NA00158712) and two females (MABIK NA00158713, MABIK NA00158714) collected Seunghan Lee at the coast of Pohang on 3rd May 2022, from Research Vessel Haeyanghwnangkyung 3.
Measurements. All measurements data and morphometric ratios are given in Table 2.
Description. Males (Fig. 2, Table 2). The body is cylindrical, gradually tapering in cervical and caudal regions, about 1,120–1,285 μm in length and 20–22 μm wide at the maximum body diameter. The cuticle is transverse striations. Somatic alae are not present in both lateral sides, caudal alae are observed in males. Six inner labial sensilla are minute setae (about 0.5 μm in length). Six outer labial setae are 3–4 μm long and four cephalic setae are positioned just behind outer labial setae, with the same length as the outer labial setae. The amphids are located 7–10 μm from the anterior end, 15–24 μm in length. The stoma is minute. The nerve ring is indistinct, situated 112–136 μm from the anterior apex, with a body diameter of 16–18 μm at the nerve ring. Secretory-excretory glands and pores are not observed. Pharynx is enlarged at posterior end, 180–207 μm in length from the anterior end. Cardia is small, inconspicuous. Reproductive system is diorchic, testes are opposed and outstretched, the anterior testis is located on right side of intestine, situated from 48% to 52% of body length, the posterior testis located on left side of intestine, positioned from 64% to 70% of body length. Spicules are equal, arcuate, 1.3–1.4 times cloacal body diameters (15–18 μm in length) with indistinct ventral ala. Spicule tips are surrounded by gubernaculum. Precloacal sensillum or pore is absent. The tail is conico-cylindrical, 12.2 to 13.3 of the cloacal body diameters long. The anterior conical portion is about 40–50% of the total tail length, the poster-

Table 2. Morphometrics of *Halalaimus gracilis* de Man, 1888 from East Sea, Korea and *H. gracilis* de Man, 1888 from North Sea and England.

Characters	*H. gracilis* from East Sea, Korea		*H. gracilis* from North Sea[a]	*H. gracilis* from England[b]
	♂; n = 3	♀; n = 2	♂; n = n/a, ♀; n = n/a	♂; n = n/a, ♀; n = n/a
L	1120–1285	1220–1315	1000–1000	800–1300
mbd	20–22	20–24	16–20	17–26
hd	3–4	3–4	n/a	3–3
cs	3–4	2–4	n/a	3–4
ampl	15–24	15–17	n/a	12–13
ampw	12–13	12	n/a	12–13
ampL	7–10	10–12	n/a	12–13
NL	112–136	120–140	n/a	n/a
N cbd	16–18	16–18	n/a	n/a
PL	180–207	205–239	263–286	n/a
P cbd	19–21	18–21	n/a	n/a
V%	n/a	51.5–53.5	n/a	50.0–50.0
abd	12–14	12–12	n/a	11
spia	15–18	n/a	18–20	17
s	1.3–1.4	n/a	n/a	1.5
TL	150–171	145	153–166	112–124
a	55–61	55–61	50–60	40–60
b	5.3–6.2	5.2	3.5–3.8	n/a
c	7.0–8.1	5.6	6.0–6.5	n/a
c′	12.2–13.3	4.8	n/a	12.0–15.0

All measurements in μm unless otherwise stated, except ratio *a*, *b*, *c*, *c′*, s. n/a: not applicable or unknown. Literature sources: [a]de Man, 1888; [b]Platt & Warwick, 1983.

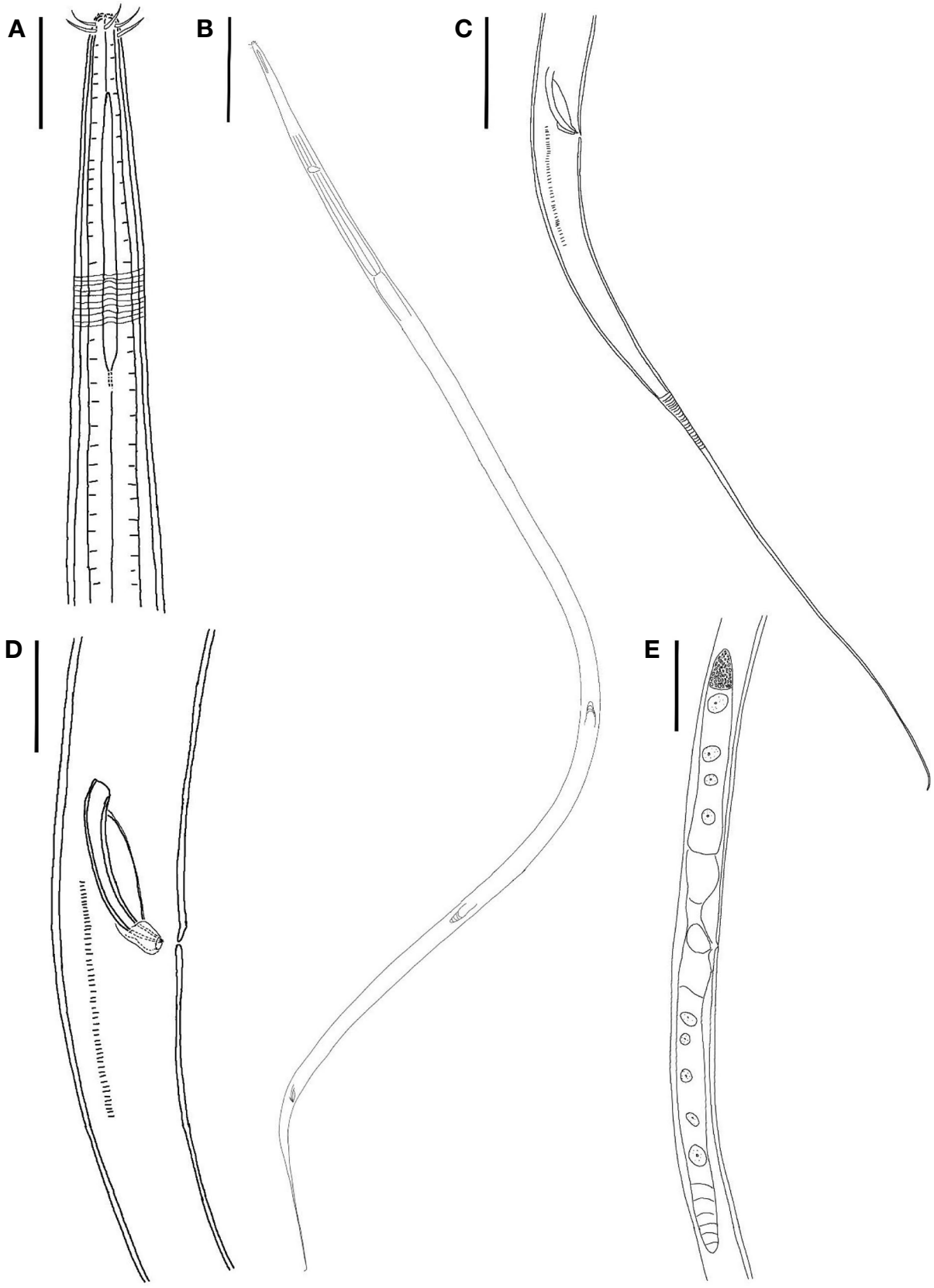


Fig. 2. *Halalaimus gracilis* de Man, 1888 from the East Sea, Korea: A, Male pharynx; B, Male habitus; C, Male tail; D, Male copulatory apparatus; E, Female vulva. Scale bars: 10 μm (A, D), 25 μm (C), 50 μm (E) and 100 μm (B).

ior cylindrical portion is filiform, with spinneret and no terminal setae. Caudal glands are indistinct, located postcloacally. Caudal sensilla are papilliform or very short setiform, and difficult to observe.

Females (Fig. 2, Table 2). Similar to males in most respects. Reproductive systems are amphidelphic, reflexed ovaries. Vulva is situated slightly posterior to mid-body at 51.5−53.5% of the body of length.

Remarks. *Halalaimus gracilis* de Man, 1888 is characterized by the presence of setiform inner labial sensilla, ornamented caudal alae in male, the absence of precloacal sensilla or pore, and simple plated gubernaculums without any apophysis or lateral extensions (Keppner, 1992). Keppner (1992) used male characteristics to categorize *halalaimus* species into four groups, specifically focusing on: the presence or absence of caudal alae: the presence or absence of precloacal supplements. *Halalaimus gracilis* de Man, 1888 belongs to group 2, members of which have the caudal alae and lack the precloacal sensillum or pore. Our specimens from East Sea, Korea are the same as the original description by de Man in 1888 and redescription by Warwick *et al*. in 1998, but slight longer than original description in the body width (20−24 μm vs. 16−26 μm) and the body length (1,120−1,315 μm vs. 800−1,300 μm). We consider such differences as variations within one species.

Class Enoplea Inglis, 1983
Subclass Enoplia Pearse, 1942
Order Enoplida Filipjev, 1929
Family Oxystominidae Chitwood, 1935
Genus *Oxystomina* Filipjev, 1918

***Oxystomina elongata* (Bütschli, 1874) Filipjev, 1921**

Original description (Bütschli, 1874: 34, fig. 18a−d, Kiel Port, Germany)

Table 3. Morphometrics of *Oxystomina elongata* (Bütschli, 1874) Filipjev, 1921 from South Sea, Korea and *O. elongata* (Bütschli, 1874) Filipjev, 1921 from Germany, New Zealand, Bering Sea, North Sea and England.

Characters	*O. elongata* from South Sea, Korea		*O. elongata* from Kiel Port, Germany[a]	*O. elongata* from New Zealand[b]	*O. elongata* from Bering Sea[c]	*O. elongata* from North Sea[d]	*O. elongata* from England[e]
	♂; n = 2	♀; n = 2	♂; n = 1, ♀; n = 0	♂; n = 1, ♀; n = 1	♂; n = 3, ♀; n = 2	♂; n = 1, ♀; n = 1	♂; n = n/a, ♀; n = n/a
L	1810−2120	1915−2185	3700	2200−2600	2400−2900	1935−2175	1800−2000
mbd	40−45	45−50	60	n/a	40−51	32−35	35−38
hd	5−6	5−6	n/a	n/a	9−10	7	6
cs	3−4	3−4	n/a	n/a	2−2.5	2−2	2.5−2.5
cer	3−4	3−4	n/a	n/a	2−2.5	2−2	2.5−2.5
ampl	10−12	10−12	n/a	n/a	15	n/a	n/a
ampw	5−5	4−5	n/a	n/a	5−5	n/a	3.5−3.5
ampL	30−35	30−35	n/a	n/a	37−52	9−10	29−30
amp cbd	15−17	19−20	n/a	n/a	12−15	12−13	12−13
NL	165−180	185−210	n/a	n/a	245−300	n/a	n/a
N cbd	27−30	30−30	n/a	n/a	28−35	n/a	n/a
EPL	135−155	149−172	n/a	n/a	170−205	n/a	n/a
PL	255−320	250−335	247	n/a	620−820	430−490	432−480
P cbd	40−45	45−50	n/a	n/a	40−47	33	n/a
V%	n/a	23.0−30.5	n/a	n/a	37.3−44.1	31	n/a
abd	28−30	25−27	n/a	n/a	25−27	24	n/a
spia	38−42	n/a	n/a	n/a	36−39	n/a	36−38
s	1.3−1.5	n/a	n/a	n/a	1.4	n/a	n/a
TL	85−92	85−95	528	n/a	115−125	84−100	87
a	40−53	38−49	62	70	50−64	55−66	51−56
b	6.6−7.0	6.5−7.7	15	4.5−5.2	3.5−3.9	4.4−4.5	4.4−4.5
c	20.9−23.0	22.5−23.0	7	21.0−25.0	18.0−23.0	22.0−23.0	22.0−23.0
c′	2.8−3.3	3.4−3.5	n/a	n/a	3.5−4.2	3.5−4.2	5

All measurements in μm unless otherwise stated, except ratio *a*, *b*, *c*, *c′*, s. n/a: not applicable or unknown. Literature sources: [a]Bütschli, 1874; [b]de Man, 1907, [c]Filipjev, 1927, [d]Lorenzen, 1969, [e]Platt & Warwick, 1983.



Fig. 3. *Oxystomina elongata* (Bütschli, 1874) Filipjev, 1921 from the South Sea, Korea: A, Male pharynx; B, Female head, pharynx, vulva; C, Male tail; D, Male habitus. Scale bars: 50 μm (A, C), 100 μm (B) and 200 μm (D).

Other descriptions [(de Man, 1907: plate 1, fig. 6, New Zealand. Filipjev, 1921: transfer *Oxystoma elongata* to the genus *Oxystomina*. Filipjev, 1927: plate 4, fig. 22a–b, Bering Sea. Kreis, 1929: 28–29, fig. 4a–b (=*Acoma brevicauda*), France. Stekhoven, 1935: fig. 82a–c, North Sea. Stekhoven, 1940: 17, fig. 11a–e, North Sea. Timm, 1952: 78, fig. 3, Chesapeake Bay, USA. Lorenzen, 1969: 232–233, fig. 30a–e, North Sea. Platt and Warwick, 1983: 194–195, fig. 86a–d, England.)]

Synonymised names [(*Acoma brevicauda* Kreis, 1929, *Oxystoma elongata* Bütschli, 1874, *Oxystomatina elongatum* (Bütschli)]

Locality. The coast of Mijo-myeon, Namhae-gun, Gyeongsangnam-do, located in the subtidal zone of eastern part of South Sea, Korea (34°40′55.0″N, 128°2′10.0″E), at a depth of 22 m, in the clay sediment.

Material. Two males (MABIK NA00158064, MABIK NA00158717) and two females (MABIK NA00158718, MABIK NA00158719) collected by Jung-Ho Hong at the coast of Namhae on 1st May 2023, from Research Vessel Haeyanghwnangkyung 2.

Measurements. All measurements data and morphometric ratios are given in Table 3.

Description. Males (Fig. 3, Table 3). The body is slender, elongated and very thin at the anterior end. The cuticle is smooth. The epidermal gland cells are scattering throughout the body. The inner and outer labial sensilla is papilliform, difficult to observe. Six cephalic setae are 3–4 μm long. Four cervical setae are 3–4 μm long, located at 10–12 μm (about two times of the head diameter) from front end of body. Amphidial fovea is longitudinal oval shape, 10–12 μm long and 5 μm wide, located at 30–35 μm from the anterior apex. The buccal cavity is minute. The pharynx is slender, posteriorly forming a well-pronounced bulb (about 0.5 cbd at the pharynx base), 255–320 μm in length, 40–45 μm in width. The pore of secretory-excretory glands is distinct and sclerotized, positioned at the 0.48–0.53 of the pharyngeal lengths from the anterior body end. The nerve ring is situated 165–180 μm from the anterior apex. The cardia is indistinct, surrounded by intestinal tissue. The ventral gland is located 65–80 μm from the junction of pharynx and intestine, about 0.4 corresponding body diameters wide. The tail is conicocylindrical with a clavate distal part, 2.8–3.3 of the cloacal body diameters long, without terminal setae. The reproductive system is monorchic with an anterior outstretched testis. The spicules arcuate, 26–27 μm long, enlarged proximal end with a velum, distal end tapered. The Gubernaculum is minute, curved, surrounding spicules. One short and one long precloacal supplementary setae are in front of the cloaca; the anterior one is short, 5–6 μm long; the posterior one is long, 10–12 μm long; located at the level of proximal end of spicule, or 20–22 μm in front of the anus.

Females (Fig. 3, Table 3). Similar to males in most respects, but the body is slightly thick. The reproductive system is monodelphic, single posterior reflexed ovary. The vulva with slightly raised lips, is situated at pre-median of body (23.0–30.5% of the body length).

Remarks. *Oxystomina elongata* (Bütschli, 1874) Filipjev, 1921 is characterized by having arcuate spicules with velum; inconspicuous or absent inner and outer labial sensilla; the presence of the gubernaculum; the width of amphidial fovea equal to or less than 0.5 corresponding body diameters; the posterior portion of tail clavate; equal to or shorter than the anterior conical portion; the absence of the precloacal papilla or seta (Platonova, 1984). The morphological data of Bütschli (1874) from Germany and de Man (1907) from New Zealand are hard to compare with Korean specimens, because of many missing characters. The specimens of Filipjev (1927) from Bering Sea are slightly bigger than Korean specimens. The South Sea, Korea specimens in general fit the redescription of Lorenzen (1969) and Warwick *et al*. (1998), except in the case of value "de Man ratio *b*" which is higher in specimens from North Sea and England ($b = 6.5–7.7$ vs. 4.4–4.5) and slight difference in the body width (40–50 μm vs. 32–38 μm). We interpret this variation as intraspecific diversity.

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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New records of freshwater algae from Korea II

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This study summarizes the distribution and taxonomic description about 26 taxa of the freshwater algae recorded for the first time in Korea collected from several swamps, reservoir and mountainous wetlands in the South Korea from 2014 to 2024. These algae classified into 3 taxa of Cyanophyceae, 1 taxon of Chlorophyceae, 13 taxa of Conjugatophyceae, 4 taxa of Euglenophyceae, 1 taxa of Raphidophyceae, 1 taxon of Dinophyceae, 2 taxon of Chrysophyceae and 1 taxon of Xanthophyceae. Among these, 3 genera of *Merotricha* of Raphidophyceae, *Ammatoidea* of Cyanophyceae and *Mischococcus* of Xanthophyceae were newly recorded in the Korean freshwater algal flora.

Keywords: algal flora, *Ammatoidea*, freshwater algae, *Merotricha*, *Mischococcus*, new record in Korea

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Introduction

Since Kawamura (1918) reported a species of *Centritractus* (Xanthophyceae) at lake Seoho, Suwon, total 6,653 taxa of algae have been described from various water bodies all over Korea (Kim, 2015; 2018; Lee and Joh, 2015; Lee and Kim, 2015a; Lee and Kim, 2015b; Kim and Kim, 2017; Kim and Lee, 2022; National Institute of Biological Resources, 2023). Of these, about 4,100 taxa have been reported as freshwater algae, which are composed of diatoms (33.1%), charophytes (24.2%), chlorophytes (17.2%), euglenophytes (9.2%), cyanobacteria (8.7%), heterokontophytes (5.3%), dinophytes (1.7%) and other taxa (0.6%) (Nakdonggang National Institute of Biological Resources, 2024). The recorded algal species from Korea is only less than 10 % of estimated 72,500 algal species worldwide (Guiry and Guiry, 2024). Also, 60–70% of some algal groups are cosmopolitan or world-widely distributed, whereas 30–40% are distributed in endemic or restricted to particular regions (Coesel, 1996; Kristiansen and Lind, 2005), although it may be hard to generalize to all of the algal species. In this light, it is presumed that there are more freshwater algae growing in Korea that have not been reported yet.

Recently, the importance of biological diversity has been increasing emphasized, with the discovery of indigenous species as biological resources recognized as an urgent national task to secure biological sovereignty.

Therefore, this make it all the more important to carry out continuous and detailed investigations of freshwater algae on diverse wetlands environments across the country including unique environments such as highland wetlands, mountain sphagnum bogs, lagoons and craters (orum) as well as lowland reservoirs, swamp and pond.

Various samples from various water bodies throughout the country were collected and thoroughly investigated. In

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the present study, 3 genera and 26 taxa of freshwater algae are reported for the first time in Korea.

Materials and Methods

Samples were collected from 18 different regions including mountainous wetlands, volcanic lakes (orum), lowland swamps, old reservoirs and pond from 2014 to 2024 (Table 1). The materials were obtained by means of plankton net (mesh size 20 μm), spuit or by squeezing submerged macrophytes, and living materials were immediately examined. After first examination living materials, they were preserved in 5% formalin solution for permanent preservation and detail identification. Microscopic examinations were made at magnification ×400−×630 using a Zeiss Microscope (Axio Imager. A2) and photographs were taken with a AxioCam HRC camera (Zeiss). pH and conductivity were measured in the field by means of a HI8314 membrane pH meter and a HI9835 EC meter (HANNA instruments, USA). All the taxa reported in the present study are illustrated with photomicrographs. The materials are deposited in the Department of Biology, Kyungpook National University.

Results and Discussion

Cyanobacteria
Cyanophyceae
Oscillatoriales
Microcoleaceae (Phormidiaceae, Microcoleoideae)

***Ammatoidea sinensis* Ley 1944 (Fig. 1A, B)**

Reference. Chu 2007, p. 66, pl. 15, fig. 4; Komárek & Anagnostidis 2008, p. 552, fig. 830.
Occurrence. Imdang weir (April 23, 2016).

Filaments isopolar, curved like arch-shaped, 13−14 μm wide in the middle part, gradually attenuated towards ends, with terminate in hair-like; trichomes not constricted at cross-walls, 8−10 μm wide in central parts, 2−4 μm long, gradually tapering towards ends, cells at terminal part longer than wide; sheath thin, colourless; hormogonia arise from central parts of trichomes.

Nostocales
Nodulariaceae

***Nodularia moravica* Hindák, Smarda & Komárek 2003 (Fig. 1C, D)**

Reference. Komárek 2013, p. 914, fig. 1187.
Occurrence. Taein reservoir (April 17, 2024).

Filaments solitary or in mucilaginous, microscopic to macroscopic mats on the substrate; individual filament 8−15 μm wide, parallel arranged or entangled. Trichomes cylindrical, constricted at the cross-walls, not attenuated towards ends. Sheath cylindrical, thin, colourless, open at both ends. Cells short barrel-shaped, always shorter than wide, with homogeneous content, without gas vesicles, blue-green, sometimes slightly granulated. Trichomes with intercalary regular distances heterocysts, occasionally

Table 1. Informations of sampling sites.

Sampling sites	Longitude/Latitude	Characteristic of sampling site	pH	EC (μS/cm)	Alt. (m)	Sampling date
Mulyoungari-orum	126°41′36″E, 33°22′09″N	Oligotrophic caldera lake	5.6	36.1	479	2015.7.17
Muljangal-orum	126°36′25″E, 33°24′28″N	Oligotrophic caldera lake	6.7	22.0	886	2015.7.17
1100m wetland	126°21′27″E, 33°21′27″N	Oligotrophic *Sphagnum* bog	6.5	24.6	1097	2015.6.17
Sumeonmulbangdi	126°26′54″E, 33°21′50″N	Oligotrophic *Sphagnum* bog	5.4	47.0	981	2016.10.16
Dongbaekdongsan	126°42′55″E, 33°31′06″N	Oligotrophic shallow rock pond	6.1	54.7	99	2016.4.22
Udo Unnamed pond	126°57′12″E, 33°30′04″N	Mesotrophic shallow agricultural pond	7.1	55.1	29	2024.2.17
Taein reservoir	127°45′13″E, 34°57′08″N	Mesotrophic agricultural reservoir	7.6	110.4	5	2024.4.17
Hwaeomneup	129°05′56″E, 35°24′22″N	Oligotrophic *Sphagnum* bog	5.6	23.5	772	2016.7.17
Mujechineup	129°08′34″E, 35°27′37″N	Oligotrophic *Sphagnum* bog	5.8	25.3	545	2016.3.24
Sajapyeong wetland	128°59′23″E, 35°32′11″N	Oligotrophic *Sphagnum* bog	6.1	17.5	774	2018.11.19
Palgongsan wetland	128°34′46″E, 36°02′12″N	Old mountainous small reservoir	6.7	43.3	844	2014.7.22
Guryong reservoir	128°57′56″E, 35°50′07″N	Mesotrophic highland small reservoir	6.8	90.6	561	2016.3.13
Mochje	128°13′43″E, 35°36′38″N	Oligotrophic mountainous shallow pond	6.6	75.0	150	2016.4.22
Sangho	128°39′38″E, 38°05′06″N	Oligotrophic shallow lagoon	6.9	65.3	4	2016.4.22
Imdang weir	128°54′58″E, 35°42′20″N	Oligotrophic stream	7.1	75.0	100	2016.4.23
Jangcheok reservoir	128°29′05″E, 35°26′10″N	Old mesotrophic reservoir	7.5	125.0	30	2016.4.23
Geomdan-ecological wetland	128°37′33″E, 35°54′03″N	River side wetland	7.2	85.2	24	2014.7.22
Namsan reservoir	128°50′16″E, 35°46′44″N	Mesotrophic reservoir	7.5	91.4	84	2016.10.16

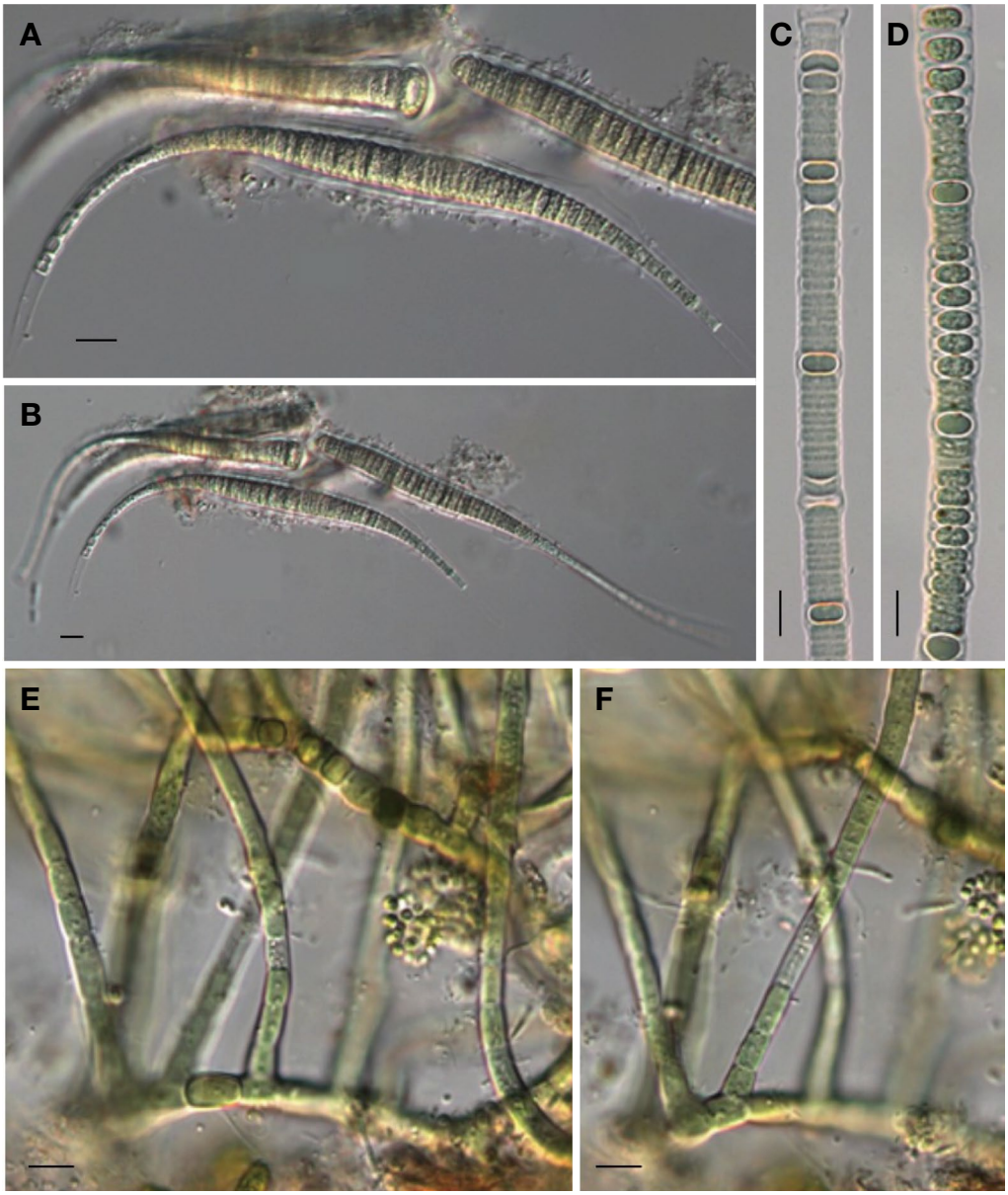


Fig. 1. A, B. *Ammatoidea sinensis*, C, D. *Nodularia moravica*, E, F. *Hapalosiphon hibernicus*. Scale bars = 10 μm.

in terminal position, solitary, shortly barrel-shaped, with greenish-yellowish, homogeneous content. Akinetes subspherical, in series, shorter than wide, with brownish granular content. Cells 8−11 μm in wide, 2−4(6) μm long, Heterocysts 8.5−11 μm in wide, 4−7 μm long, Akinetes 10−12 μm in wide, 6−8 μm long.

Hapalosiphonaceae

***Hapalosiphon hibernicus* West & G.S.West 1896 (Fig. 1E, F)**

Reference. Komárek 2013, p. 514, fig. 626.
Occurrence. 1,100 m wetland (July 17, 2015).

Filaments solitary among other algae or forming small clusters. Main axis with slightly bends and numerous narrower branches perpendicular to it. Main filament 7−10 μm in wide, branches 4.5−5.5 μm in wide; cells of the branches usually much longer than wide, typically 3−4 times, occasionally up to 8 times and sometimes almost resembling a multicellular hair. Akinete develops from several cells which from a common wall, which is thick and dark yellow-brown. Cells pale blue-green, cylindrical or very slightly barrel-shaped widened, 3−7.5 μm in wide, isometric, rarely shorter than wide; apical cells rounded, rarely slightly widened. Heterocysts intercalary, cylindrical, up to 5 times longer than wide, 3.8−6.6 μm.

Chlorophyta
Chlorophyceae
Chlamydomonadales
Chlamydomonadaceae

***Sphaerellopsis sphaerelloides* Pascher 1927 (Fig. 2A, B)**

Reference. Ettl 1983, p. 540, f. 782.
Occurrence. Mulyoungari-orum (March 25, 2015), Mochje (April 22, 2016).

Cells solitary, biflagellated, flat, broad ellipsoid, both ends rounded, covered with a broad hyaline envelop; protoplast narrow ellipsoid to spindle-shaped; cell wall smooth, flagella as long as cell length; chloroplast cup-shaped, with basal pyrenoid and without stigma; cells 17−19 μm in diameter, 28−30 μm long.

Charophyta
Conjugatophyceae
Desmidiales
Closteriaceae

***Closterium acutum* var. *variabile* (Lemmermann) W. Krieger 1935 (Fig. 2C, D)**

Reference. Coesel & Meesters 2007, p. 39, pl. 8, figs. 18, 19; Růžička 1977, p. 97, pl. 6, figs. 32−37; Prescott *et al*., 1975, p. 31, pl. 16, figs. 8−10.
Occurrence. Gasan-sanseung (July 22, 2014).

Cells slender, 10 to 36 times longer than wide, irregularly curved and mostly strongly curved (nearly semicircular), sometimes one semicell curved and the other nearly straight, sigmoid forms common; gradually tapering from the middle to ends; cells 2.5−6 μm in wide, 40−150 μm long.

Desmidiales
Desmidiaceae

***Cosmarium amoenum* var. *mediolaeve* Nordstedt 1887 (Fig. 2E−H)**

Reference. Coesel & Meesters 2007, p. 105, pl. 71, figs. 11-12; Prescott *et al*. 1981, p. 65, pl. 287, figs. 3, 11.
Occurrence. Sajapyeong wetland (November 19, 2018).

Cells medium sized, about 1.3 to 1.6 times longer than broad, moderately constricted in the middle, sinus narrowly open to almost closed; cell wall granulated, granules disposed in vertical and lateral series, just above the isthmus arranged in two transverse rows and the median part of the semicell face without granules; semicells subquadrate, lateral margins slightly convex and subparallel each other, apex straight to slightly convex, apical angles broadly rounded; side view of semicells ovate-oblong; vertical view of semicells broadly elliptic; cells 33−38 μm in broad, 50−55 μm long, isthmus 14−15 μm.

***Cosmarium quadratum* var. *willei* (Schmidle) W.Krieger & Gerloff 1969 (Fig. 2I, J)**
(Syn. *Cosmarium quadratum* f. *wellei* (Schmidle) West & G.S.West 1908)

Reference. Prescott *et al*. 1981, p. 261, pl. 293, figs. 6, 7.
Occurrence. Sajapyeong wetland (April 22, 2018).

Cells medium sized, about twice as long as broad, moderately constricted in the middle, sinus narrowly linear, almost closed; semicells subquadrate, lateral margins straight and parallel each other, apex straight to slightly convex, apical angles broadly rounded, basal angles rectangularly rounded; side view of semicells ovate; vertical view of semicells elliptic; cells 32−35 μm in broad, 55−60 μm long, isthmus 17−20 μm.

***Cosmarium quadratum* var. *minus* Förster 1965 (Fig. 2K, L)**

Reference. Yamagishi & Akiyama 1987, v. 11, p. 13.
Occurrence. Mujechi-neup (March 24, 2016), Hwaeomneup (July 17, 2019).

Cells medium sized, about 1.7−1.8 times longer than broad, moderately constricted in the middle, sinus narrowly linear and closed; semicells slightly pyramidal, lateral margins tapered to apex, apex retuse at the middle, basal angles mostly protruding and rounded; side view of semicells narrowly pyramidal; vertical view of semicells broadly elliptic; cell wall punctate; cells 23−29 μm in broad, 37−50 μm long, isthmus 10−12 μm.

***Cosmarium speciosum* f. *minus* Wille 1879 (Fig. 2M−P)**

Reference. West & West 1908, p. 251, pl. 89, figs. 8−10; Prescott *et al*. 1981, p. 289, pl. 272, fig. 6, pl. 273, fig. 4.
Occurrence. Sajapyeong wetland (April 22, 2018).

Cells medium sized, about 1.4−1.5 times longer than broad, moderately constricted in the middle, sinus narrowly linear and closed; semicells slightly pyramidal, lateral margins slightly tapered to apex and crenate, crenations 6, apex evidently truncate and 4 crenate, apical crenations 4, granulate within the margin, 3−4 granules in regular concentric and radial series, with 6−9 vertical series of granules just above the isthmus; vertical view of semicells elliptic; cells 22−23 μm in broad, 31−33 μm long, isthmus 11−13 μm. This variety differ from the typical in that the semicells rather more pyramidate, with the apex more evidently truncate and smaller size.

***Cosmarium turpinii* Brebisson 1856 (Fig. 3A−C)**

Reference. West & West 1908, p. 189, pl. 82, figs. 16−17, pl. 83, fig. 1; Prescott *et al*. 1981, p. 338, pl. 275, figs. 5, 7; Coesel & Meesters 2007, p. 148, pl. 78, fig. 1.
Occurrence. Imdang weir (May 01, 2017).

Cells medium sized, slightly longer than broad, very deep

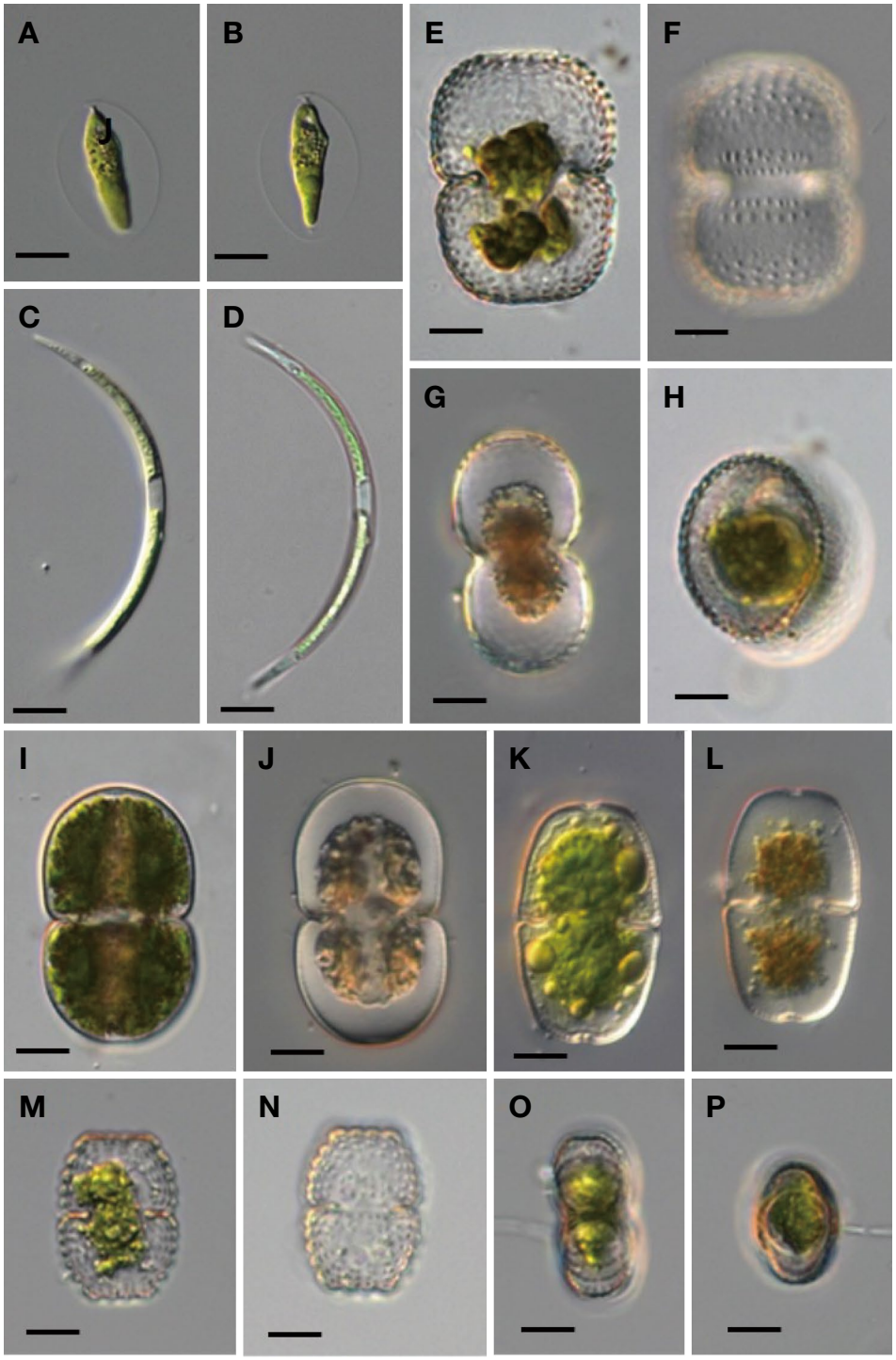


Fig. 2. A, B. *Sphaerellopsis sphaerelloides*, C, D. *Closterium acutum* var. *variabile*, E−H. *Cosmarium amoenum* var. *mediolaeve*, I, J. *Cosmarium quadratum* var. *willei*, K, L. *Cosmarium quadratum* var. *minus*, M−P. *Cosmarium speciosum* f. *minus*. Scale bars = 10 μm.

constricted in the middle, sinus narrowly linear, somewhat open outwards; semicells pyramidate to trapeziform, basal angles rounded, lateral margins slightly concave in the upper part, apical angles obtuse, apex straight to slightly retuse; cell wall with densely and regularly disposed granules, in the center of the semicells with a pair of closely adjacent tumours, each furnished with a group of verrucae; Just above the isthmus some transversal series of granules;

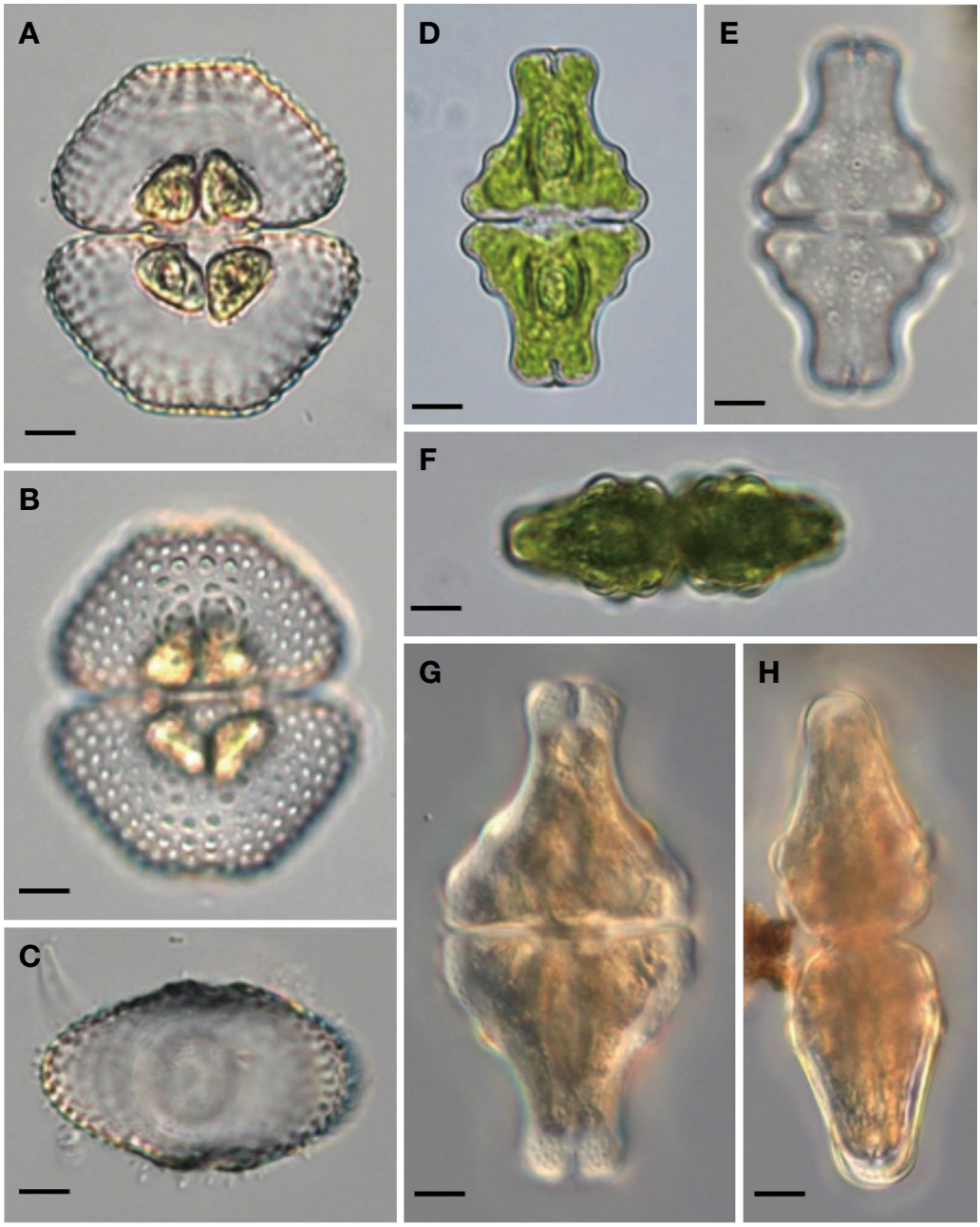


Fig. 3. A–C. *Cosmarium turpinii*, D–F, *Euastrum dedelta* var. *capitatum*, G, H. *Euastrum didelta* var. *japonicum*. Scale bars = 10 μm.

vertical view of semicells ellipsoid with a pair of adjacent granular tumours at the middle on either side; cells 50–66 μm in broad, 60–77 μm long, isthmus 12–14 μm.

***Euastrum didelta* var. *capitatum* (A.M.Scott & Prescott) Anissimova & Guiry 2021 (Fig. 3D–F)**
(Syn. *Euastrum sinuosum* var. *capitatum* A.M.Scott & Prescott 1961)

Reference. Yamagishi & Akiyama 1988, v. 8, p. 44.
Occurrence. Mulyoungari-orum (May 21, 2015), Muljangal-orum (May 21, 2015).

Cells medium sized, 1.7–1.9 times longer than broad, median constriction deep, sinus narrowly linear, somewhat delated extremity; semicells subtriangular, five lobed, polar lobe elongated, apex flat to slightly domed, with a deep and closed median incision; apical angles rounded, upper lateral lobes mamilate, lateral margins of lower lateral lobes divergent; sell wall with five protuberance, three transversely disposed at the base of semicells and two at the central part; between the central protuberances and isth-

mial protuberance a distinct mucilage pore; cells 35−40 μm in diameter, 56−70 μm long, isthmus 7−10 μm.

***Euastrum didelta* var. *japonicum* M.Hirano 1951 (Fig. 3G, H)**

Reference. Yamagishi & Akiyama 1986, v. 5, p. 33.
Occurrence. Sajapyeong wetland (September 17, 2018).

Cells large, about two times longer than broad, median constriction deep, sinus narrowly linear, somewhat delated extremity; semicells subpyramidate, polar lobe relatively short with parallel margins, apex truncately rounded to slightly domed, with a deep and closed median incision; lateral lobes trapeziform, lower lateral margins parallel and retuse at the middle; lateral view of semicells narrow pyramidate, lower lateral margins with two protrusions and broad rounded apex; semicells with a prominent protuberance just above and four more protuberances (two at the base and two near the centre); between the central protuberances usually a distinct mucilage pore; cells 55−60 μm in diameter, 110−115 μm long, isthmus 13−15 μm.

***Staurastrum botrophilum* Wolle 1881 (Fig. 4A−C)**

Reference. West & West 1912, p. 166, pl. 126, fig. 4; Prescott *et al*. 1982, p. 145, pl. 342, fig. 7; Coesel & Meesters 2013, p. 75, pl. 52, figs. 6−9.
Occurrence. Hwaeom-neup (Jun 16, 2016).

Cells medium sized, about as long as broad or slightly longer than broader, median constriction deep, sinus narrowly linear and slightly dilated extremity; semicell pyramidate-truncate, basal angles broadly rounded, lateral margins granular, subconvex, apex truncate and straight; cell wall with about 6 series of granules arranged in concentric around the angles; semicells in vertical view triangular, lateral margins slightly concave in the middle, angles broadly rounded; granules forming annular series around the lobes; cells 35−40 μm wide, 38−42 μm long, isthmus 10−11 μm.

***Staurastrum octodontum* var. *tetrodontum* Scott et Grönblad 1957 (Fig. 4D)**

Reference. Prescott *et al*. 1982, p. 263, pl. 403, fig. 9.
Occurrence. Udo unnamed pond (Feb. 17, 2024).

Cells small, about as long as broad or slightly longer than broader with processes, median constriction shallow, sinus open U-shaped in face view; semicells bowl-shaped, the extreme base of the semicells convex and with a single short spine, apical margin broadly concave, apical angles projected upward into a long nodulated process, tipped with three sharp spined, lateral margin with teeth along the midline; semicells in vertical view fusiform, angles extending into processes with spine margins; cells 28−34 μm wide, 33−36 μm long with processes, 10−13 μm long without processes, isthmus 4−5 μm.

***Staurodesmus brevispina* (Brebisson) Croasdale 1957 (Fig. 4E−G)**

(Syn. *Staurastrum brevispinum* Ralfs)

Reference. West & West 1912, p. 145, pl. 123, figs. 1−3; Coesel & Meesters 2007, p. 158, pl. 90, figs. 15−18; Prescott *et al*. 1982, p. 150, pl. 332, figs. 11, 16.
Occurrence. Imdang weir (May 01, 2017).

Cells medium sized, about as long as broad, median constriction deep, sinus open and acute-angled at the apex; semicells oblong-elliptic, ventral margin usually more convex than the dorsal margin, apex convex or subtruncate, lateral angles broadly rounded and furnished with a mucro or papilla; cell wall smooth; semicells in vertical view triangular, the sides concave, angles broadly rounded and furnished with a small mucro; cells 25−30 μm wide, 28−35 μm long, isthmus 8−10 μm.

***Xanthidium concinnum* W.Archer 1883 (Fig. 4H−K)**

Reference. West & West 1912, p. 86, pl. 112, fig. 10; Prescott *et al*. 1982, p. 61, pl. 310, fig. 24, pl. 312, fig. 7.
Occurrence. Mulyoungari-orum (May 21, 2015).

Cells small sized, about as broad as long, median constriction deep, sinus narrow and linear, acutely open outward; semicells transversely subhexagonal, apex truncate, lateral angles furnished with a single minute spine, apical angles furnished with a pair of minute spines; lateral view of semicell subcircular, with a small papilla at the middle on either side and a pair of minute spines at the apical margin; in the vertical view of semicells elliptic, with a prominent papilla on the middle on either side and with one minute spine at both poles; cell wall smooth; cells 10−12 μm in diameter without spines, 10−11 μm long, isthmus 3.5−4.5 μm.

***Xanthidium planum* (Roll) Coesel & Meesters 2023 (Fig. 4L, M)**

(Syn. *Xanthidium antilopaeum* var. *planum* Roll 1936)

Reference. Coesel & Meesters 2007, p. 153, pl. 83, figs. 4, 5; Prescott *et al*. 1982, p. 54, pl. 316, fig. 5.
Occurrence. 1,100 m wetland (May 21, 2015).

Cells medium sized, about as broad as long, median constriction deep, sinus shortly linear with a slightly dilated extremity, acutely open outward; semicells subelliptic-hexagonal, all the angles very slightly rounded, each of the four exposed angles furnished with a pair of simple, straight or slightly curved, fairly stout long spines, upper lateral margins and apex straight to slightly concave, central part of semicell thickened, round or elliptic, variously scrobiculated; lateral view of semicell circular or subcircular, with a slightly thickened at both side, and a pair of diverging spines on the apical margin; in vertical view of semicells elliptic, with a slight thickening at the middle on each side, and with a pair of slightly divergent spines on each

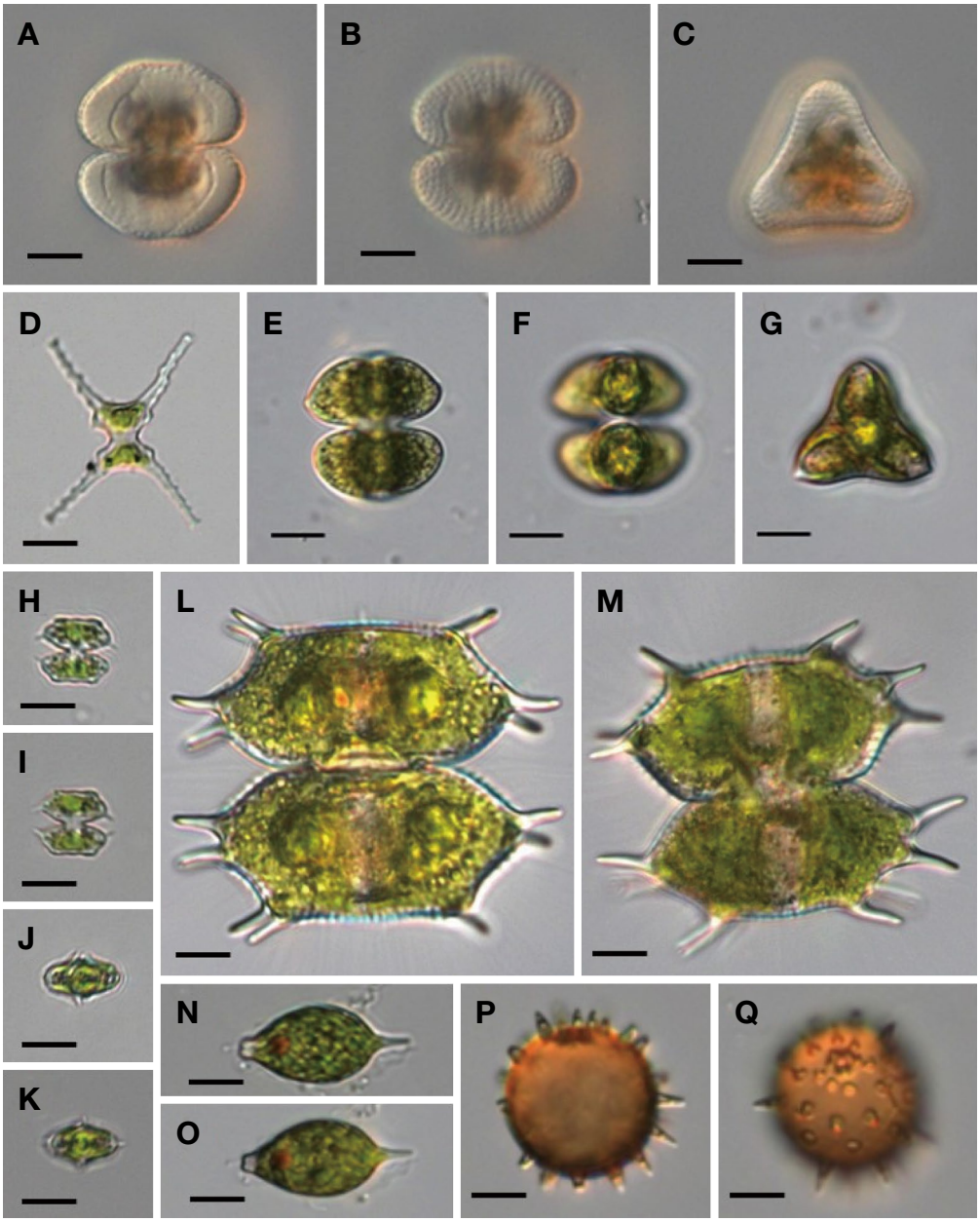


Fig. 4. A–C. *Staurastrum botrophilum*, D. *Staurastrum octodontum* var. *tetrodontum*, E–G. *Staurodesmus brevispina*, H–K. *Xanthidium concinnum*, L, M. *Xanthidium planum*, N, O. *Lepocinclis caudata* var. *wuhienweni*, P, Q. *Trachelomonas afra*. Scale bars = 10 μm.

polar margin; cell wall finely punctate; cells 48–55 μm in diameter without spines, 48–55 μm long, isthmus 15–17 μm, spines 8–10 μm long. This variety differs from the typical species in that the apical spines are widely more divergent as to form an angle of 100–135° with the apical margin of the semicell.

Euglenophyta
Euglenophyceae
Euglenales
Phacaceae

***Lepocinclis caudata* var. *wuhienweni* Chu 1935 (Fig. 4N, O)**

Reference. Yamagishi & Akiyama 1989, v. 10, p. 41.
Occurrence. Hwaeom-neup (March 25, 2016).

Cells spindle-shaped, anterior end narrowly produced, truncate and slightly bipapillated; posterior end projected into a long, straight, sometimes slightly curved cauda; periplasts spirally striated; paramylon bodies two, ring-like plate; cells 14–18 μm in diameter, 32–39 μm long with a cauda.

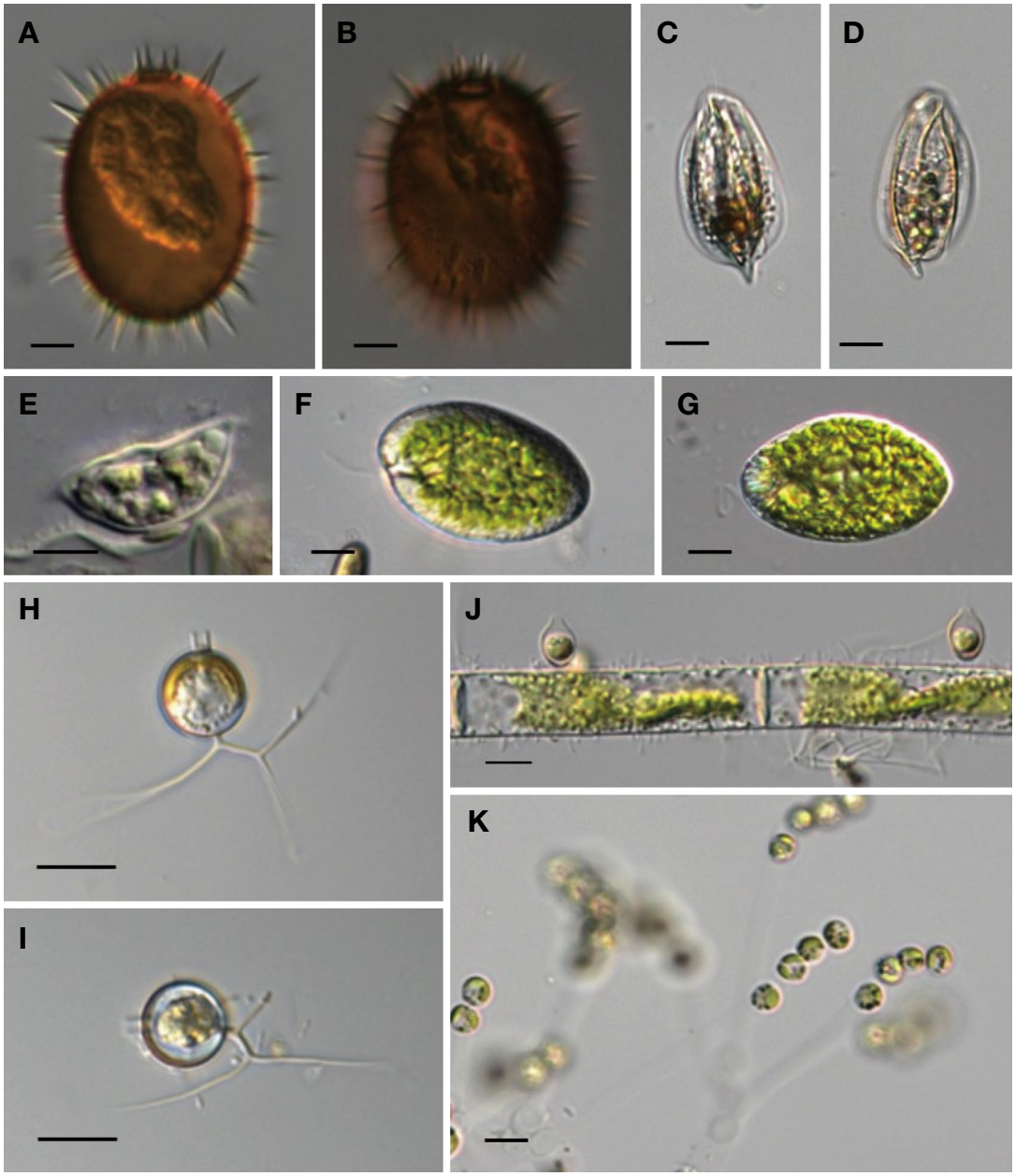


Fig. 5. A, B. *Trachelomonas megalacantha*, C, D. *Petalomonas platyrhyncha*, E. *Dinococcus oedogonii*, F, G. *Merotricha capitata*, H, I. *Chrysococcus furcatus*, J. *Chrysopyxis inaequalis*, K. *Mischococcus confervicola*. Scale bars = 10 μm.

Trachelomonas afra Rino 1981 (Fig. 4P, Q)

Reference. Yamagishi & Akiyama 1996, v. 16, p. 84.
Occurrence. Jangcheok reservoir (August 05, 2018).

Lorica spherical, brown in color; flagella apertures with a short cylindric collar having few short, blunt spines around the mouth; wall sparsely covered with short, stout, blunt spines having a clear dark-brown, transverse septa in the middle; lorica 24−28 μm in diameter, spines 4−6 μm long. This species is very similar to *Trachelomonas lismorensis* var. *mirabilis* Playfair in the shape of the lorica and stout spines covering the wall, but differs it in having the short cylindrical collar with short spines around the mouth.

Trachelomonas megalacantha A.M.Cunha 1914 (Fig. 5A, B)

Reference. Yamagishi & Akiyama 1988, v. 8, p. 90; Huber-Pestalozzi 1955, p. 307, fig. 579.
Occurrence. Guryong reservoir (May 01, 2017).

Lorica large ellipsoid, both ends narrowed and rounded; flagella apertures without a clear collar, but often surround-

ed by a circle of small spines; wall covered by many stout, long spines having a pointed apex; lorica 30−36 μm in diameter, length 55−60 μm, spines 10−12 μm long, 2−3 μm broad at the base.

Stavomonadea
Petalomonadida
Scytomonadidae

***Petalomonas platyrhyncha* Skuja 1948 (Fig. 5C, D)**

Reference. Huber-Pestalozzi 1955, p. 502, fig. 1026.
Occurrence. Dongbaekdongsan (July 17, 2016), Geomdan-ecological wetland (September 18, 2017).

Cells flat, rigid, ellipsoid; anterior end slightly narrowed and broadly rounded or truncate rounded, with a small furrow; posterior end gradually tapered and projected into a short, stout cauda; pellicle with strong longitudinal rib, with several keels with grooves on both dorsal and ventral side flat-convex; dorsal side convex and ventral side flat cells 18−25 μm in diameter, length 38−42 μm.

Dinophyta
Dinophyceae
Phytodiniales
Phytodiniaceae

***Dinococcus oedogonii* (P.G.Richter) Fott 1960 (Fig. 5E)**
(Syn. *Raciborskia bicornis* Wolozyńska 1919)

Reference. Dillard 2007, p. 84, pl. 17, fig. 10; John *et al*. 2011, p. 271, pl. 70, fig. G.
Occurrence. Mulyoungari-orum (October 12, 2014).

Cells epiphytic with broad disc-shape stock on the filamentous algae, ellipsoid in face view, both ends with a single short spine, upper margin straight, laternal margins roundly convex; cells 9−12 μm in diameter, length 25−35 μm.

Heterokontophyta
Raphidophyceae
Chattonellales
Vacuolariaceae

***Merotricha capitata* Skuja 1934 (Fig. 5F, G)**

Reference. Dillard 2007, p. 78, pl. 16, fig. 5.
Occurrence. Guryong reservoir (November 06, 2021), Namsan reservoir (October 16, 2016).

Cells solitary, free-swimming, ovoid to ellipsoid, posterior broadly round or slightly narrowed, anterior with a group of radially arranged trichocysts; flagella subapicular or lateral; cells diameter 25−28 μm, length 39−45 μm.

Chrysophyceae
Chromulinales
Chrysococcaeae

***Chrysococcus furcatus* Nicholls 1981 (Fig. 5H, I)**
(Syn. *Trachelomonas furcata* Dolgoff 1922)

Reference. Huber-Pestalozzi 1955, p. 350, fig. 752.
Occurrence. Namsan reservoir (January 31, 2021).

Lorica spherical, light brown in color; flagella apertures with a long cylindric collar; wall with a long, 1st or secondary branched spine; lorica 11−12.5 μm in diameter, spines 4−6 μm long; collar 2−2.5 μm in diameter, 2.5−3.0 μm long; spines 20−25 μm long.

Chrysosaccales
Stylococcaceae

***Chrysopyxis inaequalis* Fott 1952 (Fig. 5J)**

Reference. Yamagishi & Akiyama 1995, v. 14, p. 7.
Occurrence. Sajapyeong wetland (April 22, 2016).

Cells solitary, epiphytic on the filamentous algae, surrounded by a lorica; loricae circular to broad-ellipsoid in side view, anterior end with a short and narrow neck; attached to the host alga by two thread-like outgrowth from the rounded base; protoplasts ovoid to globose with a single laminate, golden-brown chromatophore; lorica 6−9 μm in diameter, length 9−11 μm.

Xanthophyceae
Mischococcales
Mischococcaceae

***Mischococcus confervicola* Nägeli 1849 (Fig. 5K)**

Reference. Dillard 2007, p. 60, pl. 11, fig. 2; Yamagishi & Akiyama 1985, v. 3, p. 56.
Occurrence. Sangho (February 08, 2021).

Thalli epiphytic, dendroid colony consisting of dichotomously or trichotomously branched, with cells in two or four at the apices of gelatinous tube. Cells globose, single or in pairs in the distal ends of the branching tubes; Chloroplasts single or few discoid, parietal, yellowish-green color. Cells diameter 3.5−5.5(5−8) μm.

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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Ten species of the tribe Trypetini (Insecta: Diptera: Tephritidae: Trypetinae) newly recorded in Korea

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In the process of investigating the fly family Tephritidae in Korea, we report the following ten species of the tribe Trypetini new to this country: *Anomoia apicalis* Ito, 1984, *Chetostoma esakii* (Ito, 1960), **comb. nov.**, *Chetostoma flexuosum* (Zia, 1938), **comb. nov.**, *Chetostoma melliculum* Richter, 1965, *Chenacidiella purpureiseta* (Chen, 1948), *Dryadodacryma albicostale* Ito, 1984, *Hemileoides theodori* Rohdendorf, 1955, *Ihekaze diversa* (Ito, 1952), *Morinowotome itoi* Korneyev, 1998, and *Stemonocera corruca* (Hering, 1937). Among the eight genera treated here, *Chenacidiella* Shiraki, 1968, *Dryadodacryma* Ito, 1984, *Ihekaze* Ito, 1984, and *Hemileoides* Rohdendorf, 1955 are recorded for the first time in Korea. As a result, 67 genera and 116 species are recognized for the Korean tephritid fauna. We provided a new Korean name, synonymy, distribution, taxonomic diagnosis, and color photographs for each newly recognized Korean species. When possible, we mentioned their biology and discussed intraspecific variability, sexual dimorphism, and systematic status. In addition, we acknowledge here the genus *Sinacidia* Chen, 1948, as a junior synonym of the genus *Chetostoma* Rondani, 1856. On the other hand, we here resurrect the genera *Dryadodacryma* and *Hemileoides* from the synonymy of *Hemilea* Loew, 1862, and the genus *Ihekaze* from the synonymy of *Acidiella* Hendel, 1914. We also recognize Japanese *Hemileoides continuum* (Ito, 1984) as a **comb. nov.** from the genus *Dryadodacryma*.

Keywords: *Anomoia*, *Chenacidiella*, *Chetostoma*, *Dryadodacryma*, *Hemileoides*, *Ihekaze*, *Morinowotome*, *Stemonocera*

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Introduction

The Tephritidae is a large family of acalyptrate flies including over 5,200 valid species and 490 genera worldwide (Norrbom *et al*., 1999; Catalogue of Life as of December 2024 - www. Catalogueoflife.org). They are primarily phytophagous flies that contain some of the most significant global agricultural pests, and others are significant for their role in the biological control of weeds (White and Elson-Harris, 1992; Han and Ro, 2019). In the latest molecular phylogenetic analysis of the superfamily Tephritoidea (Han and Ro, 2016), we suggested that the concept of the family Tephritidae should be expanded to include parasitic tephritoid families (i.e., Pyrgotidae and Ctenostylidae). If this happens (Han and Ro, in prep.), the estimated number of valid tephritid species could exceed 5,500.

Han (2022) previously enumerated a total of 56 genera and 112 species of Tephritidae in Korea. As a result of our recent reclassification of this list (Han and Ro, in prep.) and the additional four genera and ten species listed in the following paragraph, we now recognize 67 genera and 116 species for the Korean tephritid fauna.

In the present study, we report ten newly recorded species of the tribe Trypetini in the Korean Peninsula: *Anomoia apicalis* Ito, 1984, *Chetostoma esakii* (Ito, 1960), *Chetostoma flexuosum* (Zia, 1938), *Chetostoma mellic-*

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ulum Richter, 1965, *Chenacidiella purpureiseta* (Chen, 1948), *Dryadodacryma albicostale* Ito, 1984, *Hemileoides theodori* Rohdendorf, 1955, *Ihekaze diversa* (Ito, 1952), *Morinowotome itoi* Korneyev, 1998, and *Stemonocera corruca* (Hering, 1937). Among the eight genera listed here, *Chenacidiella* Shiraki, 1968, *Dryadodacryma* Ito, 1984, *Ihekaze* Ito, 1984, and *Hemileoides* Rohdendorf, 1955 are recognized for the first time for the Korean tephritid fauna. We provided a new Korean name, synonymy, distribution, taxonomic diagnosis, and color photographs for each species included. When possible, we mentioned their biology and discussed intraspecific variability, sexual dimorphism, and systematic status.

Materials and Methods

The morphological terminology and interpretations used in this study follow White *et al*. (1999). Photographs were taken with a Panasonic (Osaka, Japan) DMC G5 and G7 cameras with a Panasonic Lumix 45−175 mm lens and a Raynox (Yoshida Inc., Tokyo, Japan) MSN-202 macro conversion lens. The consecutive digital images in different focal planes (usually 50−100 shots per a single figure) were Z-stacked using Helicon Focus software (Helicon Soft, Ltd., Khirkov, Ukraine). Some photographs of live specimens (kept in a glass cage) were taken with a Nikon (Tokyo, Japan) D7000 camera with a macro lens and extension tubes.

Most of the specimens used in this study are deposited in the Division of Biological Science and Technology, Yonsei University, Wonju, Korea (YSUW), and some are in the National Institute of Biological Resources, Incheon, Korea (NIBR) and Korea National Arboretum, Gwangneung, Korea (KNA). Abbreviations of the other institutions mentioned in the text are as follows: EUMJ, Ehime University, Entomological Laboratory, Matsuyama, Japan; IZAS, Institute of Zoology, Academia Sinica, Insect Collection, Beijing, China; UOPJ, Entomological Laboratory, University of Osaka Prefecture, Osaka, Japan; ZISP, Zoological Museum, Academy of Sciences, Russian Academy of Sciences, Universitetskaya, Naberzhnayal B-164, St. Petersburg, Russia; ZMHU, Museum fur Naturkunde der Humboldt Universitat zu Berlin, Bereich Zoologisches Museum, Invalidenstrasse 43, Berlin, D-1040, Germany; ZMM, Zoological Museum, University of Moscow, Herzen str. 6, Moscow 103009, Russia.

Systematic Accounts

Order Diptera Linnaeus, 1758
Family Tephritidae Newman, 1834
Subfamily Trypetinae Loew, 1861
Tribe Trypetini
Subtribe Chetostomatina Han, 1999
Genus *Anomoia* Walker, 1835

1. *Anomoia apicalis* Ito, 1984
끝검정부채과실파리 (신칭) (Fig. 1A−C)

Anomoia apicalis Ito 1984: 84 (type locality: Japan, Shikoku, Iyo, Sugitate, near Matuyama; holotype ♀ EUMJ); Wang 1998: 149 (diagnosis, distribution); Norrbom *et al*. 1999: 84 (in world catalog); Sueyoshi 2000 (Tokyo, Im-

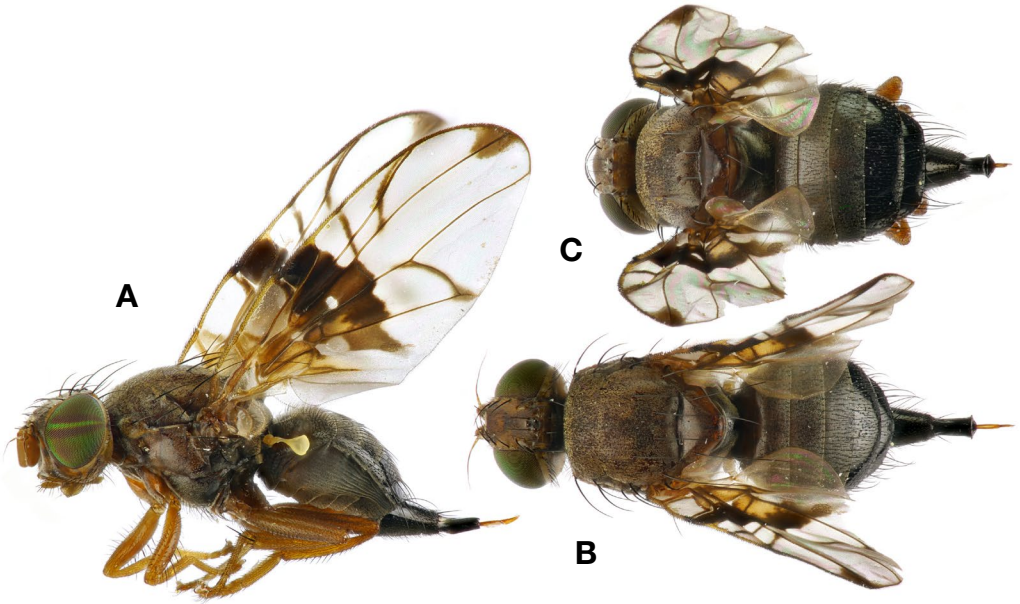


Fig. 1. *Anomoia apicalis* Ito, 1984. A. female, lateral view; B. female, dorsal view; C. female, dorso-caudal view.

perial Palace); Sueyoshi *et al*. 2003: 190 (Ibaraki Pref., Japan); Korneyev & Ovchinnikova 2004: 483 (in Russian FE key); Yamauchi *et al*. 2010: 16 (Mt. Sara, Shikoku, Japan); Sueyoshi 2014: 574 (in Japanese catalog).

Phagocarpus apicalis Ito 1956: 24 (*nomen nudum*, published after 1930 without a description).

Diagnosis. All four known Korean species of *Anomoia* can be easily recognized by their peculiar narrow medially interrupted C-shaped apical to subapical wing bands (Fig. 1C). *Anomoia apicalis* can be further distinguished from Korean congeners by the combination of the following characteristics (Fig. 1): 1) body entirely brown to dark brown with orange-brown legs; 2) dark brown spot on apex of vein R_{2+3}; 3) C-band completely interrupted in cell r_{4+5}; 4) C-band dorsally terminated at apex of vein R_1; and 5) cell c almost entirely hyaline except narrow brownish basal and apical areas.

Description of Korean material. Wing length 5.4−5.8 mm, body brown to dark brown with orange-brown head and legs, with dark brown setae and setulae. Head brown with 3 frontal and 2 orbital setae; ocellar triangle dark brown with ocellar seta as long as anterior orbital seta; genal setae strong, dark brown; scutum matte brown; dorsocentral setae about same level as postsutural supra-alar setae; dorsocentral setae well above level of intra-alar setae; postpronotal lobe similar color as scutum; scutellum subshiny brown, almost bare with sparse lateral setulae; 2 pairs of long scutellar setae with apical pair slightly shorter and crossed subapically; mediotergite shiny dark brown; anatergite and katatergite dark brown; anepisternum brown with lower seta slightly shorter than upper seta; remaining mesopleura dark brown. Legs orange-brown with dark brown setae and setulae. Wing hyaline with narrow C-shaped apical to subapical band interrupted completely in cell r_{4+5}, dorsally ended at apex of vein R_1; large dark brown spot on apex of vein R_{2+3}; dark subcostal band broadly formed from dark brown pterostigma, basal to crossvein R-M, basal half of cell dm, cell bm, narrowly in anal lobe ended at about 2/5−1/3 to wing margin; cell bc hyaline, cell c almost hyaline except for narrow brownish basal and apical areas; cell br dark brown with round hyaline spot basal 1/3 between crossveins BM-Cu and DM-Cu. Abdominal tergites dark brown; oviscape dark brown cylindrical; aculeus laterally flattened and apico-ventrally serrated. Male unknown.

Material examined. KOREA: Jeollanam-do: Haenam-gun, Haenam-eup, Gugyo-ri, Mt. Geumgangsan, N34°35′28″ E126°36′7″, 19.V.2019, S.S. Euo *et al*., 1♀ (YSUW); Gwangyang-si, Ongnyong-myeon, Mt. Baegunsan from Hanjae hill, N35°6′23″, E127°37′17″ 23.V.2019, S.-S. Euo *et al*., 2♀ (NIBR); *ditto*, 1♀ (YSUW); *ditto*, 6.V.2020, 3♀ (YSUW).

Distribution. Korea (Jeollanam-do), Japan (Honshu, Shikoku, Ryukyu Is.)

Biology. Unknown.

Remarks. We were not able to obtain male specimens in Korea. Coincidentally, Ito's (1984) type series also includes only females. The new Korean name refers to its peculiar dark spot at the apex of wings (Fig. 1A).

Genus *Chetostoma* Rondani, 1856

2. *Chetostoma esakii* (Ito, 1960), comb. nov.
에사키턱가시과실파리 (신칭) (Fig. 2A−E)

Euleia (*Sinacidia*) *esakii* Ito 1960: 1 (type locality: Japan, Kyushu, Buzen, Hikosan; holotype ♀ UOPJ); Ito 1956: 25 (*nomen nudum* - published after 1930 without a description).

Euleia esakii: Foote 1984: 88 (in Palaearctic catalog).

Sinacidia esakii: Ito 1984: 174 (in Japanese identification manual); Han 1992: 172 (listed as an unconfirmed taxon of Trypetini); Ichita 1994: 61 (Aomori Pref., Japan); Wang 1998: 198 (in East Asian identification manual); Norrbom *et al*. 1999: 205 (in world catalog); Yamauchi & Kagesawa 2000: 112 (Hiraka town, Iwate Pref., Honshu, Japan); Korneyev & Ovchinnikova 2004: 486 (in Russian FE key); Sueyoshi & Inoue 2004: 4 (Fukui Pref., Honshu, Japan); Yamauchi *et al*. 2010 (Mt. Sara, Ehime Pref., Shikoku, Japan); Sueyoshi 2014: 586 (in Japanese catalog).

Diagnosis. *Chetostoma esakii* can be distinguished from Korean congeners by the combination of the following characteristics (Fig. 2): 1) mediotergite completely dark brown (Fig. 2D); 2) oviscape orange-brown (Fig. 2C, D); 3) discal band and accessory costal band merged to form more or less Y-shaped band; 4) stem of this Y-shaped band widely separated from subapical band in anal lobe; and 5) dark brown subapical and anterior apical band touching or slightly separated to form inverted L-shaped band.

Description of Korean material. Wing length 5−5.9 mm, body almost entirely orange-brown with dark brown setae and setulae. Head orange-brown with 3 frontal and 2 orbital setae; ocellar triangle dark brown with ocellar seta strong, about as long as posterior orbital seta; genal seta strong, dark brown; anterior corner of gena with stronger setulae in male (slightly shorter than genal seta), but normal (mostly shorter than half as long as genal seta) in female (Fig. 2A vs. 2C); scutum matte orange-brown; dorsocentral setae about same level as postsutural supra-alar setae; acrostichal setae slightly above level of intra-alar setae; postpronotal lobe similar color as scutum; scutellum subshiny orange-brown, almost bare with sparse lateral setulae; 2 pairs of long scutellar setae with apical pair slightly shorter and parallel; mediotergite completely subshiny dark brown; anatergite and katatergite orange-brown; ane-

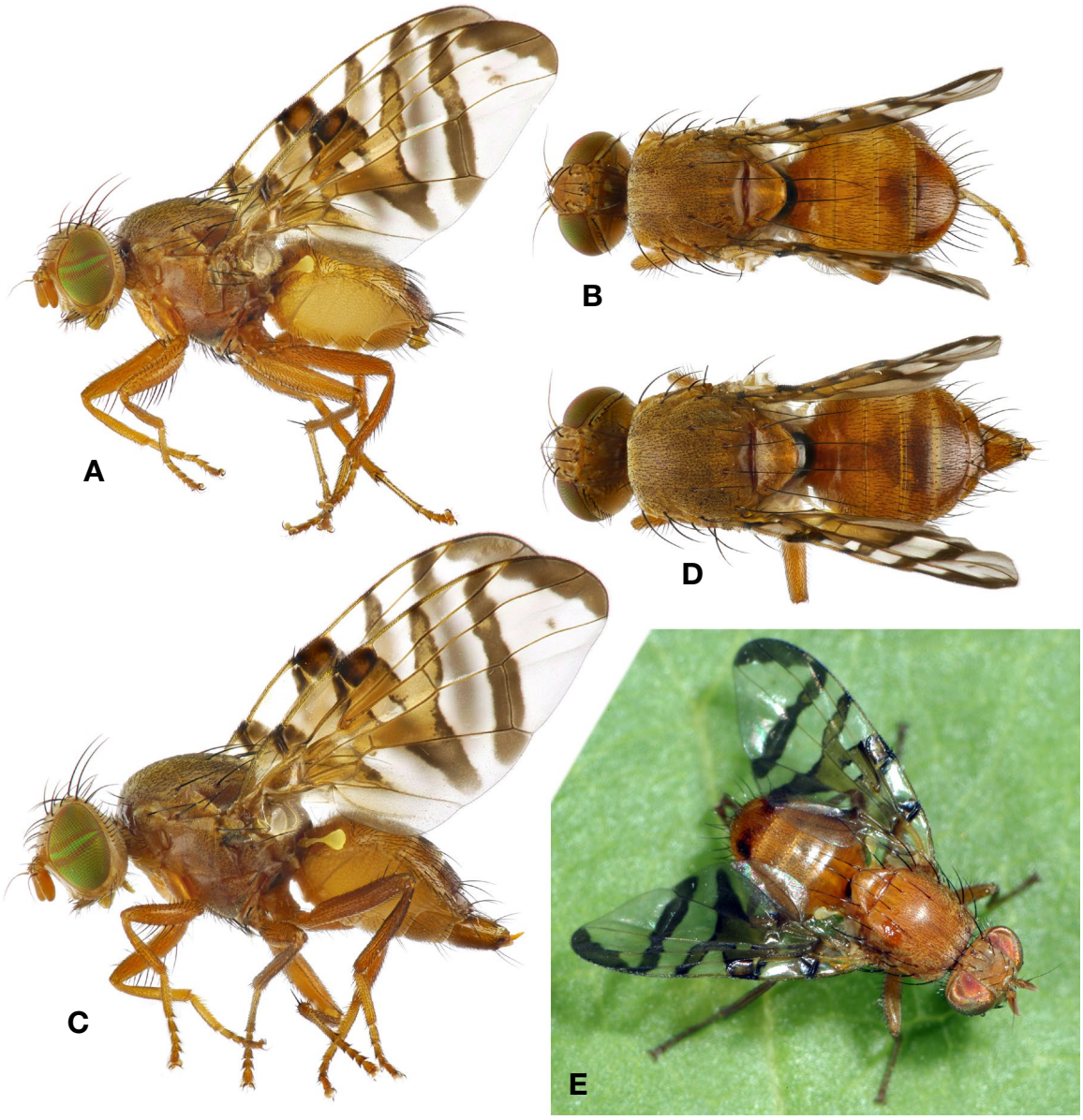


Fig. 2. *Chetostoma esakii* (Ito, 1960). A. male, lateral view; B. male, dorsal view; C. female, lateral view; D. female, dorsal view; E. live male.

pisternum orange-brown with lower seta slightly shorter than upper seta; remaining mesopleura orange-brown except katepisternum and meron with dark brown tinge ventrally. Legs orange-brown with dark brown setae and setulae. Wing hyaline with dark brown anterior apical band and subapical band slightly touching or separated to form inverted L-shaped band, subapical band in cell r_{4+5} variably yellowish brown in middle; tiny postero-medial brown spot in hyaline area of cell r_{4+5} between subapical and anterior apical bands; discal and accessory costal bands merged to form more or less Y-shaped band, cells r_1, r_{2+3} portion of Y-band yellowish brown margined with dark brown color; cell br yellowish brown with more or less rectangular hyaline spot at basal 1/5 to apical 1/2 between crossveins BM-Cu and R-M, this spot margined outside with darker color; basal 3/5 of cell dm yellowish brown except for apical dark brown margin; stem of Y-band in anal lobe dark brown, slightly separated from wing margin and widely separated from subapical band; cell bc hyaline with narrow dark brown area anterior to crossvein H; cell c hyaline except basal 1/5 and apical 1/10 dark brown; pterostigma dark brown. Abdominal tergites orange-brown except pair of small dark brown sublateral spots on male tergite 5 (missing in some specimens); oviscape orange-brown, cylindrical, shorter than 2 preceding tergites; aculeus laterally flattened and api-

co-ventrally serrated.

Material examined. KOREA: Gangwon-do: Jeongseon-gun, Mt. Mindungsan, from Yupyeong-ri to 1,119 m peak, N37°16′15″ E128°46′30″, 16.VII.2005, H.-Y. Han *et al*., 1♂ (YSUW); *ditto*, 19.VII.2005, 1♂ (NIBR); Yeongwol-gun, Yeongwol-eup, Heungwol-ri, Mt. Taehwasan, N37° 07′03.3″ E128°29′07.4″, 1.VIII.2018, S.-S. Euo & C.-O. Kim, 3♂ 2♀ (YSUW).

Distribution. Korea, Japan (Honshu, Shikoku, Kyushu).

Biology. Unknown.

Remarks. See Remarks of *C. flexuosum*. The new Korean name refers to the specific epithet.

3. *Chetostoma flexuosum* (Zia, 1938), comb. nov.

지아턱가시과실파리 (신칭) (Fig. 3A–E)

Myiolia flexuosa Zia 1938: 43 (type locality: China, Gansu, Tsien-Ou [Tsienou]; holotype ♀ IZAS).

Myoleja flexuosa: Foote 1984: 98 (in Palaearctic catalog; listed also as *Sinacidia flexuosa* in same publication, p. 119).

Euleia (*Sinacidia*) *flexsim* [*sic*]: Ito 1956: 25 (in Japanese list).

Sinacidia flexuosa: Chen 1948: 74 (in Chinese list); Foote 1984: 119 (in Palaearctic catalog; listed also as *Myoleja flexuosa* in same publication, p. 98); Ito 1984: 173 (in Japanese identification manual); Wang 1998: 198 (in East Asian identification manual); Norrbom *et al*. 1999: 205 (in world catalog); Korneyev & Ovchinnikova 2004: 486 (in Russian FE key); Sueyoshi 2014: 586 (in Japanese catalog).

Diagnosis. *Chetostoma flexuosum* can be distinguished from Korean congeners by the combination of the following characteristics (Fig. 3): 1) mediotergite dark brown with narrow medial longitudinal orange-brown stripe (Fig. 3B); 2) oviscape orange-brown; 3) discal band and accessory costal band merged to form more or less Y-shaped band; and 4) dark brown subapical and anterior apical band merged to form uninterrupted inverted L-shaped band.

Description of Korean material. Wing length 5.4–5.5 mm, body almost entirely orange-brown with dark brown setae and setulae. Head orange-brown with 3 frontal and 2 orbital setae; ocellar triangle dark brown with ocellar seta strong, about as long as posterior orbital seta; genal seta strong, dark brown; anterior corner of gena with relatively strong setulae (about 2/3 as long as or shorter than genal seta) in both sexes; scutum matte orange-brown; dorsocentral setae slightly above level as postsutural supra-alar setae; acrostichal setae slightly above level of intra-alar setae; postpronotal lobe similar color as scutum; scutellum subshiny orange-brown, almost bare with sparse lateral setulae; 2 pairs of long scutellar setae with apical pair slightly shorter and parallel; mediotergite subshiny dark brown with narrow medial longitudinal orange-brown stripe; anatergite and katatergite orange-brown; anepisternum orange-brown with lower seta slightly shorter than upper seta; remaining mesopleura orange-brown. Legs orange-brown with dark brown setae and setulae. Wing hyaline with dark brown anterior apical band and subapical band merged to form inverted L-shaped band, subapical band in cell r_{4+5} and over crossvein DM-Cu variably yellowish brown medially; discal and accessory costal bands merged to form clear Y-shaped band, cells r_1, r_{2+3}, br, and dm portion of Y-band yellowish brown margined with darker color; cell br yellowish brown with more or less rectangular hyaline spot at basal 1/10 to apical 1/2 between crossveins BM-Cu and R-M; stem of Y-band in anal lobe largely dark brown, either separated or merged with subapical band; cell bc hyaline with narrow brown area anterior to crossvein H; cell c hyaline except basal 1/5 brown; pterostigma dark brown. Abdominal tergites orange-brown; oviscape orange-brown, cylindrical, shorter than 2 preceding tergites; aculeus laterally flattened and apico-ventrally serrated.

Material examined. KOREA: Gangwon-do: Wonju-si, Heungeop-myeon, Maeji-ri, Yonsei Univ. Mirae Campus, N37°17′10″ E127°54′01″, 3.IV.2006, H.-W. Byun, 1♀ (NIBR); Hongcheon-gun, Nae-myeon, Gwangwon-ri, Woldun-gol, N37°50′52″ E128°25′24″, 13.X.2018, S.-S. Euo *et al*., 1♂ (YSUW).

Distribution. Korea, China (Gansu), Japan (Hokkaido).

Biology. Unknown.

Remarks. We here recognize the genus *Sinacidia* Chen, 1948, as a junior synonym of *Chetostoma* Rondani, 1856. Therefore, the two known *Sinacidia* species (the type species, *flexuosum* Zia, and subsequently included species, *esakii* Ito) are newly recorded in Korea and placed under the genus *Chetostoma*. Both species are not only morphologically similar to *Chetostoma curvinerve* Rondani, 1856, (the type species of *Chetostoma*) but also genetically close, tightly forming a monophyletic group together with another Korean species, *C. melliculum* (an unpublished analysis including the majority of Trypetini genera based on over 5,000 bp mitochondrial DNA; Han and Ro, in prep.). In males of the type species, *C. curvinerve*, the anterior corner of gena has 4–8 greatly enlarged hone-like setae. In *C. esakii*, anterior genal setulae are significantly stronger in males (as Fig. 2A vs. 2C). Still, in *C. flexuosum*, such sexual dimorphism was not observed in the only available pair (Fig. 3A vs. 3C). No male is currently known for *C. melliculum*. The new Korean name of *C. flexuosum* refers to the original describer of this species.

4. *Chetostoma melliculum* Richter, 1965

리히터턱가시과실파리 (신칭) (Fig. 4A–C)

Chaetostoma melliculum Richter 1965: 136 (type locality; Russia, Primorskiy, Suputinsk Reservation; holotype ♀ ZISP).

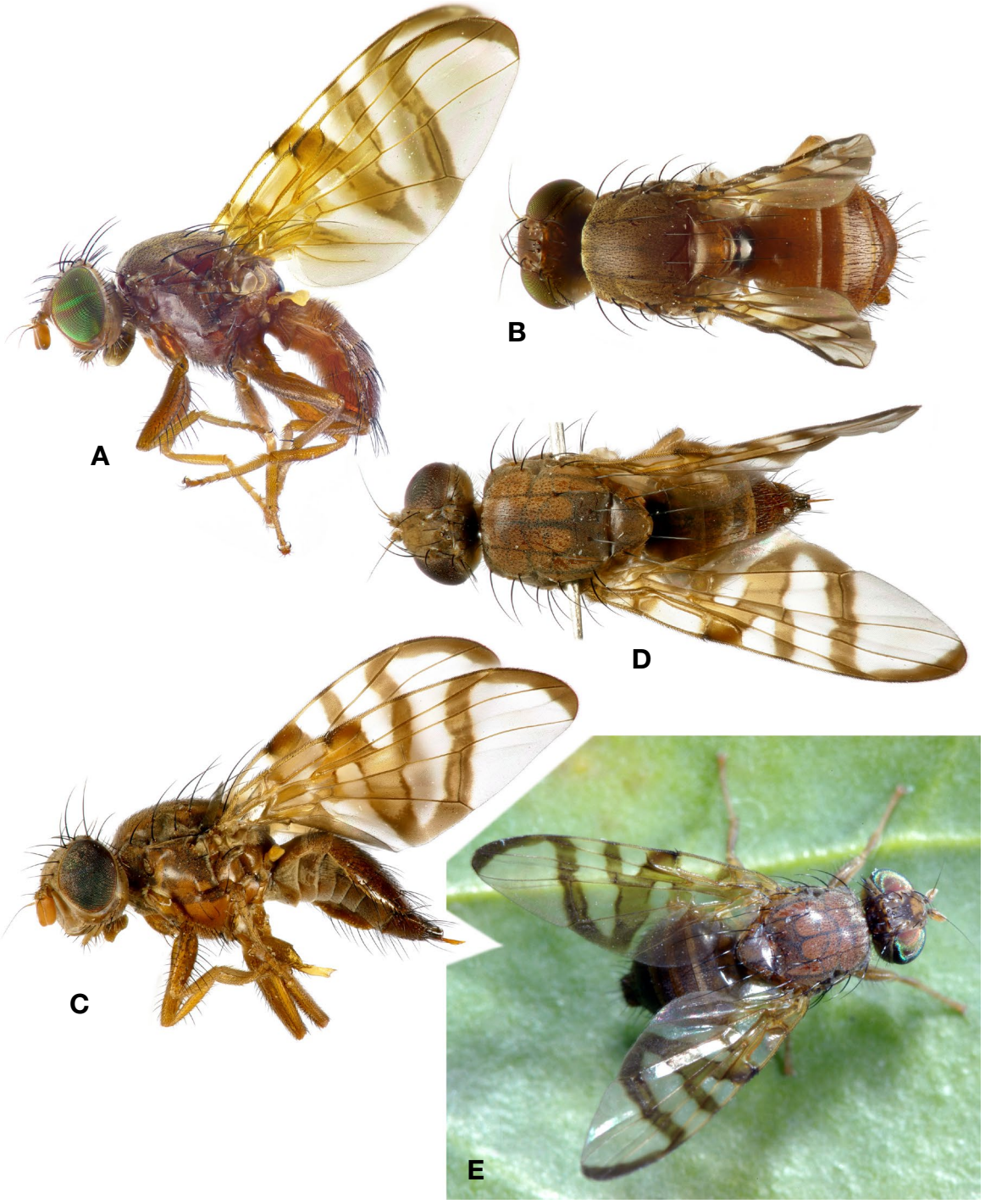


Fig. 3. *Chetostoma flexuosum* (Zia, 1938). A. male, lateral view; B. male, dorsal view; C. female, lateral view; D. female, dorsal view; E. live female.

Chetostoma melliculum: Foote 1984: 80 (in Palaearctic catalog); Han 1992: 54 (in Trypetini list, Ph.D. dissertation); Korneyev 1998: 7 (in Russian FE list); Norrbom *et al*. 1999: 124 (in world catalog); Korneyev & Ovchinnikova 2004: 486 (in Russian FE key).

Diagnosis. *Chetostoma melliculum* can be distinguished from Korean congeners by the combination of the following characteristics (Fig. 4): 1) mediotergite dark brown with narrow medial longitudinal orange-brown stripe (Fig. 4B); 2) oviscape orange-brown; 3) accessory costal band

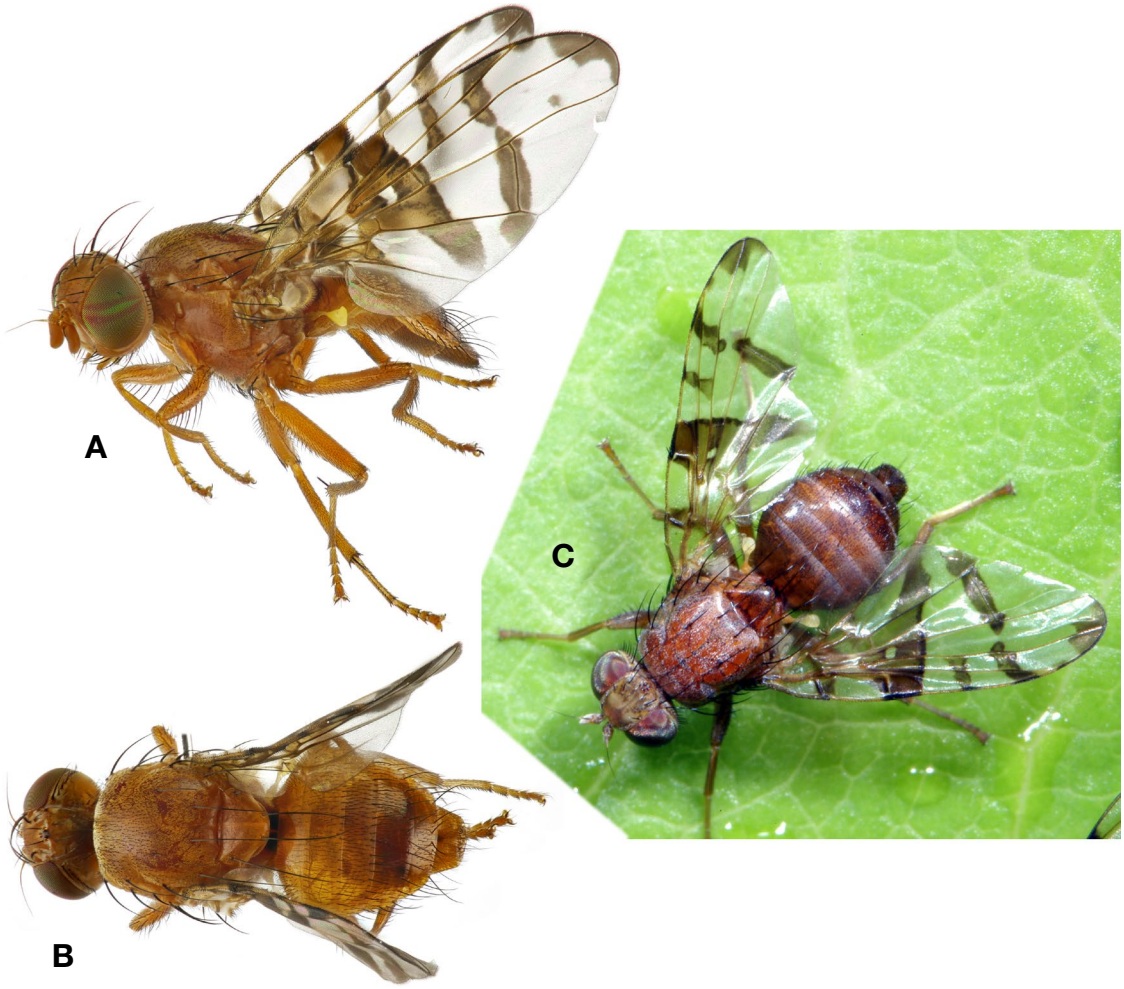


Fig. 4. *Chetostoma melliculum* Richter, 1965. A. female, lateral view; B. female, dorsal view; C. live female.

separated from discal band; 4) posterior stem of discal band separated from subapical band in anal lobe; 5) dark brown subapical band slightly to completely interrupted in cell r_{4+5}; and 6) anterior apical band as small spot posterior to apex of vein R_1 plus larger spot from mid-point between veins R_1 and R_{2+3} to apex of vein R_{4+5}.

Description of Korean material. Wing length 5.6−6.7 mm, body almost entirely orange-brown with dark brown setae and setulae. Head orange-brown with 3 frontal and 2 orbital setae; ocellar triangle dark brown with ocellar seta strong, about as long as posterior orbital seta; genal seta strong, dark brown; scutum matte orange-brown; dorsocentral setae about same level as postsutural supra-alar setae; acrostichal setae slightly above level of intra-alar setae; postpronotal lobe similar color as scutum; scutellum subshiny orange-brown, almost bare with sparse lateral setulae; 2 pairs of long scutellar setae with apical pair slightly shorter and parallel; mediotergite subshiny dark brown with narrow medial longitudinal orange-brown stripe; anatergite and katatergite orange-brown; anepisternum orange-brown with lower seta slightly shorter than upper seta; remaining mesopleura orange-brown. Legs orange-brown with dark brown setae and setulae. Wing hyaline with dark brown subapical band slightly to completely interrupted in cell r_{4+5}; anterior apical band reduced to small spot posterior to apex of vein R_1 plus larger spot from mid-point between veins R_1 and R_{2+3} to apex of vein R_{4+5}; tiny postero-medial brown to faint spot in hyaline area of cell r_{4+5} between subapical and anterior apical bands; accessory costal band separated from discal band; posterior stem of discal band separated from subapical band in anal lobe; cells r_1, r_{2+3} portion of discal band yellowish brown margined with dark brown color; cell br yellowish brown with more or less rectangular hyaline spot at basal 1/3 to apical 1/2 between crossveins BM-Cu and R-M, this spot margined outside with darker color; basal half of cell dm yellowish brown except apical dark brown margin; posterior stem of discal band in anal lobe dark brown, slightly

separated from wing margin and widely separated from subapical band; cell bc hyaline with narrow dark brown area anterior to crossvein H; cell c hyaline except basal 1/4 brown and apical margin dark brown; pterostigma dark brown; halter yellowish white. Abdominal tergites orange-brown; oviscape orange-brown, cylindrical, distinctly shorter than 2 preceding tergites; aculeus laterally flattened and apico-ventrally serrated. Male unknown.

Material examined. KOREA: Gangwon-do: Jeongseon-gun, Mt. Mindungsan, from Yupyeong-ri to 1,119 m peak, N37°16′15″ E128°46′30″, 6.VI.2006, H.Y. Han *et al*., 1♀ (NIBR); Yeongwol-gun, Yeongwol-eup, Heungwol-ri, Mt. Taehwasan, N37°07′03.3″ E128°29′07.4″, 1.VIII.2018, S.-S. Euo & C.-O. Kim, 1♀ (YSUW); *ditto*, 16.VIII.2018, H.-Y. Han *et al*., 1♀ (YSUW).

Distribution. Korea, Russian Far East.

Biology. Unknown.

Remarks. See Remarks of *C. flexuosum*. The new Korean name refers to the original describer of this species.

Subtribe Trypetina
Genus *Chenacidiella* Shiraki, 1968

5. *Chenacidiella purpureiseta* (Chen, 1948)
얼룩무늬과실파리 (신칭) (Fig. 5A–D)

Acidiella purpureiseta Chen 1948: 115 (type locality: Formosa [Taiwan]; holotype ♂ IZAS; sex of the holotype was not specified in the original description but Wang (1998: 160) indicated that he examined the holotype ♂ and paratypes 1♂ 1♀); Ito 1952: 7 (Shikoku, Japan).

Acidiella (*Umibenowotome*) *purpureiseta*: Ito 1956: 25 (in Japanese list; *Umibenowotome - nomen nudum*).

Chenacidiella purpureiseta: Shiraki 1968: 34 (redescription); Hardy 1977: 108 (in Oriental catalog); Foote 1984: 79 (in Palaearctic catalog); Ito 1984: 191 (in Japanese identification manual); Han 1992: 108 (in Trypetini list, Ph.D. dissertation); Wang 1998: 160 (in East Asian identification manual); Norrbom *et al*. 1999: 123 (in world catalog); Sueyoshi & Inoue 2004: 3 (Fukui Pref., Honshu, Japan); Sueyoshi 2012: 219 (Shikoku, Japan); Sueyoshi 2014: 580 (in Japanese catalog).

Diagnosis. *Chenacidiella purpureiseta* can be distinguished from other Korean tephritids by its peculiar wing pattern; largely dark brown with irregular anterior and posterior hyaline margins (Fig. 5A, D). In addition, this species can be further separated by: 1) ivory white humeral stripe and scutellum; 2) apical half of hind femur dark brown; and 3) scutum with 3 wide longitudinal dark stripes joined together at about posterior 1/3 of scutum (Fig. 5B, C).

Description of Korean material. Wing length 4.4–5.1 mm, body yellow to dark brown with dark brown setae and setulae. Head orange-brown with upper half of occiput dark brown; vertex, posterior 1/3 of frons often darker than face and gena; 3 frontal and 2 orbital setae; ocellar triangle dark brown with ocellar seta strong, about as long as posterior orbital seta; genal seta strong, dark brown, nearby setulae mostly about half as long as genal seta; scutum matte brown ground color with wide dark brown median and sublateral stripes joined together at about posterior 1/3 of scutum; dark stripes faded at about posterior 1/5 of scutum; dorsocentral setae slightly above level of postsutural supra-alar setae; acrostichal setae slightly above level of intra-alar setae; postpronotal lobe and upper katepisternum form wide ivory white humeral stripe; scutellum subshiny ivory white, bare; 2 pairs of long scutellar setae with apical pair slightly shorter and parallel; mediotergite orange brown ground color with wide, rectangular medial longitudinal dark brown stripe; anatergite dark brown; katatergite orange-brown; anepisternum orange brown except upper 1/3 ivory white, with lower seta slightly shorter than upper seta; remaining mesopleura orange-brown. Legs mostly yellowish brown except for apical half of hind femur and short base of hind tibia dark brown. Wing (Fig. 5A, C) largely dark brown with irregular anterior and posterior hyaline margins; halter yellowish white. Abdominal T1 + 2, T3 orange-brown; T4, T5 basally dark brown with orange-brown ground color; female T6 orange-brown; oviscape basally dark brown and apically orange-brown, cylindrical, about as long as 2 preceding tergites; aculeus dorsoventrally flattened with apico-lateral serration.

Material examined. KOREA: Jeju-do: Jeju-si, Mt. Sarabong near parking lot, N33°31′09″ E126°33′31″, 1.VIII. 2016, H.-Y. Han *et al*., 1♂ (NIBR); *ditto*, 2♂ 3♀ (YSUW); *ditto*, 1♂ 1♀ (KNA); Seogwipo-si, Mt. Gogeunsan, N33° 15′54″ E126°30′35″, 271 m, 2.VIII.2016, H.-Y. Han *et al*., 1♀ (KNA); *ditto*, 1♂ 1♀ (YSUW); Seogwipo-si, Seogwipohang, 2.V.2007, McPhail trap, S.Y. Kim, 1♀ (YSUW).

Distribution. Korea (Jeju Is.), Taiwan, China (Zhejiang), Japan (Honshu, Shikoku, Kyushu).

Biology. Unknown.

Remarks. Based on a morphological cladistic analysis, Han (1999) postulated that *Chenacidiella* is closely related to the genera *Vidalia* Robineau-Desvoidy, 1830, and *Hoplandriomyia* Bezzi, 1923, both of which have enlarged horn-like male frontal setae. Our unpublished analysis including the majority of Trypetini genera based on over 5,000 bp mitochondrial DNA (Han and Ro, in prep.), however, resulted in a tightly clustered monophyletic group including *Chenacidiella*, *Hoplandromyia*, *Calosphenisca* Hendel, 1914, *Itosigo* Ito, 1984, and *Pseudovidalia* Han, 2012, while *Vidalia* was displaced from this group. This means that the similar-looking male horns in *Vidalia* and *Hoplandromyia* are likely to be the results of convergent evolution. The new Korean name refers to its irregularly patched wing pattern.

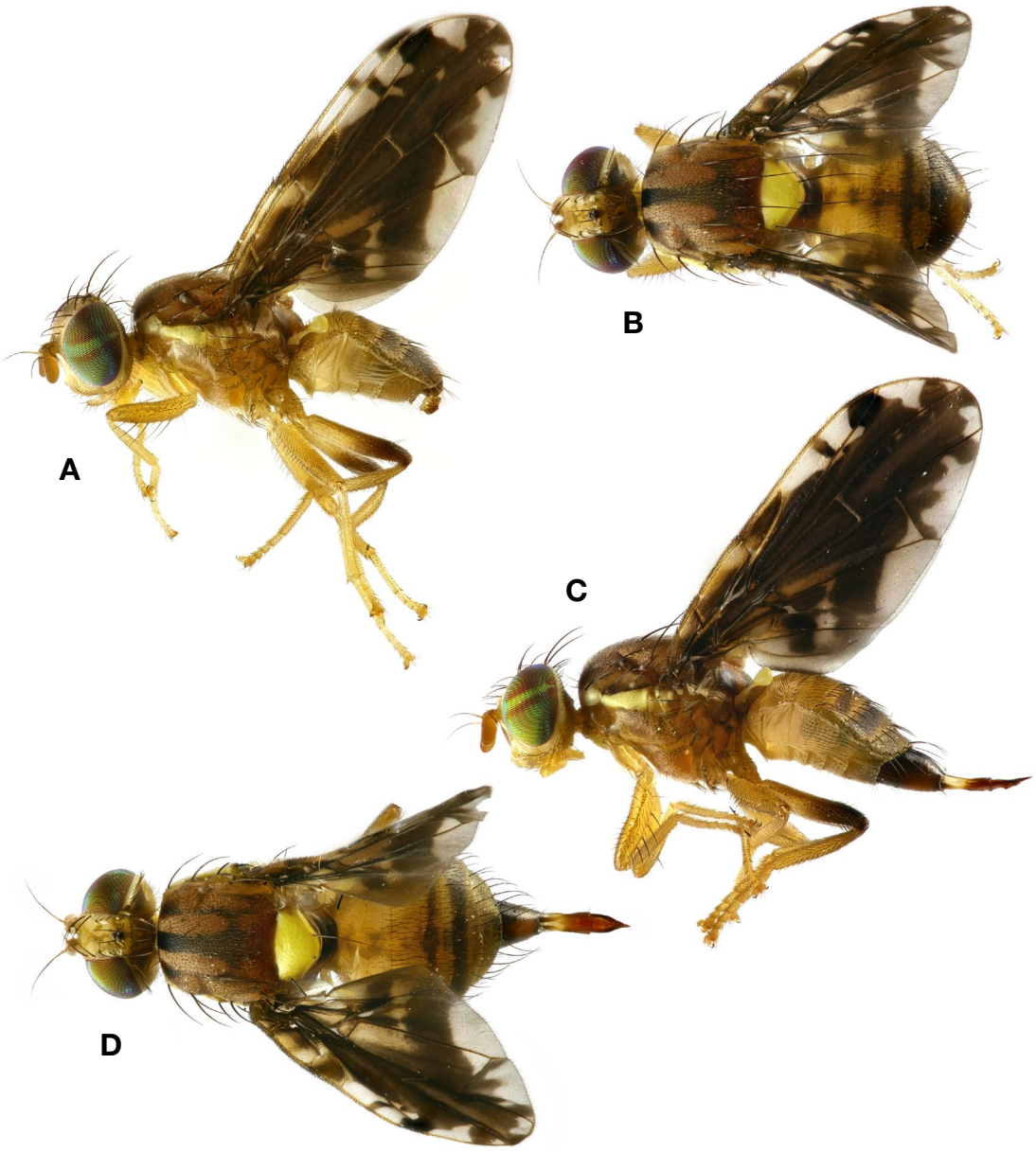


Fig. 5. *Chenacidiella purpureiseta* (Chen, 1948). A. male, lateral view; B. male, dorsal view; C. female, lateral view; D. female, dorsal view.

Genus *Dryadodacryma* Ito, 1984

6. *Dryadodacryma albicostale* Ito, 1984
앞흰테큰띠과실파리 (신칭) (Fig. 6A–D)

Dryadodacryma albicostale Ito 1984: 199 (type locality: Japan, Honshu, Tanba, Seryo; holotype ♂ UOPJ); Korneyev 1998: 23 (in Russian FE list; as unconfirmed taxon of Trypetini); Korneyev & Ovchinnikova 2004: 468, 506 (in Russian FE key); Sueyoshi 2014: 581 (in Japanese catalog).

Acidiella albicostalis Ito 1956: 25 (*nomen nudum* - published after 1930 without a description).

Hemilea albicostale: Han 1992: 117 (n. comb. from *Dryadodacryma*; Ph.D. dissertation); Wang 1998: 170 (in East Asian identification manual); Norrbom *et al*. 1999: 156 (in world catalog).

Diagnosis. *Dryadodacryma albicostale* can be readily distinguished by the combination of the following characteristics (Fig. 6): 1) anterior 2/3 of wing almost completely dark brown with very narrow anterior transverse hyaline streak starting from pterostigma to about basal 3/5–4/5 of costal vein between veins R_1 and R_{2+3} (Fig. 6A, C); 2) mediotergite entirely orange-brown (Fig. 6B, D); and 3)

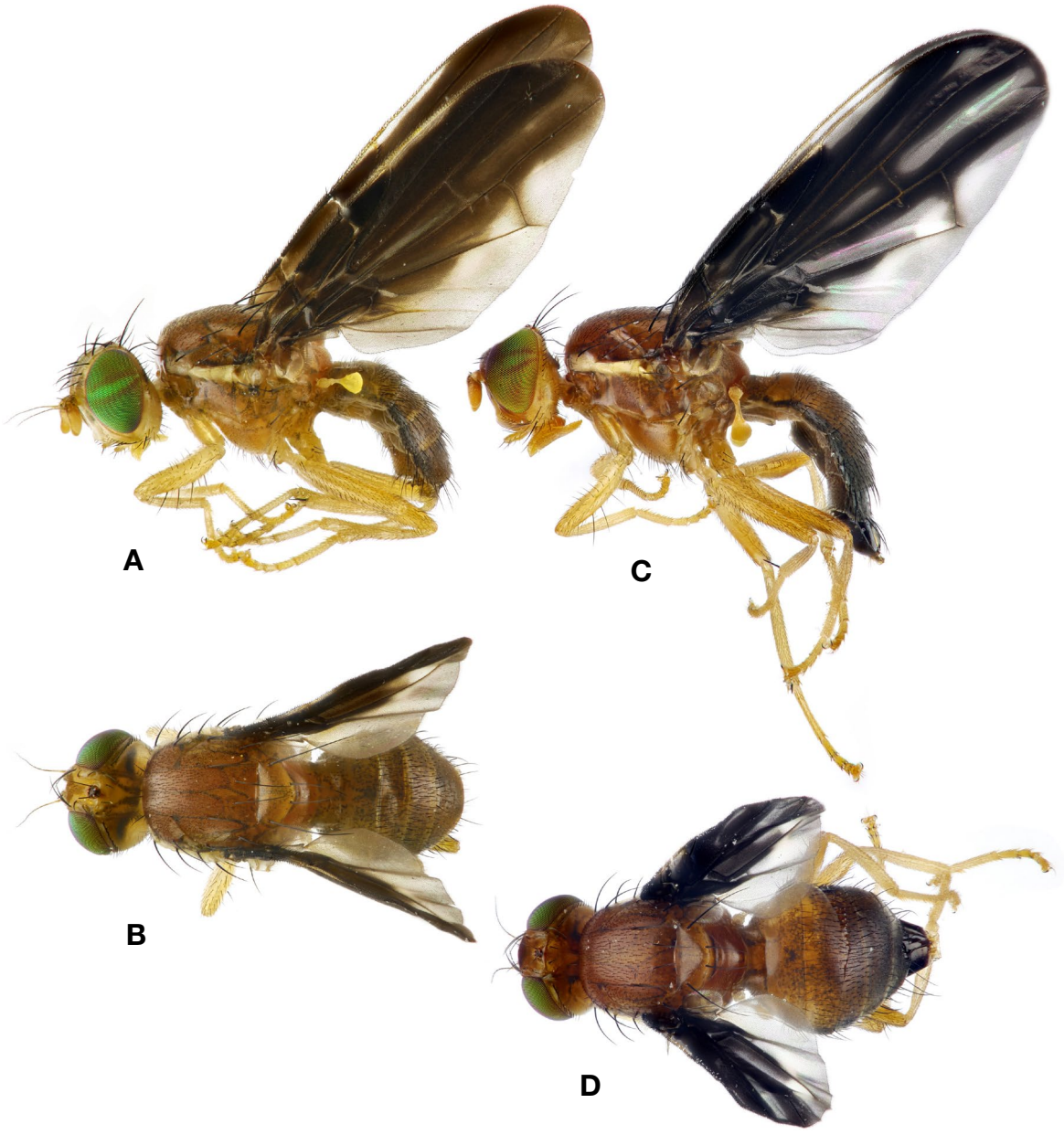


Fig. 6. *Dryadodacryma albicostale* Ito, 1984. A. male, lateral view; B. male, dorsal view; C. female, lateral view; D. female, dorsal view.

preabdominal tergites dorsally with pair of narrow dark brown lateral longitudinal bands (Fig. 6A, C). In Korea, the wing of this species is similar to that of *Hemilea infuscata* Hering, 1937 and *Pseudhemilea longistigma* (Shiraki, 1933), but can be easily distinguished by the above character 1 as well as other characteristics.

Description of Korean material. Wing length 5.0−5.7 mm, yellowish brown to orange-brown body with dark brown setae and setulae. Head yellowish brown; 3 frontal and 2 orbital setae; ocellar triangle dark brown with ocellar seta about as long as posterior orbital seta; genal seta strong, dark brown, nearby setulae about half as long as genal seta. Thorax with scutum orange-brown with dorsocentral setae about same level as postsutural supra-alar setae; acrostichal setae slightly above intra-alar setae; ivory white humeral stripe from postpronotal lobe, about upper 1/3 of anepisternum, anterior to wing base; scutellum subshiny orange-brown, bare; 2 pairs of long scutellar setae with apical pair about 2/3 as long as basal one, parallel; mediotergite orange-brown; anatergite and katatergite orange-brown; pleura entirely orange brown; anepisternum with upper seta strong, but lower seta about half as long as upper one. Legs yellowish brown with dark brown setae and setulae. Anterior 2/3 of wing almost completely dark

brown with narrow anterior transverse hyaline streak starting from pterostigma to about basal 3/5−4/5 of costal vein between veins R_1 and R_{2+3}; posterior hyaline parts of wing include alula, anal lobe, apical 2/3 of cell cu_2, postero-apical corner of cell DM-Cu, posterior 4/5 of cell m; narrow dark brown band over crossvein DM-Cu; halter yellowish white. Abdomen orange-brown but female T4−6 often darker than T1−3; with pair of narrow dark brown lateral longitudinal bands on tergites 2 to 5 in male and to 6 in female; oviscape shiny dark brown, about 1.5x as long as preceding tergite when measured latero-ventrally.

Material examined. KOREA: Gangwon-do: Jeongseon-gun, Nam-myeon, Mt. Mindungsan, from Yupyeong-ri to 1,119 m peak, N37°16′15″ E128°46′30″, 3.VI.2013, H.-S. Lee *et al*., 2♀ (YSUW); *ditto*, 17.VI.2013, H.-Y. Han *et al*., 1♀ (NIBR); *ditto*, 17.V.2015, H.-Y. Han & S.-S. Euo, 1♀ (YSUW); *ditto*, 17.VI.2016, H.-Y. Han *et al*., 1♀ (YSUW); Hoengseong-gun, Anheung-myeon, Mt. Chiaksan from Gangrim 4-ri to Cheonjibong, N37°23′51″ E128°05′23″, 1,086 m, 17.VII.2018, S.-W. Suk *et al*., 1♂ (YSUW); Inje-gun, Girin-myeon, Seo-ri, Mt. Maebongsan, N37°56′43.1″ E128°13′40″, 20.V.2017, S.-S. Euo *et al*., 1♀ (YSUW).

Distribution. Korea, Japan (Honshu).

Biology. Unknown.

Remarks. At a glance, *Dryododacryma albicostile* closely resembles *Hemilea dimidiata* (Costa, 1844), the type species of the genus *Hemilea* Loew, 1862, and that is why *Dryododacryma* was synonymized with *Hemilea* (Han, 1992; Norrbom *et al*., 1999). However, our molecular analyses (Han, 2012; Han and Ro, in prep. - an analysis including the majority of Trypetini genera based on over 5,000 bp mitochondrial DNA) clearly indicated that the dark *Hemilea*-like wing patterns have convergently evolved multiple times within the Trypetini. Therefore, we here resurrect *Dryododacryma* from the synonymy of *Hemilea*. The new Korean name refers to the wing pattern similar to *Hemilea infuscata* except with a narrow anterior transverse hyaline streak.

Genus *Hemileoides* Rohdendorf, 1955

7. *Hemileoides theodori* Rohdendorf, 1955

점박이검정날개과실파리 (신칭) (Fig. 7A−F)

Hemileoides theodori Rohdendorf 1955: 327 (type locality: Russia, Primorskiy, Vladivostok; holotype ♀ ZISP); Foote 1984: 92 (in Palaearctic catalog); Korneyev 1998: 23 (in Russian FE list); Korneyev & Ovchinnikova 2004: 505 (in Russian FE key).

Hemilea theodori: Han 1992: 120 (n. comb. from *Hemileoides*; Ph.D. dissertation); Norrbom *et al*. 1999: 157 (in world catalog).

Diagnosis. *Hemileoides theodori* can be readily distinguished by the largely dark brown wing with peculiar hyaline spots and areas (sexually dimorphic; Fig. 7A, C vs. 7D, F); see also Description). In addition, the following characteristics further distinguish this species: 1) 4 frontal setae; 2) 3 narrow dark brown longitudinal bands (medial + 2 sublateral); 3) mediotergite dark brown; 4) with only single anepisternal seta; 5) male abdomen with thick and straight longitudinal band (Fig. 7C); and 6) female abdomen with similar dark band on T1 + 2, but, from T3, dark band gradually widened toward the entire margin of T4 (Fig. 7F) and T5−6 turns entirely dark brown.

Description of Korean material. Wing length 4.4−5.6 mm, body yellowish brown to orange-brown with dark brown setae and setulae. Head yellowish brown; 4 frontal and 2 orbital setae; ocellar triangle dark brown with ocellar seta slightly shorter than posterior orbital seta; genal seta strong, dark brown, nearby setulae shorter than genal seta. Thorax with scutum orange-brown with 3 narrow dark brown longitudinal bands (medial + 2 sublateral); dorsocentral setae about same level as postsutural supra-alar setae; acrostichal setae about same level as intra-alar setae; ivory white humeral stripe from postpronotal lobe, about upper 1/3 of anepisternum, to underneath of wing base; scutellum subshiny orange-brown, bare; 2 pairs of long scutellar setae with apical pair shorter than basal ones; mediotergite dark brown; anatergite and katatergite yellowish brown; pleura entirely yellowish brown except for ivory humeral stripe; anepisternum with only strong upper seta. Legs yellowish brown with dark brown setae and setulae. Wing largely dark brown (sexually dimorphic; Fig. 7A, C vs. 7D, F) except for following areas: anterior part of cells bc and c hyaline; pterostigma pale grey; narrow (half of cell r_1 width) anterior transverse hyaline streak starting from pterostigma apex to about basal 2/3 of costal vein between veins R_1 and R_{2+3}, this streak constricted at about basal 3/5; small round posterior hyaline spot at basal 1/4 of cell r_{4+5}, in addition, male with tiny medial round spot at basal 1/2; round hyaline spot at medio-basal 2/3 of cell DM-Cu; triangular hyaline spot at postero-basal 1/3 of cell m; cell cu_2 largely dark with longitudinal hyaline streak at basal 2/3 of cell; alula and anal lobe hyaline; halter yellowish white. Male abdomen in yellowish brown ground color with thick and straight longitudinal band; female abdomen with similar band only on T1 + 2; from T3, dark band gradually widened toward entire margin of T4; T5−6 entirely dark brown; oviscape shiny dark brown, about as long as 2 preceding tergites.

Material examined. KOREA: Gangwon-do: Jeongseon-gun, Mt. Mindungsan, from Yupyeong-ri to 1,119 m peak, N37°16′15″ E128°46′30″ 24.VI.2005, H.Y. Han *et al*., 1♂ 1♀ (YSUW); *ditto*, 8.VII.2005, 1♂ 1♀ (YSUW); *ditto*, 19.VII.2005, 1♂ (NIBR); *ditto*, 1♂ (YSUW).

Distribution. Korea, Russian Far East.

Biology. The majority of specimens were collected from

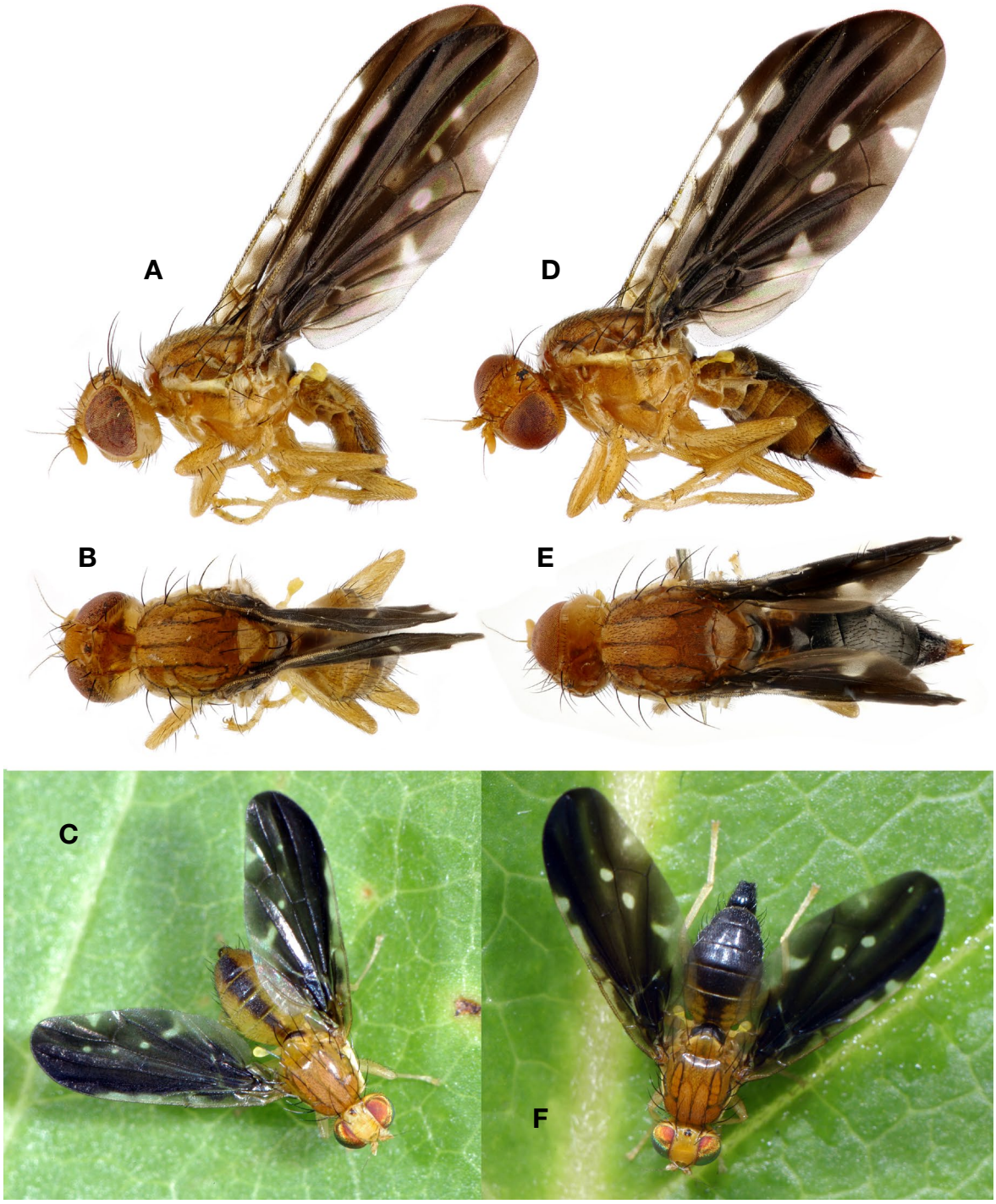


Fig. 7. *Hemileoides theodori* Rohdendorf, 1955. A. male, lateral view; B. male, dorsal view; C. live male; D. female, lateral view; E. female, dorsal view; F. live female.

the shaded oak forest near the peak of Mt. Mindungsan (see Material examined). Both sexes were swept from oak branches at about 1–1.5 m high, sticking out from relatively mature oak trees.

Remarks. *Hemileoides theodori* is the type species of the genus. Since its dark wing pattern resembles typical *Hemilea*, it was regarded as a synonym with the latter having seniority (Han, 1992; Norrbom, 1999). However, our molecular analyses (Han, 2012; Han and Ro, in prep. - an analysis including the majority of Trypetini genera based on

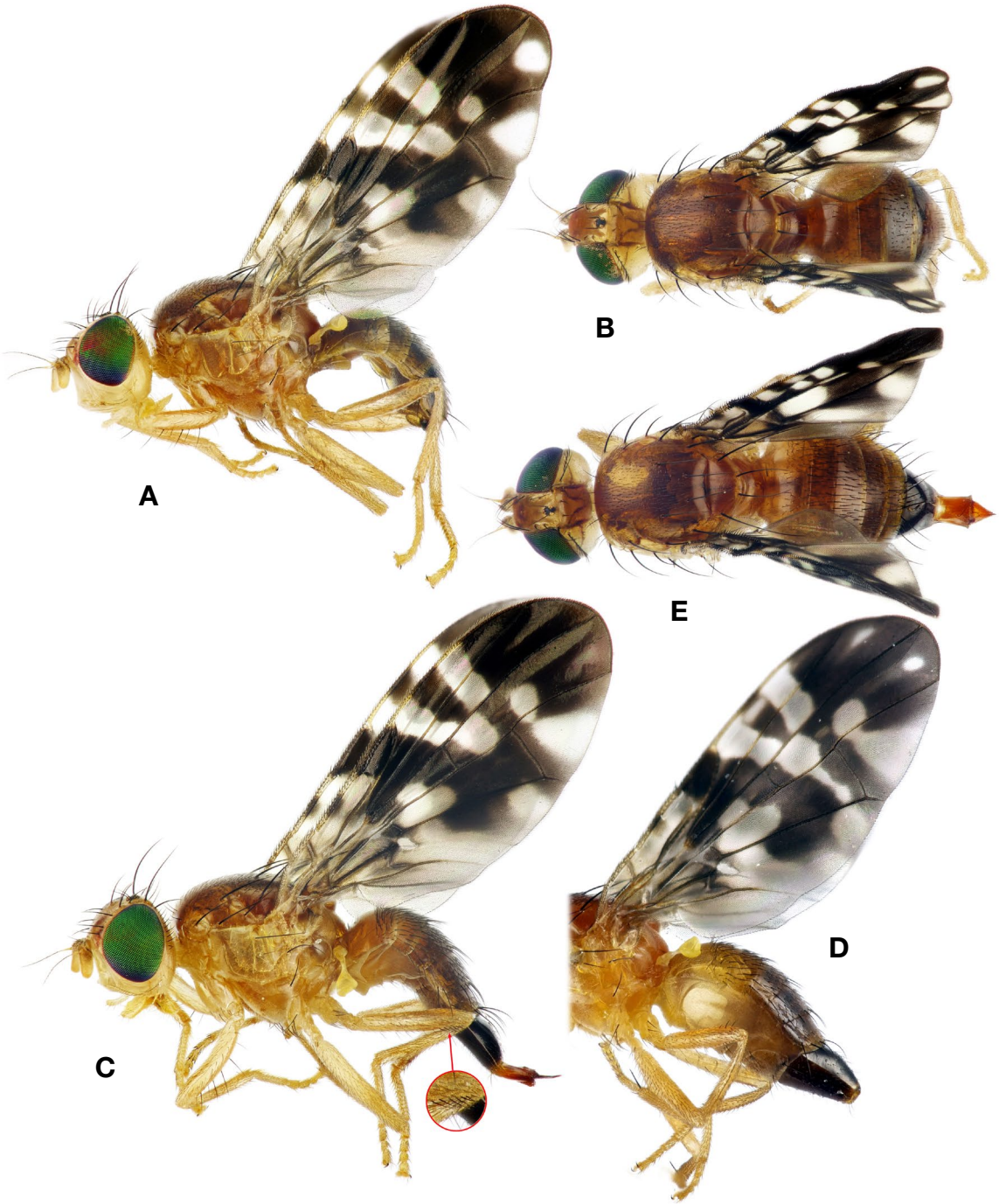


Fig. 8. *Ihekaze diversa* (Ito, 1952). A. male, lateral view; B. male, dorsal view; C. female with typical wing pattern; D. female with aberrant wing pattern; E. female, dorsal view.

over 5,000 bp mitochondrial DNA) indicated that the dark *Hemilea*-like wing patterns have convergently evolved multiple times within the Trypetini. Therefore, we here resurrect *Hemileoides* from the synonymy of *Hemilea*. In this analysis, we recognized Japanese *Hemileoides continuum* (Ito, 1984), comb. nov., as a sister species of *H. theodori*.

Genus *Ihekaze* Ito, 1984

8. *Ihekaze diversa* (Ito, 1952)

남해과실파리 (신칭) (Fig. 8A–E)

Acidiella diversa Ito 1952: 5 (type locality: Japan, Kyushu, Osumi, Sata; holotype ♂ UOPJ); Ito 1956: 25 (type species of *Ihekaze* - *nomen nudum*); Foote 1984: 69 (in

Palaearctic catalog); Han 1992: 156 (in world checklist of Trypetini; Ph.D. dissertation); Wang 1998: 129 (in East Asian identification manual); Norrbom *et al*. 1999: 68 (in world catalog); Korneyev & Ovchinnikova 2004: 510 (in Russian FE key); Sueyoshi 2012: 218 (Imperial Palace, Tokyo); Sueyoshi 2014: 577 (in Japanese catalog).

Ihekaze diversa: Ito 1984: 181 (in Japanese identification manual; designated as type species of *Ihekaze*).

Diagnosis. *Ihekaze diversa* can be distinguished from other Korean Trypetini by the combination of the following characteristics (Fig. 8): 1) genal seta pale yellow; 2) hind femur apically with 6 short anteroventral setae forming comb-shape (Fig. 8C; see inset); 3) wing with Y-shaped hyaline band across cells r_1, r_{2+3}, r_{4+5}; and 4) round postero-medial hyaline spot in cell r_{4+5}. This species shows sexual dimorphism in wing pattern by presence (in males; Fig. 8A) or absence (in females; Fig. 8C, or rarely much smaller - Fig. 8D) of apical round hyaline spot in cell r_{4+5}.

Description of Korean material. Wing length 4.2−4.7 mm, body pale yellow to brown with mostly dark brown setae and setulae. Head with frons and median occiput brown; antennae, face, parafacial and gena pale yellow; 3 frontal and 2 orbital setae; ocellar triangle dark brown with ocellar seta about as long as posterior orbital seta; genal seta strong, pale yellow, nearby setulae also pale yellow mostly about half as long as genal seta. Thorax with postpronotal lobe yellowish brown; scutum brown with dorsocentral setae about same level as postsutural supra-alar setae; acrostichal setae about same level as intra-alar setae; scutellum subshiny orange-brown, bare; 2 pairs of long scutellar setae with apical pair about 2/3 as long as basal one, parallel; mediotergite brown; anatergite and katatergite yellowish brown; pleura entirely yellowish brown; anepisternum with upper seta strong, but lower seta about half as long as upper one. Legs yellowish brown with dark brown setae and setulae; hind femur apically with 6 short anteroventral setae forming comb-shape. Wing largely dark brown with following hyaline areas: cell bc, cell c with small pale brown medial spot, basal area up to fork of Rs more or less hyaline with brownish tinge; apical to dark pterostigma, hyaline band across cells r_1, r_{2+3}, r_{4+5}, this band as wide as each cell width; about same width apical to this band, similar hyaline band across cells r_1, r_{2+3}; these two band loosely form Y-shaped band together; cell r_{4+5} with subasal rectangular spot (stem of Y-band), median round posterior spot, large apical round spot in male but absent or rarely as much smaller spot in female; cell br with hyaline spot medially between fork and crossvein R-M; basal 2/5 of cell dm hyaline; cell cu_2 with basal 1/3 and subapical 1/4 hyaline; anal lobe hyaline; cell m medially with large hyaline spot touching about 1/2−3/5 of wing margin; halter yellowish white. Abdominal tergites brown, T5 in both sexes with pair of large loosely defined dark brown sublateral spots; oviscape shiny dark brown, about as long as 2 preceding tergites.

Material examined. KOREA: Jeollanam-do: Wando-gun, Wando-eup, from Sosepo Port to Sanghwangbong, N34°20′02″ E126°40′19″, 7.VI.2013, Y.-B. Lee & H.-S. Lee, 1♂ 1♀ (NIBR); *ditto*, 8♂ 3♀ (YSUW); *ditto*, 15.VI. 2024, S.-W. Suk & Y.-B. Lee, 1♀ (YSUW); *ditto*, 28.V. 2017, S.-S. Euo, 1♂ (YSUW). Jeju-do: Jeju-si, Aewol-eup, Bongseong-ri, Handae Oreum, N33°21′23″ E126° 25′29″, 19.VI.2017, Coll. H.-Y. Han *et al*., 1♀ (YSUW); Jeju-si, Mt. Sarabong, N33°31′06″ E126°32′42″, 11.VI. 2018, H.-Y. Han *et al*., 1♀ (YSUW).

Distribution. Korea (Jeju Is., Jeollanam-do), Japan (Honshu, Shikoku, Kyushu).

Biology. Unknown.

Remarks. Ito (1952) originally described this species as a member of the genus *Acidiella* Hendel, 1914, but later (Ito, 1984) described the new genus *Ihekaze* with this species as the type species. Han (1992) synonymized *Ihekaze* with *Acidiella* for their superficial similarity. However, our molecular analysis (Han and Ro, in prep. - an analysis including the majority of Trypetini genera based on over 5,000 bp mitochondrial DNA) indicated that *Acidiella* should be restricted to a much smaller monophyletic group, and *Ihekaze* should be resurrected for a monophyletic group including at least five East Asian species within the *Trypeta* group of the tribe Trypetini (Han and Ro, in prep.). The new Korean name of this species refers to the southern coastal area of Korea, where the majority of this species were collected.

Genus *Morinowotome* Ito, 1984

9. *Morinowotome itoi* Korneyev, 1998

닮은모리노과실파리 (신칭) (Fig. 9A−E)

Morinowotome itoi Korneyev 1998: 31 (type locality: Primorskiy, Khasan distr., Ryazanovka; holotype ♀ ZMM); Korneyev & Ovchinnikova 2004: 512 (in Russian FE key); Sueyoshi 2014: 583 (in Japanese catalog as distributed in Chishima Island, Hokkaido = currently in Kuril Islands, Russia).

Morinowotome egregia: Han & Kwon 2000: 103 (Fig. 38; misidentified male photo).

Diagnosis. *Morinowotome itoi* can be distinguished from other tephritids in Korea by the combination of the following characteristics (Fig. 9): 1) ocellar seta strong, as long as anterior orbital seta; 2) mediotergite dark brown with wide medial longitudinal orange-brown strip about 1/3 as wide as mediotergite (Fig. 9C, E); and 3) wing with largely yellowish brown inverted L-shaped apical band with isolated subapical band placed perpendicular to vein R_{2+3} toward crossvein DM-Cu. This species is very similar to

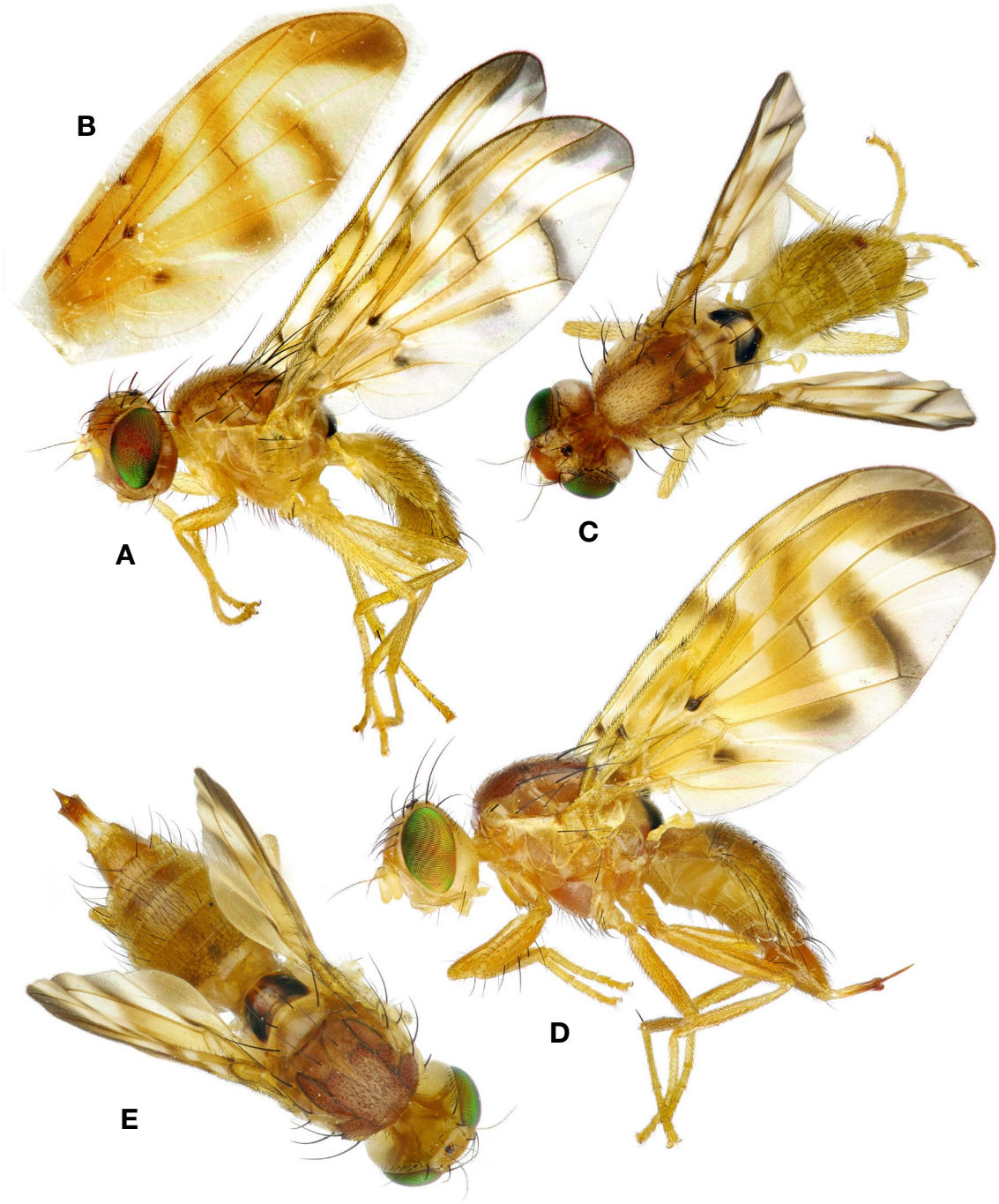


Fig. 9. *Morinowotome itoi* Korneyev, 1998. A. male with teneral wing, lateral view; B. fully darkened male wing; C. male, dorsal view; D. female, lateral view; E. female, dorsal view.

the type species of *Morinowotome*, *M. egregia* (Shiraki, 1933), but can be separated by the above characteristics 2 and 3. In *M. egregia*, the orange-brown band on mediotergite is much narrower, the wing with L-band interrupted medially, and the subapical band slightly but clearly acute angle from vein R_{2+3} toward crossvein DM-Cu.

Description of Korean material. Wing length 4.8−6.0 mm, body predominantly yellowish brown with dark brown setae and setulae. Head yellowish brown with 3 frontal and 2 orbital setae; ocellar triangle dark brown with strong ocellar seta, as long as posterior orbital seta; genal seta strong, dark brown, nearby setulae at most half as long as genal seta. Thorax with scutum yellowish brown with dorsocentral setae about same level as postsutural supra-alar

setae; acrostichal setae about same level as intra-alar setae; ivory white humeral stripe from postpronotal lobe, about upper 1/4 of anepisternum; scutellum yellowish brown, bare except sparse maginal setulae; 2 pairs of long scutellar setae with apical pair slightly shorter and crossed near apex; mediotergite shiny dark brown with wide orange brown median longitudinal streak about 1/3 as wide as mediotergite; anatergite and katatergite yellowish brown; pleura entirely yellowish brown; anepisternum with lower seta about half as long as upper one. Legs yellowish brown with dark brown setae and setulae. Wing pattern pale yellow to dark brown: antero-basal half largely yellow except for mostly hyaline cell br, pterostigma yellow with apical 1/3 brown, node of RS and extension of cell bcu dark brown; anterior apical band and radial medial band merged to form inverted L-shaped band, L-band largely pale yellow except for brown to dark brown R_{4+5} plus apex of R_{2+3} portion and cell cu_2 portion; subapical band disconnected from L-band, yellow except for brown to dark brown area around crossvein DM-Cu, perpendicular to vein R_{2+3} toward crossvein DM-Cu; halter yellowish white. Abdominal tergites yellowish brown; oviscape yellowish brown, about as long as two preceding tergites.

Material examined. KOREA: Gangwon-do: Wonju-si, Panbu-myeon, Seogok-ri, Mt. Baegunsan, from Yongsugol to 1,087.1 m peak, N37°14′59″ E127°57′46″, 23.VI. 1998, H.-Y. Han & D.-S. Choi, 1♂ (YSUW); Inje-gun, Yongneup Swamp area, N38°12′48″ E128°7′19″, 1,204 m, 11.VII.2015, H.-Y. Han *et al*., 1♀ (YSUW); Inje-gun, Girin-myeon, Mt. Jeombongsan, from Jindong-ri to Gombaeryeong, N38°1′40″ E128°25′5″, 1,091 m, 9.VI.2016, H.-Y. Han *et al*., 1♂ (YSUW). Gyeongsangnam-do: Hamyang-gun, Mt. Jirisan National Park, Saeseoksanjang, Malaise trap, 26.VI–26.VII.2001, D.S. Ku, 1♀ (YSUW).

Distribution. Korea, Russian Far East including the Kuril Islands.

Biology. Unknown.

Remarks. We obtained two Korean males (Fig. 9A–C), which are the only known males of *M. itoi*. Fig. 9A and B represent the lateral and dorsal view of a teneral male, which shows a somewhat reduced wing pattern. Fig. 9C represents the wing pattern of a fully darkened male, which is similar to that of a female (Fig. 9D). There seems to be no detectable sexual wing dimorphism in both species of the genus *Morinowotome* in Korea. This is a very rarely collected species, but the type species *M. egregia* is relatively common in Korea. Our molecular analysis (Han and Ro, in prep. - an analysis including the majority of Trypetini genera based on over 5,000 bp mitochondrial DNA) indicated that the genus *Morinowotome* is a monophyletic group.

Genus *Stemonocera* Rondani, 1870

10. *Stemonocera corruca* (Hering, 1937)

긴뿔과실파리 (신칭) (Fig. 10A–E)

Trypeta corruca Hering 1937: 248 (type locality: Russland [Russia]; holotype ♂ ZMHU).

Myiolia lucens Zia 1938: 47 (type locality: China, sw. Shanxi, Ho-Chan, 2,255 m; Tsi-li-yu [Tsiliyu], 2,100 m; lectotype ♀ IZAS, designated by Wang 1998: 201); Han 1992: 149 (new synonym of *Stemonocera corruca*); Wang 1998: 201 (listed as synonym of *S. corruca*).

Stemonocera corruca: Han 1992: 149 (new combination from *Trypeta* & *Vidalia*; Ph.D. dissertation); Wang 1998: 200 (in East Asian identification manual); Norrbom *et al*. 1999: 210 (in world catalog); Korneyev & Ovchinnikova 2004: 501 (in Russian FE key); Sueyoshi 2014: 586 (new record in Kuril Islands).

Diagnosis. *Stemonocera corruca* can be distinguished from other Korean tephritid species by the combination of the following characteristics (Fig. 10): 1) single orbital seta; 2) ocellar seta reduced (hair-like); and 3) male frontal setae enlarged and situated on antler-like anterior frontal process (Fig. 10A–C); 4) scutum without pair of short and prominent anterior-most dark longitudinal bands; and 5) mediotergite shiny dark brown with yellowish brown median longitudinal streak about half as wide as mediotergite. This species closely resembles *S. mica* but can be distinguished by not having the above characteristics 4 and 5.

Description of Korean material. Wing length 6.4–7.1 mm, body predominantly yellowish brown with dark brown setae and brown to yellowish brown setulae, males particularly show sexually dimorphic frontal enlargement. Head yellowish brown, usually with 4 frontal setae; male frontal setae enlarged, blunt-tipped, and situated on antler-like anterior frontal process (posterior-most seta rarely reduced to normal seta); female usually with 4 normal frontal setae but sometimes 3 or 5, often different number in different side; always with single orbital seta; ocellar triangle dark brown with ocellar seta reduced to tiny hair; genal seta strong, yellowish brown to brown, nearby setulae at most half as long as genal seta. Thorax with scutum yellowish brown with pair of very narrow longitudinal, irregular dark brown streaks from behind outer scapular setae to above scuto-scutellar suture, posterior tip of this streak outwardly curved and thickened; dorsocentral setae clearly behind level of postsutural supra-alar setae; acrostichal setae about same level as intra-alar setae; ivory white humeral stripe from postpronotal lobe, about upper 1/4 of anepisternum, anterior to wing base; scutellum yellowish brown, bare except sparse maginal setulae; 2 pairs of long scutellar setae with apical pair slightly shorter and parallel; mediotergite shiny dark brown with yellowish brown median longitudinal streak about half as wide as

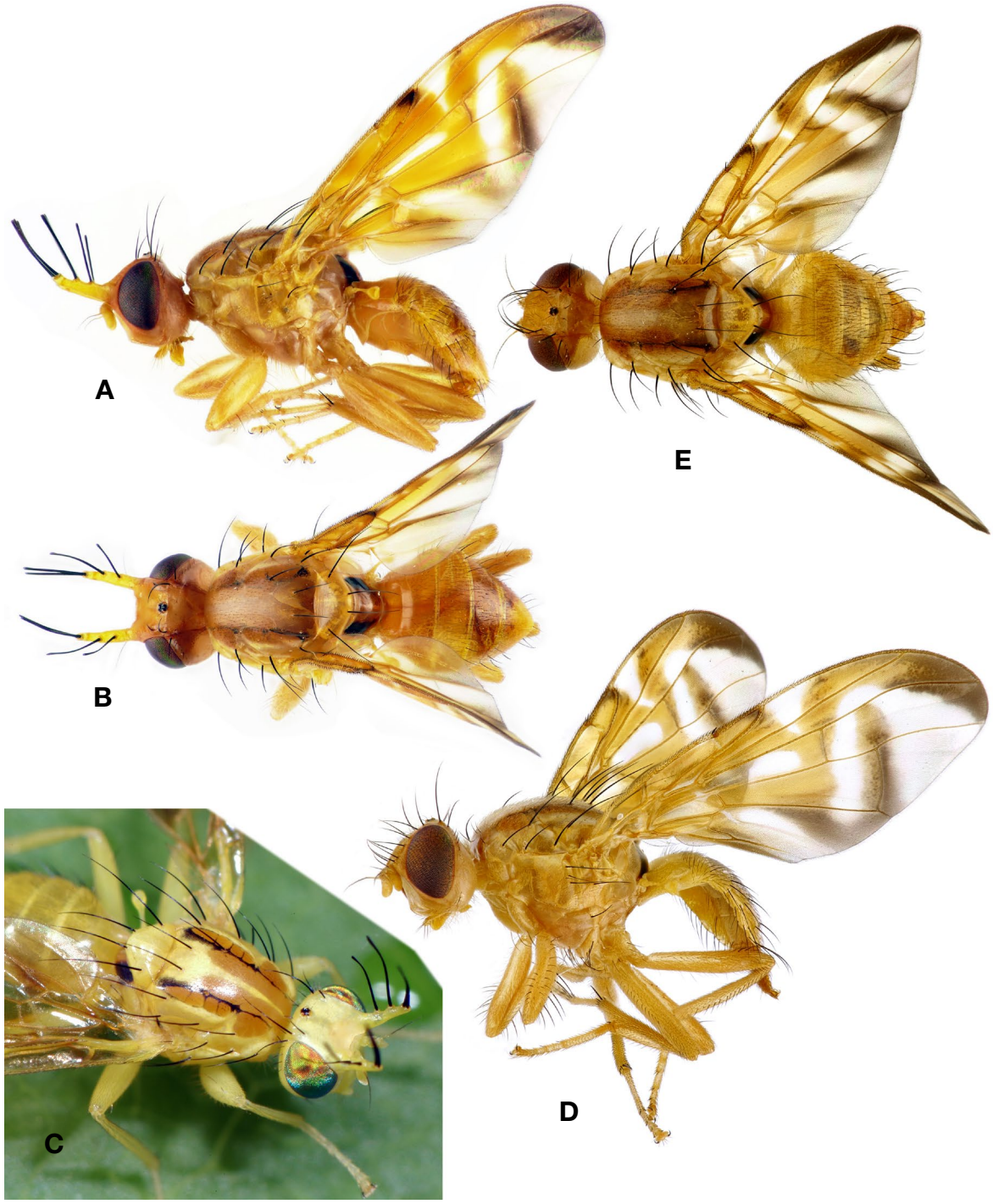


Fig. 10. *Stemonocera corruca* (Hering, 1937). A. male, lateral view; B. male, dorsal view; C. live male; D. female, lateral view; E. female, dorsal view.

mediotergite; anatergite and katatergite yellowish brown; pleura entirely yellowish brown; anepisternum with lower seta at most half as long as upper seta. Legs yellowish brown with most setae and setulae yellowish brown in males but largely brown to dark brown in females; front femur swollen in males but normal in females; claws and mid femoral spur dark brown. Wing pattern largely yellow with some dark brown areas: antero-basal part largely yellow except for mostly hyaline cell br; pterostigma yellow with apical 1/3 brown to dark brown; anterior apical band

and radial medial band merged to form inverted L-shaped band, L-band largely yellow except for brown to dark brown R_{4+5} plus apex of R_{2+3} portion and cell cu_2 portion; subapical band disconnected from L-band, yellow except for brown to dark brown area around crossvein DM-Cu. Abdominal tergites yellowish brown; oviscape yellowish brown, about as long as two preceding tergites.

Material examined. KOREA: Gangwon-do: Jeongseon-gun, Mt. Mindungsan, from Yupyeong-ri to 1,119 m peak, N37°16′15″ E128°46′30″, 8.VII.2005, H.-Y. Han *et al*., 1♂ (YUW); *ditto*, 16.VII.2005, 1♂ 2♀ (YSUW); *ditto*, 19.VII.2005, 1♀ (YSUW); *ditto*, 1♀ (NIBR); *ditto*, 4.VIII. 2005, 1♂ 2♀ (YSUW); *ditto*, 28.VI.2012, 1♂ (YSUW); *ditto*, 1♂ (NIBR).

Distribution. Korea, Russian Far East, China (Heilongjiang, Jilin, Shanxi, Beijing).

Biology. Unknown, but likely to be a leaf-miner of Asteraceae plant as in other species of the genus *Stemonocera* (see host records by Han, 1998).

Remarks. The new Korean name refers to the longer frontal horns than those of the similar-looking *S. mica*.

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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Report of 14 unrecorded bacterial species in Korea belonging to the phyla *Bacteroidota*, *Acidobacteriota* and *Verrucomicrobiota*, excavated during the survey in 2023

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In this study, a total of 14 bacterial strains belonging to the phyla *Bacteroidota*, *Acidobacteriota* and *Verrucomicrobiota* isolated in 2023 are reported as unrecorded species in Korea. Among 14 bacterial strains, 12 strains were assigned to the phylum *Bacteroidota*, including 5 species belonging to the family *Flavobacteriaceae*, 3 species to the family *Weeksellaceae*, 2 species to the family *Cyclobacteriaceae* and 1 species each to the families *Prolixibacteraceae* and *Sphingobacteriaceae*. At genus level, *Flavobacterium* (5 species) was the most abundant genus, which was then followed by *Chryseobacterium* (3 species) and *Algoriphagus* (2 species). Single species were obtained for the genera *Sunxiuqinia* and *Mucilaginibacter*. In addition, one isolate assigned to the phylum *Acidobacteriota* belonged to the genus *Edaphobacter* of the family *Acidobacteriaceae*, and the other assigned to the phylum *Verrucomicrobiota* belonged to the genus *Verrucomicrobium* of the family *Verrucomicrobiaceae*.

Keywords: *Acidobacteriota*, *Bacteroidota*, *Flavobacterium*, unrecorded species, *Verrucomicrobiota*

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Introduction

The phyla *Bacteroidota*, *Acidobacteriota* and *Verrucomicrobiota* share several common characteristics. They are all Gram-stain-negative bacteria and exhibit diverse cellular morphologies, including rod-shaped, coccoid, and filamentous forms. These bacteria can be aerobic, facultative anaerobic, or obligate anaerobic, and they do not form endospores. They are widely distributed across various environments, including soil, aquatic ecosystems and host-associated microbiomes, and play significant roles in ecological processes such as carbon and nitrogen cycling, nutrient degradation, and host interactions.

Bacteroidota are primarily found in the gut and skin of animals, as well as in marine and terrestrial environments. They are known for their role in nutrient digestion, calorie absorption, immune regulation, metabolic processes, and the gut-brain axis. These bacteria contribute significantly to host-microbiome interactions, particularly in the breakdown of complex carbohydrates (Krieg *et al*., 2010;

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Thomas *et al*., 2011; Wang *et al*., 2016).

Acidobacteriota are predominantly soil-dwelling bacteria, and are particularly abundant in acidic environments. They have a remarkable tolerance to low pH and play a crucial role in carbon and nitrogen cycling within soil ecosystems. Some species are capable of metabolizing complex carbohydrates, thus promoting soil health and plant growth (Thrash and Coates, 2010; Dedysh and Sinninghe Damsté, 2018; Kalam *et al*., 2020).

Verrucomicrobiota are found in a wide range of habitats, including soil, freshwater, marine environments, and extreme conditions such as hot springs. They contribute to carbon cycling by degrading complex carbohydrates, and some species are even involved in methane production. Notably, *Akkermansia muciniphila*, a representative species of this phylum, plays a key role in gut health by degrading mucin, an essential glycoprotein in mucus, thereby influencing host metabolism and immune function (Hedlund, 2010; Derrien *et al*., 2017; Orellana *et al*., 2021).

In a series of extensive surveys on the prokaryotic diversity in Korea in the year 2023, 14 novel strains belonging the phyla *Bacteroidota*, *Acidobacteriota* and *Verrucomicrobiota* were isolated from various environmental sources, and their taxonomic properties were analyzed. As a result, a total of 14 unrecorded species of Korea were identified, and their taxonomic properties are presented.

Materials and Methods

The strains were isolated from various environmental samples such as soil, mudflat, wetland, stream, agricultural soil, and mud (Table 1). The samples were processed or treated separately, diluted and spread onto diverse culture media, namely R2A, marine agar (MA) or peptone-tryptone-yeast extracts-glucose (PTYG) agar, and incubated at 25−37°C for 2−5 days. The designated strain codes, sources of isolation, culture media, and incubation conditions are provided in the descriptions and Table 1. All strains were purified as single colonies and stored in 10−20% glycerol suspension at −80°C as well as lyophilized ampoules.

Colony characteristics of the isolates were observed on the same agar media for cultivation. Cellular morphology and cell size were examined using either a transmission electron microscope or a scanning electron microscope. Gram staining was performed using standard procedures (Bartholomew and Mittwer, 1952). Biochemical characteristics were tested by using API 20NE galleries (bio Mérieux) according to the manufacturer's instructions.

The extraction of genomic DNA, PCR amplification of 16S rRNA gene and sequencing were performed using the procedures as described previously (Weisburg *et al*., 1991). The EzBioCloud database (Yoon *et al*., 2017) was

Table 1. Taxonomic affiliations of isolated strains belong to the phyla *Bacteroidota*, *Acidobacteriota* and *Verrucomicrobiota*

Affiliation	Strain ID	NIBR[a] ID	Identification	Similarity (%)[b]	Isolation source	Medium[c]	Culture conditions (°C, days)
Acidobacteriota	MA-22	NIBRBAC000510756	*Edaphobacter modestus*	98.94	Soil	R2A	25°C, 3 d
Bacteroidota	MMS23-Q5	NIBRBAC000510827	*Algoriphagus roseus*	99.09	Soil	R2A	30°C, 3 d
	JPR4	NIBRBAC000510805	*Algoriphagus kandeliae*	99.93	Mudflat	MA	28°C, 3 d
	AN795	NIBRBAC000510616	*Flavobacterium amnicola*	100.00	Wetland	R2A	28°C, 3 d
	CA1-11	NIBRBAC000510743	*Flavobacterium johnsoniae* subsp. *johnsoniae*	99.86	Soil	R2A	25°C, 3 d
	DL8	NIBRBAC000510651	*Flavobacterium ajazii*	99.16	Stream	R2A	25–30°C, 4 d
	FW4	NIBRBAC000510789	*Flavobacterium hercynium*	98.95	Agricultural soil	PTYG	28°C, 4 d
	MMS23-HJ70	NIBRBAC000510812	*Flavobacterium zaozhuangense*	99.37	Soil	R2A	30°C, 3 d
	CAU 1723	NIBRBAC000510780	*Sunxiuqinia elliptica*	99.93	Mud	MA	30°C, 3 d
	AR1	NIBRBAC000510794	*Mucilaginibacter rubeus*	100.00	Agricultural soil	R2A	28°C, 3 d
	ST11	NIBRBAC000510744	*Chryseobacterium polytrichastri*	99.24	Soil	R2A	25°C, 3 d
	WK20	NIBRBAC000510653	*Chryseobacterium aahli*	99.22	Soil	R2A	30°C, 2 d
	NW27	NIBRBAC000510634	*Chryseobacterium piscicola*	99.10	Stream	R2A	30°C, 3 d
Verrucomicrobiota	JDC8	NIBRBAC000510582	*Verrucomicrobium spinosum*	99.86	Soil	R2A	30°C, 2 d

[a]National Institute of Biological Resources.
[b]Sequence similarity based on 16S rRNA gene.
[c]R2A, Reasoner's 2A agar; MA, marine agar; PTYG, peptone-tryptone-yeast extract-glucose agar.

used for search of closest species, and their sequence were aligned using EzEditor2 (Jeon *et al*., 2014). Phylogenetic trees were generated by Jukes-Cantor distance mode (Jukes and Cantor, 1969) and neighbor-joining method (Saitou and Nei, 1987) using MEGA 7.0 (Kumar *et al*., 2016). The phylogenetic trees were evaluated using the bootstrap analysis (Felsenstein, 1985) based on 1,000 resampled datasets.

Results and Discussion

A total of 14 bacterial strains belonging to the phyla *Bacteroidota* (12 strains), *Acidobacteriota* (1 strain), and *Verrucomicrobiota* (1 strain) were isolated (Table 1). These strains represented 14 unrecorded species in Korea, belonging to 7 genera in 7 families. The 12 strains assigned to the phylum *Bacteroidota*, included 5 species belonging to the family *Flavobacteriaceae*, 2 species each to the families *Cyclobacteriaceae* and *Weeksellaceae*, and 1 species each to the families *Prolixibacteraceae* and *Sphingobacteriaceae*. At genus level, *Flavobacterium* (5 species) was the most abundant genus, which was then followed by *Chryseobacterium* (3 species) and *Algoriphagus* (2 species). Single species were obtained for the *Sunxiuqinia* and *Mucilaginibacter*. Among the remaining strains, one strain assigned to *Acidobacteriota* belonged to the genus *Edaphobacter* of the family *Acidobacteriaceae*, and the other assigned to *Verrucomicrobiota* belonged to the genus *Verrucomicrobium* of the family *Verrucomicrobiaceae*. The electron microscopic images of the isolates are provided in Fig. 1, and the phylogenetic relationship between the isolates and closely related species are presented in Figs. 2, 3 and 4. The detailed descriptions of each unrecorded species are provided.

Description of *Edaphobacter modestus* MA-22

Cells are Gram-stain-negative and rod-shaped. Motile by flagella. Colonies are circular, slightly convex, glistening and cream orange-colored after incubation for 3 days on R2A at 25°C. Positive for esculin hydrolysis and β-galactosidase, and weakly positive for nitrate reduction, but negative for indole production, glucose fermentation, arginine dihydrolase, urease 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 not utilized as sole carbon sources. Strain MA-22 (=NIBRBAC000510756) was isolated from a soil sampled at Inje-gun, Gangwon-do, Republic of Korea (37°57′49.1″ N 128°19′53.7″E). The GenBank accession number for the 16S rRNA gene sequence of strain MA-22 is OR342862.

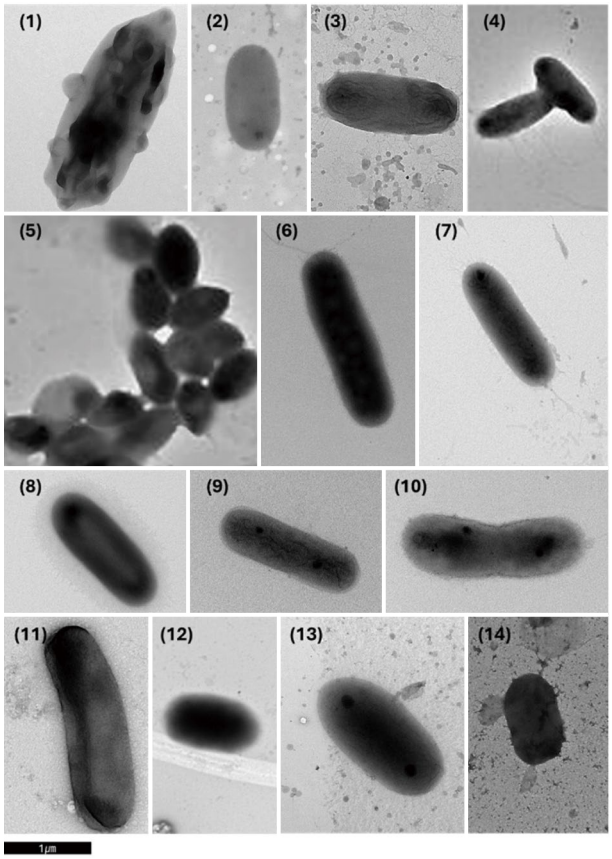


Fig. 1. Transmission electron or scanning electron micrographs of cells of the strains isolated in the study. Strain: 1, MA-22; 2, MMS23-Q5; 3, JPR4; 4, AN795; 5, CA1-11; 6, DL8; 7, FW4; 8, MMS23-HJ70; 9, CAU 1723; 10, AR1; 11, ST11; 12, WK20; 13, NW27; 14, JDC8. Scale bar, 1 μm.

Description of *Algoriphagus roseus* MMS23-Q5

Cells are Gram-stain-negative and ovoid-shaped. Colonies are circular, flat and pink-colored after incubation for 3 days on R2A at 30°C. Positive for esculin hydrolysis, gelatin hydrolysis and β-galactosidase, but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase and urease. 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 MMS23-Q5 (=NIBR BAC000510827) was isolated from a soil sampled at Heukseok-dong, Seo-gu, Daejeon, Republic of Korea (36° 16′15″N 127°21′21″E). The GenBank accession number for the 16S rRNA gene sequence of strain MMS23-Q5 is OR789442.

Description of *Algoriphagus kandeliae* JPR4

Cells are Gram-stain-negative and short rod-shaped. Colonies are circular, entire convex, smooth and red-color-

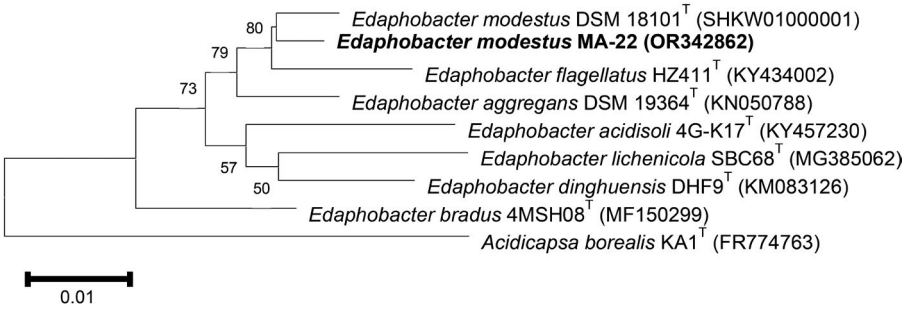


Fig. 2. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences showing the relationship between the strains isolated in this study and their relatives in the family *Acidobacteriaceae* of the phylum *Acidobacteriota*. Bootstrap values (>50%) are shown at branching points. *Acidicapsa borealis* KA1^T used as an outgroup. Scale bar, 0.01 substitutions per nucleotide.

ed after incubation for 3 days on Marine agar at 28°C. Positive for esculin hydrolysis and β-galactosidase, but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease 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 not utilized as sole carbon sources. Strain JPR4 (=NIBRBAC000510805) was isolated from a mudflat sampled at Samsan-myeon, Ganghwa-gun, Incheon, Republic of Korea (37°70′95″N 126°30′99″E). The GenBank accession number for the 16S rRNA gene sequence of strain JPR4 is OR751828.

Description of *Flavobacterium amnicola* AN795

Cells are Gram-stain-negative and rod-shaped. Colonies are round, entire, convex and yellow-colored after incubation for 3 days on R2A at 28°C. Negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis, gelatin hydrolysis, β-galactosidase and cytochrome oxidase. 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 AN795 (=NIBR BAC000510616) was isolated from a wetland sampled at Dogi-dong, Anseong-si, Gyeonggi-do, Republic of Korea (37°01′02.6″N 127°15′48.9″E). The GenBank accession number for the 16S rRNA gene sequence of strain AN795 is OR527152.

Description of *Flavobacterium johnsoniae* subsp. *johnsoniae* CA1-11

Cells are Gram-stain-negative and rod-shaped. Colonies are circular, slightly convex, glistening and yellow-colored after incubation for 3 days on R2A at 25°C. Positive for esculin hydrolysis, gelatin hydrolysis and β-galactosidase, but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase and urease. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, adipic acid, malic acid and trisodium citrate are utilized as sole carbon sources, but not potassium gluconate, capric acid and phenylacetic acid. Strain CA1-11 (=NIBRBAC000510743) was isolated from a soil sampled at Cheonan-si, Chungcheongnam-do, Republic of Korea (36°48′58.3″N 127°07′17.4″E). The GenBank accession number for the 16S rRNA gene sequence of strain CA1-11 is OR346149.

Description of *Flavobacterium ajazi* DL8

Cells are Gram-stain-negative and short rod-shaped. Colonies are circular, convex, opaque and bright yellow-colored after incubation for 4 days on R2A at 25–30°C. Positive for nitrate reduction, esculin hydrolysis, gelatin hydrolysis and β-galactosidase, but negative for indole production, glucose fermentation, arginine dihydrolase and urease. D-Glucose, L-arabinose, D-mannose and D-maltose are utilized as sole carbon sources, but not D-mannitol, *N*-acetyl-glucosamine, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. Strain DL8 (=NIBRBAC000510651) was isolated from a stream sampled at Gongneungcheon, Neungan-ro, Jori-eup, Paju-si, Gyeonggi-do, Republic of Korea (37°44′ 29.6″N 126°47′35.2″E). The GenBank accession number for the 16S rRNA gene sequence of strain DL8 is OR251 346.

Description of *Flavobacterium hercynium* FW4

Cells are Gram-stain-negative and short rod-shaped. Colonies are circular, undulate, convex, smooth and white-colored after incubation for 4 days on PTYG agar at 28°C. Positive for nitrate reduction, esculin hydrolysis, gelatin hydrolysis and β-galactosidase, but negative for indole production, glucose fermentation, arginine dihydrolase and urease. D-Glucose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, malic acid and

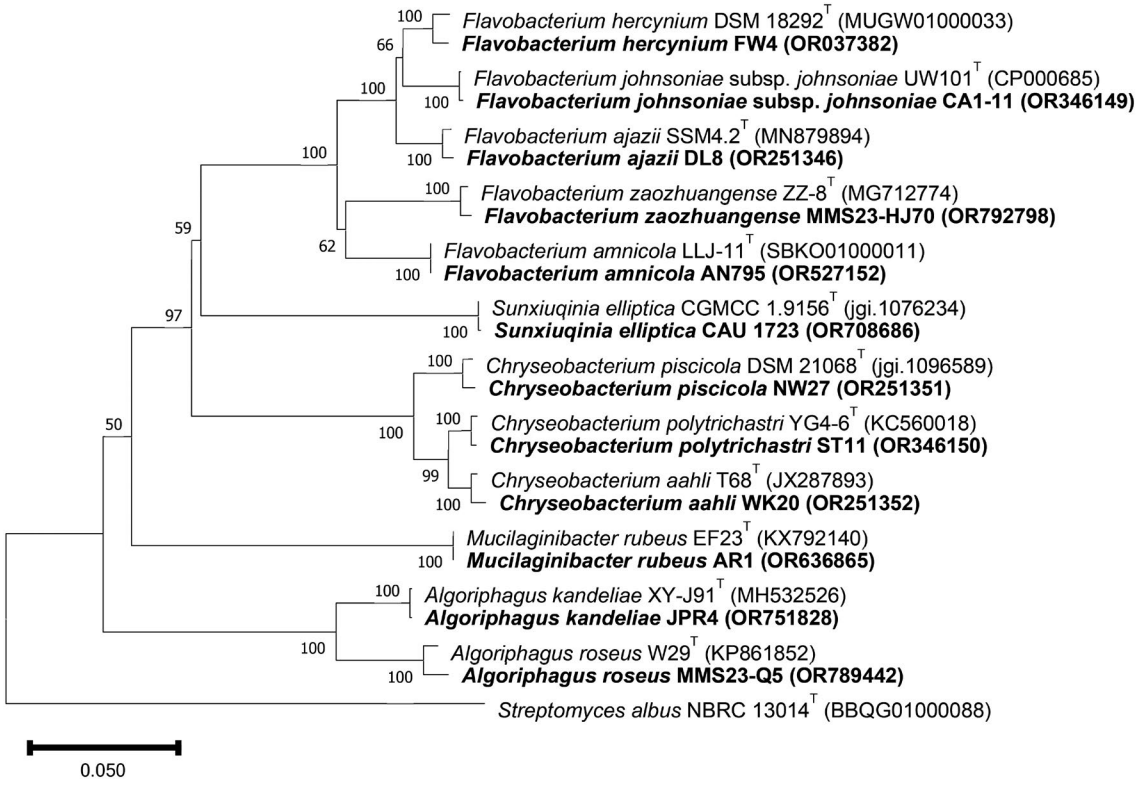


Fig. 3. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences showing the relationship between the strains isolated in this study and their relatives in the families *Cyclobacteriaceae*, *Flavobacteriaceae*, *Prolixibacteraceae*, *Sphingobacteriaceae* and *Weeksellaceae* of the phylum *Bacteroidota*. Bootstrap values (>50%) are shown at branching points. *Streptomyces albus* NBRC 13014^T used as an outgroup. Scale bar, 0.05 substitutions per nucleotide.

trisodium citrate are utilized as sole carbon sources, but not L-arabinose, capric acid, adipic acid and phenylacetic acid. Strain FW4 (=NIBRBAC000510789) was isolated from an agricultural soil sampled at 994-1 Geumsan-ri, Seomyeon, Chuncheon-si, Gangwon-do, Republic of Korea (37°89′77″N 127°69′35″E). The GenBank accession number for the 16S rRNA gene sequence of strain FW4 is OR037382.

Description of *Flavobacterium zaozhuangense* MMS23-HJ70

Cells are Gram-stain-negative and rod-shaped. Colonies are circular, smooth, glistening and yellow-colored after incubation for 3 days on R2A at 30°C. Positive for β-galactosidase, but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis and gelatin hydrolysis. D-Glucose is utilized as sole carbon sources, but not 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 MMS23-HJ70 (=NIBRBAC000510812) was isolated from a soil sampled at Gyesan-dong, Gyeyang-gu, Incheon, Republic of Korea (37°54′49″N 126°72′96″E). The GenBank accession number for the 16S rRNA gene sequence of strain MMS23-HJ70 is OR792798.

Description of *Sunxiuqinia elliptica* CAU1723

Cells are Gram-stain-negative and short rod-shaped. Colonies are circular, smooth, entire, convex, opaque and coral-colored after incubation for 3 days on Marine agar at 30°C. Positive for esculin hydrolysis and β-galactosidase, but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease 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 not utilized as sole carbon sources. Strain CAU 1723 (=NIBRBAC000510780) was isolated from a mud sampled at 1531, Daebuhwanggeum-ro, Danwon-gu, Ansan-si, Gyeonggi-do, Republic of Korea (37°17′19.8″N 126°34′57.1″E). The GenBank accession number for the 16S rRNA gene sequence of strain CAU 1723 is OR708686.

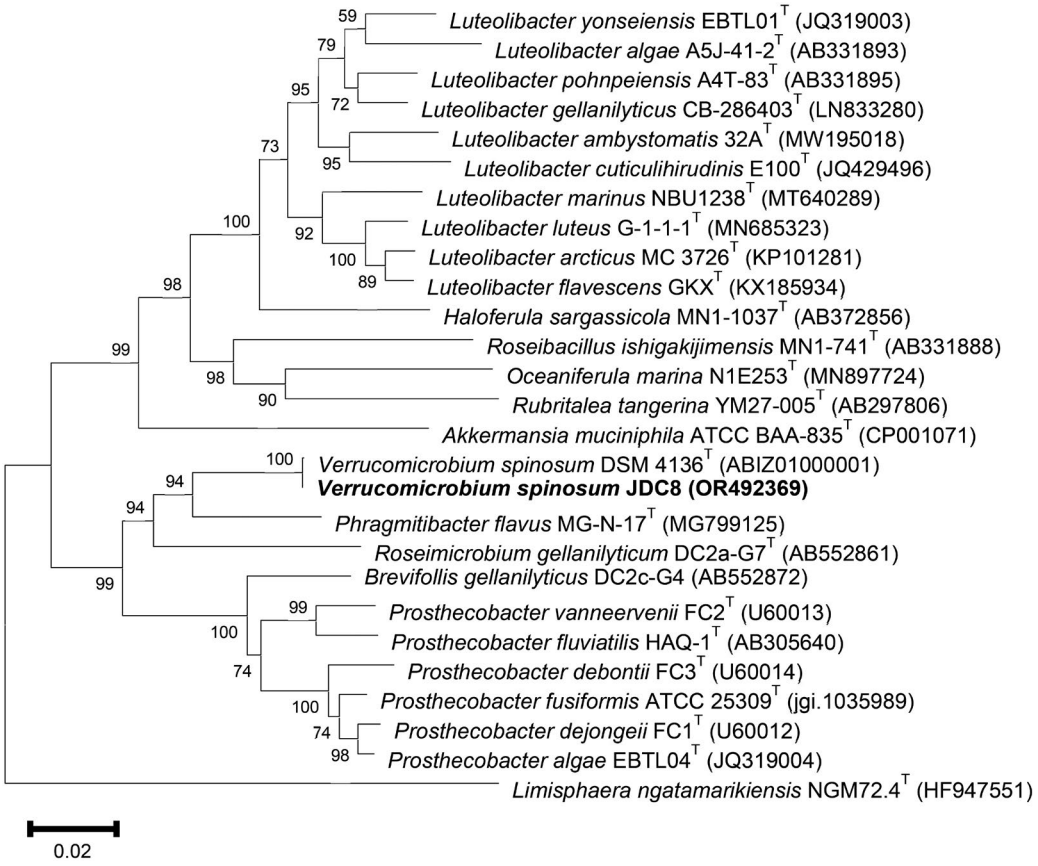


Fig. 4. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences showing the relationship between the strains isolated in this study and their relatives in the family *Verrucomicrobiaceae* of the phylum *Verrucomicrobiota*. Bootstrap values (>50%) are shown at branching points. *Limisphaera ngatamarikiensis* NGM72.4^T used as an outgroup. Scale bar, 0.02 substitutions per nucleotide.

Description of *Mucilaginibacter rubeus* AR1

Cells are Gram-stain-negative and short rod-shaped. Colonies are circular, entire, convex, smooth and pink-colored after incubation for 3 days on R2A at 28°C. Positive for nitrate reduction, esculin hydrolysis, gelatin hydrolysis and β-galactosidase, but negative for indole production, glucose fermentation, arginine dihydrolase and urease. D-Glucose and L-arabinose are utilized as sole carbon sources, but not D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. Strain AR1 (=NIBRBAC000510794) was isolated from an agricultural soil sampled at Sunhwan-ro, Danwon-gu, Ansan-si, Gyeonggi-do, Republic of Korea (37°34′14″N 126°84′36″E). The GenBank accession number for the 16S rRNA gene sequence of strain AR1 is OR636865.

Description of *Chryseobacterium polytrichastri* ST11

Cells are Gram-stain-negative and rod-shaped. Colonies are circular, slightly convex, glistening and yellow-colored after incubation for 3 days on R2A at 25°C. Positive for esculin hydrolysis and gelatin hydrolysis, and weakly positive for β-galactosidase, but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase and urease. 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 ST11 (=NIBRBAC000510744) was isolated from a soil sampled at Nowon-gu, Seoul, Republic of Korea (37°38′20.4″N 127°02′53.3″E). The GenBank accession number for the 16S rRNA gene sequence of strain ST11 is OR346150.

Description of *Chryseobacterium aahli* WK20

Cells are Gram-stain-negative and short rod-shaped. Colonies are circular, low convex and golden yellow-colored after incubation for 2 days on R2A at 30°C. Positive for esculin hydrolysis and gelatin hydrolysis, but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease and β-galactosidase. D-Glucose is utilized as sole carbon source, but not 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 WK20 (=NIBRBAC000510653) was isolated from a soil sampled at Siksa-dong, Ilsandong-gu, Goyang-si, Gyeonggi-do, Republic of Korea (37°40′47.1″N 126°48′20.3″E). The GenBank accession number for the 16S rRNA gene sequence of strain WK20 is OR251352.

Description of *Chryseobacterium piscicola* NW27

Cells are Gram-stain-negative and rod-shaped. Colonies are round and yellow colored after incubation for 3 days on R2A at 30°C. Positive for esculin hydrolysis and gelatin hydrolysis, but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease 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 NW27 (=NIBRBAC000510634) was isolated from a stream sampled at Gongneungcheon, Neungan-ro, Jori-eup, Paju-si, Gyeonggi-do, Republic of Korea (37° 44′29.6″N 126°47′35.2″E). The GenBank accession number for the 16S rRNA gene sequence of strain NW27 is OR251351.

Description of *Verrucomicrobium spinosum* JDC8

Cells are Gram-stain-negative and having wart-like prosthecae in the cell surface. Colonies are circular and yellow-colored after incubation for 2 days on R2A at 30°C. Positive for nitrate reduction, esculin hydrolysis and cytochrome oxidase, but negative for indole production, glucose fermentation, arginine dihydrolase, urease, gelatin hydrolysis, β-galactosidase and cytochrome oxidase. D-Glucose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, malic acid and trisodium citrate are utilized as sole carbon sources, but not L-arabinose, potassium gluconate, capric acid, adipic acid and phenylacetic acid. Strain JDC8 (=NIBRBAC000510582) was isolated from a soil sampled at Jeongwangcheon-ro, Siheung-si, Gyeonggi-do, Republic of Korea (37°19′54″N 126°44′25″E). The Gen Bank accession number for the 16S rRNA gene sequence of strain JDC8 is OR492369.

Conflicts of Interest

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

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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

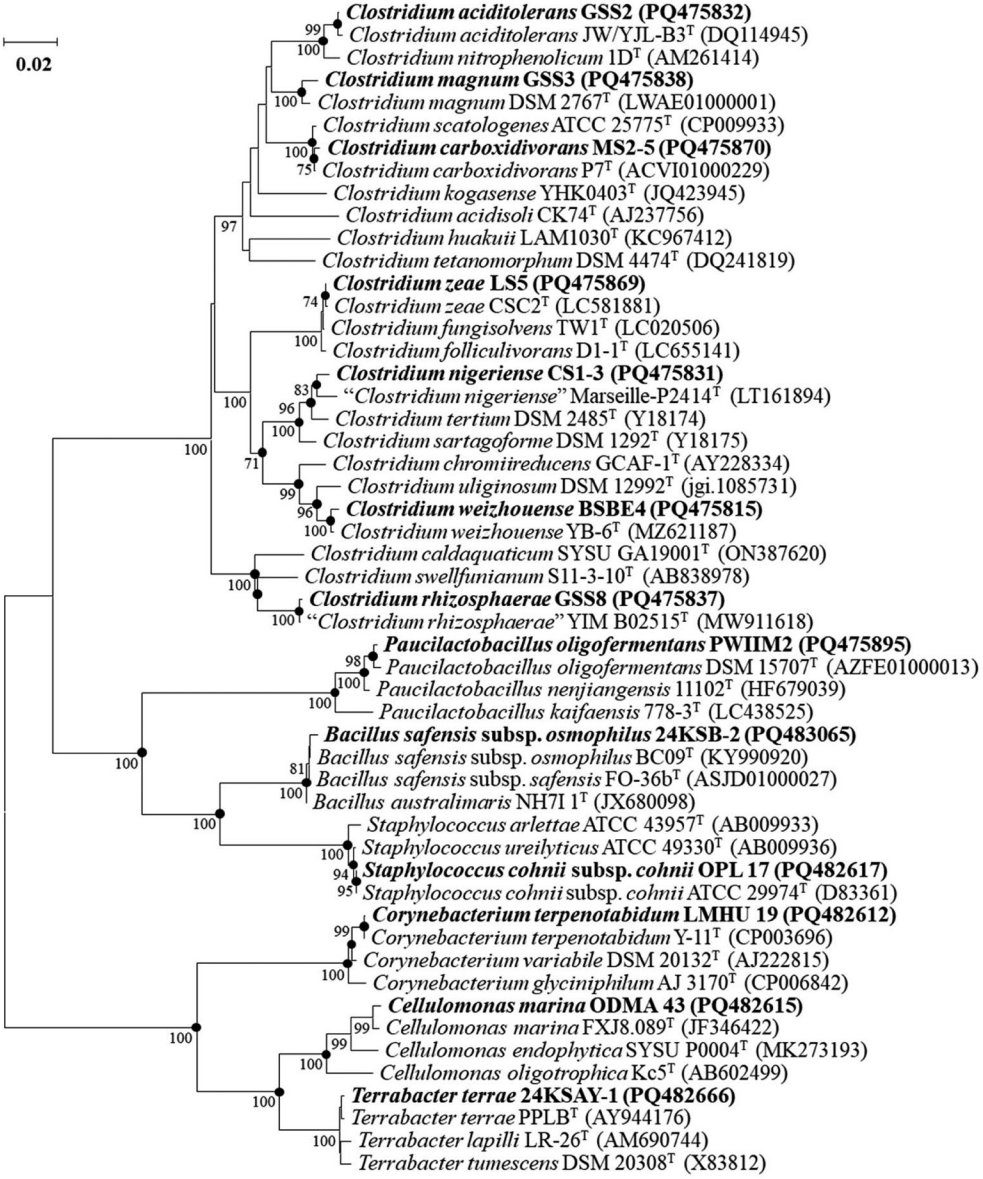


Fig. 1. Neighbor-joining (NJ) phylogenetic tree based on 16S rRNA gene sequences, showing the relationships between bacterial strains isolated in this study and their relatives in the phylum *Actinomycetota*, *Bacillota*. Bootstrap values (>70%) based on 1,000 replications are shown at branch points. 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

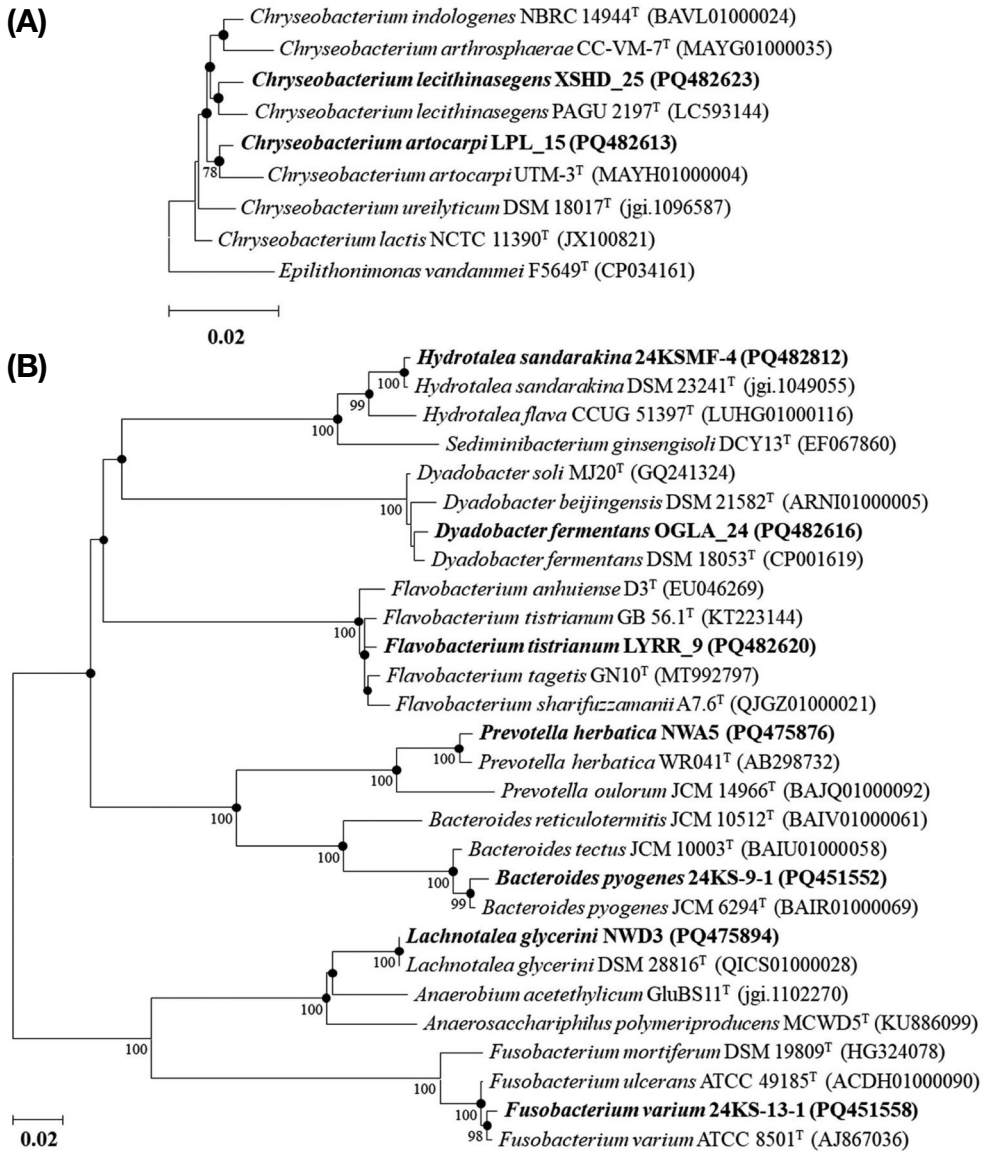


Fig. 2. Neighbor-joining (NJ) phylogenetic trees based on 16S rRNA gene sequences, showing the relationships between bacterial strains isolated in this study and their relatives in the genus *Chryseobacterium* (A) and the phyla *Bacteroidota* and *Fusobacteriota* (B). Bootstrap values (>70%) based on 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-

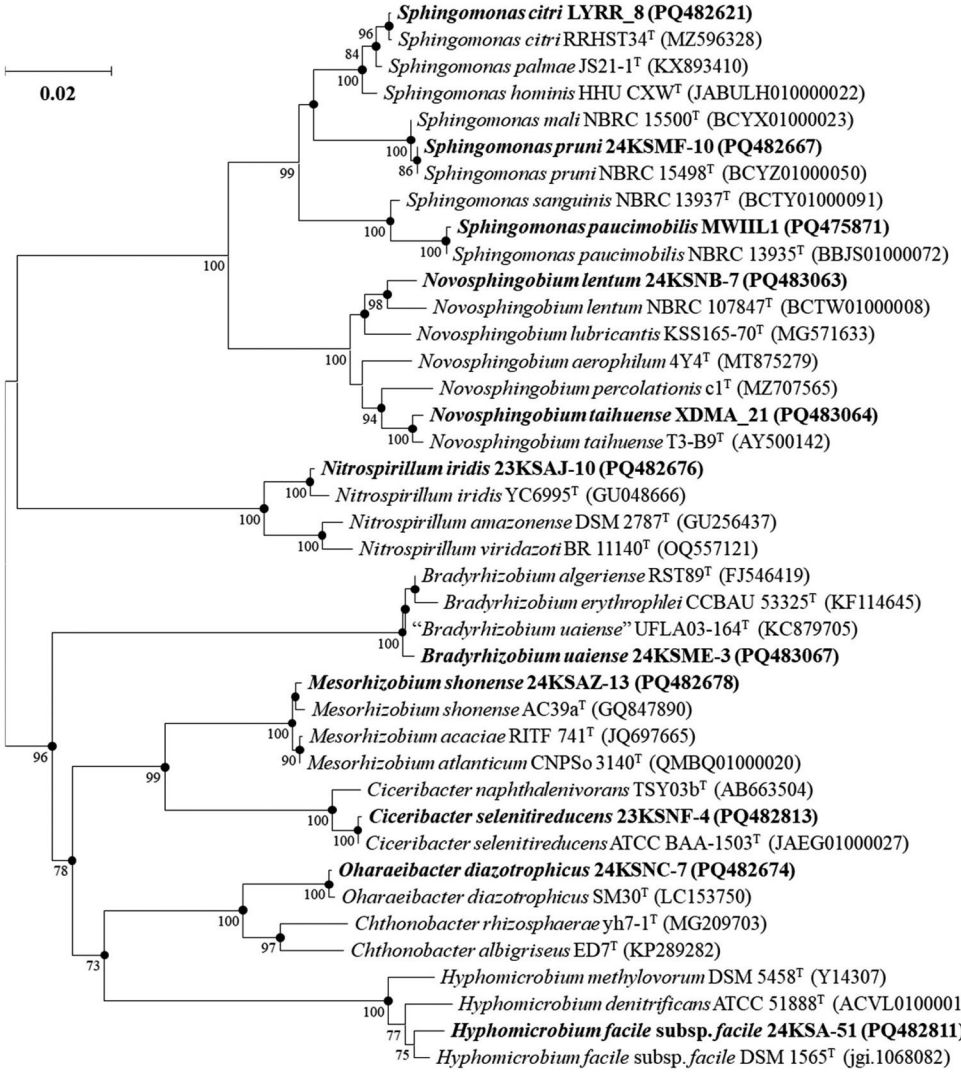


Fig. 3. Neighbor-joining (NJ) phylogenetic tree based on 16S rRNA gene sequences, showing the relationships between bacterial strains isolated in this study and their relatives in the class *Alphaproteobacteria*. Bootstrap values (>70%) based on 1,000 replications are shown at branch points. Filled circles 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

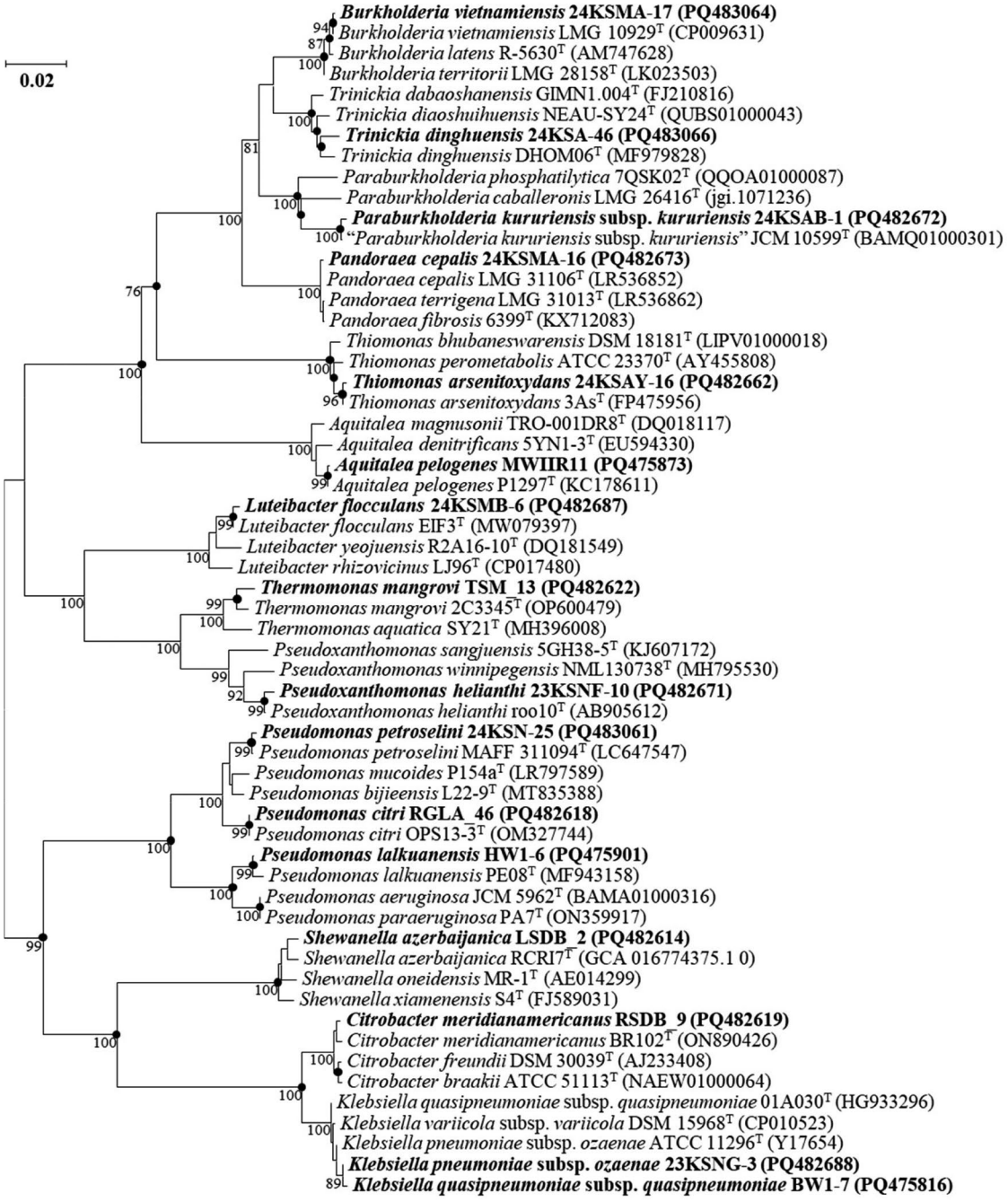


Fig. 4. Neighbor-joining (NJ) phylogenetic tree based on 16S rRNA gene sequences, showing the relationships between bacterial strains isolated in this study and their relatives in the class *Betaproteobacteria* and *Gammaproteobacteria*. Bootstrap values (>70%) based on 1,000 replications are shown at 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

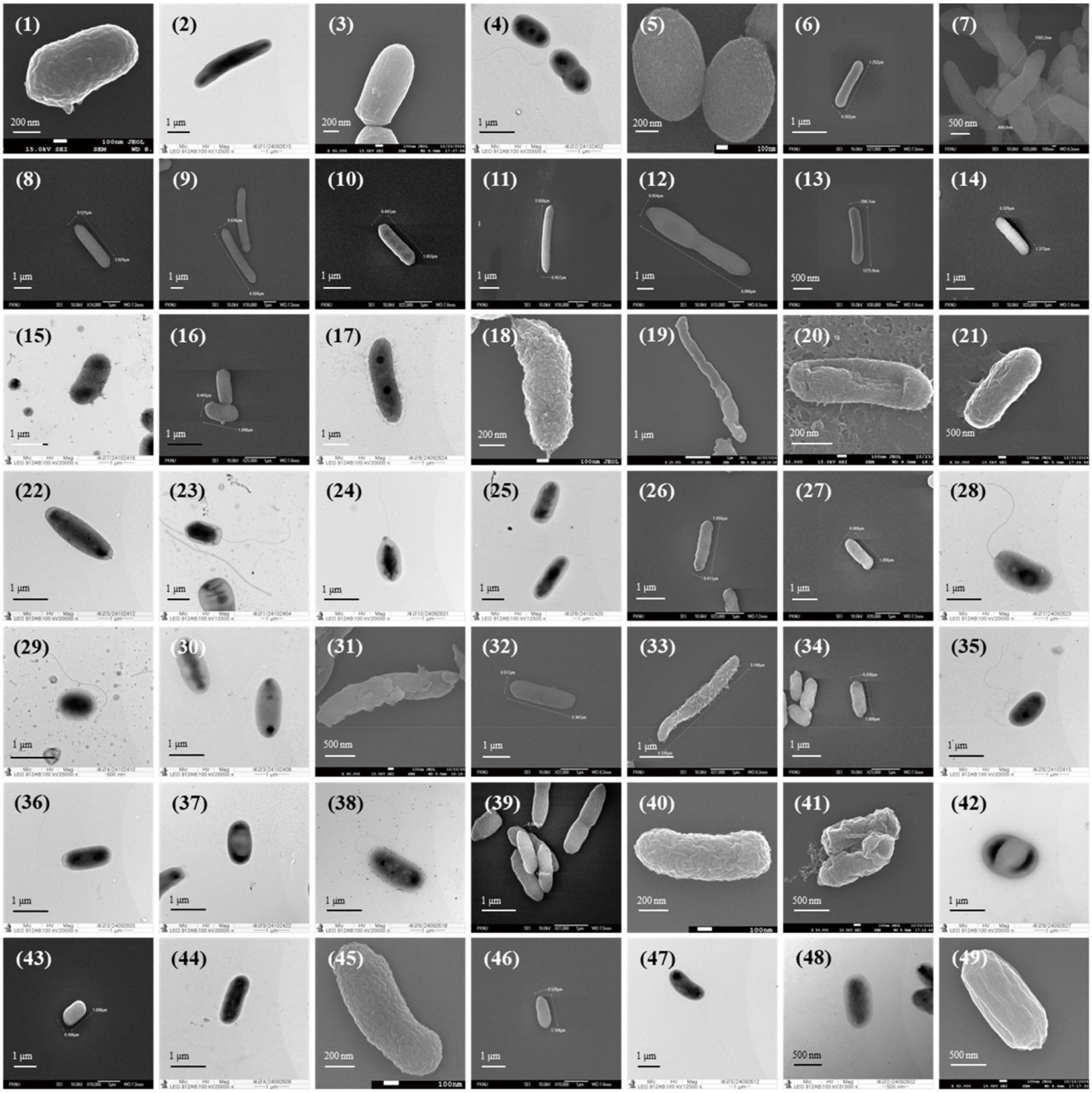


Fig. 5. Transmission electron or scanning electron micrographs of cells of the strains isolated in this study. Strains: 1, ODMA_43; 2, 24KSAY-1; 3, LMHU_19; 4, 24KSB-2; 5, OPL_17; 6, PWIIM2; 7, GSS2; 8, MS2-5; 9, GSS3; 10, CS1-3; 11, GSS8; 12, BSBE4; 13, LS5; 14, NWD3; 15, 24KS-9-1; 16, NWA5; 17, 24KSMF-4; 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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Identification of silver vine, *Actinidia polygama* flower bud gall midge (Diptera: Cecidomyiidae) in Korea and its ecological traits

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The mature galled flower buds of the silver vine *Actinidia polygama* (Actinidiaceae) are used in traditional oriental medicine in Korea. In Japan, a similar gall maker of *A. polygama* is *Pseudasphondylia matatabi*. However, few taxonomic studies exist on gall makers in Korea. Comprehensive morphological and molecular analyses confirmed that the Korean specimens were identical to *P. matatabi* from Japan. Morphological characteristics, particularly the male genital structure and pupal horn morphology, matched the original description from Japan. Molecular phylogenetic analysis of the DNA barcode region revealed that the Korean and Japanese populations formed a monophyletic clade distinctly separated from other congeners, including the recently described *P. kiwiphila* from Taiwan, which induces galls in *A. rufa*. Life history observations showed that adult emergence occurred from September to October, when no suitable oviposition sites were available for the deciduous host plant, suggesting the existence of an unknown winter host plant.

Keywords: *Actinidia polygama*, gall midge, *Pseudasphondylia*

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Introduction

Galls are abnormally modified plant tissues or organs resulting from chemical and mechanical stimulation by gall-inducing organisms (Shorthouse and Rohfritsch, 1992). Several herbivorous insect groups include gall-inducing species (such as Hymenoptera, Lepidoptera, Diptera, and Hemiptera). Gall shape and host information represent an "extended phenotype" of the gall-inducing cecidomyiid (Yukawa, 2000). Cecidomyiid species can be easily distinguished based on gall morphology and host taxonomy. Certain cecidomyiid galls are used as herbal medicines in East Asia. The most prominent examples are the fruit galls of *Ampelopsis glandulosa* var. *heterophylla* (Vitaceae) and the flower bud gall of *Actinidia polygama* (Actinidiaceae). In Oriental Medicine, the gall of *A. polygama*, known as Mokcheonryoza (목천료자; 木天蓼子), has been used as a popular herbal medicine (Kim *et al*., 2023) (Fig. 1).

The gall inducer of flower buds on *A. polygama* is *Pseudasphondylia matatabi* in Japan, whereas in Taiwan, *Pseudasphondylia kiwiphila* is known to induce galls on *Actinidia rufa*, which belongs to the same genus as *A. polygama* (Yuasa and Kumazawa, 1938; Lin *et al*., 2022). A total of 14 described species of the genus *Pseudasphondylia* are known globally (Gagné and Jaschhof, 2021; Matsuda *et al*., 2021; Lin *et al*., 2022; Elsayed *et al*., 2023). Congeners and related genera exhibit alternating host behaviors (Tokuda and Yukawa, 2005; Uechi *et al*., 2004; Elsayed *et al*., 2019). *P. matatabi* is also a potential host-alternating species because its adult stage occurs from September to October. However, *A. polygama* is deciduous and leaves no oviposition sites on its host plants from autumn to winter. Winter host plant species are not yet identified in Japan (Tokuda and Yukawa, 2005). The similarity between the host plant and the gall shape suggests that the Korean species may be related to *P. matatabi*

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Fig. 1. Flower bud gall of *Actinidia polygama*; a: investigation site in Japan (Inumaki, Hisayama Town, Fukuoka), b: Early flower bud of *A. polygama*, c: Early stage of gall (12 June 2016), d: Bloomed flower bud gall.

(Hashim and Yukawa, 1992).

This study aimed to confirm whether the gall midge species on *A. polygama* in Korea are identical to *P. matatabi* in Japan and to provide basic ecological information on *P. matatabi* in Japan. This study contributes to a better understanding of this gall-inducing species and its relationship with *A. polygama* in East Asia.

Materials and Methods

Morphological studies, terminology, and depository of specimens

For morphological observation, pupal cases and adults stored in 80–85% ethanol were mounted on slides in Canada balsam, following Yukawa (1971) and Gagné (1989). Adult morphological terminology followed Cumming and Wood, 2017, except for the thoracic sclerites, which followed Yukawa and Ohsaki (1988). The pupal morphological terminology followed Gagné (1994). Specimens used in this study were deposited in the National Institute of Biological Resources, Korea.

Ecological surveys

In 2015 and 2016, from April to June, surveys were conducted at a colony of *Actinidia polygama* in Inumaki, Hisayama Town, Fukuoka, Japan (N33°40′33″, E130°32′46″), to confirm gall development and adult oviposition (Fig. 1a). The site was visited every two days; however, as the buds became more prominent, visits for daily observations increased. Sticky traps were placed near flowers to collect females for oviposition.

Molecular analysis

DNA samples were extracted from 80–85% ethanol-stored specimens using a DNeasy Blood and Tissue Kit (Qiagen, Tokyo, Japan) following the manufacturer's instructions. The 658 bp region of the COI gene used for the DNA barcoding project (Hebert *et al.*, 2003) was amplified, purified, and sequenced following the method described in Yukawa *et al.* (2003). The primers used for this analysis were: forward; LCO1490 5′-GGT CAA CAA ATC ATA AAG ATA TTG G -3′ and reverse; HCO2198 5′-TAA ACT TCA GGG TGA CCA AAA AAT CA-3′ (Folmer *et al.*, 1994). Sanger sequencing was performed

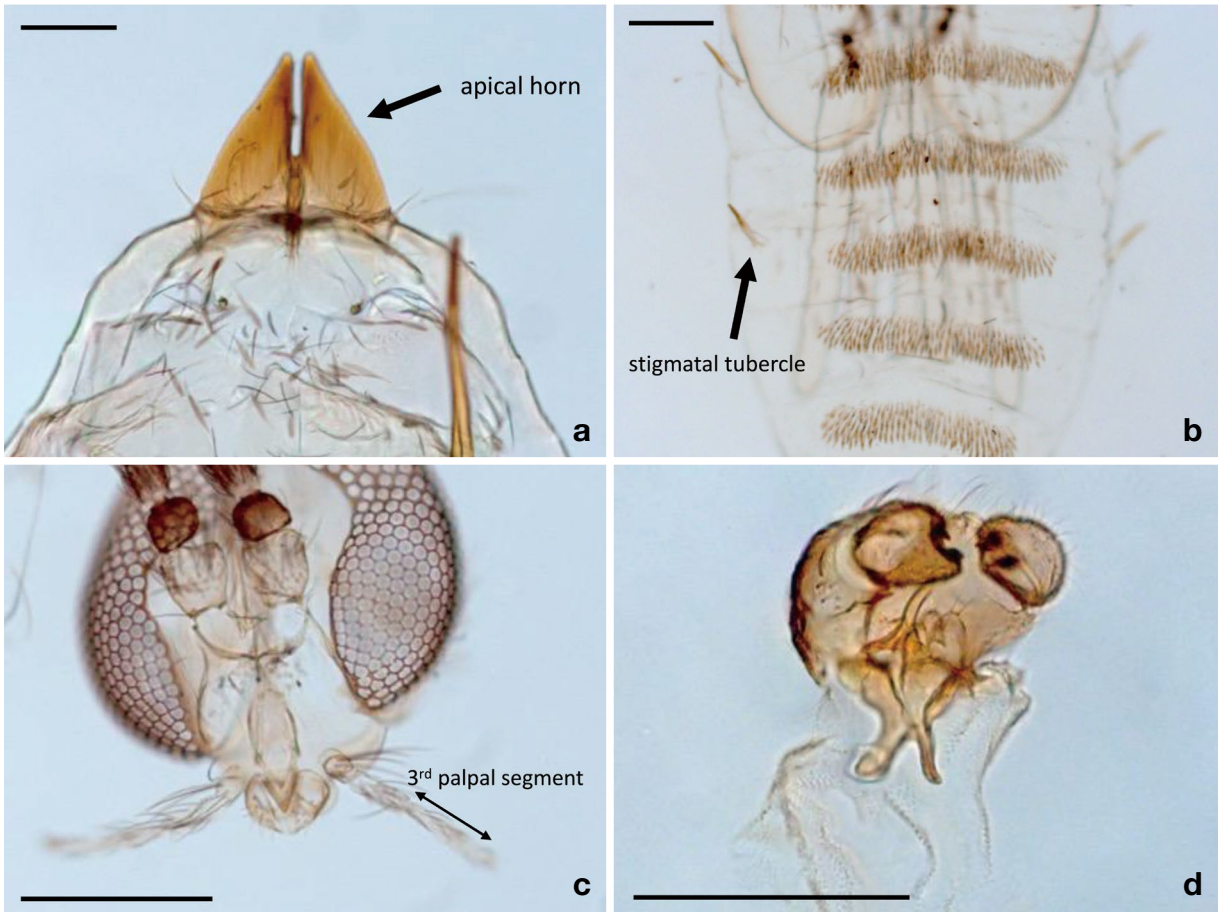


Fig. 2. Morphology of *Pseudasphondylia matatabi* in Korea; a: pupal head (ventral), b: pupal abdomen (dorsal), c: female head, d: male genitalia. Scale bar indicates 200 μm.

by Macrogen, Inc. (Seoul, Korea). Sequence data were aligned using MAFFT version 7 with the G-INS-I method (Golubchik *et al*., 2007) on the Geneious Prime program 2025.0.2 (https://www.geneious.com). Five species belonging to the same genus as *Pseudasphondylia* (*P. neolitseae*, *P. elaeocarpi*, *P. saohimea*, *P. tominagai*, and *P. kiwiphila*) were included and *Kiefferia pericarpiicola* was used as the outgroup taxon. Maximum likelihood trees were obtained using IQ-TREE (Trifinopoulos *et al*., 2016) with the TIM + F + G4 substitution model. The most suitable maximum likelihood model was chosen for the IQ-TREE using the Bayesian information criterion (BIC).

The nucleotide sequence data reported in this study were deposited in the NCBI GenBank database (https://www.ncbi.nlm.nih.gov).

Results

Taxonomic accounts
Family Cecidomyiidae
Subfamily Cecidomyiinae
Tribe Asphondyliini
Subtribe Asphondyiina
Genus *Pseudasphondylia* Monzen, 1955

Pseudasphondylia matatabi
(Yuasa and Kumazawa, 1938) (Fig. 2)
개다래꽃봉오리혹파리 (신칭)

Examined specimens. 2♂1♀ 3 pupa (NIBR, voucher number: 2019-IN-265-001−006), Chilbong-ro, Hojeo-myeon, Wonju-si, Gangwon-do, South Korea (N37°27′43″, E127°53′59″), 5 Oct. 2019, Coll. Junheon Kim (National Institute of Forest Science).

Diagnosis. Pupal apical horn 290−300 μm in length, acutely pointed, with finely denticulate outer margin; stigmatal tubercles long, 175−185 μm, present on second to fifth abdominal segments. Palpus three-segmented; third palpal segment about 2 times as long as second. Wing about 2 times as long as wide. Male genitalia cerci deeply emarginated with V-shaped incision, each lobe bearing numerous

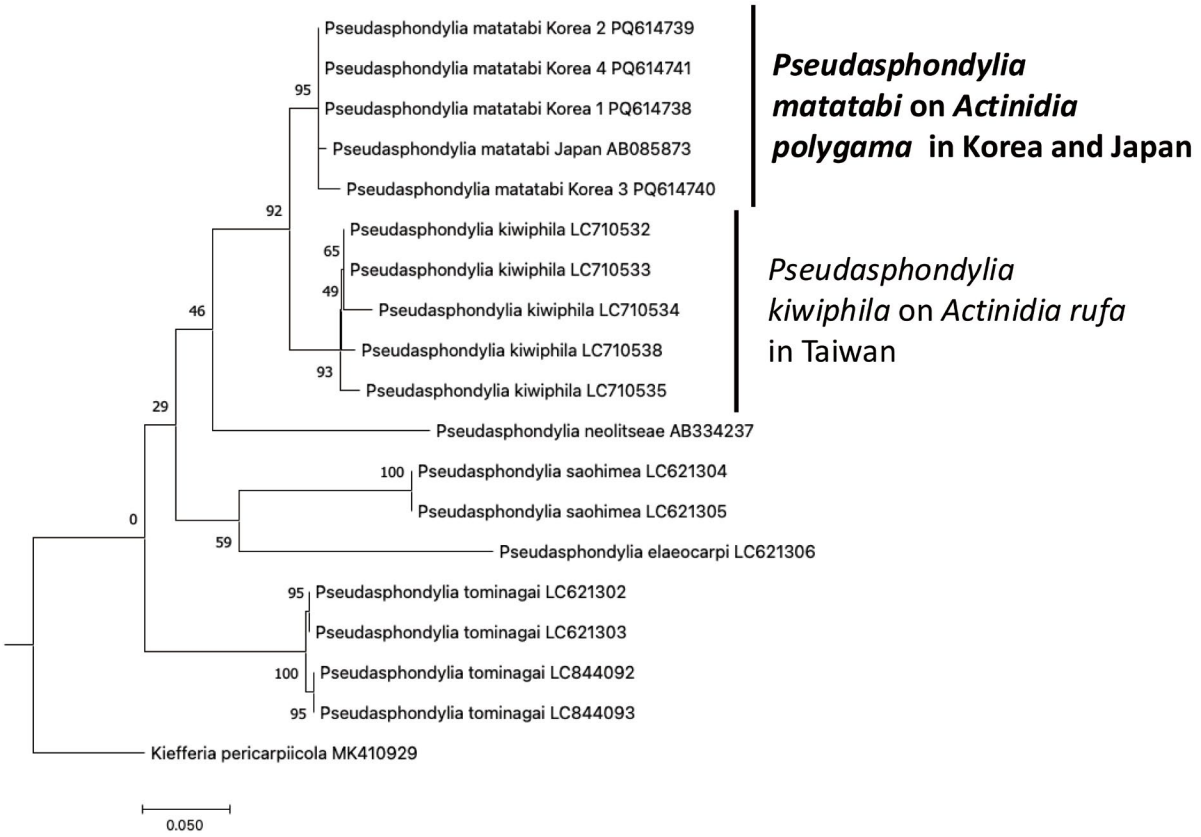


Fig. 3. Maximum likelihood tree of *Pseudasphondylia matatabi* and their congeners based on mtDNA COI sequences. Bootstrap values are indicated for nodes.

setae; gonostylus oval in shape, bearing two distinct sclerotized teeth at distal end; gonocoxite elongate in form, extending ventrally past gonostylar insertion point, with distinctive finger-like basal lobe; aedeagus narrow, gradually tapering toward apex. Needle part of ovipositor long about 1.5 mm (Fig. 2).

Gall. The ovary of the flower enlarged and swelled irregularly. Each gall contained multiple larval chambers with a maximum diameter of 15−38 mm and a height of 10−22 mm, which were larger than those of normal fruit (Yukawa and Masuda, 1996). Galls could form on flower buds before or during the flowering process. Considering their developmental characteristics, they should be classified as flower bud galls rather than fruit galls (Fig. 1c).

Distribution. Japan (Honshu, Shikoku, Kyushu) and Korea.

Life history. In Kyushu, Japan, the flower buds of *A. polygama* begin to develop during April and reach full bloom in June. The gall midge is assumed to lay eggs in early flower buds, although oviposition behavior was not observed during the daytime surveys (2015, 2016) (Fig. 1b). Galls developed from June to July, although the larvae remained in the first-instar stage until late August. Larval growth accelerates from September, with pupation and emergence occurring from late September to October (Yukawa and Masuda, 1996). However, from October onwards, no flower buds or fruits were available on *A. polygama* for oviposition, suggesting that the gall midge must move to a winter host; however, this process remains unknown.

Molecular analysis. Maximum likelihood tree analysis revealed that *P. matatabi* specimens from Korea and Japan formed a well-supported monophyletic clade with high bootstrap support (Fig. 3). The Korean population (NCBI accessions: PQ614738−PQ614741) clustered closely with the Japanese population (AB085873), indicating a close genetic relationship. This clade was distinctly separated from its congeners, including *P. kiwiphila* from Taiwan and other *Pseudasphondylia* species (*P. neolitseae*, *P. elaeocarpi*, *P. saohimea*, and *P. tominagai*). The tree topology strongly supported the genetic uniformity of *P. matatabi* populations across Korea and Japan.

Discussion

This study confirmed the identity of the flower bud gall midge of *A. polygama* in Korea as *P. matatabi* through comprehensive morphological and molecular analyses.

This identification was particularly crucial, given the recent discovery of *P. kiwiphila*, a closely related species inducing galls on *A. rufa* in Taiwan. The morphological characteristics of the Korean specimens aligned perfectly with those of the description of *P. matatabi* from Japan, particularly in terms of the male genitalia structure and pupal horn morphology (Yukawa, 1971). Molecular phylogenetic analysis strongly supported this identification.

Life history observations in Japan revealed synchronized development with host plant phenology, particularly during the flowering period. The absence of suitable oviposition sites on *A. polygama* during winter strongly suggests the existence of an alternative host plant, similar to that of the host-alternation behavior observed in other Asphondyliini species. Further research is required to identify the winter host plants of *P. matatabi*.

Conflicts of interest

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

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First record of the family Sebidae (Crustacea: Malacostraca: Amphipoda) from Korean waters, with description of newly recorded species, *Seba chiltoni*

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This study aims to discover and document amphipods from Korea, contributing to the clarification of the taxonomy of Korean amphipod species. As part of this effort, a newly recorded species, *Seba chiltoni* Moore, 1987, belonging to the family Sebidae Walker, 1907, was collected from the southern subtidal area of Jeju-do, Korea and is reported herein. The family Sebidae is notable for comprising only a single genus, *Seba* Spence Bate, 1862. In this paper, the morphological characteristics of the genus *Seba* and the newly recorded species *Seba chiltoni* are provided. The species is described and fully illustrated in the present study. This is the first record of the family Sebidae from Korea.

Keywords: Amphilochidea, amphipod, Korea, sebid, taxonomy

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Introduction

The family Sebidae Walker, 1907 is a small family group containing a single genus, *Seba* Spence Bate, 1862. Spence Bate established the genus *Seba* under Amphipoda, designating *Seba innominata* as the type species. Later, in 1906, Walker proposed the family Sebidae and considered *S. innominata* a nomen dubium, designating *Seba saundersii* Stebbing, 1875 as the new type species. Currently, five previously established genera—*Caribseba* Shaw, 1989, *Grimaldia* Chevreux, 1889, *Paravalettia* K.H. Barnard, 1916, *Seba* Spence Bate, 1862, and *Teraticum* Chilton, 1884—have been synonymized with *Seba*, which now comprises 27 recognized species (Horton *et al*., 2025). The known species of *Seba* are predominantly found in shallow subtidal zones and are ecologically associated with benthic marine organisms such as sponges and macroalgae (Ariyama, 2009).

The family Sebidae and its sole genus *Seba* can be distinguished from related taxa by the following characteristics: antennae subequal in length; accessory flagellum present with two articles (except in *S. tropica* McKinney, 1980, where it is absent); eyes absent (except in *S. typica* (Chilton, 1884), where they are present); gnathopod 1 weakly chelate or subchelate; gnathopod 2 strongly chelate with elongate ischium; urosomites 2–3 coalesced (except in *S. aloe* Karaman, 1971, where segments are distinct); uropod 3 uniramus with a biarticulated ramus (Holman and Watling, 1983; Barnard and Karaman, 1991; Ariyama, 2009).

In this paper, we describe and illustrate a newly recorded species, *S. chiltoni*, in the Korean amphipod fauna. This is the first record of the family Sebidae from Korean waters.

Materials and Methods

Specimens were collected by SCUBA diving from the subtidal waters at Mun-island, Seogwipo-si, Jeju-do, Korea on 24 May 2018. For preservation, the specimens were

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fixed with 95% ethanol and later dissected in glycerol on Cobb's aluminum hollow slides. Permanent mounts were made using polyvinyl lactophenol with lignin pink as a staining agent. Pencil drawing and measuring were performed with the aid of a drawing tube, mounted on an SZX 12 stereomicroscope (Olympus) and BX 51 interference contrast compound microscope (Olympus). Line drawings were produced using the program Clip Studio Paint (Celsys, Japan). Body length was measured from the tip of the rostrum to the posterior end of the urosome, along the dorsal parabolic line of the body. Specimens are deposited at the National Institute of Biological Resources (NIBR), Incheon, Korea and the Department of Biological Science, Dankook University (DKU), Cheonan, Korea.

Systematic Accounts

Order Amphipoda Latreille, 1816 단각목
Family Sebidae Walker, 1907
작은집게손옆새우과 (신칭)
Genus *Seba* Spence Bate, 1862
작은집게손옆새우속 (신칭)

***Seba chiltoni* Moore, 1987 (Figs. 1–3)**
제주작은집게손옆새우 (신칭)

Seba chiltoni Moore, 1987: 258, figs. 14–15; Ariyama, 2009: 45, figs. 1–4.

Seba typica - Chilton, 1921: 56, fig. 6a–d; Chilton, 1924: 269; Ledoyer, 1978: 314, fig. 42; Ledoyer, 1986: 948, fig. 374.

Material examined. 2♂♂, Munseom island, Seogwipo-si, Jeju-do, Korea 33°13′38″N, 126°34′4″E, 24 May 2018. The specimens were collected by SCUBA diving, collected by Y.H. Kim.

Description. Male (cat no. NIBRIV0000837772): Body (Figs. 1, 2A) dorsally smooth, 2.4 mm long. Head subquadrate, longer than pereonite 1; cephalic lobe blunt; eye absent; rostrum not elongated; pereonite 2 longest, subequal in length with cephalon and pereonite 1 combined.

Epimera (Fig. 2B), epimeron 1 rounded posteroventrally, with one robust seta; epimeron 2 subquadrate, weakly produced posteroventrally; epimeron 3 produced posteroventrally with small cusp, four robust setae ventrally.

Antenna 1 (Fig. 2C) short, about quarter of body length; peduncular article 1 subrectangular, with ventrodistal robust seta, peduncular article 2 slender, rectangular, peduncular article 3 short, callynophorate ventrodistally; length ratio of peduncular articles 1–3 = 1.00 : 1.02 : 0.28; flagellum 4-articulate, articles 1, 2 callynophorate ventrodistally; accessory flagellum present, slender, 2-articulate.

Antenna 2 (Fig. 2D) slender, shorter than antenna 1; peduncular articles 1, 2 short; peduncular article 4 slender, rectangular; length ratio of peduncular articles 3–5 = 1.00 : 3.61 : 2.52; flagellum short, 3-articulate.



Fig. 1. *Seba chiltoni* Moore, 1987. Adult male, 2.6 mm (DKU202505), habitus. Scale bar = 1.0 mm

Gnathopod 1 (Fig. 2E) subchelate; coxa subquadrate, widening ventrally, posteroventral corner slightly notched, each corner with setule; basis elongate, narrowing proximally, ischium and merus pubescent posteriorly; carpus subtriangular, with ventrodistal setae; propodus widening distally, hind margin pubescent, palm steeply angled, middle portion with 2 large blunt processes, palmar corner distinctly produced, with two stout robust setae; dactylus falcate, fitting palm.

Gnathopod 2 (Fig. 2F) slender, chelate; coxa subquadrate, wider, about 0.95× as wide as long, posteroventral corner slightly notched, each corner with setule; basis slightly curved anteriorly, 0.84 times as long as that of gnathopod 1; ischium elongate, subrectangular, 0.59 times as long as basis; carpus subequal in length to ischium; propodus elongate, forming a chela with fitted dactylus, each margin straight, distal tip slightly curved anteriorly; dactylus falcate, fitting palm.

Pereopod 3 (Fig. 2G), coxa subovate; basis subrectangular, slightly curved posteriorly; merus produced anterodistally; carpus and propodus subrectangular, with posterior robust setae; dactylus falcate; length ratio of articles 2–7 = 1.00 : 0.33 : 0.89 : 0.62 : 0.60 : 0.31.

Pereopod 4 (Fig. 2H) similar to pereopod 3; length ratio of articles 2–7 = 1.00 : 0.28 : 0.82 : 0.56 : 0.58 : 0.30.

Pereopod 5 (Fig. 3A), coxa wider than long, bilobate; basis subovate, anterior margin with two robust setae, posterior margin weakly crenulate; merus broad, produced posterodistally; carpus and propodus subrectangular; dactylus falcate; length ratio of articles 2–7 = 1.00 : 0.25 : 0.71 : 0.50 : 0.52 : 0.22.

Pereopod 6 (Fig. 3B) similar to pereopod 5, except basis much larger, anterior margin with six robust setae, poster-

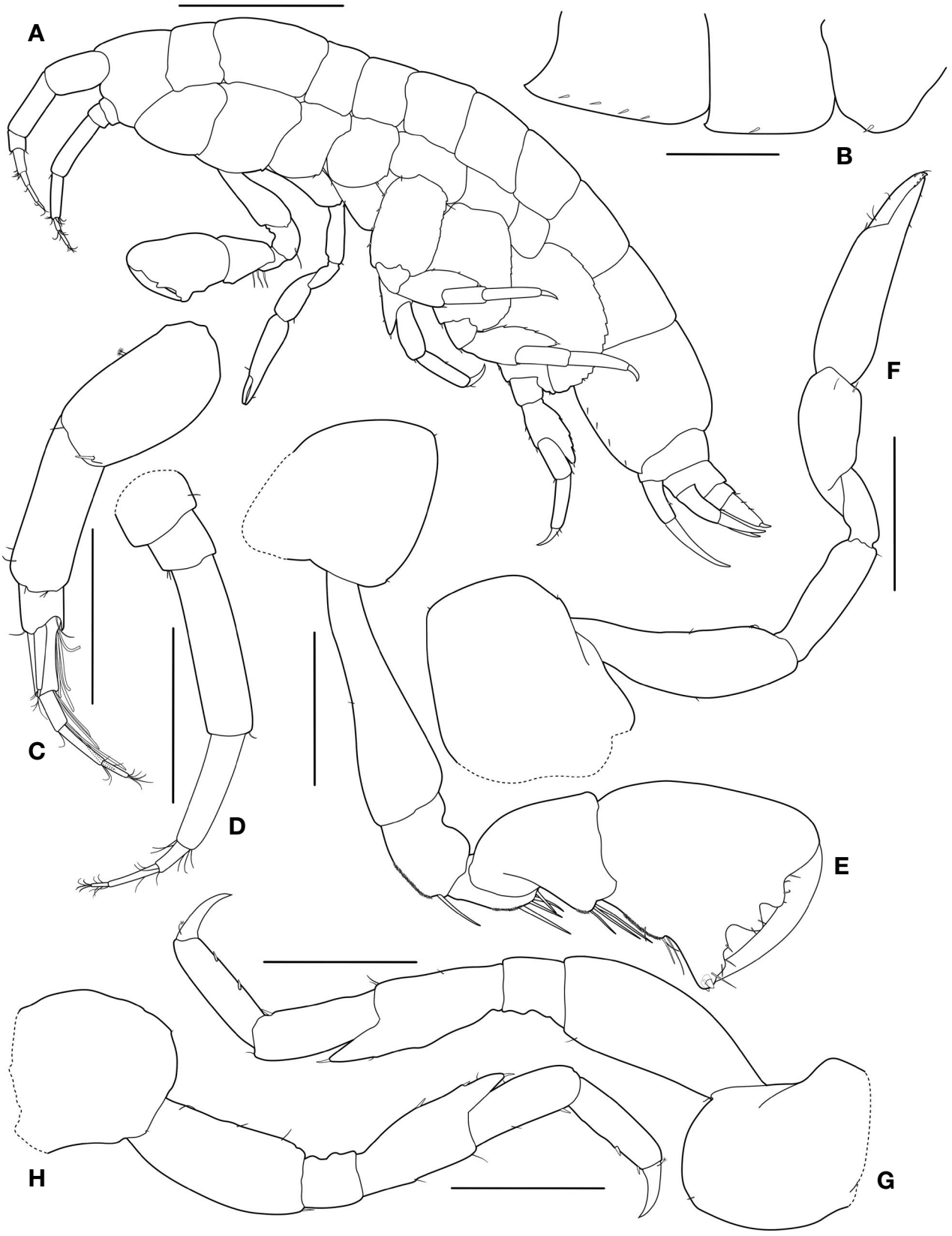


Fig. 2. *Seba chiltoni* Moore, 1987. Adult male, 2.4 mm (NIBRIV0000837772): A, habitus; B, epimera; C, antenna 1 (medial view); D, antenna 2; E, gnathopod 1; F, gnathopod 2; G, pereopod 3; H, pereopod 4. Scale bars: A = 0.5 mm, B–H = 0.2 mm.

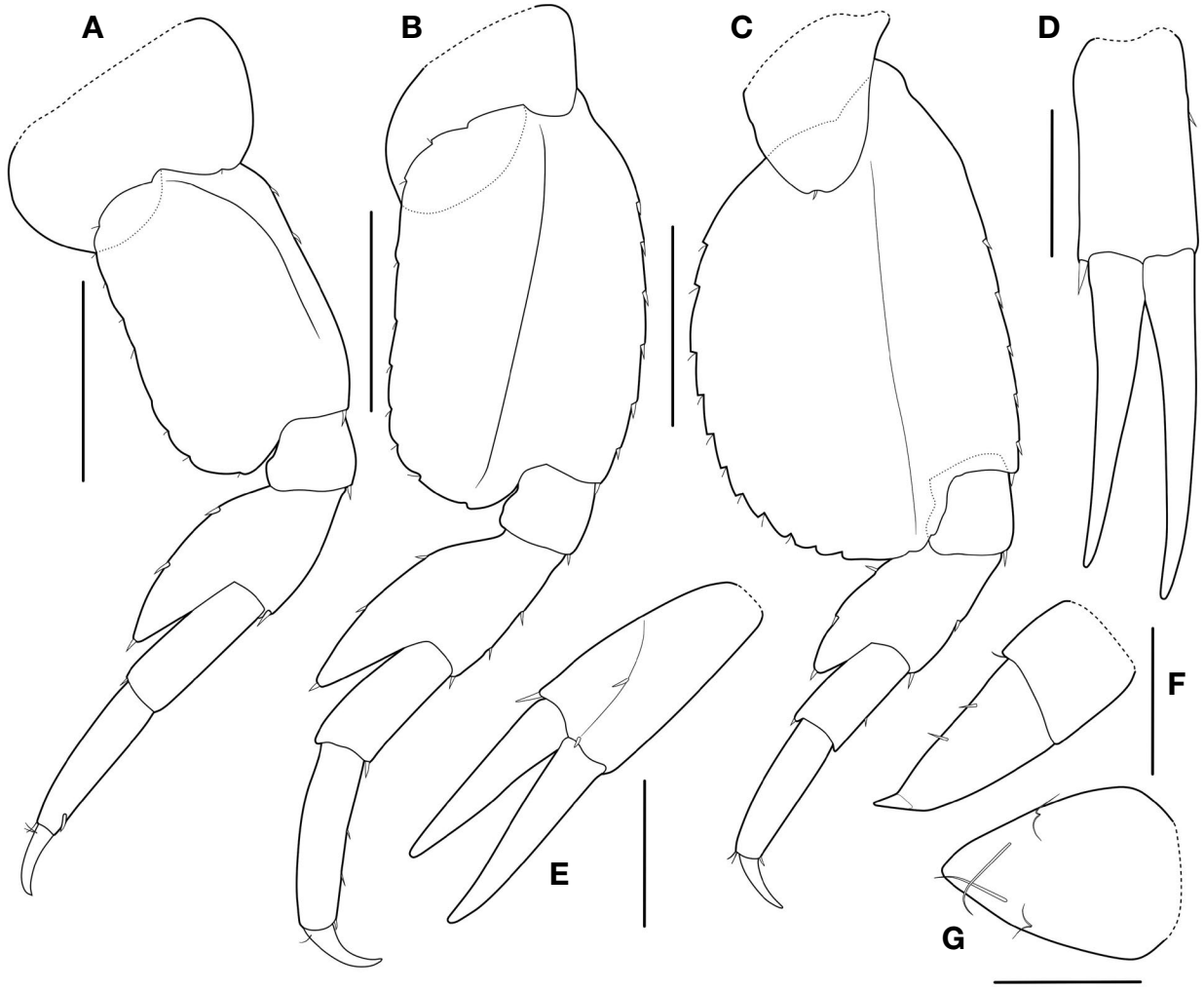


Fig. 3. *Seba chiltoni* Moore, 1987. Adult male (NIBRIV0000837772), 2.4 mm. A, pereopod 5; B, pereopod 6; C, pereopod 7; D, uropod 1; E, uropod 2; F, uropod 3; G, telson. Scale bars: A–C = 0.2 mm, D–G = 0.1 mm.

ior margin weakly crenulate; length ratio of articles 2–7 = 1.00 : 0.19 : 0.64 : 0.38 : 0.46 : 0.21.

Pereopod 7 (Fig. 3C) coxa small, unilobate, subtriangular; basis broad, semicircular, expanded posteriorly, anterior margin with five robust setae, posterior margin serrulate; length ratio of articles 2–7 = 1.00 : 0.22 : 0.41 : 0.23 : 0.34 : 0.17.

Uropod 1 (Fig. 3D), peduncle subrectangular, with mediodistal robust seta; rami slender, longer than peduncle, unarmed, outer ramus slightly longer than inner one.

Uropod 2 (Fig. 3E) subsimilar to uropod 1, peduncle subrectangular, subequal in length to outer ramus, with distolateral and distomedial robust setae; rami unarmed, outer ramus slightly longer than inner one.

Uropod 3 (Fig. 3F) uniramus, peduncle short, subquadrate; ramus triangular, biarticulate, article 2 short, upturned distally.

Telson (Fig. 3G) subtriangular, entire, bearing two setules on each side and two dorsal setae.

Remarks. *Seba chiltoni* Moore, 1987 shows considerable variation in the morphology of the gnathopod 1 and pereopods across different studies (Chilton, 1921; Ledoyer, 1978; 1986; Ariyama, 2009). These variations are primarily attributed to age-related changes. Since members of the genus *Seba* are small-sized species, even minor differences in body size may lead to notable morphological discrepancies. *Seba chiltoni* is characterized by expanded pereonite 2, subequal in length with head-pereonite 1 combined. The male gnathopod 1 large, subchelate, propodus palm angled, being slanted with age, palmar margin with two blunt and one minute processes, palm corner defined by a blunt process with two stout robust setae. Pereopod 7, merus posterodistally expanded in adult male, reaching the distal end of the carpus in specimens measuring 3.1 mm (Ariyama, 2009). However, in smaller specimens, the degree of merus expansion varies depending on the level of

development (Chilton, 1921; Ledoyer, 1978; 1986). Our specimens align well with previous studies in the morphology of gnathopod 1 but differ in the degree of merus expansion, likely due to their smaller size and the resulting developmental variation.

Distribution. Australia (Tasmania), Japan (Shirahama), Korea (Jeju-do island), New Zealand.

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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Open Access

A report of seven unrecorded lactic acid bacteria species isolated from freshwater, freshwater sediment, and plant samples in Korea

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To isolate indigenous lactic acid bacteria (LAB) strains from the environment, multiple samples including freshwater, freshwater sediment, freshwater aquatic plants, and plants around freshwater ecosystems were collected in Korea. Bacterial isolates were obtained using the conventional culture method with MRS media supplemented with cyclohexamide and sodium azide and subjected to 16S rRNA gene sequencing to identify previously unrecorded bacterial species in Korea. Analysis of the 16S rRNA gene sequences indicated that seven isolates exhibited more than 98.65% sequence similarity with validly published bacterial type strains, which had not previously been officially reported in Korea. These isolates were classified within the *Bacillota* phylum as species *Ligilactobacillus acidipiscis*, *Pediococcus ethanolidurans*, *Pediococcus inopinatus*, *Weissella muntiaci*, *Fructobacillus fructosus*, *Vagococcus penaei*, and *Paucilactobacillus nenjiangensis*. In this study, we provide details on the seven newly discovered LAB species, including their phylogenetic positions, as well as their morphological, physiological, and biochemical characteristics.

Keywords: 16S rRNA gene sequence, bacterial diversity, envioronment, indigenous lactic acid bacteria, unrecorded bacterial species in Korea

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Introduction

Microorganisms are ubiquitously present in the environment and significantly influence the establishment and functionality of terrestrial, marine, and freshwater ecosystems (Gupta *et al*., 2016). These microorganisms play vital roles such as biogeochemical cycling, climate regulation, and water purification (Arora-Williams *et al*., 2018; Linz *et al*., 2018; Cavicchioli *et al*., 2019; Mydeen *et al*., 2023). In addition, they are closely associated with complex multicellular organisms, such as humans, other animals, plants, and insects, and are crucial for the health of their hosts (Zilber-Rosenberg and Rosenberg, 2008). Microbiome transfer has been documented within abiotic environments such as air, soil, and water, as well as within biotic environments and between these environments, resulting in beneficial effects on both planetary and human health through the introduction of novel functions (Sessitsch *et al*., 2023).

Environmental microorganisms are a source of hydrolytic enzymes, secondary metabolites, pollutant-degrading enzymes, bioflocculants, and biopolymers, and are being used in a variety of industries, including foods, pharmaceuticals, and biofuels (Hernández-Carlos and Gamboa-Angulo, 2011; Vitorino and Bessa, 2017; Chantarasiri, 2021; Prihanto *et al*., 2022). Lactic acid bacteria (LAB) are Gram-positive, catalase-negative, and facultatively anaerobic bacteria that produce a diverse array of metabolites,

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including organic acids, antimicrobial peptides, exopolysaccharides, enzymes, and bioactive compounds (Salvetti *et al*., 2012; Anumudu *et al*., 2024). LAB are primarily associated with various types of fermented products and are also found in a broad range of environmental habitats including the human and animal body, plants, seeds, soil, and water (Liu *et al*., 2014). LAB have a long history of safe usage in human, foods, and animal feeds, spanning centuries, with numerous commercial probiotic agents derived from diverse LAB species (Tannock, 1997; Bhogoju and Nahashon, 2022). LAB are also being investigated for the development of biological control agents to detoxify hazardous chemicals (Ma, 2024), and for roles in regulating soil organic matter and biochemical cycles in soil, plant, and agricultural systems (Raman *et al*., 2022; Murindangabo *et al*., 2023).

As part of the research program conducted by the Nakdonggang National Institute of Biological Resources (NNIBR), many bacterial strains were isolated from various environmental samples to enhance the understanding of bacterial diversity and their functional properties. Several novel and/or unrecorded bacterial species, not yet identified in the Republic of Korea, were discovered. Here, we announce seven unrecorded lactic acid bacteria species, isolated from freshwater, freshwater sediment, and plant samples.

Materials and Methods

To isolate lactic acid bacteria (LAB) in environment, various samples including freshwater, freshwater sediment, freshwater aquatic plants, and plants around freshwater ecosystems were collected in Korea. The freshwater and freshwater sediment samples were serially diluted in 1X phosphate-buffered saline (PBS, pH 7.4) and the aliquots were spread onto MRS agar (Difco BD, USA) supplemented with 0.1 g/L of cyclohexamide and 0.2 g/L of sodium azide to inhibit fungi and yeast, and Gram negative bacteria. The agar plates were incubated at 30°C for 2−3 days. For the plant samples, the aerial parts or flowers of the plant were transferred directly into MRS broth supplemented with 0.1 g/L of cyclohexamide and 0.2 g/L of sodium azide at a 10% (w/v) concentration and incubated at 30°C for 7 days. After incubation, the culture was diluted with 1X PBS and the aliquots were spread onto MRS agar. All resulting colonies were sub-cultured on MRS agar followed by aerobic incubation at 30°C for 2−3 days to obtain pure cultures. The purified strains were preserved in 15% (v/v) glycerol at −80°C.

The 16S rRNA genes from the purified bacterial cells were individually PCR-amplified and sequenced as previously described by Jung *et al*. (2024). The resulting 16S rRNA gene sequences were compared with those of all reported bacterial type strains in the EzBioCloud database (Yoon *et al*., 2017) to calculate pairwise sequence similarities. Isolates exhibiting similarity percentage above the 16S rRNA gene sequence similarity threshold of 98.65% for prokaryote species delineation (Kim *et al*., 2014) and identified as unreported in Korea with the respective valid bacterial type strain names were classified as unrecorded bacterial species in Korea.

The isolates related to the unrecorded bacterial species underwent phylogenetic as well as morphological and phenotypic analyses as detailed below. The almost complete 16S rRNA gene sequences of these unrecorded bacterial species and their closely related type strains were aligned using CLUSTAL W (Thompson *et al*., 1994). Phylogenetic trees were generated utilizing the neighbor-joining (NJ) (Saitou and Nei, 1987), maximum-likelihood (ML) (Felsenstein, 1981), and maximum-parsimony (MP) methods (Fitch, 1971) employing MEGA version 11.0 software (Tamura *et al*., 2021). Evolutionary distances for the NJ and ML trees were computed applying the Kimura two-parameter (K2P) model (Kimura, 1980). The MP tree was constructed using the Subtree-Pruning-Regrafting (SPR) algorithm with partial deletion. Bootstrap analysis involving 1,000 replications (Felsenstein, 1985) was utilized to assess the robustness of the topologies for NJ, ML and MP trees. Colony morphology of the bacterial isolates was characterized using cultures grown on MRS agar at 30°C for three days. Cellular morphology and flagellation were observed by transmission electron microscopy (TEM) following uranyl acetate staining of samples cultured on MRS agar for three days. Gram staining was performed using a commercially available kit (BD Difco, USA). Oxidase and catalase activities were tested based on production of indophenol blue with of 1% (w/v) tetramethyl-p-phenylenediamine (Merck) and production of oxygen bubbles with 3% (v/v) aqueous hydrogen peroxide solution, respectively. Physiological and biochemical traits were analyzed employing the API 50CHL and API ZYM systems as per the manufacturer's instructions (bioMérieux).

Results and Discussion

Through 16S rRNA gene sequence analysis of bacterial isolates obtained from multiple samples, including freshwater, freshwater sediment, freshwater aquatic plants, and plants around freshwater ecosystems, a total of seven strains were identified as previously unrecorded bacterial species in Korea. Each strain is designated by an ID, along with its 16S rRNA gene sequence similarity (%) and isolation source, as detailed in Table 1. The phylogenetic tree, derived from 16S rRNA gene sequences, revealed the closest relationships between the isolates and the type

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

Phylum	Family	Genus	Strain ID	NNIBR ID	Genbank accession #	Closely related species	Similarity (%)	Isolation source (Species name)	Optimal medium and growth temperature
Bacillota	*Lactobacillaceae*	*Ligilactobacillus*	24SJ07S1-3	NNIBR202411BA1913	PP800336	*Ligilactobacillus acidipiscis*	100.0	Freshwater sediment	MRS (30°C)
	Lactobacillaceae	*Pediococcus*	24SJ08S1-21	NNIBR202411BA1919	PP800335	*Pediococcus ethanolidurans*	99.5	Freshwater sediment	
	Lactobacillaceae	*Pediococcus*	23ND39W-MRS1	NNIBR202411BA1920	PP800325	*Pediococcus inopinatus*	100.0	Freshwater	
	Lactobacillaceae	*Weissella*	chma1	NNIBR202411BA1928	PP800313	*Weissella muntiaci*	100.0	Aerial parts (*Chelidonium majus*)	
	Lactobacillaceae	*Fructobacillus*	Prnu1-6	NNIBR202411BA1929	PP800326	*Fructobacillus fructosus*	99.7	Flower (*Prunus mume*)	
	Enterococcaceae	*Vagococcus*	24SJ18W-MRS6	NNIBR202411BA1930	PP800339	*Vagococcus penaei*	99.7	Freshwater	
	Lactobacillaceae	*Paucilactobacillus*	24SH02S-MRS2	NNIBR202411BA1931	PP800337	*Paucilactobacillus nenjiangensis*	99.9	Freshwater sediment	

strains of validly published species, as shown in Fig. 1. At the genus level, these newly identified lactic acid bacteria species were classified into the genera *Ligilactobacillus*, *Pediococcus*, *Weissella*, *Fructobacillus*, and *Paucilactobacillus* within the family *Lactobacillaceae* of the Bacillota phylum; *Vagococcus* is part of the family *Enterococcaceae* within the same Bacillota phylum. Of the seven lactic acid bacteria strains, three were coccus-shaped and four were rod-shaped (Fig. 2). Comprehensive morphological, physiological, and biochemical characteristics of these seven bacterial species, which had not been previously recorded in Korea, are provided in the strain descriptions. Based on our findings, these seven bacterial isolates have been classified into *Ligilactobacillus acidipiscis*, *Pediococcus ethanolidurans*, *Pediococcus inopinatus*, *Weissella muntiaci*, *Fructobacillus fructosus*, *Vagococcus penaei*, and *Paucilactobacillus nenjiangensis*, none of which have been officially reported in Korea until now. Consequently, we provide detailed descriptions of these seven unreported lactic acid bacteria species.

Description of *Ligilactobacillus acidipiscis* 24SJ07S1-3

Cells are gram-stain-positive, non-flagellated, and rod-shaped. Colonies appear circular, flat, smooth, and creamy white with entire margins after incubation at 30°C for 2−3 days on MRS agar. Cells are negative for oxidase and catalase activities. Glycerol (weakly), L-arabinose, D-ribose, D-galactose, D-glucose, D-fructose, D-mannose, D-mannitol, methyl-α-D-mannopyranoside, methyl-α-D-glucopyranoside, *N*-acetylglucosamine, arbutin, esculin, salicin, D-cellobiose, D-maltose, D-trehalose, gentiobiose, and potassium gluconate (weakly) are utilized as carbon sources. Cells are positive for leucine arylamidase, valine arylamidase, naphthol-AS-BI-phosphohydrolase (weakly), and starch hydrolysis, but negative for alkaline phosphatase, esterase (C4), esterase lipase (C8), lipase (C14), cystine arylamidase, trypsin, α-chymotrypsin, acid phosphatase, α-galactosidase, β-galactosidase, β-glucuronidase, α-glucosidase, β-glucosidase, *N*-acetyl-β-glucosaminidase, α-mannosidase, and α-fucosidase. Strain 24SJ07S1-3 (=NNIBR 202411BA1913=FBCC-B18228) was isolated from a freshwater sediment sample collected in Gurye-gun, Jeollanam-do, Republic of Korea (35°15′47.7″N 127°26′54.2″E). The GenBank accession number for the 16S rRNA gene sequence of strain 24SJ07S1-3 is PP800336.

Description of *Pediococcus ethanolidurans* 24SJ08S1-21

Cells are gram-staining-positive, non-flagellated, and coccus-shaped. Colonies appear circular, flat, smooth, and creamy white with entire margins after incubation at 30°C for 2−3 days on MRS agar. Cells are negative for

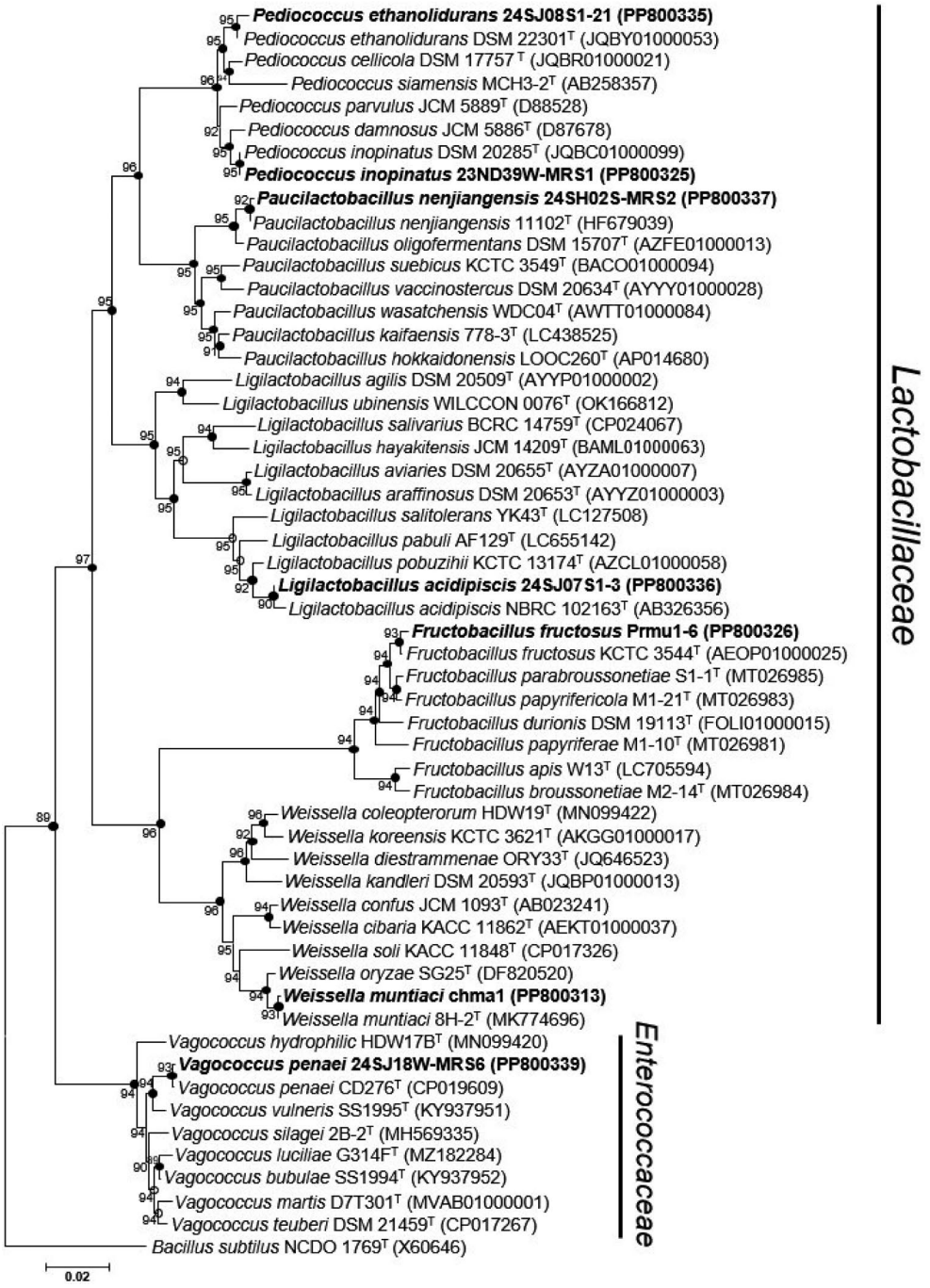


Fig. 1. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences of *Ligilactobacillus acidipiscis* 24SJ07S1-3, *Pediococcus* (*P*.) *ethanolidurans* 24SJ08S1-21, *P. inopinatus* 23ND39W-MRS1, *Weissella muntiaci* chma1, *Fructobacillus fructosus* Prmu1-6, *Vagococcus penaei* 24SJ18W-MRS6, and *Paucilactobacillus nenjiangensis* 24SH02S-MRS2. Trees were constructed by the neighbor joining (NJ) algorithm and filled circles indicate that the corresponding nodes that were also recovered in the trees reconstructed with both the maximum parsimony (MP) and maximum likelihood (ML) algorithms. Bootstrap values over 50% are shown. *Bacillus subtilis* NCDO 1769^{T} (X60646) was used as a outgroup. Scale bar = 0.02 substitutions per nucleotide position.

oxidase and catalase activities. L-arabinose, D-ribose, D-xylose, D-galactose, D-glucose, D-fructose, D-mannose, *N*-acetylglucosamine, amygdalin, arbutin (weakly), esculin, salicin, D-cellobiose, D-maltose, D-saccharose, D-trehalose, gentiobiose, D-tagatose, potassium gluconate, and potassium 2-ketogluconate (weakly) are utilized as carbon sources. Cells are positive for esterase (C4) (weakly), esterase lipase (C8) (weakly), lipase (C14) (weak-

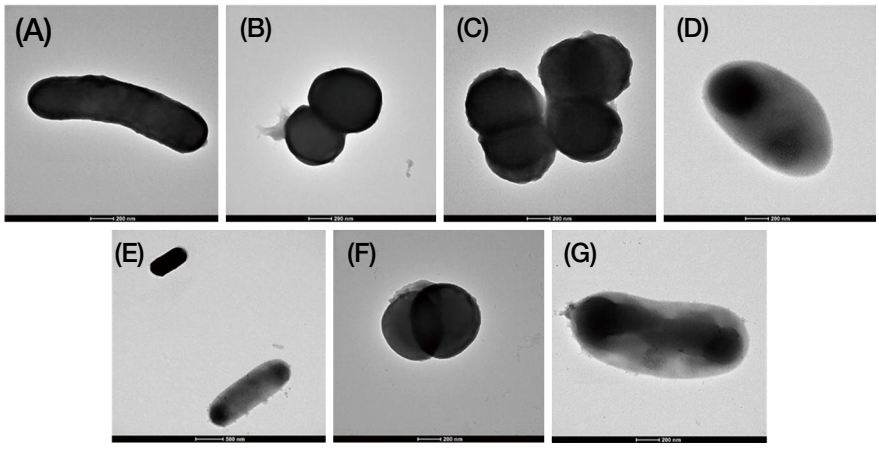


Fig. 2. Transmission electron micrographs (TEM) of (A) *Ligilactobacillus acidipiscis* 24SJ07S1-3, (B) *Pediococcus* (*P.*) *ethanolidurans* 24SJ08S1-21, (C) *P. inopinatus* 23ND39W-MRS1, (D) *Weissella muntiaci* chma1, (E) *Fructobacillus fructosus* Prmu1-6, (F) *Vagococcus penaei* 24SJ18W-MRS6, and (G) *Paucilactobacillus nenjiangensis* 24SH02S-MRS2, cultured at 30°C for three days on MRS agar plates.

ly), leucine arylamidase, valine arylamidase, cystine arylamidase (weakly), acid phosphatase (weakly), naphthol-AS-BI-phosphohydrolase (weakly), α-glucosidase, and β-glucosidase, but negative for alkaline phosphatase, trypsin, α-chymotrypsin, α-galactosidase, β-galactosidase, β-glucuronidase, *N*-acetyl-β-glucosaminidase, α-mannosidase, and α-fucosidase. Strain 24SJ08S1-21 (=NNIBR 202411BA1919=FBCC-B18233) was isolated from a freshwater sediment sample collected in Gurye-gun, Jeollanam-do, Republic of Korea (35°13′27.5″N 127°27′37.1″ E). The GenBank accession number for the 16S rRNA gene sequence of strain 24SJ08S1-21 is PP800335.

Description of *Pediococcus inopinatus* 23ND39W-MRS1

Cells are gram-staining-positive, non-flagellated, and coccus-shaped. Colonies appear circular, flat, smooth, and creamy white with entire margins after incubation at 30°C for 2–3 days on MRS agar. Cells are negative for oxidase and catalase activities. D-galactose, D-glucose, D-fructose, D-mannose, *N*-acetylglucosamine, amygdalin, esculin, salicin, D-cellobiose, D-maltose, D-lactose, D-saccharose, D-trehalose, gentiobiose, and D-turanose (weakly) are utilized as carbon sources. Cells are positive for leucine arylamidase, valine arylamidase, naphthol-AS-BI-phosphohydrolase (weakly), α-glucosidase, and β-glucosidase, but negative for alkaline phosphatase, esterase (C4), esterase lipase (C8), lipase (C14), cystine arylamidase, trypsin, α-chymotrypsin, acid phosphatase, α-galactosidase, β-galactosidase, β-glucuronidase, *N*-acetyl-β-glucosaminidase, α-mannosidase, and α-fucosidase. Strain 23ND39W-MRS1 (=NNIBR202411BA1920=FBCC-B18234) was isolated from a freshwater sample collected in Taebaek-si, Gangwon-do, Republic of Korea (37°05′54.7″N 129°01′ 9.5″E). The GenBank accession number for the 16S rRNA gene sequence of strain 23ND39W-MRS1 is PP800 325.

Description of *Weissella muntiaci* chma1

Cells are gram-staining-positive, non-flagellated, and rod-shaped. Colonies appear circular, flat, smooth, and creamy white with entire margins after incubation at 30°C for 2–3 days on MRS agar. Cells are positive for casein and starch hydrolysis, and negative for oxidase and catalase activities. L-arabinose, D-ribose, D-xylose, D-glucose, D-fructose, D-mannose, *N*-acetylglucosamine, D-trehalose, potassium gluconate, and potassium 2-ketogluconate (weakly) are utilized as carbon sources. Cells are positive for esterase lipase (C8) (weakly), leucine arylamidase, acid phosphatase, naphthol-AS-BI-phosphohydrolase (weakly), but negative for alkaline phosphatase, esterase (C4), lipase (C14), valine arylamidase, cystine arylamidase, trypsin, α-chymotrypsin, α-galactosidase, β-galactosidase, β-glucuronidase, α-glucosidase, β-glucosidase, *N*-acetyl-β-glucosaminidase, α-mannosidase, and α-fucosidase. Strain chma1 (=NNIBR202411BA1928=FBCC-B18242) was isolated from the aerial parts of *Chelidonium majus* collected in Sangju-si, Gyeongsangbuk-do, Republic of Korea (36°26′39.4″N 128°15′17.1″E). The GenBank accession number for the 16S rRNA gene sequence of strain chma1 is PP800313.

Description of *Fructobacillus fructosus* Prmu1-6

Cells are gram-staining-positive, non-flagellated, and rod-shaped. Colonies appear circular, flat, smooth, and creamy white with entire margins after incubation at 30°C for 2–3 days on MRS agar. Cells are negative for oxidase and catalase activity. D-glucose, D-fructose, D-mannitol

(weakly), and esculin (weakly) are utilized as carbon sources. Cells are positive for leucine arylamidase, α-chymotrypsin (weakly), acid phosphatase, and naphthol-AS-BI-phosphohydrolase (weakly), but negative for alkaline phosphatase, esterase (C4), esterase lipase (C8), lipase (C14), valine arylamidase, cystine arylamidase, trypsin, α-galactosidase, β-galactosidase, β-glucuronidase, α-glucosidase, β-glucosidase, *N*-acetyl-β-glucosaminidase, α-mannosidase, and α-fucosidase. Strain Prmu1-6 (=NNIBR202411 BA1929=FBCC-B18243) was isolated from the flower of *Prunus mume* in Sangju-si, Gyeongsangbuk-do, Republic of Korea (36°26′34.8″N 128°15′20.8″E). The Gen Bank accession number for the 16S rRNA gene sequence of strain Prmu1-6 is PP800326.

Description of *Vagococcus penaei* 24SJ18W-MRS6

Cells are Gram-staining-positive, non-flagellated, and coccus-shaped. Colonies appear circular, flat, smooth, and creamy white with entire margins after incubation at 30°C for 2−3 days on MRS agar. Cells are negative for oxidase and catalase activities. Glycerol, D-ribose, D-galactose, D-glucose, D-fructose, D-mannose, inositol, methyl-α-D-glucopyranoside, *N*-acetylglucosamine, arbutin, esculin, salicin, D-maltose, D-saccharose, D-trehalose, D-melezitose, D-raffinose, and D-turanose (weakly) are utilized as carbon sources. Cells are positive for esterase (C4), esterase lipase (C8), leucine arylamidase, valine arylamidase (weakly), cystine arylamidase (weakly), α-chymotrypsin (weakly), acid phosphatase, β-galactosidase (weakly), α-glucosidase (weakly), and naphthol-AS-BI-phosphohydrolase, but negative for alkaline phosphatase, lipase (C14), trypsin, α-galactosidase, β-glucuronidase, α-glucosidase, *N*-acetyl-β-glucosaminidase, α-mannosidase, and α-fucosidase. Strain 24SJ18W-MRS6 (=NNIBR202411 BA1930=FBCC-B18244) was isolated from a freshwater sample in Wando-gun, Jeollanam-do, Republic of Korea (34°23′37.9″N 126°42′14.4″E). The GenBank accession number for the 16S rRNA gene sequence of strain 24SJ 18W-MRS6 is PP800339.

Description of *Paucilactobacillus nenjiangensis* 24SH02S-MRS2

Cells are Gram-staining-positive, non-flagellated, and rod-shaped. Colonies appear circular, flat, smooth, and creamy white with entire margins after incubation at 30°C for 2−3 days on MRS agar. Cells are negative for oxidase and catalase activities. L-arabinose, D-ribose, D-xylose, D-galactose, D-glucose, D-fructose (weakly), D-mannose, *N*-acetylglucosamine, D-maltose, D-saccharose, amidon, potassium gluconate, potassium 2-ketogluconate, and potassium 5-ketogluconate (weakly) are utilized as carbon sources. Cells are positive for leucine arylamidase, valine arylamidase, acid phosphatase (weakly), and naphthol-AS-BI-phosphohydrolase, but negative for alkaline phosphatase, esterase (C4), esterase lipase (C8), lipase (C14), cystine arylamidase, trypsin, α-chymotrypsin, α-galactosidase, β-galactosidase, β-glucuronidase, α-glucosidase, β-glucosidase, *N*-acetyl-β-glucosaminidase, α-mannosidase, and α-fucosidase. Strain 24SH02S-MRS2 (=NNIBR 202411BA1931=FBCC-B18245) was isolated from a freshwater sediment sample in Gangneung-si, Gangwon-do, Republic of Korea (37°47′52.2″N 128°54′40.8″E). The GenBank accession number for the 16S rRNA gene sequence of strain 24SH02S-MRS2 is PP800337.

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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Invited article

NOTE

Annual trends in the 2024 National Species List of Korea: Update and implications for biodiversity management

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The National Species List of Korea was established to reinforce national sovereignty over biological resources, supporting compliance with international agreements such as the Nagoya Protocol, the Convention on Biological Diversity and standardized species names. As of 2024, the list includes 61,230 wild species in inhabiting the Korean Peninsula, reflecting the taxonomic identification and classification progress since its initial publication in 1996. The greatest increases in the number of species added to the list are among insects, invertebrates, fungi, and algae. Annual updates are made according to international nomenclatural codes, incorporating new species discoveries, synonym revisions, and taxonomic refinements. In 2024, 1,220 species are added, including synonymization and species re-identification. Since 2023, over 40 species originating from tropical regions (i.e., type locality) have been added each year, potentially indicating biodiversity shifts caused by climate change. Despite a recent decline in species discovery rates, national efforts such as the Korean Indigenous Species Investigation Project continue to play a key role in understanding the biodiversity of Korea and contributing to conservation policies. The full list is updated annually and is publicly accessible via the CBD-CHM Korea portal (https://www.kbr.go.kr).

Keywords: biodiversity, CBD-CHM Korea portal, climate change, taxonomic revision

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The National Species List of Korea was established to reinforce the nation's sovereignty over its biological resources in response to international frameworks such as the Nagoya Protocol (Secretariat of the Convention on Biodiversity, 2011) and the Convention on Biological Diversity (UNEP, 1992). In addition to its role in compliance with international agreements, the list provides standardized scientific and Korean name for species, supporting national biodiversity monitoring, and conservation planning for species management in Korea.

The first comprehensive compilation of species in Korea was published documenting 28,462 species by the Korean National Council for Conservation of Nature (1996). By 2007, prior to the establishment of the National Institute of Biological Resources, this number had increased to 29,916 species (Ministry of Environment, 2007). As of 2024, 61,230 species had been recorded on the National Species List, according to the latest report (https://www.kbr.go.kr) (Fig. 1).

The National Species List encompasses all the wild

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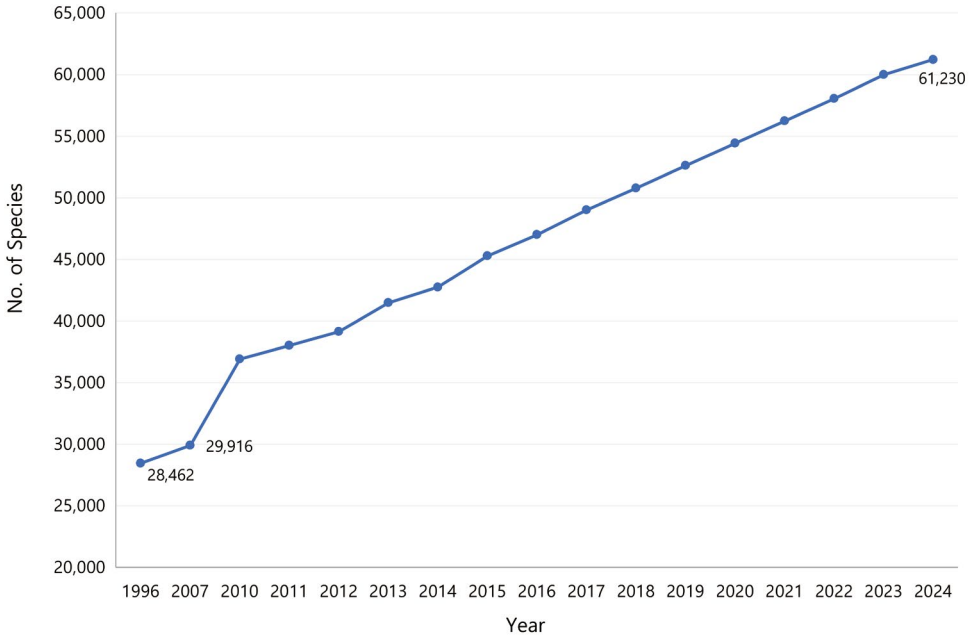


Fig. 1. Cumulative number of species recorded in the National Species List of Korea (1996–2024).

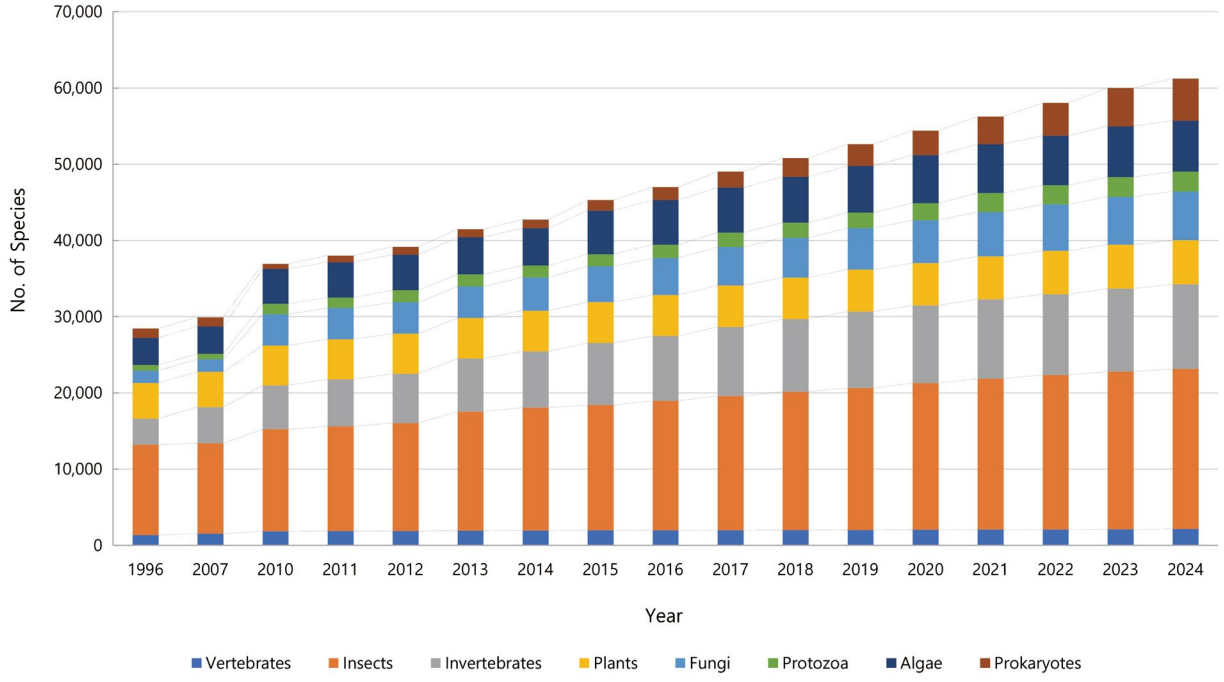


Fig. 2. Cumulative number of species by taxonomic groups in the National Species List of Korea (1996–2024).

species discovered on the Korean Peninsula. Since 1996, the most significant increase has occurred on the number of insect species (approximately 9,000 newly listed species), followed by invertebrates, fungi, algae, prokaryotes, plants, protozoa, and vertebrates (Fig. 2).

The National Species List is primarily based on the Eukaryota classification of the Catalogue of Life and follows a seven-kingdom system (https://www.catalogueoflife.org). The traditional six-kingdom Protista was an artificial assemblage that grouped together all eukaryotes not classified as plants, animals or fungi. Recent phylogenetic studies have reclassified these organisms into two king-

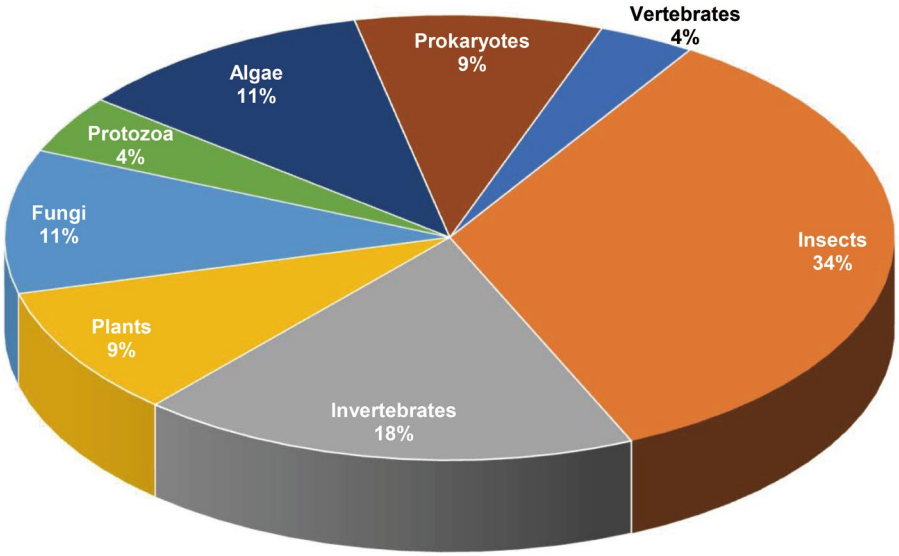


Fig. 3. Taxonomic composition of the 2024 National Species List of Korea.

doms: Chromista and Protozoa (Whittaker and Margulis, 1978; Ruggiero *et al*., 2015). Although algae constitute a polyphyletic group, the term remains widely used in biodiversity conservation and management. The term is used in biodiversity indicators and statistics-such as the Status of Species in the Korean Peninsula-for practical purpose in tracking biodiversity trends over time. In this context, "algae" encompasses Chlorophyta, Charophyta, and Rhodophyta (Plantae): Bacillariophyta, Dinophyta, Ochrophyta, Cryptophyta, Haptophyta, and Pyrrophyta (Chromista): Euglenophyta (Protozoa): and Cyanobacteria (Bacteria).

In the current National Species List (2024), the number of species by major taxonomic groups is 20,975 insects, 11,118 invertebrates, 6,703 algae, 6,402 fungi, 5,781 plants, 5,509 prokaryotes, 2,590 protozoa, and 2,152 vertebrates (Fig. 3).

The compilation and maintenance of the National Species List comply with Internationally recognized nomenclatural codes, including the International Code of Nomenclature for Algae, Fungi, and Plants, the International Code of Zoological Nomenclature, and the International Code of Nomenclature for Prokaryotes. The guidelines for compiling the list incorporate the principle of priority in determining valid names, the proper treatment of synonyms, and application of standardized formats for scientific names.

The National Species List is revised annually to reflect the updated accepted scientific names as determined by international nomenclatural codes, and synonymization. These updates are essential for the effective use of global species information, verification of imported and exported biological resources, and consistent comparisons of species composition across countries or regions.

In 2024, the list was updated with 327 newly described species, 925 species newly recorded in Korea, and 32 species removed. The net increase compared with the list in the previous year was 1,220 species (Table 1). Of the removed species, 23 were deleted because of synonymization, according to the International Code of Zoological Nomenclature. Synonyms were excluded if the valid name was already included in the list or if multiple names were consolidated into a single species. Nine species were excluded after they were confirmed as not distributed in Korea. 279 species records were updated due to synonymization.

Since 2023, the type locality and distribution data of newly added species in the National Species List have been examined to assess whether these species occur in tropical regions. In 2023 and 2024, 45 and 23 species, respectively were investigated as having type localities in tropical regions. While these findings represent only a conservative estimate based on available literature, they could tentatively suggest the occurrences of species under climate change and shift ecological condition.

Taxonomic studies in Korea have begun relatively recently compared with those in many developed countries. Nonetheless, significant advances have been achieved through Korean Indigenous Species Investigation Project, led by the Ministry of Environment. At its peak, this initiative identified over 1,300 new or previously unrecorded species per year (Bae *et al*., 2021). In recent years, the discovery rate has declined to approximately 950 species annually, reflecting the growing challenges in identifying novel taxa. Despite this decline, continued field investigations are critical for monitoring Korean biodiversity and supporting updates to the National Species List.

Table 1. The number of newly-added/excluded species in the 2024 National Species List of Korea.

Major taxon classification		Species newly included (excluded)	Details (higher taxonomic groups, species number, Korean name)
National species list	Management groups		
Plantae	Plants	22	Magnoliophyta 19 (제주사약채 등), Bryophyta 3 (태백담뱃대이끼 등)
Animalia	Vertebrates	62	Anguilliformes 1 (별꽃곰치), Blenniiformes 1 (뿔베도라치), Carcharhiniformes 1 (흑상어), Perciformes 7 (노랑무늬양쥐돔 등), Scorpaeniformes 1 (긴머리달재), Siluriformes 1 (금강자가사리), Anseriformes 2 (큰기러기 등), Charadriiformes 4 (뿔바다오리 등), Ciconiiformes 3 (중대백로 등), Falconiformes 5 (참매 등), Passeriformes 35 (오목눈이 등), Piciformes 1 (크낙새)
	Insects	296 (−31)	Coleoptera 98 (애기버섯벌레 등), Diptera 69 (독도점등에모기 등), Entomobryomorpha 1 (나도붓톡토기), Hemiptera 12 (까마중진딧물 등), Hymenoptera 51 (대한별쌍살벌 등), Lepidoptera 54 (한국창날개뿔나방 등), Orthoptera 1, Plecoptera 7 (가시민무늬강도래 등), Symphypleona 2종, Thysanoptera 1 (느티나무관총채벌레)
	Invertebrates	226 (−1)	Annelida 8 (나도홍점갯지렁이 등), Arthropoda 140 (굵은발꽃왕거미 등), Bryozoa 15 (쇠스랑가시바구니이끼벌레 등), Chordata 2 (황록세줄멍게 등), Cnidaria 15 (주황깃히드라 등), Echinodermata 4 (삼각애기불가사리 등), Hemichordata 1, Mollusca 10 (큰돌기배고둥붙이 등), Nematoda 12 (왕버들뿌리썩이선충 등), Platyhelminthes 11, Porifera 5, Rotifera 3
Protozoa	Protozoa	15	Apicomplexa 1, Ciliophora 13 (부리고개돌린섬모충 등), Foraminifera 1 (원판더미유공충)
Chromista	Algae	50	Bacillariophyceae 49, Coscinodiscophyceae 1
Fungi	Fungi	111	Ascomycota 58 (진녹색두건버섯 등), Basidiomycota 42 (줄무늬졸각버섯 등), Mucoromycota 7, Zygomycota 4
Bacteria	Prokaryotes	470	Acidobacteriota 1, Actinobacteria 1, Actinomycetota 111, Bacillota 47, Bacteroidota 69, Deinococcota 1, Pseudomonadota 237, Verrucomicrobiota 3
Total		1,252 (−32)	

The National Species List of Korea is publicly available and updated annually through the CBD-CHM Korea portal (https://www.kbr.go.kr) (Available under the "National Biodiversity Information" section).

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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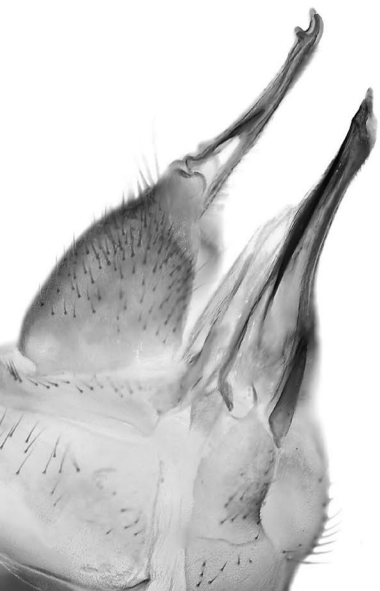
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Front Cover

This cover is a microscopic photograph of *Leptocotis tenuirostris* (Claus, 1871), a newly recorded pelagic amphipod (Hyperiidea) in Korea. A related article can be found on pages 248-253. Photo by June Kim