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A report of 42 unrecorded bacterial species isolated from fish intestines and clams in freshwater environments

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Abstract: Nine fish and one clam species were collected from freshwater environments in Korea, including four lakes, two streams, and the Nakdong River, to investigate the host-associated bacteria. Hundreds of bacterial strains were isolated from the samples using a cell sorter and a dilution plating method. After identification of the bacterial strains using 16S rRNA gene sequences, 42 strains with greater than 98.7% sequence similarity with validly published species were determined to be unrecorded bacterial species in Korea. These strains were phylogenetically diverse and assigned to four phyla, six classes, 17 orders, 27 families, and 32 genera. At the genus level, the unrecorded species were classified as *Corynebacterium*, *Mycobacterium*, *Mycolicibacterium*, *Gordonia*, *Williamsia*, *Modestobacter*, *Brachybacterium*, *Sanquibacter*, *Arthrobacter*, and *Mycolicibacterium* of the class *Actinobacteria*; *Empedobacter*, and *Flavobacterium* of the class *Flavobacteriia*; *Fictibacillus*, *Psychrobacillus*, *Cohnella*, *Paenibacillus*, *Rummeliibacillus*, *Enterococcus*, and *Vagococcus* of the class *Bacilli*; *Aquamicrobium*, *Paracoccus*, and *Sphingomonas* of the class *Alphaproteobacteria*; *Achromobacter*, *Delftia*, and *Deefgea* of the class *Betaproteobacteria*; and *Aeromonas*, *Providencia*, *Yersinia*, *Marinomonas*, *Acinetobacter*, and *Pseudomonas* of the class *Gammaproteobacteria*. The 42 unrecorded species were subjected to further taxonomic characterization using gram staining, cellular and colony morphological determination, biochemical analyses, and phylogenetic analyses. This paper provides detailed descriptions of the 42 previously unrecorded bacterial species.

Keywords: freshwater, fish intestine, clam, unrecorded bacteria, 16S rRNA gene, host-associated bacteria

INTRODUCTION

The composition of microbial flora depends on external environmental factors, like pH, temperature, seasonality, humidity, and nutrient availability, in the regions in which they are found (Fierer and Jackson 2006), and ecological environments (i.e., habitats) are also impacted by microbes. Eukaryotic hosts are important habitats for microbes, and each has a unique and intimate interaction with microbes. Host-associated bacteria can be divided into two major groups: autochthonous (able to colonize within the host) and allochthonous (considered to be free-living). Many symbiotic bacteria (autochthonous) form specific and, on occasion, obligate interactions with hosts, while other symbiotic bacteria (allochthonous) show less dependent associations. The latter can multiply freely in the environment while also colonizing plant or animal hosts when an opportunity arises (Sullam *et al.* 2012). Animal intestines and plant roots, where complex metabolic processes occur that are necessary for growth

and health, contain the most abundant and diverse symbiotic bacteria. Host-associated bacteria play critical roles in nutritional provisioning, metabolic homeostasis, and immune defense.

The bacterial communities in the intestines of aquatic animals are much denser than those of terrestrial animals, as water is an ideal medium for bacterial growth (Banerjee and Ray 2017) and is a reservoir for bacteria. The development of high-throughput sequencing technology has allowed for analyses of the intestinal bacterial compositions of numerous fish species in an effort to increase production and conserve endangered species. The results suggest that the bacterial population of fish intestines may vary by host species, nutritional status, age (life cycle), surrounding water type, and other environmental conditions (Sullam *et al.* 2012; Wong and Rawls 2012; Llewellyn *et al.* 2014; Ringø *et al.* 2015; Liu *et al.* 2016). Conventional culture-based methods are limited by the required culture conditions and types of culture media, particularly for fastidious and obligate anaerobes. However, the cultivation of bacterial strains is still essential because the ecological role of bacteria in natural environments and the potential industrial applications of bacterial resources can only be revealed after successful cultivation and characterization.

During the investigation of host associated bacteria from 2017 to 2019, we collected fish species that have unique aquatic habitats or are associated with human lifestyles. A large number of bacterial strains were isolated from the intestines of diverse fish species and freshwater clams collected from different geographic locations, including those with freshwater and brackish water. A total of 42 unrecorded species are among the host-associated bacterial strains described here.

MATERIALS AND METHODS

1. Sampling and bacterial isolation

A total of nine fish species and one freshwater clam species were collected from freshwater and brackish water environments (Table 1). Each intestine of fish and the entire clam insides samples were processed separately by spreading onto the following agar media after homogenization and serial dilution: Reasoner's 2A agar (R2A), Lactobacillus selection agar (LBS), eosine methylene blue agar (EMB), International Streptomyces Project 4 agar (ISP 4), marine agar (MA), trypticase soy agar (TSA), nutrient agar (NA), and 1/10 medium dilution agar of each. The intestinal tissues of three fish species (*Hypomesus nipponensis*, *Micropterus salmoides*, and *Silurus asotus*) were also used for isolation via a single-cell sorting method using a flow cytometer (FACS Aria II, Becton Dickinson) to remove fast-growing and culture-dominant bacteria. After aerobic incubation at 15−30°C for 7−14 days, the bacterial strains were purified by subculturing a single colony onto fresh media. The pure cultures were preserved at −80°C in 20% (w/v) glycerol.

2. Identification and characterization of unrecorded species

PCR amplification with universal primers 27F and

Table 1. List of collected host species in this study

No.	Host species		Collection site
	Scientific name	Common name	
1	*Anquilla japonica*	Japanese eel	Fishery, Gochang, Jeollabuk-do
2	*Corbicula fluminea*	Asian clam	Yeongok stream, Gangneung, Gangwon-do
3	*Coreoperca herzi*	Korean aucha perch	Nakdong River, Sangju, Gyeongsangbuk-do
4	*Hypomesus nipponensis*	Wakasagi smelt	Soyang Lake, Chuncheon and Inje, Gangwon-do Songrim reservoir, Gyeongsan, Gyeongsangbuk-do Pangok reservoir, Sangju, Gyeongsangbuk-do
5	*Iksookimia koreensis*	Korean spine loach	Keum River, Geumsan, Chungcheongnam-do
6	*Leucopsarion petersii*	Ice goby	Jangji stream, Goseong, Gyeongsangnam-do
7	*Micropterus salmoides*	Largemouth bass	Nakdong River, Sangju, Gyeongsangbuk-do
8	*Pseudorasbora parva*	False dace	Yeongok stream, Gangneung, Gangwon-do
9	*Silurus asotus*	Far eastern catfish	Fishery, Jeongeup, Jeollabuk-do
10	*Takifugu niphobles*	Grass puffer	Jangji stream, Goseong, Gyeongsangnam-do

1492R and 16S rRNA gene sequencing with primers 518F and 800R were performed using standard procedures for bacterial identification. The 16S rRNA gene sequences of the bacterial strains were compared with those of other bacterial strains using the EZ Biocloud server (Yoon *et al.* 2017). Bacterial strains showing 98.7% or higher sequence similarity with those of validly published species that had not previously been reported in Korea were designated as unrecorded bacterial species. For the phylogenetic analyses, the alignment of the 16S rRNA gene sequences obtained from the isolated strains and those of closely related strains was carried out using EZ Editor (Jeon *et al.* 2014). Phylogenetic trees were constructed using the neighbor-joining (Saitou and Nei 1987), maximum parsimony (Fitch 1971), and maximum likelihood (Felsenstein 1981) methods, and evolutionary distances were calculated using the Jukes and Cantor one-parameter model (Jukes and Cantor 1969) with the MEGA package ver. 7.0 (Kumar *et al.* 2016). Bootstrap analysis was carried out using 1,000 resampled datasets (Felsenstein 1985), which were also used to test the topology of the phylogenetic tree.

The colony morphology of the strains was observed on agar plates with a magnifying glass after the cells had grown to stationary phase. Cellular morphology and size were examined by transmission electron microscopy (JEM-1400Plus, JEOL, Japan or HT7700, Hitachi, Japan). Gram staining was performed using a Gram staining kit (Sigma, USA), and oxidase activity was determined using 1% (w/v) tetramethyl ρ-phenylenediamine. Biochemical characteristics were tested using API-20NE galleries (bioMérieux, France) according to the manufacturer's instructions.

RESULTS AND DISCUSSION

The fast-growing and culture-dominant bacteria isolated from fish intestines and clams belonged to the genera *Aeromonas* (freshwater) and *Shewanella* (brackish water). These two genera are common and abundant in aquatic environments, and this finding suggests that the host-associated bacterial strains isolated in this study originated from water as allochthonous bacteria. We used a cell sorter to obtain numerous bacterial strains because culture dominance restricted the isolation of diverse bacterial strains. Most of the strains obtained in this way belonged to the genus *Pseudomonas* (class *Gammaproteobacteria*), as well as diverse genera of the class *Actinobacteria*; the strains were primarily isolated from the fish species *Hypomesus nipponensis* and *Micropterus salmoides*, respectively. In particular, strains belonging to the genus *Pseudomonas* were classified to 28 different species and included six unrecorded species. These results indicate that isolation of host-associated bacteria using a cell sorter can increase the diversity of identified bacterial strains and could assist in overcoming the problem of culture dominance.

Based on the comparison of the 16S rRNA gene sequences and phylogenetic analyses, a total of 42 strains were assigned to four phyla, six classes, 17 orders, 26 families, and 32 genera. The taxonomic affiliation and identification results are summarized in Table 2.

A phylogenetic tree of the 19 unrecorded Gram-positive species assigned to the phyla *Actinobacteria* (ten species) and *Firmicutes* (nine species) is shown in Figure 1. At the genus level, these 19 unrecorded species belong to 17 genera: *Corynebacterium*, *Mycobacteroides*, *Mycolicibacterium*, *Gordonia*, *Williamsia*, *Medestobacter*, *Brachybacterium*, *Sanguibacter*, *Arthrobacter*, and *Mycolicibacterium* of the class *Actinobacteria* and *Fictibacillus* (two species), *Psychrobacillus*, *Cohnella*, *Paenibacillus* (two species), *Rummeliibacillus*, *Enterococcus*, and *Vagococcus* of the class *Bacilli*. The phylogenetic positions of the 23 unrecorded Gram-negative strains assigned to the phyla *Bacteroidetes* and *Proteobacteria* are shown in Figure 2. These 23 unrecorded species belong to 15 genera: *Empedobacter* and *Flavobacterium* of the class *Flavobacteriia*; *Aquamicrobium*, *Paracoccus*, and *Sphingomonas* of the class *Alphaproteobacteria*; *Achromobacter*, *Delftia*, and *Deefgea* of the class *Betaproteobacteria*; and *Aeromonas*, *Providencia*, *Yersinia* (three species), *Marinomonas*, *Acinetobacter*, *Pseudomonas* (six species), and *Proteus* of the class *Gammaproteobacteria*.

These 42 unrecorded species displayed diverse cellular morphologies, including rods, short rods, and cocci (Fig. 3), with or without flagella. The colony colors were white, cream, ivory, yellow, or pink. All species grew aerobically, and some strains produced spores. The enzymatic and physiological properties examined using API 20NE kits varied depending on the species. Detailed cultural, morphological, and biochemical characteristics are shown in the species description section. Some physiological characteristics of the 42 unrecorded species differed from those of previously identified species; however, the morphologies and phylogenetic analyses proved that they were of the same species. The presence of these 42 species has been reported overseas, but until now, were unrecorded in Korea. Their phenotypic properties are described here.

Table 2. Summary of bacterial strains isolated from the intestines of fish and freshwater clams and their taxonomic affiliations

Host	Class	Order	Family	Most closely related species	Strain ID	NNIBR No.	Sim. (%)	GenBank no.	Medium	Incubation condition
Anquilla japonica	*Actinobacteria*	*Micrococcales*	*Dermabacteraceae*	*Brachybacterium huguangmaarense*	FEB3-24	NNIBR2017301BA49	99.86	MG780346	R2A	30°C, 2–3 days
	Flavobacteria	*Flavobacteriales*	*Flavobacteriaceae*	*Empedobacter falsenii*	FEB3-06	NNIBR2017301BA48	99.16	MG780344	R2A	30°C, 2–3 days
	Betaproteobacteria	*Burkholderiales*	*Comamonadaceae*	*Delftia lacustris*	FEB3-05	NNIBR2017301BA47	100.00	MG780343	NA	25°C, 2–3 days
Corbicula fluminea	*Alphaproteobacteria*	*Sphingomonadales*	*Sphingomonadaceae*	*Sphingomonas olei*	19SCL-58	NNIBR2019642BA185	99.79	MN559812	R2A	25°C, 2–3 days
	Gammaproteobacteria	*Pseudomonadales*	*Pseudomonadaceae*	*Proteus terrae*	19SCL-27	NNIBR2019642BA166	100.00	MN559811	R2A	25°C, 2–3 days
Coreoperca herzi	*Actinobacteria*	*Corynebacteriales*	*Nocardiaceae*	*Williamsia serinedens*	S8-55	NNIBR2017301BA50	99.85	MG780347	TSA	25°C, 2–3 days
Hypomesus nipponensis	*Actinobacteria*	*Corynebacteriales*	*Nocardiaceae*	*Gordonia polyisoprenivorans*	CFH1-11	NNIBR2019642BA20	99.58	MN559440	R2A	25°C, 2–3 days
		Micrococcales	*Micrococcaceae*	*Arthrobacter stackebrandtii*	IFH1-28	NNIBR2019642BA78	98.83	MN559455	NA	25°C, 2–3 days
	Flavobacteria	*Flavobacteriales*	*Flavobacteriaceae*	*Flavobacterium frigidimaris*	CFH1-34	NNIBR2019642BA36	99.86	MN559444	R2A	25°C, 2–3 days
	Bacilli	*Bacillales*	*Bacillaceae*	*Fictibacillus enclensis*	FH1-17	NNIBR2018142BA16	99.01	MK396594	TSA	30°C, 2–3 days
				Psychrobacillus soli	FH1-09	NNIBR2018142BA8	99.38	MK396593	R2A	30°C, 2–3 days
			Paenibacillaceae	*Paenibacillus mendelii*	IFH1-14	NNIBR2019642BA74	99.24	MN559453	R2A	25°C, 2–3 days
				Paenibacillus silvae	FH1-05	NNIBR2018142BA4	99.09	MK396592	TSA	30°C, 2–3 days
			Planococcaceae	*Rummeliibacillus pycnus*	FH4-10	NNIBR2018142BA84	99.52	MK396595	TSA	30°C, 2–3 days
		Lactobacillales	*Enterococcaceae*	*Enterococcus faecalis*	CFHS-18	NNIBR2019642BA52	99.32	MN559450	1/10 MA	25°C, 2–3 days
				Vagococcus fluvialis	FH5-03	NNIBR2018142BA119	100.00	MK396597	TSA	37°C, 2–3 days
	Alphaproteobacteria	*Rhodobacterales*	*Rhodobacteraceae*	*Paracoccus sphaerophysae*	IFH1-29	NNIBR2019642BA79	99.93	MN559456	R2A	25°C, 2–3 days
	Betaproteobacteria	*Neisseriales*	*Neisseriaceae*	*Deefgea rivuli*	IFH1-02	NNIBR2019642BA68	98.97	MN559452	R2A	25°C, 2–3 days
	Gammaproteobacteria	*Aeromonadales*	*Aeromonadaceae*	*Aeromonas sobria*	CFH1-09	NNIBR2019642BA18	99.93	MN559439	NA	25°C, 2–3 days
		Enterobacterales	*Morganellaceae*	*Providencia heimbachae*	FH5-02	NNIBR2017301BA51	99.93	MK396596	NA	30°C, 2–3 days
			Yersiniaceae	*Yersinia entomophaga*	CFH1-25	NNIBR2019642BA29	99.93	MN559442	R2A	25°C, 2–3 days
				Yersinia enterocolitica subsp. *palearctica*	IFH1-18	NNIBR2019642BA75	99.51	MN559454	R2A	25°C, 2–3 days

Table 2. Continued

Host	Class	Order	Family	Most closely related species	Strain ID	NNIBR No.	Sim. (%)	GenBank no.	Medium	Incubation condition
Hypomesus nipponensis	*Gammaproteobacteria*	*Pseudomonadales*	*Pseudomonadaceae*	*Pseudomonas aeruginosa*	CFHS-01	NNIBR2019642BA40	99.79	MN559445	R2A	25°C, 2–3 days
				Pseudomonas lundensis	CFHS-10	NNIBR2019642BA45	99.66	MN559447	R2A	25°C, 2–3 days
				Pseudomonas paralactis	CFH1-01	NNIBR2019642BA11	99.93	MN559438	TSA	25°C, 2–3 days
				Pseudomonas synxantha	CFHS-02	NNIBR2019642BA41	100.00	MN559446	R2A	25°C, 2–3 days
				Pseudomonas versuta	CFHS-14	NNIBR2019642BA49	99.79	MN559449	R2A	25°C, 2–3 days
				Pseudomonas weihenstephanensis	CFHS-12	NNIBR2019642BA47	100.00	MN559448	R2A	25°C, 2–3 days
Iksookimia koreensis	*Gammaproteobacteria*	*Enterobacterales*	*Yersiniaceae*	*Yersinia ruckeri*	FI2-07	NNIBR2018142BA242	100.00	MK396587	NA	25°C, 2–3 days
		Pseudomonadales	*Moraxellaceae*	*Acinetobacter pittii*	FI1-01	NNIBR2018142BA228	100.00	MK396586	TSA	37°C, 2–3 days
Leucopsarion petersii	*Flavobacteria*	*Flavobacteriales*	*Flavobacteriaceae*	*Flavobacterium frigidarium*	FEB2-04	NNIBR2017301BA46	99.31	MG780342	MA	15°C, 3–4 days
Micropterus salmoides	*Actinobacteria*	*Corynebacteriales*	*Corynebacteriaceae*	*Corynebacterium stationis*	FMD-28	NNIBR2018142BA300	99.10	MK396590	R2A	30°C, 2–3 days
			Mycobacteriaceae	*Mycobacteroides saopaulense*	FMS-15	NNIBR2018142BA318	100.00	MK396591	R2A	37°C, 2–3 days
				Mycolicibacterium sarraceniae	FMD-25	NNIBR2018142BA298	99.18	MK396589	NA	30°C, 2–3 days
		Geodermatophilales	*Geodermatophilaceae*	*Modestobacter versicolor*	FMS-37	NNIBR2018142BA338	99.37	MK396600	NA	30°C, 2–3 days
		Micrococcales	*Jonesiaceae*	*Sanguibacter inulinus*	19FMS-10	NNIBR2019642BA87	99.52	MN559813	R2A	25°C, 2–3 days
	Bacilli	*Bacillales*	*Paenibacillaceae*	*Cohnella damuensis*	FMD-08	NNIBR2018142BA285	99.62	MK396588	NA	30°C, 2–3 days
Pseudorasbora parva	*Actinobacteria*	*Mycobacteriales*	*Mycobacteriaceae*	*Mycolicibacterium bacteremicum*	19FPP-03	NNIBR2019642BA105	99.86	MN559459	R2A	25°C, 2–3 days
	Bacilli	*Bacillales*	*Bacillaceae*	*Fictibacillus aquaticus*	19FPP-20	NNIBR2019642BA114	99.05	MN559460	R2A	25°C, 2–3 days
Silurus asotus	*Alphaproteobacteria*	*Rhizobiales*	*Phyllobacteriaceae*	*Aquamicrobium lusatiense*	P4N-04	NNIBR2018142BA270	99.86	MK396598	NA	30°C, 2–3 days
	Betaproteobacteria	*Burkholderiales*	*Alcaligenaceae*	*Achromobacter pulmonis*	PI3-03	NNIBR2018142BA279	100.00	MK396599	TSA	30°C, 2–3 days
Takifugu niphobles	*Gammaproteobacteria*	*Oceanospirillales*	*Oceanospirillaceae*	*Marinomonas pontica*	FEB1-13	NNIBR2017301BA45	100.00	MG780341	MA	20°C, 2–3 days

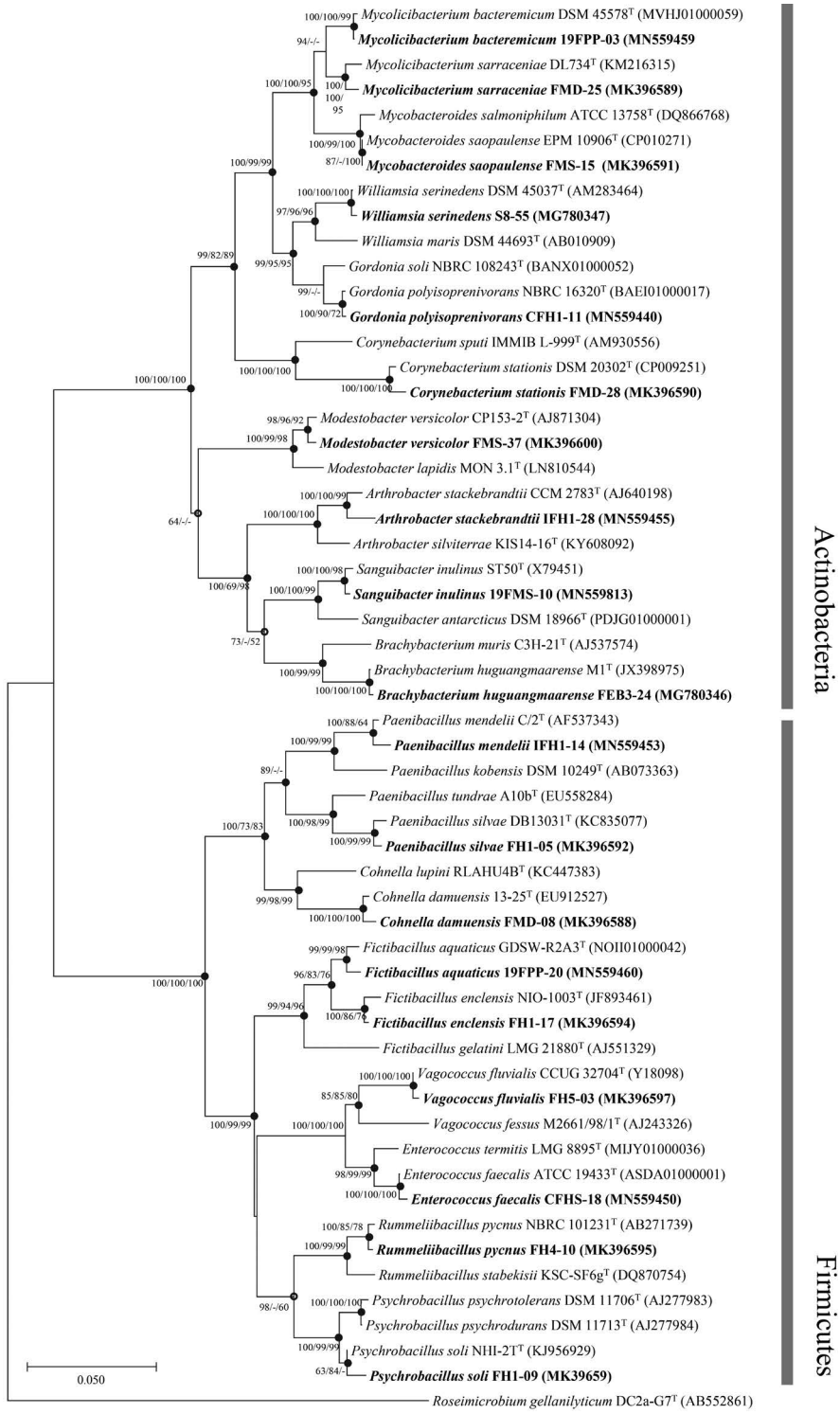

Fig. 1. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences showing the relationship between the strains isolated in this study and their gram-positive bacterial relatives including phyla *Actinobacteria* and *Firmicutes*. The bootstrap values (expressed as percentages of 1,000 replications) for neighbor-joining, maximum parsimony, maximum likelihood over 50% are shown at the nodes. The filled circles indicate that the corresponding nodes were also recovered in the trees generated with the maximum likelihood and maximum parsimony algorithms, while the open circles indicate that the corresponding nodes were also recovered in the tree generated with one of these algorithms. Bar, 0.05 substitutions per nucleotide position.

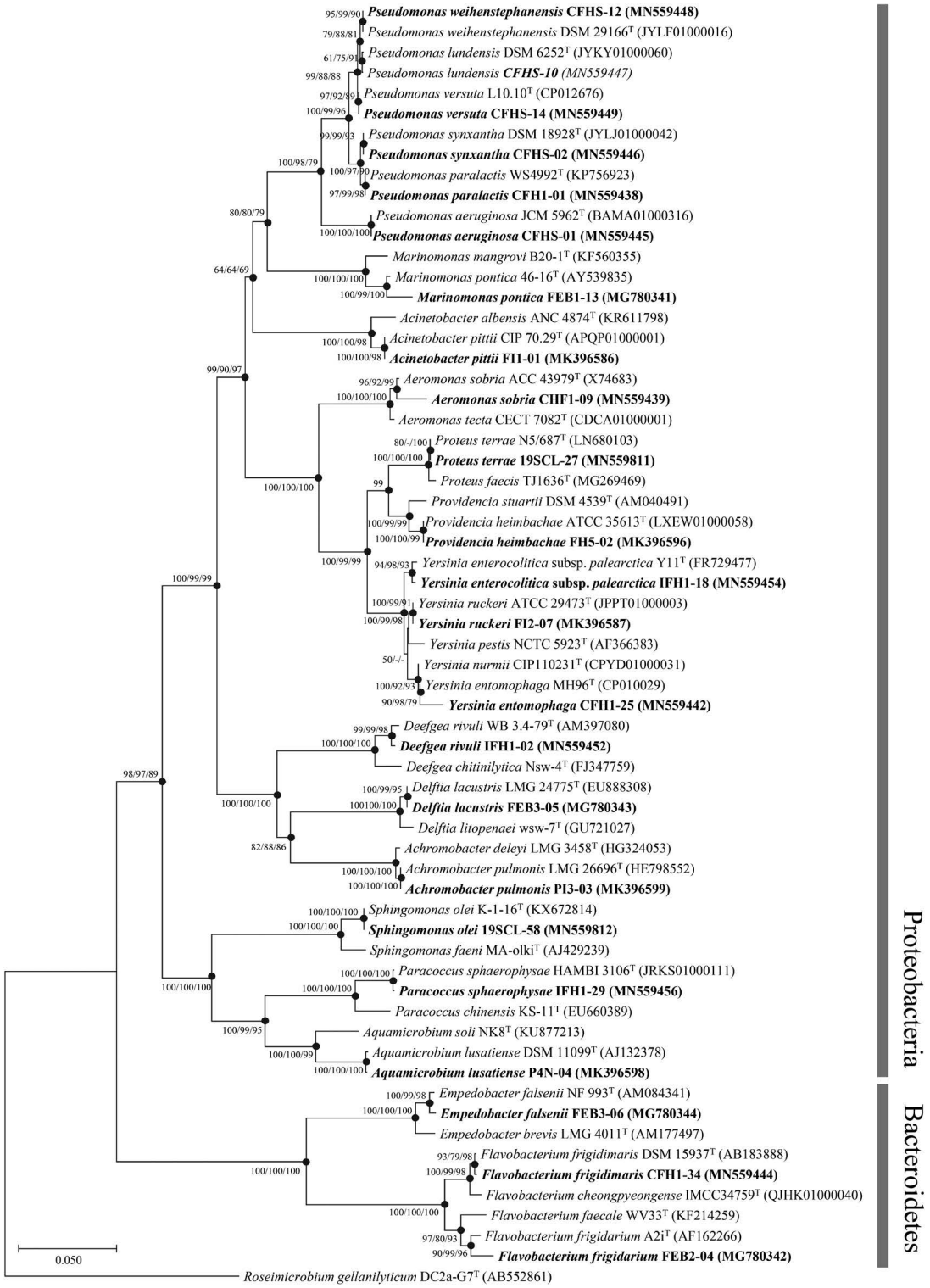

Fig. 2. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences showing the relationship between the strains isolated in this study and their gram-negative bacterial relatives including phyla *Bacteroidetes* and *Proteobacteria*. The bootstrap values (expressed as percentages of 1,000 replication) for neighbor-joining, maximum parsimony, maximum likelihood over 50% are shown at the nodes. The filled circles indicate that the corresponding nodes were also recovered in the trees generated with the maximum likelihood and maximum parsimony algorithms. Bar, 0.05 substitutions per nucleotide position.

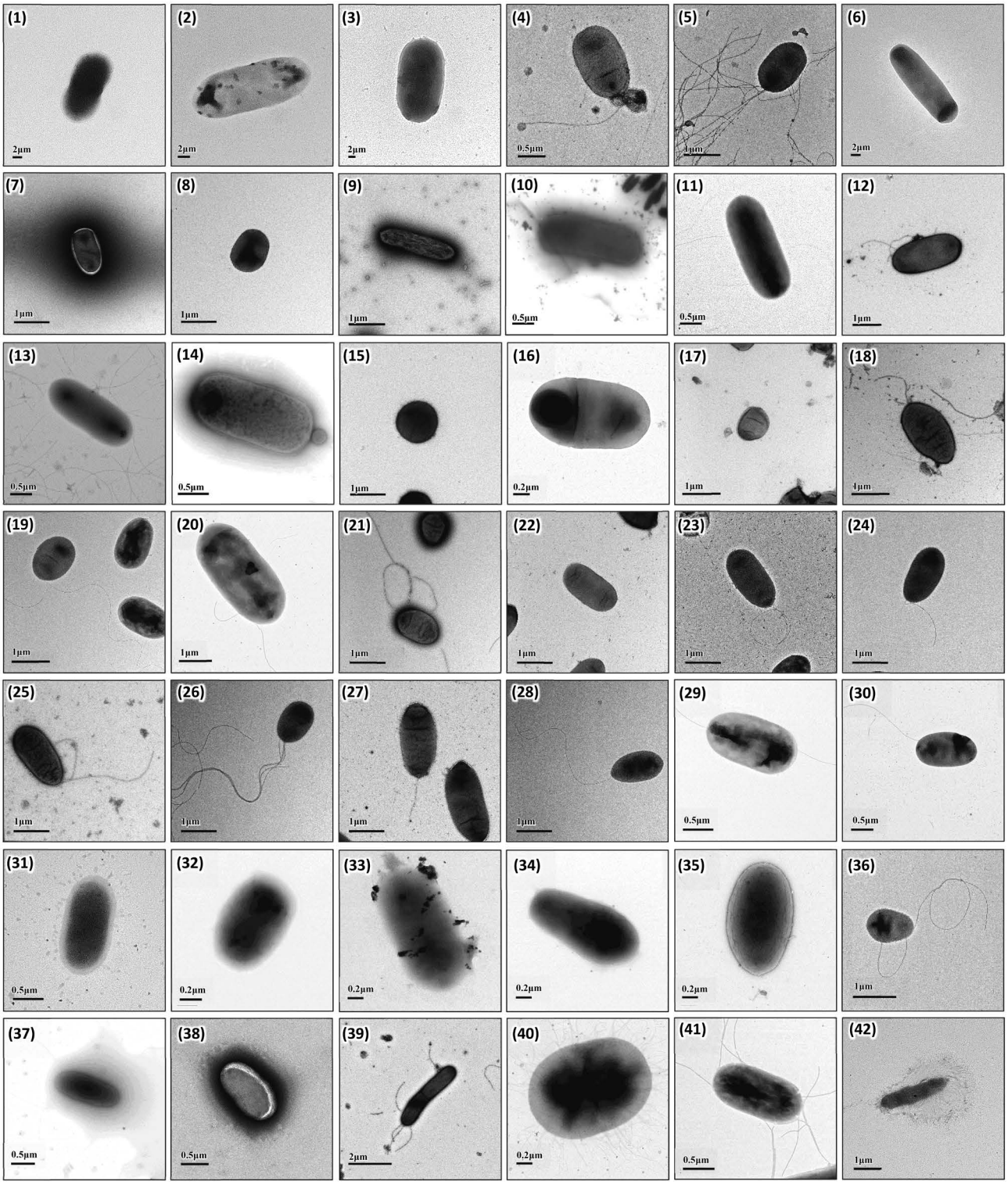

Fig. 3. Transmission electron micrographs of cells of the strains isolated in this study. Strains : 1, FEB3-24; 2, FEB3-06; 3, FEB3-05; 4, 19SCL-58; 5, 19SCL-27; 6, S8-55; 7, CFH1-11; 8, IFH1-28; 9, CFH1-35; 10, FH1-17; 11, FH1-09; 12, IFH1-14; 13, FH1-05; 14, FH4-10; 15, CFHS-18; 16, FH5-03; 17, IFH1-29; 18, IFH1-02; 19, CFH1-09; 20, FH5-02; 21, CFH1-25; 22, IFH1-18; 23, CFHS-01; 24, CFHS-10; 25, CFH1-01; 26, CFHS-02; 27, CFHS-14; 28, CFHS-12; 29, FI2-07; 30, FI1-01; 31, FEB2-04; 32, FMD-28; 33, FMS-15; 34, FMD-25; 35, FMS-37; 36, 19FMS-10; 37, FMD-08; 38, 19FPP-03; 39, 19FPP-20; 40, P4N-04; 41, PI3-03; 42, FEB1-13.

Description of *Brachybacterium huguangmaarense* FEB3-24

Cells are Gram-stain-positive, aerobic, non-flagellated, and coccoid to short rod-shaped. Colonies grown on R2A are circular, convex, smooth, and ivory colored after incubation for 2−3 days at 30°C. Esculin is hydrolyzed, but not gelatin. Nitrate is not reduced. Glucose is not fermented and indole is not produced. Enzyme activity of β-galactosidase is observed, but not oxidase, arginine dihydrolase, and urease. D-glucose, D-mannose (weakly), D-mannito l (weakly), *N*-acetyl-glucosamine (weakly), D-maltose, and potassium gluconate are utilized as sole carbon sources, but not L-arabinose, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain FEB3-24 (=NNIBR2017301BA49) was isolated from intestine of *Anquilla japonica* collected from fishery, Gochang, Jeollabuk-do, Korea. The GenBank accession number for the 16S rRNA gene sequence is MG780346.

Description of *Empedobacter falsenii* FEB3-06

Cells are Gram-stain-negative, aerobic, non-flagellated, and rod-shaped. Colonies grown on R2A are circular, convex, smooth, and ivory colored after incubation for 2−3 days at 30°C. Esculin and gelatin are hydrolyzed. Nitrate is not reduced and glucose is not fermented. Indole is produced. Enzyme activities of oxidase and β-galactosidase are observed, but not arginine dihydrolase and urease. D-glucose, *N*-acetyl-glucosamine (weakly), D-maltose (weakly), trisodium citrate (weakly), and phenylacetic acid (weakly) are utilized as sole carbon sources, but not L-arabinose, D-mannose, potassium gluconate, capric acid, adipic acid, and malic acid. Strain FEB3-06 (=NNIBR2017BA48) was isolated from intestine of *Anquilla japonica* collected from from fishery, Gochang, Jeollabuk-do, Korea. The GenBank accession number of 16S rRNA gene sequence is MG780344.

Description of *Delftia lacutris* FEB3-05

Cells are Gram-stain-negative, aerobic, flagellated, and rod-shaped. Colonies grown on NA are circular, convex, smooth, and ivory colored after incubation for 2−3 days at 25°C. Esculin and gelatin are not hydrolyzed and nitrate is reduced to nitrite. Glucose is not fermented and indole is not produced. Enzyme activities of oxidase, arginine dihydrolase, and urease are observed, but not β-galactosidase. D-mannitol, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid are utilized as sole carbon sources, but not D-glucose, L-arabinose, D-mannose, *N*-acetyl-glucosamine, and D-maltose. Strain FEB3-05 (=NNIBR2017BA47) was isolated from intestine of *Anquilla japonica* collected from fishery, Gochang, Jeollabuk-do, Korea. The GenBank accession number of 16S rRNA gene sequence is MG780343.

Description of *Sphingomonas olei* 19SCL-58

Cells are Gram-stain-negative, aerobic, flagellated, and rod-shaped. Colonies grown on R2A are circular, convex, smooth, and yellow colored after incubation for 2−3 days at 25°C. Esculin is hydrolyzed, but not gelatin. Nitrate is not reduced. Glucose is not fermented and indole is not produced. Enzyme activities of oxidase, arginine dihydrolase, urease, and β-galactosidase are not observed. D-glucose and capric acid are utilized as sole carbon sources, but not L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain 19SCL-58 (=NNIBR2019642BA185) was isolated from *Corbicula leana* collected from the Yeongok stream, Gangneung, Gangwon-do, Korea. The GenBank accession number of 16S rRNA gene sequence is MN559812.

Description of *Proteus terrae* 19SCL-27

Cells are Gram-stain-negative, aerobic, flagellated, and rod-shaped. Colonies grown on R2A are circular, convex, smooths and cream white colored after incubation for 2−3 days at 25°C. Esculin and gelatin are hydrolyzed and nitrate is reduced to nitrite. Glucose is fermented and indole is produced. Enzyme activity of urease is observed, but not oxidase, arginine dihydrolase, and β-galactosidase. D-glucose, *N*-acetyl-glucosamine, D-maltose, and adipic acid are utilized as sole carbon sources, but not L-arabinose, D-mannose, D-mannitol, potassium gluconate, capric acid, malic acid, trisodium citrate, and phenylacetic acid. Strain 19SCL-27 (=NNIBR2019642BA166) was isolated from *Corbicula leana* collected from the Yeongok stream, Gangneung, Gangwon-do, Korea. The GenBank accession number of 16S rRNA gene sequence is MN559811.

Description of *Williamsia serinedens* S8-55

Cells are Gram-stain-positive, aerobic, non-flagellated, and rod-shaped. Colonies grown on TSA are circular, convex, smooth, and pinkish ivory colored after incubation for

2−3 days at 25°C. Esculin is hydrolyzed, but not gelatin. Nitrate is reduced to nitrogen. Glucose is not fermented and indole is not produced. Enzyme activities of urease and β-galactosidase are observed, but not oxidase and arginine dihydrolase. D-mannitol, malic acid and trisodium citrate are utilized as sole carbon sources, but not D-glucose, L-arabinose, D-mannose, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, and phenylacetic acid. Strain S8-55 (=NNIBR2017BA51) was isolated from intestine of *Coreoperca herzi* collected from the Nakdong River, Sangju, Gyeonsangjuk-do, Korea. The GenBank accession number of 16S rRNA gene sequence is MG780347.

Description of *Gordonia polyisoprenivorans* CFH1-11

Cells are Gram-stain-negative, aerobic, non-flagellated, and rod-shaped. Colonies grown on R2A are circular with entire margin, brittle, opaque, and pinkish white colored after incubation for 2−3 days at 25°C. Esculin is hydrolyzed, but not gelatin. Nitrate is not reduced and indole is not produced. Glucose is fermented. Enzyme activities of urease and β-galactosidase are observed, but not oxidase and arginine dihydrolase. D-glucose, L-arabinose, D-mannose, D-mannitol, potassium gluconate, malic acid, trisodium citrate and phenylacetic acid are utilized as sole carbon sources, but not *N*-acetyl-glucosamine, D-maltose, capric acid, and adipic acid. Strain CFH1-11 (=NNIBR2019642BA20) was isolated from intestine of *Hypomesus nipponensis* collected from the Soyang Lake, Chuncheon, Gangwon-do, Korea. The GenBank accession number of 16S rRNA gene sequence is MN559440.

Description of *Arthrobacter stackebrandtii* IFH1-28

Cells are Gram-stain-positive, aerobic, non-flagellated, and coccoid to short rods shaped. Colonies grown on NA are circular entire margin, smooth, and ivory to yellow colored after incubation for 2−3 days at 25°C. Esculin is hydrolyzed, but not gelatin. Nitrate is reduced and glucose is fermented. Indole is not produced. Enzyme activities of oxidase (weakly) and β-galactosidase are observed, but not arginine dihydrolase and urease. 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 not adipic acid and phenylacetic acid. Strain IFH1-28 (=NNIBR2019642BA78) was isolated from intestine of *Hypomesus nipponensis* collected from the Soyang Lake, Inje, Gangwon-do, Korea. The GenBank accession number of 16S rRNA gene sequence is MN559455.

Description of *Flavobacterium frigidimaris* CFH1-34

Cells are Gram-stain-negative, aerobic, non-flagellated, and rod-shaped. Colonies grown on Reasoner's 2A agar (R2A) are circular, smooth, undulate margin, opaque, and yellow colored after incubation for 2−3 days at 25°C. Esculin is hydrolyzed, but not gelatin. Nitrate is reduced to nitrogen. Glucose is not fermented and indole is not produced. Enzyme activities of urease and β-galactosidase are observed, but not oxidase and arginine dihydrolase. The strain does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid as sole carbon sources. Strain CFH1-34 (=NNIBR2019642BA36) was isolated from intestine of *Hypomesus nipponensis* collected from the Soyang Lake, Chuncheon, Gangwon-do, Korea. The GenBank accession number of 16S rRNA gene sequence is MN559444.

Description of *Fictibacillus enclensis* FH1-17

Cells are Gram-stain-positive, aerobic, flagellated, and rod-shaped. Colonies grown on TSA are circular, smooth, convex, opaque, and cream colored after incubation for 2−3 days at 30°C. Esculin is hydrolyzed, but not gelatin. Nitrate is not reduced and indole is not produced. Glucose is fermented. Enzyme activity of β-galactosidase is observed, but not oxidase, urease, and arginine dihydrolase. 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 not capric acid. Strain FH1-17 (=NNIBR2018142BA16) was isolated from intestine of *Hypomesus nipponensis* collected from the Soyang Lake, Chuncheon, Gangwon-do, Korea. The GenBank accession number of 16S rRNA gene sequence is MK396594.

Description of *Psychrobacillus soli* FH1-09

Cells are Gram-stain-positive, aerobic, non-flagellat-

ed, and rod-shaped. Colonies grown on R2A are circular, raised, moist, and ivory colored after incubation for 2−3 days at 30°C. Esculin and gelatin are hydrolyzed. Nitrate is reduced to nitrogen. Glucose is not fermented and indole is not produced. Enzyme activity of urease is observed, but not oxidase, arginine dihydrolase, and β-galactosidase. D-glucose, potassium gluconate, and adipic acid are utilized as sole carbon sources, but not L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, capric acid, malic acid, trisodium citrate, and phenylacetic acid. Strain FH1-09 (=NNIBR2018142BA8) was isolated from intestine of *Hypomesus nipponensis* collected from the Soyang Lake, Chuncheon, Gangwon-do, Korea. The GenBank accession number of 16S rRNA gene sequence is MK396593.

Description of *Paenibacillus mendelii* IFH1-14

Cells are Gram-stain-positive, aerobic, flagellated, and rod-shaped. Colonies grown on R2A are circular with entire margin, smooth, and ivory colored after incubation for 2−3 days at 25°C. Esculin is hydrolyzed, but not gelatin. Nitrate is not reduced and indole is not produced. Glucose is fermented. Enzyme activities of oxidase and arginine dihydrolase are observed, but not urease and β-galactosidase. D-glucose, L-arabinose, D-mannose, D-mannitol, potassium gluconate, capric acid, malic acid, and trisodium citrate are utilized as sole carbon sources, but not *N*-acetyl-glucosamine, D-maltose, adipic acid, and phenylacetic acid. Strain IFH1-14 (=NNIBR2019642BA74) was isolated from intestine of *Hypomesus nipponensis* collected from the Soyang lake, Inje, Gangwon-do, Korea. The GenBank accession number of 16S rRNA gene sequence is MN559453.

Description of *Paenibacillus silvae* FH1-05

Cells are Gram-stain-positive, aerobic, flagellated, and rod-shaped. Colonies grown on TSA are circular, raised, and ivory colored after incubation for 2−3 days at 30°C. Esculin and gelatin are hydrolyzed. Nitrate is not reduced and indole is not produced. Glucose is fermented. Enzyme activities of oxidase and β-galactosidase are observed, but not arginine dihydrolase and urease. D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, and potassium gluconate are utilized as sole carbon sources, but not capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain FH1-05 (=NNIBR2018142BA4) was isolated from intestine of *Hypomesus nipponensis* collected from the Soyang Lake, Chuncheon, Gangwon-do, Korea. The GenBank accession number of 16S rRNA gene sequence is MK396592.

Description of *Rummeliibacillus pycnus* FH4-10

Cells are Gram-stain-positive, aerobic, flagellated, and rod-shaped. Colonies grown on TSA are circular, smooth, convex, translucent, and yellowish cream colored after incubation for 2−3 days at 30°C. Esculin and gelatin are not hydrolyzed. Nitrate is not reduced and indole is not produced. Glucose is not fermented. Enzyme activity of oxidase is observed, but not arginine dihydrolase, urease, and β-galactosidase. Potassium gluconate, adipic acid, malic acid, trisodium citrate and phenylacetic acid are utilized as sole carbon sources, but not D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose and capric acid. Strain FH4-10 (=NNIBR2018142BA84) was isolated from intestine of *Hypomesus nipponensis* collected from the Pangok Reservoir, Sangju, Gyeongsangbuk-do, Korea. The GenBank accession number of 16S rRNA gene sequence is MK396595.

Description of *Enterococcus faecalis* CFHS-18

Cells are Gram-stain-positive, facultative anaerobic, non-flagellated, and coccoid-shaped. Colonies grown on 1/10 diluted MA are circular with entire margin, convex, smooth, and ivory colored after incubation for 2−3 days at 25°C. Gelatin is hydrolyzed, but not esculin. Nitrate is not reduced and indole is not produced. Glucose is not fermented. Enzyme activities of arginine dihydrolase, urease, and oxidase (weakly) are observed, but not β-galactosidase. D-glucose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, adipic acid, and trisodium citrate are utilized as sole carbon sources, but not L-arabinose, D-mannose, capric acid, malic acid, and phenylacetic acid. Strain CFHS-18 (=NNIBR2019642BA52) was isolated from intestine of *Hypomesus nipponensis* collected from the Soyang Lake, Chuncheon, Gangwon-do, Korea. The GenBank accession number of 16S rRNA gene sequence is MN559450.

Description of *Vagococcus fluvialis* FH5-03

Cells are Gram-stain-positive, aerobic, flagellated, and coccoid-shaped. Colonies grown on TSA are circular, smooth, convex, opaque, and cream colored after incubation for 2−3 days at 37°C. Esculin is hydrolyzed, but not

gelatin. Nitrate is not reduced and indole is not produced. Glucose is fermented. Enzyme activity of β-galactosidase is observed, but not arginine dihydrolase, urease, and oxidase. D-glucose and trisodium citrate are 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 and phenylacetic acid. Strain FH5-03 (=NNIBR2018142BA119) was isolated from intestine of *Hypomesus nipponensis* collected from the Songnim Reservoir, Gyeongsan, Gyeongsangbuk-do, Korea. The GenBank accession number of 16S rRNA gene sequence is MK396597.

Description of *Paracoccus sphaerophysae* IFH1-29

Cells are Gram-stain-negative, aerobic, non-flagellated, and coccoid-shaped. Colonies grown on R2A are circular with entire margin, smooth, and ivory to yellow colored after incubation for 2−3 days at 25°C. Esculin is hydrolyzed weakly, but not gelatin. Nitrate is not reduced. Indole is not produced and glucose is not fermented. Enzyme activity of oxidase is observed, but not arginine dihydrolase, urease, and β-galactosidase. D-glucose, L-arabinose, potassium gluconate and malic acid are utilized as sole carbon sources, but not D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, capric acid, adipic acid, trisodium citrate, and phenylacetic acid. Strain IFH1-29 (=NNIBR2019642BA79) was isolated from intestine of *Hypomesus nipponensis* collected from the Soyang Lake, Inje, Gangwon-do, Korea. The GenBank accession number of 16S rRNA gene sequence is MN559456.

Description of *Deefgea rivuli* IFH1-02

Cells are Gram-stain-negative, aerobic, flagellated, and rod-shaped. Colonies grown on R2A are circular entire margin, flat, smooth, and ivory colored after incubation for 2−3 days at 25°C. Esculin is hydrolyzed weakly, but not gelatin. Nitrate is not reduced to nitrogen and indole is not produced. Glucose is fermented. Enzyme activity of oxidase is observed, but not arginine dihydrolase, urease, and β-galactosidase. D-mannose, *N*-acetyl-glucosamine, and potassium gluconate are utilized as sole carbon sources, but not D-glucose, L-arabinose, D-mannitol, D-maltose, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain IFH1-02 (=NNIBR2019642BA68) was isolated from intestine of *Hypomesus nipponensis* collected from the Soyang Lake, Inje, Gangwon-do, Korea. The GenBank accession number of 16S rRNA gene sequence is MN559452.

Description of *Aeromonas sobria* CFH1-09

Cells are Gram-stain-negative, aerobic, flagellated, and short rod-shaped. Colonies grown on NA are circular with entire margin, smooth, translucent, and cream white colored after incubation for 2−3 days at 25°C. Esculin and gelatin are hydrolyzed and nitrate is reduced. Indole is produced and glucose is fermented. Enzyme activities of oxidase, arginine dihydrolase, and β-galactosidase are observed, but not urease. D-glucose, L-arabinose (weakly), 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 not adipic acid and phenylacetic acid. Strain CFH1-09 (=NNIBR2019642BA19) was isolated from intestine of *Hypomesus nipponensis* collected from the Soyang Lake, Chuncheon, Gangwon-do, Korea. The GenBank accession number of 16S rRNA gene sequence is MN559439.

Description of *Providencia heimbachae* FH5-02

Cells are Gram-stain-negative, aerobic, flagellated, and rod-shaped. Colonies grown on NA are circular, smooth, convex, opaque, and cream colored after incubation for 2−3 days at 25°C. Esculin is hydrolyzed, but not gelatin. Nitrate is reduced and glucose is fermented. Indole is not produced. Enzyme activity of arginine dihydrolase is observed, but not urease, β-galactosidase, and oxidase. D-glucose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, malic acid, trisodium citrate, and phenylacetic acid are utilized as sole carbon sources, but not L-arabinose, capric acid, and adipic acid. Strain FH5-02 (=NNIBR2018142BA118) was isolated from *Hypomesus nipponensis* collected from the Songnim Reservoir, Gyeongsan, Gyeongsangbuk-do, Korea. The GenBank accession number of 16S rRNA gene sequence is MK396596.

Description of *Yersinia entomophaga* CFH1-25

Cells are Gram-stain-negative, aerobic, flagellated, and rod-shaped. Colonies grown on R2A are circular with entire margin, convex, smooth, and cream white colored after incubation for 2−3 days at 25°C. Esculin and gelatin are hydrolyzed. Nitrate is reduced and indole is produced. Glu-

cose is not fermented. Enzyme activities of arginine dihydrolase and β-galactosidase are observed, but not oxidase and urease. D-glucose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, adipic acid, malic acid, and trisodium citrate are utilized as sole carbon sources, but not L-arabinose, capric acid, and phenylacetic acid. Strain CFH1-25 (=NNIBR2019642BA29) was isolated from intestine of *Hypomesus nipponensis* collected from the Soyang Lake, Chuncheon, Gangwon-do, Korea. The GenBank accession number of 16S rRNA gene sequence is MN559442.

Description of *Yersinia enterocolitica* subsp. *palearctica* IFH1-18

Cells are Gram-stain-negative, aerobic, non-flagellated, and rod-shaped. Colonies grown on R2A are circular entire margin, smooth, and ivory colored after incubation for 2–3 days at 25°C. Esculin is hydrolyzed, but not gelatin. Nitrate is not reduced and indole is not produced. Glucose is fermented. Enzyme activities of arginine dihydrolase, urease, β-galactosidase, and oxidase (weakly) are observed. 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 not capric acid, adipic acid and phenylacetic acid. Strain IFH1-18 (=NNIBR2019642BA75) was isolated from intestine of *Hypomesus nipponensis* collected from the Soyang Lake, Inje, Gangwon-do, Korea. The GenBank accession number of 16S rRNA gene sequence is MN559454.

Description of *Pseudomonas aeruginosa* CFHS-01

Cells are Gram-stain-negative, aerobic, flagellated, and rod-shaped. Colonies grown on R2A are circular with entire margin, smooth, and ivory colored after incubation for 2–3 days at 25°C. Esculin is hydrolyze, but not gelatin. Nitrate is reduced to nitrogen. Indole is not produced and glucose is not fermented. Enzyme activities of arginine dihydrolase, urease, and oxidase are observed, but not β-galactosidase. D-glucose, D-mannitol, *N*-acetyl-glucosamine, potassium gluconate, capric acid, adipic acid, malic acid, and trisodium citrate are utilized as sole carbon sources, but not L-arabinose, D-mannose, D-maltose and phenylacetic acid. Strain CFHS-01 (=NNIBR2019642BA40) was isolated from intestine of *Hypomesus nipponensis* collected from the Soyang Lake, Chuncheon, Gangwon-do, Korea. The GenBank accession number of 16S rRNA gene sequence is MN559445.

Description of *Pseudomonas lundensis* CFHS-10

Cells are Gram-stain-negative, aerobic, flagellated, and rod-shaped. Colonies grown on R2A are circular with entire margin, smooth, and ivory colored after incubation for 2–3 days at 25°C. Gelatin is hydrolyzed, but not esculin. Nitrate is not reduced and indole is not produced. Glucose is fermented. Enzyme activities of arginine dihydrolase, urease, and oxidase (weakly) are observed, but not β-galactosidase. D-glucose, L-arabinose, D-mannose, potassium gluconate, capric acid, malic acid, and trisodium citrate are utilized as sole carbon sources, but not D-mannitol, *N*-acetyl-glucosamine, D-maltose, adipic acid, and phenylacetic acid. Strain CFHS-10 (=NNIBR2019642BA45) was isolated from intestine of *Hypomesus nipponensis* collected from the Soyang Lake, Chuncheon, Gangwon-do, Korea. The GenBank accession number of 16S rRNA gene sequence is MN559447.

Description of *Pseudomonas paralactis* CFH1-01

Cells are Gram-stain-negative, aerobic, flagellated, and rod-shaped. Colonies grown on TSA are circular, flat, smooth, opaque, and ivory colored after incubation for 2–3 days at 25°C. Gelatin is hydrolyzed, but not esculin. Nitrate is not reduced and indole is not produced. Glucose is not fermented. Enzyme activities of arginine dihydrolase, urease, and oxidase are observed, but not 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 not adipic acid and phenylacetic acid. Strain CFH1-01 (=NNIBR2019642BA11) was isolated from intestine of *Hypomesus nipponensis* collected from the Soyang Lake, Chuncheon, Gangwon-do, Korea. The GenBank accession number of 16S rRNA gene sequence is MN559438.

Description of *Pseudomonas synxantha* CFHS-02

Cells are Gram-stain-negative, aerobic, flagellated, and rod-shaped. Colonies grown on R2A are circular with entire margin, smooth, and ivory colored after incubation for 2–3 days at 25°C. Gelatin and esculin are hydrolyzed and

nitrate is reduced. Indole is not produced and glucose is not fermented. Enzyme activities of arginine dihydrolase and oxidase are observed, but not urease and β-galactosidase. D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, potassium gluconate, capric acid, malic acid, and trisodium citrate are utilized as sole carbon sources, but not D-maltose, adipic acid, and phenylacetic acid. Strain CFHS-02 (=NNIBR2019642BA41) was isolated from intestine of *Hypomesus nipponensis* collected from the Soyang Lake, Chuncheon, Gangwon-do, Korea. The GenBank accession number of 16S rRNA gene sequence is MN559446.

Description of *Pseudomonas versuta* CFHS-14

Cells are Gram-stain-negative, aerobic, flagellated, and rod-shaped. Colonies grown on R2A are circular with entire margin, smooth, and ivory colored after incubation for 2−3 days at 25°C. Esculin is hydrolyzed, but not gelatin. Nitrate is not reduced and indole is not produced. Glucose is fermented. Enzyme activities of arginine dihydrolase and oxidase are observed, but not urease and β-galactosidase. D-glucose, L-arabinose, D-mannose, D-mannitol, potassium gluconate, capric acid, malic acid, and trisodium citrate are utilized as sole carbon sources, but not *N*-acetyl-glucosamine, D-maltose, adipic acid and phenylacetic acid. Strain CFHS-14 (=NNIBR2019642BA49) was isolated from intestine of *Hypomesus nipponensis* collected from the Soyang Lake, Chuncheon, Gangwon-do, Korea. The GenBank accession number of 16S rRNA gene sequence is MN559449.

Description of *Pseudomonas weihenstephanensis* CFHS-12

Cells are Gram-stain-negative, aerobic, flagellated, and rod-shaped. Colonies grown on R2A are circular with entire margin, smooth, and ivory colored after incubation for 2−3 days at 25°C. Gelatin is hydrolyzed, but not esculin. Nitrate is not reduced and indole is not produced. Glucose is fermented. Enzyme activities of arginine dihydrolase, urease, and oxidase (weakly) are observed, but not β-galactosidase. D-glucose, D-mannose (weakly), potassium gluconate, capric acid, malic acid, and trisodium citrate are utilized as sole carbon sources, but not L-arabinose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, adipic acid, and phenylacetic acid. Strain CFHS-12 (=NNIBR2019642BA47) was isolated from intestine of *Hypomesus nipponensis* collected from the Soyang Lake, Chuncheon, Gangwon-do, Korea. The GenBank accession number of 16S rRNA gene sequence is MN559448.

Description of *Yersinia ruckeri* FI2-07

Cells are Gram-stain-negative, aerobic, flagellated, and rod-shaped. Colonies grown on NA are circular, convex, smooth, and cream colored after incubation for 2−3 days at 25°C. Esculin and gelatin are hydrolyzed. Nitrate is reduced and glucose is fermented. Indole is not produced. Enzyme activities of arginine dihydrolase and β-galactosidase are observed, but not oxidase and urease. 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 not L-arabinose, capric acid, and phenylacetic acid. Strain FI2-07 (=NNIBR2018142BA242) was isolated from intestine of *Iksookimia koreensis* collected from the Geum River, Geumsan, Chungcheongnam-do, Korea. The GenBank accession number of 16S rRNA gene sequence is MK396587.

Description of *Acinetobacter pittii* FI1-01

Cells are Gram-stain-negative, aerobic, non-flagellated, and diplococoid or short rods-shaped. Colonies grown on TSA are circular, convex, smooth, opaque, and ivory colored after incubation for 2−3 days at 37°C. Esculin and gelatin are hydrolyzed weakly. Nitrate is not reduced and indole is not produced. Glucose is fermented. Enzyme activities of oxidase, urease, arginine dihyrolase, and β-galactosidase are not observed. L-arabinose, capric acid, adipic acid, malic acid, and trisodium citrate are utilized as sole carbon sources, but not D-glucose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, and phenylacetic acid. Strain FI1-01 (=NNIBR2018142BA228) was isolated from intestine of *Iksookimia koreensis* collected from the Geum River, Geumsan, Chungcheongnam-do, Korea. The GenBank accession number of 16S rRNA gene sequence is MK396586.

Description of *Flavobacterium frigidarium* FEB2-04

Cells are Gram-stain-negative, aerobic, non-flagellated, and rod-shaped. Colonies grown on MA are circular, convex, smooth, and yellow colored after incubation for 3−4 days at 15°C. Esculin and gelatin are hydrolyzed. Nitrate is not reduced and indole is not produced. Glucose is not fermented. Enzyme activity of β-galactosidase is ob-

served, but not arginine dihydrolase, urease, and oxidase. D-glucose, D-mannose, D-mannitol, and D-maltose are utilized as sole carbon sources, but not L-arabinose, *N*-acetyl-glucosamine, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain FEB2-04 (=NNIBR2017BA46) was isolated from intestine of *Leucopsarion petersii* collected from the Jangji Stream, Goseong, Gyeongsangnam-do, Korea. The GenBank accession number of 16S rRNA gene sequence is MG780342.

Description of *Corynebacterium stationis* FMD-28

Cells are Gram-stain-positive, aerobic, non-flagellated, and rod-shaped. Colonies grown on R2A are circular, smooth, convex, and ivory colored after incubation for 2–3 days at 30°C. Esculin is hydrolyzed weakly, but not gelatin. Nitrate is reduced and glucose is fermented. Indole is not produced. Enzyme activities of oxidase, urease, arginine dihydrolase, and β-galactosidase is not observed. D-glucose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, malic acid, trisodium citrate, and phenylacetic acid are utilized as sole carbon sources, but not L-arabinose, potassium gluconate, capric acid, and adipic acid. Strain FMD-28 (=NNIBR2018142BA300) was isolated from intestine of *Micropterus salmoides* collected from the Nakdong River, Sangju, Gyeongsangbuk-do, Korea. The GenBank accession number of 16S rRNA gene sequence is MK396590.

Description of *Mycobacteroides saopaulense* FMS-15

Cells are Gram-stain-positive, aerobic, non-flagellated, and rod-shaped. Colonies grown on R2A are irregular, dry, brittle, opaque, and white colored after incubation for 2–3 days at 37°C. Esculin is hydrolyzed, but not gelatin. Nitrate is reduced. Indole is not produced and glucose is not fermented. Enzyme activities of arginine dihydrolase, urease, β-galactosidase, and oxidase are not observed. The strain does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid as sole carbon sources. Strain FMS-15 (=NNIBR2018142BA318) was isolated from intestine of *Micropterus salmoides* collected from the Nakdong River, Sangju, Gyengsangbuk-do, Korea. The GenBank accession number of 16S rRNA gene sequence is MK396591.

Description of *Mycolicibacterium sarraceniae* FMD-25

Cells are Gram-stain-positive, aerobic, non-flagellated, and rod-shaped. Colonies grown on NA are circular, smooth, convex, and yellowish ivory colored after incubation for 2–3 days at 30°C. Esculin and gelatin are not hydrolyzed. Nitrate is reduced. Indole is not produced and glucose in not fermented. Enzyme activity of urease is observed, but not arginine dihydrolase, β-galactosidase, and oxidase. D-glucose, D-mannitol, potassium gluconate, and malic acid are utilized as sole carbon sources, but not L-arabinose, D-mannose, *N*-acetyl-glucosamine, D-maltose, capric acid, adipic acid, trisodium citrate, and phenylacetic acid. Strain FMD-25 (=NNIBR2018142BA298) was isolated from intestine of *Micropterus salmoides* collected from the Nakdong River, Sangju, Gyeongsangbuk-do, Korea. The GenBank accession number of 16S rRNA gene sequence is MK396589.

Description of *Modestobacter versicolor* FMS-37

Cells are Gram-stain-positive, aerobic, flagellated, and rod-shaped. Colonies grown on NA are circular, crateriform, and pinkish ivory colored after incubation for 2–3 days at 30°C. Esculin and gelatin are hydrolyzed. Nitrate is not reduced and indole is not produced. Glucose is not fermented. Enzyme activity of β-galactosidase is observed, but not arginine dihydrolase, urease, and oxidase. D-glucose, D-maltose, potassium gluconate, adipic acid (weakly), malic acid (weakly), and phenylacetic acid are utilized as sole carbon sources, but not L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, capric acid, and trisodium citrate. Strain FMS-37 (=NNIBR2018142BA338) was isolated from intestine of *Micropterus salmoides* collected from the Nakdong River, Sangju, Gyeongsangbuk-do, Korea. The GenBank accession number of 16S rRNA gene sequence is MK396600.

Description of *Sanguibacter inulinus* 19FMS-10

Cells are Gram-stain-positive, aerobic, flagellated, and rod-shaped. Colonies grown on R2A are circular, convex, smooth, and lemon colored after incubation for 2–3 days at 25°C. Esculin is hydrolyzed, but not gelatin. Nitrate is not reduced and indole is not produced. Glucose is fermented. Enzyme activities of β-galactosidase and oxidase (weakly) is observed, but not arginine dihydrolase and ure-

ase. D-glucose, L-arabinose, D-mannose, *N*-acetyl-glucosamine, D-maltose, and potassium gluconate are utilized as sole carbon sources, but not D-mannitol, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. Strain 19FMS-10 (=NNIBR2019642BA87) was isolated from intestine of *Micropterus salmoides* collected from the Yeongok stream, Gangneung, Gangwon-do, Korea. The GenBank accession number of 16S rRNA gene sequence is MN559813.

Description of *Cohnella damuensis* FMD-08

Cells are Gram-stain-positive, aerobic, flagellated, and rod-shaped. Colonies grown on NA are circular, flat, opaque, and cream white colored after incubation for 2−3 days at 30°C. Esculin is hydrolyzed weakly, but not gelatin. Nitrate is reduced to nitrogen. Indole is not produced and glucose is not fermented. Enzyme activities of urease and oxidase are observed, but not arginine dihydrolase and *β*-galactosidase. D-mannitol, *N*-acetyl-glucosamine, potassium gluconate, capric acid, adipic acid, and malic acid are utilized as sole carbon sources, but not D-glucose, L-arabinose, D-mannose, D-maltose, trisodium citrate, and phenylacetic acid. Strain FMD-08 (=NNIBR2018142BA285) was isolated from intestine of *Micropterus salmoides* collected from the Nakdong River, Sangju, Gyeongsangbuk-do, Korea. The GenBank accession number of 16S rRNA gene sequence is MK396588.

Description of *Mycolicibacterium bacteremicum* 19FPP-03

Cells are Gram-stain-positive, aerobic, non-flagellated, and rod-shaped. Colonies grown on R2A are circular, convex, smooth, and yellowish ivory colored after incubation for 2−3 days at 25°C. Esculin is hydrolyzed weakly, but not gelatin. Nitrate is reduced. Indole is not produced and glucose is not fermented. Enzyme activities of urease and *β*-galactosidase are observed, but not arginine dihydrolase and oxidase. D-mannitol, potassium gluconate, and malic acid are utilized as sole carbon sources, but not D-glucose, L-arabinose, D-mannose, *N*-acetyl-glucosamine, D-maltose, capric acid, adipic acid, trisodium citrate, and phenylacetic acid. Strain 19FPP-03 (=NNIBR2019642BA105) was isolated from intestine of *Pseudorasbora parva* collected from the Yeongok stream, Gangneung, Gangwon-do, Korea. The GenBank accession number of 16S rRNA gene sequence is MN559459.

Description of *Fictibacillus aquaticus* 19FPP-20

Cells are Gram-stain-positive, aerobic, flagellated, and rod-shaped. Colonies grown on R2A are circular with entire margin, flat, smooth, and cream white colored after incubation for 2−3 days at 25°C. Esculin and gelatin are hydrolyzed. Nitrate is not reduced and indole is not produced. Glucose is not fermented. Enzyme activity of *β*-galactosidase is observed, but not arginine dihydrolase, urease, and oxidase. D-glucose and D-maltose are utilized as sole carbon sources, but not L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain 19FPP-20 (=NNIBR2019642BA114) was isolated from intestine of *Pseudorasbora parva* collected from the Yeongok stream, Gangneung, Gangwon-do, Korea. The GenBank accession number of 16S rRNA gene sequence is MN559460.

Description of *Aquamicrobium lusatiense* P4N-04

Cells are Gram-stain-negative, aerobic, flagellated, and rod-shaped. Colonies grown on NA are irregular with undulate margins, umbonate, and cream colored after incubation for 2−3 days at 30°C. Esculin is hydrolyzed, but not gelatin. Nitrate is not reduced and indole is not produced. Glucose is not fermented. Enzyme activity of *β*-galactosidase is observed, but not arginine dihydrolase, urease, and oxidase. D-glucose and trisodium citrate are 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, and phenylacetic acid. Strain P4N-04 (=NNIBR2018142BA270) was isolated from intestine of *Silurus asotus* collected from fishery, Jeongeup, Jeollabuk-do, Korea. The GenBank accession number of 16S rRNA gene sequence is MK396598.

Description of *Achromobacter pulmonis* PI3-03

Cells are Gram-stain-negative, aerobic, flagellated, and rod-shaped. Colonies grown on TSA are circular, smooth, convex, opaque, and cream colored after incubation for 2−3 days at 30°C. Esculin and gelatin are not hydrolyzed. Nitrate is reduced. Indole is not produced and glucose is not fermented. Enzyme activities of urease and oxidase, but not arginine dihydrolase and *β*-galactosidase. *N*-acetyl-glucosamine (weakly), potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phe-

nylacetic acid are utilized as sole carbon sources, but not D-glucose, L-arabinose, D-mannose, D-mannitol and D-maltose. Strain PI3-03 (=NNIBR2018142BA279) was isolated from intestine of *Silurus asotus* collected from fishery, Jeongeup, Jeollabuk-do, Korea. The GenBank accession number of 16S rRNA gene sequence is MK396599.

Description of *Marinomonas pontica* FEB1-13

Cells are Gram-stain-negative, aerobic, flagellated, and rod-shaped. Colonies grown on MA are irregular, convex, smooth, and ivory colored after incubation for 2–3 days at 20°C. Esculin is hydrolyzed, but not gelatin. Nitrate is not reduced and indole is not produced. Glucose is fermented. Enzyme activities of urease (weakly) and β-galactosidase are observed, but not arginine dihydrolase and oxidase. D-glucose, D-mannose, D-mannitol, D-maltose, potassium gluconate, malic acid, and trisodium citrate are utilized as sole carbon sources, but not L-arabinose, *N*-acetyl-glucosamine, capric acid, adipic acid and phenylacetic acid. Strain FEB1-13 (=NNIBR2017BA45) was isolated from intestine of *Takifugu niphobles* collected from the Jangji Stream, Goseong, Gyeongsangbuk-do, Korea. The GenBank accession number of 16S rRNA gene sequence is MG780341.

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REFERENCES

Banerjee G and AK Ray. 2017. Bacterial symbiosis in the fish gut and its role in health and metabolism. Symbiosis 72:1–11.

Felsenstein J. 1981. Evolutionary trees from DNA sequences: a maximum likelihood approach. J. Mol. Evol. 17:368–376.

Felsenstein J. 1985. Confidence limits on phylogenies: An approach using the bootstrap. Evolution 39:783–791.

Fierer N and RB Jackson. 2006. The diversity and biogeography of soil bacterial communities. Proc. Natl. Acad. Sci. USA 103:626–631.

Fitch WM. 1971. Toward defining the course of evolution: minimum change for a specific tree topology. Syst. Zool. 20:406–416.

Jeon YS, K Lee, SC Park, BS Kim, YJ Cho, SM Ha and J Chun. 2014. EzEditor: a versatile sequence alignment editor for both rRNA- and protein-coding genes. Int. J. Syst. Evol. Microbiol. 64:689–691.

Jukes TH and CR Cantor. 1969. Evolution of protein molecules pp. 21–213. In: Mammalian Protein Metabolism Vol. 3. (Munro HN, ed.). Academic Press. New York.

Kumar S, G Stecher and K Tamura. 2016. MEGA7: Molecular Evolutionary Genetics Analysis version 7.0 for bigger datasets. Mol. Biol. Evol. 33:1870–1874.

Liu H, X Guo, R Gooneratne, R Lai, C Zeng, F Zhan and W Wang. 2016. The gut microbiome and degradation enzyme activity of wild freshwater fishes influenced by their trophic levels. Sci. Rep. 6:24340.

Llewellyn MS, S Boutin, SH Hoseinifar and N Derome. 2014. Teleost microbiomes: the state of the art in their characterization, manipulation and importance in aquaculture and fisheries. Front. Microbiol. 5:207.

Ringø E, Z Zhou, JLG Vecino, S Wadsworth, J Romero, Å Krogdahl, RE Olsen, A Dimitroglou, A Foey, S Davies, M Owen, HL Lauzon, LL Martinsen, PD Schryver, P Bossier, S Sperstad and DL Merrifield. 2015. Effect of dietary components on the gut microbiota of aquatic animals. A never-ending story? Aquac. Nutr. 22:219–282.

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

Sullam KE, SD Essinger, CA Lozupone, MP O'Connor, GL Rosen, R Knight, SS Kilham and JA Russell. 2012. Environmental and ecological factors that shape the gut bacterial communities of fish: a meta-analysis. Mol. Ecol. 21:3363–3378.

Wong S and JF Rawls. 2012. Intestinal microbiota composition in fishes is influenced by host ecology and environment. Mol. Ecol. 21:3100–3102.

Yoon SH, SM Ha, S Kwon, J Lim, Y Kim, H Seo and J Chun. 2017. Introducing EzBioCloud: A taxonomically united database of 16S rRNA and whole genome assemblies. Int. J. Syst. Evol. Microbiol. 67:1613–1617.