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A report of 36 unrecorded bacterial species belonging to the phyla *Actinomycetota*, *Bacillota*, *Bacteroidota*, *Deinococcota*, and *Pseudomonadota* isolated in Republic of Korea

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As part of a comprehensive investigation of indigenous prokaryotic species in the Republic of Korea, 37 bacterial strains belonging to 36 species were isolated from diverse environmental habitats. These strains were assigned to five phyla, namely *Deinococcota*, *Actinomycetota*, *Bacillota*, *Bacteroidota*, and *Pseudomonadota*. Each strain was identified based on 16S rRNA gene sequence similarity (>98.7%) and the formation of definite phylogenetic clades with their closest reported species. Among isolates, there is one species belonging to the phylum *Deinococcota*, five species belonging to the phylum *Actinomycetota*, four species belonging to the phylum *Bacillota*, nine species belonging to the phylum *Bacteroidota*, and 17 species belonging to the phylum *Pseudomonadota* (comprising eight species of the class *Alphaproteobacteria*, one species of the class *Betaproteobacteria*, and eight species of the class *Gammaproteobacteria*). Based on 16S rRNA gene sequence analysis, each strain was assigned to independent and predefined bacterial species. Since there were no published or official reports regarding these 36 species in the Republic of Korea, they have been reported as unrecorded species in the Republic of Korea. Their Gram stain, cell morphology, colony, basic biochemical characteristics, strain ID, and isolation source of each species are described in the species descriptions.

Keywords: 16S rRNA, *Actinomycetota*, *Bacteroidota*, *Bacillota*, *Deinococcota*, indigenous prokaryotic species in Republic of Korea, *Pseudomonadota*, taxonomy, unrecorded species

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Introduction

Deinococcota is a bacterial phylum, renamed from '*Deinococcus-Thermus*' in 2021 (Oren and Garrity, 2021). At the time of writing, the phylum *Deinococcota* consists of only one class *Deinococci*, and three orders are in the class *Dinococci*, including *Deinococcales*, Thermales, and Trueperales. Most bacteria species have a thick layer of peptidoglycan, and they contain outer membranes (Griffiths and Gupta, 2007).

Actinomycetota is a bacterial phylum that was renamed from '*Actinobacteria*' in 2021 (Oren and Garrity, 2021). Most members of the *Actinomycetota* are Gram-positive and isolated from diverse environments, including soil, freshwater, and marine environments. They also have relatively high G+C content (Gao and Gupta, 2012). At the time of writing, taxonomic classification based on 16S rRNA gene sequences indicated that the phylum *Actino-*

mycetota has five classes: *Acidimicrobiia*, *Actinomycetes*, *Coriobacteriia*, *Nitriliruptoria*, *Rubrobacteria*, and *Thermoleophilia*.

The *Bacillota* is a bacterial phylum that was renamed from '*Firmicutes*' in 2021 (Oren and Garrity, 2021). Most species of the phylum *Bacillota* are Gram-positive with low G+C content (Wolf *et al*., 2004), and are prevalent in diverse environments. At the time of writing, the 16S rRNA gene sequences based on taxonomic classification indicated that the phylum *Bacillota* has seven classes including *Bacilli*, *Clostridia*, *Culicoidibacteria*, *Erysipelotrichia*, *Limnochordia*, *Negativicutes*, and *Thermolithobacteria*.

Bacteroidota is a bacterial phylum that was renamed from '*Bacteroidetes*' in 2021 (Oren and Garrity, 2021). At the time of writing, according to the 16S rRNA gene sequences-based taxonomic classification, there are six classes, including *Bacteroidia*, *Chitinophagia*, *Cytophagia*, *Flavobacteriia*, *Saprospiria*, and *Sphingobacteriia*. Bacteria of the phylum *Bacteroidota* are one of the most abundant bacteria in the adult gastrointestinal tract (Rajilić-Stojanović and de Vos, 2014), but also found in diverse environments on Earth (Thomas *et al*., 2011).

The *Pseudomonadota* is a bacterial phylum that was renamed from '*proteobacteria*' in 2021 (Oren and Garrity, 2021). Most species of the phylum *Pseudomonadota* are Gram-negative. According to the 16S rRNA gene sequences based taxonomic classification, there are eight classes with validly published names including *Acidithiobacillia*, *Alphaproteobacteria*, *Betaproteobacteria*, *Deltaproteobacteria*, *Epsilonproteobacteria*, *Gammaproteobacteria*, *Hydrogenophilia*, and *Oligoflexia*. Many pathogenic genera such as *Vibrio* and *Salmonella* are in this phylum, they can cause gastrointestinal inflammation, diarrhea (Jantsch *et al*., 2011), and gastroenteritis (Cabanillas-Beltrán *et al*., 2006).

In the present study, we collected several samples from various environments in the Republic of Korea and isolated many novel and unrecorded bacteria. As part of the study, we describe 36 bacterial species belonging to the phyla *Deinococcota*, *Actinomycetota*, *Bacillota*, *Bacteroidota*, and *Pseudomonadota*, which have not been reported in Republic of Korea before.

Materials and Methods

A total of 37 bacterial strains were isolated from environmental samples including soil, agricultural soil, mud, tidal flat, solar saltern, seawater, marine algae, seaweed, marine sand, sediment, lake water, brackish water, breast milk, and healthy human urine (Table 1). Each sample was processed separately, spread onto several culture media including R2A agar (R2A), glucose yeast extract agar (GYE), marine agar 2216 (MA), brain heart infusion agar (BHI), De Man-Rogosa-Sharpe agar (MRS) or trypticase soy agar (TSA), and incubated at 20, 25, 30 or 37°C for 2−5 days (Table 1). The designated strain ID, taxonomic information, isolation sources, culture media, and incubation conditions are summarized in Table 1. All strains were purified as single colonies after streaking and maintained at −80°C in a glycerol solution (20%, w/v) as well as lyophilized ampoules for long-term preservation.

Colony morphology of isolated strains was observed on agar plates after their cells were grown up to stationary phase. Cellular morphology and cell size were examined by light microscopy or transmission electron microscopy. Gram stain was performed using a Gram-stain kit (bioMérieux) or the standard procedures. Phenotypic characteristics were tested by using API 20NE galleries (bioMérieux) according to the manufacturer's instructions.

DNA extraction, PCR amplification of 16S rRNA gene, and Sanger sequencing were performed using the standard procedures described elsewhere (Lee *et al*., 2023). The 16S rRNA gene sequences of the strains assigned to the phylum *Bacteroidota* were compared with those of other bacterial species with validly published names using the EzBioCloud database (Yoon *et al*., 2017). For phylogenetic analyses, alignment of sequences was carried out with CLUSTAL W software (Thompson *et al*., 1994). Phylogenetic trees were inferred by using the neighbour-joining algorithm (Saitou and Nei, 1987) implemented within the PHYLIP package (Felsenstein, 1993). Evolutionary distance matrices for the neighbour-joining method were calculated by using the algorithm of Jukes and Cantor (1969) with the program DNADIST. The stability of relationships was assessed by bootstrap analysis based on 1000 resamplings of the neighbour-joining dataset by using the programs SEQBOOT, DNADIST, NEIGHBOR, and CONSENSE of the PHYLIP package.

Results and Discussion

Strain assigned to the phylum *Deinococcota*

Based on the 16S rRNA gene sequence comparison and phylogenetic analysis, strain CAU-S6 was assigned to the order *Deinococcales*, phylum *Deinococcota*, family *Deinococcaceae*, and genus *Deinococcus* (Table 1; Parte *et al*., 2020). Phylogenetic analysis based on 16S rRNA gene sequences show that strain CAU-S6 was identified as a member of *Deinococcus taklimakanensis* (Fig. 1). This strain was isolated from soil. For morphological information, the transmission electron microscope image of the strain is presented in Fig. 2. Colony color, morphology, and other phenotypic characteristics are shown in the species description.

Table 1. Summary of 37 isolates belonging to the phyla *Deinococcota*, *Actinomycetota*, *Bacillota*, *Bacteroidota* and *Pseudomonadota* and their taxonomic affiliations, isolations sources and culture conditions.

Order	Family	Genus	Strain No.	NIBR[a] ID	Closest species	16S rRNA gene sequence similarity (%)	Isolation source	Medium for incubation	Condition for incubation
Phylum *Deinococcota*									
Deinococcales	*Deinococcaceae*	*Deinococcus*	CAU-S6	NIBRBAC000501286	*Deinococcus taklimakanensis*	100	Soil	R2A	37°C, 3d
Phylum *Actinomycetota*									
Cellulomonadales	*Oerskoviaceae*	*Paraoerskovia*	SB3	NIBRBAC000002203	*Paraoerskovia sediminicola*	100	Tidal flat	MA	25°C, 2d
Microbacteriales	*Microbacteriaceae*	*Agromyces*	CAU 1452	NIBRBAC000501246	*Agromyces kandeliae*	99.24	Soil	GYE	30°C, 2d
		Microbacterium	NDK-63	NIBRBAC000497860	*Microbacterium sorbitolivorans*	99.72	Gut of Burmese Python	TSA	25°C, 3d
Mycobacteriales	*Corynebacteriaceae*	*Corynebacterium*	CAU 1463	NIBRBAC000501259	*Corynebacterium sanguinis*	100	Urine	BHI	37°C, 2d
Streptomycetales	*Streptomycetaceae*	*Streptomyces*	MMS16-UL617	NIBRBAC000498612	*Streptomyces geranii*	98.79	Soil	TSA	30°C, 5d
Phylum *Bacillota*									
Bacillales	*Bacillaceae*	*Bacillus*	CAU 11110	NIBRBAC000498489	*Bacillus gobiensis*	99.59	Soil	MA	37°C, 3d
		Metabacillus	LM3308	NIBRBAC000501180	*Metabacillus malikii*	98.85	Gut of Swinhoe's Pheasant	MA	37°C, 3d
Lactobacillales	*Carnobacteriaceae*	*Jeotgalibaca*	PTS2502	NIBRBAC000498383	*Jeotgalibaca arthritidis*	99.79	Feces	TSA	30°C, 2d
	Lactobacillaceae	*Lactobacillus*	HY_M_2_4	NIBRBAC000002176	*Lactobacillus apis*	99.65	Gut of insect	MRS	25°C, 2d
Phylum *Bacteroidota*									
Cytophagales	*Cyclobacteriaceae*	*Algoriphagus*	KYW691	NIBRBAC000002267	*Algoriphagus sanaruensis*	99.86	Seawater	MA	25°C, 3d
Flavobacteriales	*Flavobacteriaceae*	*Arenibacter*	CAU 1462	NIBRBAC000501258	*Arenibacter aquaticus*	99.72	Marine sand	MA	30°C, 2d
		Flavobacterium	RSG-18	NIBRBAC000002469	*Flavobacterium plurextorum*	100	Gut of Sebastes schlegeli	R2A	20°C, 3d
			WW92	NIBRBAC000002550	*Flavobacterium endophyticum*	99.86	Fresh water	R2A	25°C, 3d
		Lacinutrix	KYW850	NIBRBAC000002269	*Lacinutrix venerupis*	99.93	Seawater	MA	25°C, 2d
		Mesonia	IMCC25659	NIBRBAC000498556	*Mesonia oceanica*	99.86	Plant root	MA	20°C, 3d
	Weeksellaceae	*Chryseobacterium*	BSSK-MA29	NIBRBAC000506377	*Chryseobacterium subflavum*	100	Tidal flat	MA	25°C, 5d
			JPSW-R7	NIBRBAC000509638	*Chryseobacterium aquaeductus*	98.82	Seawater	R2A	25°C, 3d
Sphingobacteriales	*Sphingobacteriaceae*	*Pedobacter*	BY5	NIBRBAC000497881	*Pedobacter schmidteae*	98.77	Soil	R2A	30°C, 2d

Table 1. Continued.

Order	Family	Genus	Strain No.	NIBR[a] ID	Closest species	16S rRNA gene sequence similarity (%)	Isolation source	Medium for incubation	Condition for incubation
Phylum *Pseudomonadota* (alpha)									
Rhizobiales	*Cohaesibacteraceae*	*Cohaesibacter*	CAU 1516	NIBRBAC000502383	*Cohaesibacter intestini*	100	Tidal flat	MA	30°C, 3d
Rhodobacterales	*Rhodobacteraceae*	*Litorivita*	G7-2	NIBRBAC000002485	*Litorivita pollutaquae*	99.84	Tidal flat	MA	25°C, 2d
		Sinirhodobacter	SJ5-2	NIBRBAC000502467	*Sinirhodobacter huangdaonensis*	100	Sludge	TSA	30°C, 2d
			H1Y	NIBRBAC000498408	*Sinirhodobacter huangdaonensis*	100	Sludge	R2A	30°C, 3d
		Thioclava	6-2	NIBRBAC000002501	*Thioclava sediminum*	100	Tidal flat	MA	25°C, 2d
	Roseobacteraceae	*Shimia*	CAU 1190	NIBRBAC000498495	*Shimia thalassica*	99.71	Soil	MA	30°C, 3d
Rhodospirillales	*Thalassobaculaceae*	*Oceanibaculum*	Gri0127	NIBRBAC000502472	*Oceanibaculum nanhaiense*	99.92	Algae of seawater	MA	30°C, 3d
Sphingomonadales	*Erythrobacteraceae*	*Croceicoccus*	J2	NIBRBAC000002260	*Croceicoccus pelagius*	99.93	Seawater	MA	25°C, 3d
	Sphingomonadales	*Novosphingobium*	CAU 1464	NIBRBAC000501261	*Novosphingobium ovatum*	98.70	Dead mine water	R2A	30°C, 3d
Phylum *Pseudomonadota* (beta)									
Neisseriales	*Neisseriaceae*	*Vitreoscilla*	NSG-13	NIBRBAC000002465	*Vitreoscilla massiliensis*	98.87	Gut of Sebastes schlegeli	NA	20°C, 3d
Phylum *Pseudomonadota* (gamma)									
Cellvibrionales	*Microbulbiferaceae*	*Microbulbifer*	TATF-M118	NIBRBAC000508890	*Microbulbifer okhotskensis*	99.44	Tidal flat	MA	25°C, 3d
Chromatiales	*Chromatiaceae*	*Rheinheimera*	SyP7R	NIBRBAC000502479	*Rheinheimera coerulea*	98.94	Algae of seawater	R2A	30°C, 3d
Enterobacterales	*Yersiniaceae*	*Rahnella*	RSG-8	NIBRBAC000002468	*Rahnella inusitata*	99.72	Gut of Sebastes schlegeli	R2A	20°C, 3d
Lysobacterales	*Rhodanobacteraceae*	*Dyella*	CAU 1486	NIBRBAC000502380	*Dyella halodurans*	99.32	Tidal flat	GYE	30°C, 3d
Oceanospirillales	*Halomonadaceae*	*Halomonas*	BSW10-2	NIBRBAC000002768	*Halomonas litopenaei*	99.93	Tidal flat	MA	25°C, 2d
	Oceanospirillaceae	*Nitrincola*	KA17	NIBRBAC000002263	*Nitrincola schmidtii*	99.59	Seawater	MA	25°C, 3d
Pseudomonadales	*Aestuariirhabdaceae*	*Spartinivicinus*	CAU 1596	NIBRBAC000503246	*Spartinivicinus ruber*	99.79	Marine sans	MA	30°C, 3d
	Marinobacteraceae	*Marinobacter*	SAG5	NIBRBAC000497878	*Marinobacter shengliensis* subsp. *alexandrii*	98.86	Algae of seawater	MA	30°C, 2d

[a]National Institute of Biological Resources.

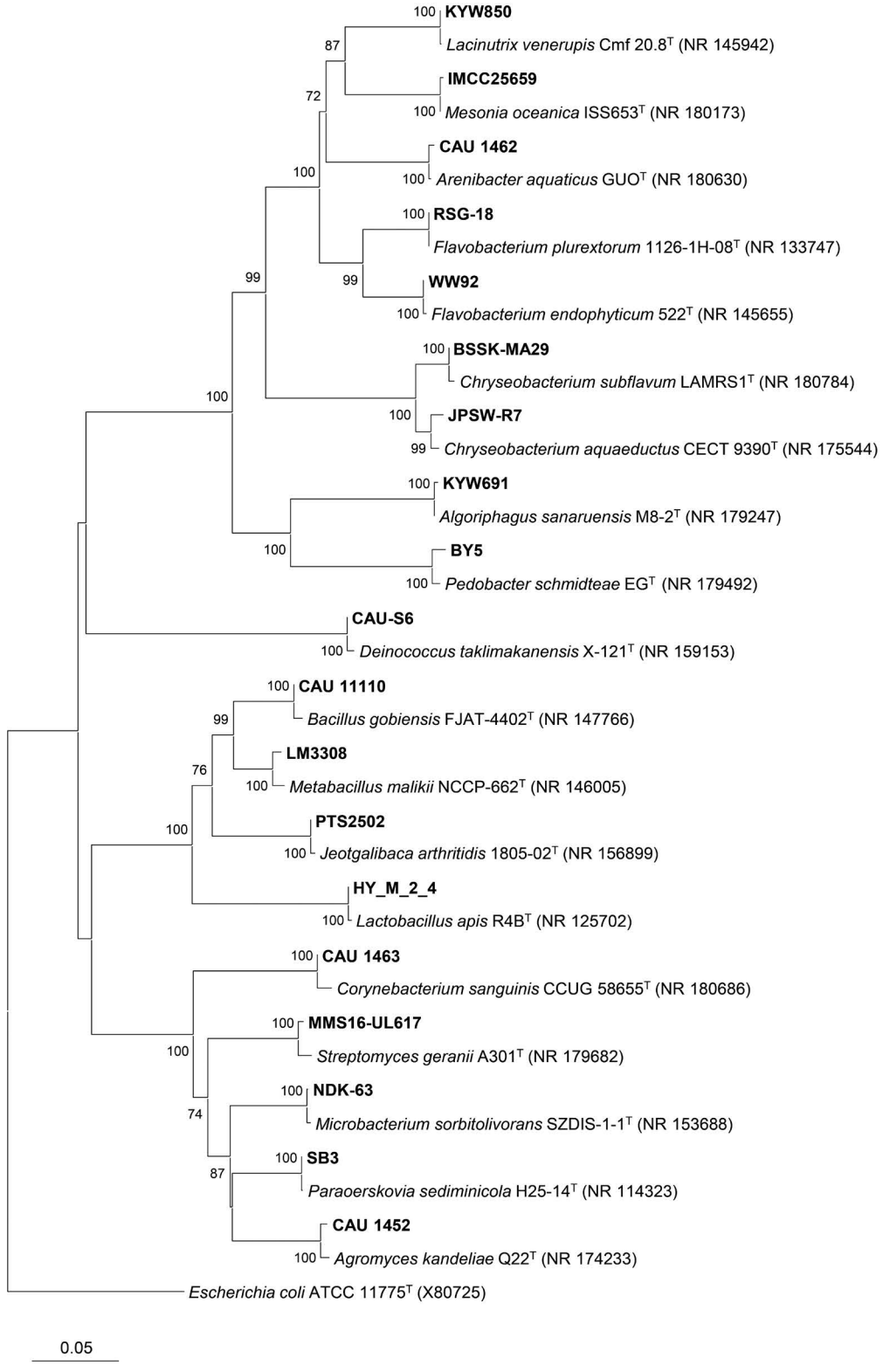

Fig. 1. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences showing the relationships between 19 strains isolated in this study and their relatives in the phyla *Actinomycetota*, *Bacillota*, *Bacteroidota* and *Deinococcota*. *Escherichia coli* ATCC 11775^T (GenBank accession no. X80725) was used as an outgroup. Bootstrap values greater than 70% are shown at branching points. Bar, 0.05 substitutions per nucleotide position.

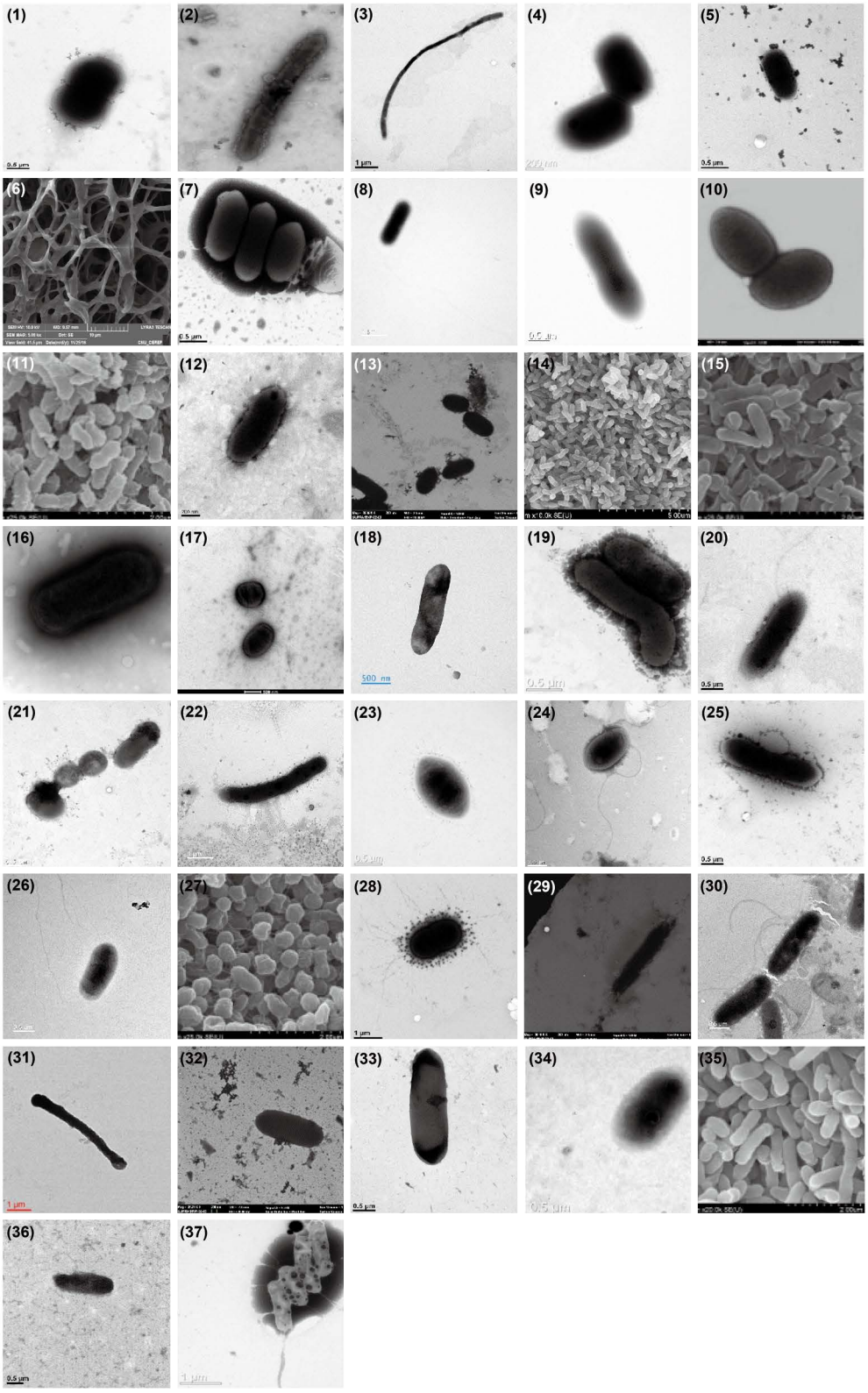

Fig. 2. Transmission electron or scanning electron micrographs of cells of the strains isolated in this study. Strains: 1, CAU-S6; 2, SB3; 3, CAU 1452; 4, NDK-63; 5, CAU 1463; 6, MMS16-UL617; 7, CAU 11110; 8, LM3308; 9, PTS2502; 10, HY_M_2_4; 11, KYW691; 12, CAU 1462; 13, RSG-18; 14, WW92; 15, KYW850; 16, IMCC25659; 17, BSSK-MA29; 18, JPSW-R7; 19, BY5; 20, CAU 1516; 21, G7-2; 22, SJ5-2; 23, H1Y; 24, 6-2; 25, CAU 1190; 26, Gri0127; 27, J2; 28, CAU 1464; 29, NSG-13; 30, SyP7R; 31, TATF-M118; 32, RSG-8; 33, CAU 1486; 34, BSW10-2; 35, KA17; 36, CAU 1596; 37, SAG5.

Strains assigned to the phylum *Actinomycetota*

Based on the 16S rRNA gene sequence comparison and phylogenetic analyses, five strains were assigned to four orders in the phylum *Actinomycetota*: one strain in the order *Cellulomonadales*, two strains in the order *Microbacteriales*, one strain in the order *Mycobacteriales*, and the other strain in the order *Streptomycetales* (Table 1; Fig. 1; Parte *et al*., 2020). In the order *Cellulomonadales*, one strain belongs to the genus *Paraoerskovia* in the family *Oerskoviaceae*. In the order *Microbacteriales*, two strains belong to the family *Microbacteriaceae* that includes the genera *Agromyces* and *Microbacterium*. In the order *Mycobacteriales*, one strain belongs to the genus *Corynebacterium* in the family *Corynebacteriaceae*. In the order *Streptomycetales*, one strain was assigned to the genus *Streptomyces* in the family *Streptomycetaceae*. The five strains were isolated from tidal flat, soil, gut of Burmese python, and urine. For morphological information, the transmission or scanning electron microscope images of the strains are presented in Fig. 2. Colony color, morphology, and other phenotypic characteristics are shown in the species descriptions.

Strains assigned to the phylum *Bacillota*

Based on the 16S rRNA gene sequence comparison and phylogenetic analyses, four strains were assigned to two orders in the phylum *Bacillota*: two strains in the order *Bacillales* and two strains in the order *Lactobacillales* (Table 1; Fig. 1; Parte *et al*., 2020). In the order *Bacillales*, two strains were assigned to the family *Bacillaceae* that includes the genera *Bacillus* and *Metabacillus*. In the order *Lactobacillales*, one strain belongs to the genus *Jeotgalibaca* in the family *Carnobacteriaceae* and the other strain belongs to the genus *Lactobacillus* in the family *Lactobacillaceae*. The four strains were isolated from soil, gut of Swinhoe's pheasant, feces, and gut of insect. For morphological information, the transmission or scanning electron microscope images of the strains are presented in Fig. 2. Colony color, morphology, and other phenotypic characteristics are shown in the species descriptions.

Strains assigned to the phylum *Bacteroidota*

Based on the 16S rRNA gene sequence comparison and phylogenetic analyses, nine strains were assigned to three orders in the phylum *Bacteroidota*: one strain in the order *Cytophagales*, seven strains in the order *Flavobacteriales*, and one strain in the order *Sphingobacteriales* (Table 1; Fig. 1; Parte *et al*., 2020). In the order *Cytophagales*, 1 strain belongs to the genus *Algoriphagus* in the family *Cyclobacteriaceae*. In the order *Flavobacteriales*, five strains were assigned to the family *Flavobacteriaceae* that includes the genera *Arenibacter*, *Flavobacterium*, *Lacinutrix*, and *Mesonia* and two strains belonging to the genus *Chryseobacterium* in the family *Weeksellaceae*. In the order *Sphingobacteriales*, one strain was assigned to the genus *Pedobacter* in the family *Sphingobacteriaceae*. The nine strains were isolated from seawater, marine sand, gut of fish (*Sebastes schlegeli*), freshwater, plant root, and soil. For morphological information, the transmission or scanning electron microscope images of the strains are presented in Fig. 2. Colony color, morphology, and other phenotypic characteristics are shown in the species descriptions.

Strains assigned to the phylum *Pseudomonadota* (alpha)

Based on the 16S rRNA gene sequence comparison and phylogenetic analyses, nine strains were assigned to four orders in the phylum *Pseudomonadota* (alpha): one strain in the order *Rhizobiales*, five strains in the order *Rhodobacterales*, one strain in the order *Rhodospirillales*, and two strains in the order *Sphingomonadales* (Table 1; Fig. 3; Parte *et al*., 2020). In the order *Rhizobiales*, one strain belongs to the genus *Cohaesibacter* in the family *Cohaesibacteraceae*. In the order *Rhodobacterales*, four strains belong to the family *Rhodobacteraceae*, which includes the genera *Litorivita*, *Sinirhodobacter*, and *Thioclava*, and one strain belongs to the genus *Shimia* in the family *Roseobacteraceae*. In the order *Rhodospirillales*, one strain was assigned to the genus *Oceanibaculum* in the family *Thalassobaculaceae*. In the order *Sphingomonadales*, one strain was assigned to the genus *Oceanibaculum* in the family *Erythrobacteraceae*, and the other strain belongs to the genus *Novosphingobium* in the family *Sphingomonadales*. The nine strains were isolated from tidal flat, sludge, soil, algae of seawater, dead mine water, and seawater. For morphological information, the transmission or scanning electron microscope images of the strains are presented in Fig. 2. Colony color, morphology, and other phenotypic characteristics are shown in the species descriptions.

Strains assigned to the phylum *Pseudomonadota* (beta)

Based on the 16S rRNA gene sequence comparison and phylogenetic analyses, one strain was assigned to the order *Neisseriales* in the phylum *Pseudomonadota* (beta): the strain belongs to the genus *Vitreoscilla* in the family *Neisseriaceae* (Table 1; Fig. 3; Parte *et al*., 2020). This strain was isolated from the gut of a fish (*Sebastes schlegeli*). For morphological information, the transmission electron microscope image of the strain is presented in Fig. 2. Colony color, morphology, and other phenotypic characteristics are shown in the species description.

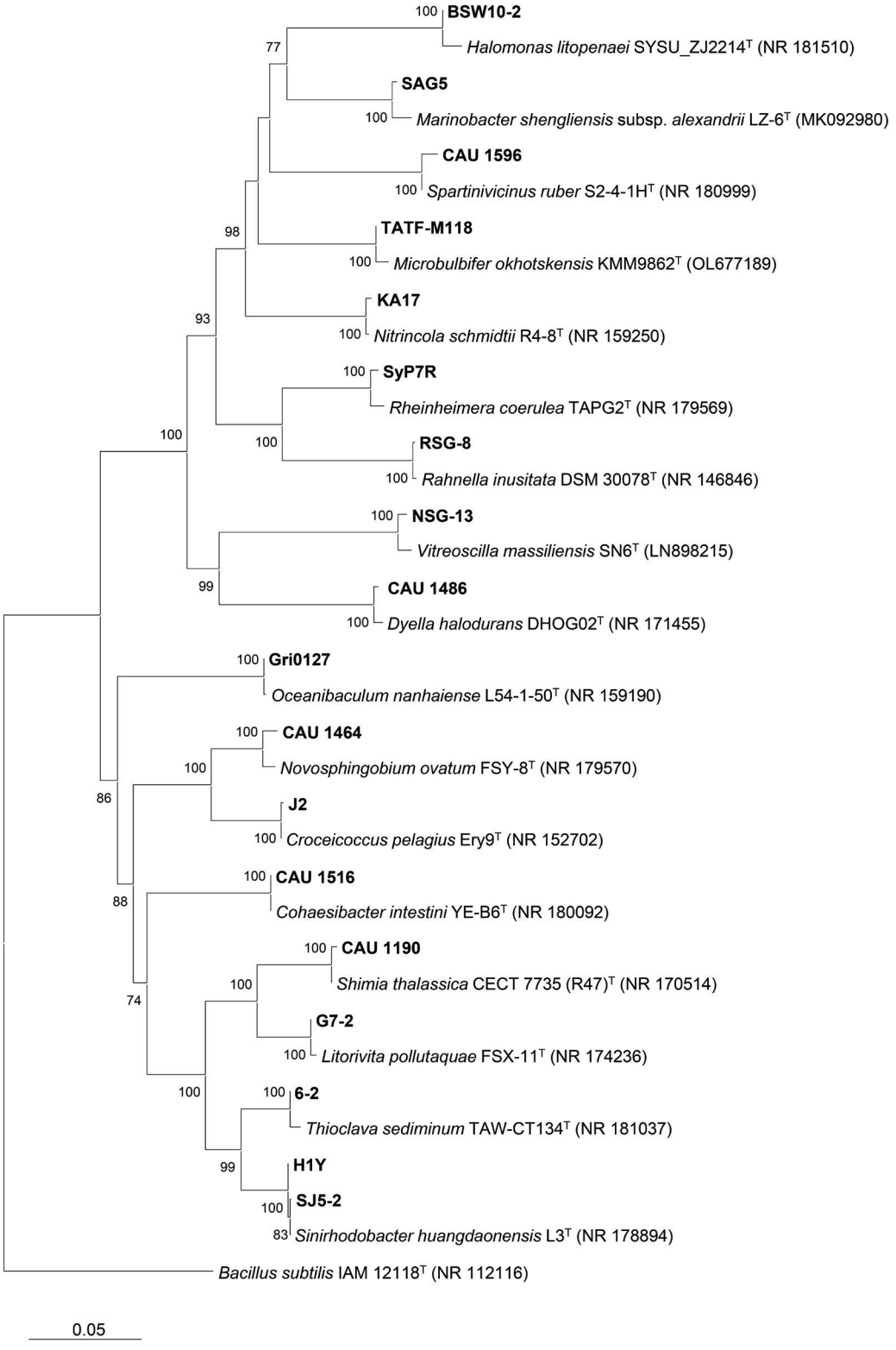

Fig. 3. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences showing the relationships of 18 strains isolated in this study and their relatives in the phylum *Proteobacteria*. Bootstrap values greater than 70% are shown at branching points. *Bacillus subtilis* IAM 12118^T (GenBank accession no. NR_112116) was used as an outgroup. Bar, 0.05 substitutions per nucleotide position.

Strains assigned to the phylum *Pseudomonadota* (gamma)

Based on the 16S rRNA gene sequence comparison and phylogenetic analyses, eight strains were assigned to six orders in the phylum *Pseudomonadota* (gamma): one strain in the order *Alteromonadales*, one strain in the order *Cellvibrionales*, one strain in the order *Enterbacterales*, one strain in the order *Lysobacterales*, two strains in the order *Oceanospirillales*, and two strains in the order *Pseudomonadales* (Table 1; Fig. 3; Parte *et al*., 2020). In the order *Cellivibrionales*, one strain was assigned to the genus *Microbulbifer* in the family *Microbulbiferaceae*. In the order *Chromatiales*, one strain was assigned to the genus *Rheinheimera* in the family *Chromatiaceae*. In the order *Enterobacterales*, one strain belongs to the genus *Rahnella* in the family *Yersiniaceae*. In the order *Lysobacterales*, one strain belongs to the genus *Dyella* in the family *Rhodanobacteraceae*. In the order *Oceanospirillales*, one strain was assigned to the genus *Halomonas* in the family *Halomonadaceae* and the other strain was assigned to the genus *Nitrincola* in the family *Oceanospirillaceae*. In the order *Pseudomonadales*, one strain belongs to the genus *Spartinivicinus* in the family *Aestuariirhabdaceae* and the other strain belongs to the genus *Marinobacter* in the family *Marinobacteraceae*. The eight strains were isolated from algae of seawater, tidal flat, gut of *Sebastes schlegeli*, and marine sands. For morphological information, the transmission or scanning electron microscope images of the strains are presented in Fig. 2. Colony color, morphology, and other phenotypic characteristics are shown in the species descriptions.

In conclusion, there is no official report that the above-mentioned 36 species have been isolated in the Republic of Korea; therefore, one species of the phylum *Deinococcota*, five species of the phylum *Actinomycetota*, four species of the phylum *Bacillota*, nine species of the phylum *Bacteroidota* and 17 species of the phylum *Pseudomonadota* are proposed as unrecorded prokaryotic species found in the Republic of Korea.

Description of *Deinococcus taklimakanensis* CAU-S6

Cells are Gram-staining-positive, non-flagellated, and coccoid shaped. Colonies are round, convex, smooth, and white colored after incubation for 3 days on R2A at 37°C. In the API 20NE system, positive for arginine dihydrolase, urease activity, esculin hydrolysis, gelatin hydrolysis, and oxidase activity; but negative for nitrate reduction, indole production, glucose acidification, 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 CAU-S6 (=NIBRBAC000501286) was isolated from a soil sample in Dongjak-gu, Seoul, Republic of Korea.

Description of *Paraoerskovia sediminicola* SB3

Cells are Gram-staining-positive, non-flagellated, and rod shaped. Colonies are circular, raised, entire, and yellow colored after incubation for 2 days on MA at 25°C. In the API 20NE system, positive for nitrate reduction, glucose acidification, esculin hydrolysis, β-galactosidase activity, oxidase activity, utilization of D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, and potassium gluconate;l; but negative for indole production, arginine dihydrolase, urease activity, gelatin hydrolysis, utilization of capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain SB3 (=NIBRBAC000002203) was isolated from a tidal flat sample in Taean-gun, Chungcheongnam-do, Republic of Korea.

Description of *Agromyces kandeliae* CAU 1452

Cells are Gram-staining-positive, non-flagellated, and rod shaped. Colonies are irregular, raised, and yellow colored after incubation for 2 days on GYE at 30°C. In the API 20NE system, positive for nitrate reduction and esculin hydrolysis; but negative for indole production, glucose acidification, arginine dihydrolase, urease activity, gelatin hydrolysis, β-galactosidase activity, and oxidase activity. 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 are not utilized as sole carbon sources. Strain CAU 1452 (=NIBRBAC000501246) was isolated from a soil sample in Wando-gun, Jeollanam-do, Republic of Korea.

Description of *Microbacterium sorbitolivorans* NDK-63

Cells are Gram-staining-positive, non-flagellated, and oval shaped. Colonies are irregular and cream colored after incubation for 3 days on TSA at 25°C. In the API 20NE system, positive for esculin hydrolysis and β-galactosidase activity; but negative for nitrate reduction, indole production, glucose acidification, arginine dihydrolase, urease activity, gelatin hydrolysis, and oxidase activity. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, and potassium gluconate are not utilized as sole carbon sources while capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid are not. Strain NDK-63 (=NIBRBAC000497860) was isolated from a gut of a Burmese python in Gwacheon-si, Gyeonggi-do, Republic of Korea.

Description of *Corynebacterium sanguinis* CAU 1463

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

rod shaped. Colonies are circular, convex, smooth, opaque, and cream colored after incubation for 2 days on BHI at 37°C. In the API 20NE system, positive for arginine dihydrolase, urease activity, esculin hydrolysis, gelatin hydrolysis; but negative for nitrate reduction, indole production, glucose acidification, β-galactosidase activity, and oxidase activity. Potassium gluconate is utilized as a sole carbon source; while 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 are not. Strain CAU 1463 (=NIBR BAC000501259) was isolated from a urine sample in Dongdaemun-gu, Seoul, Republic of Korea

Description of *Streptomyces geranii* MMS16-UL617

Cells are Gram-staining-positive, non-flagellated, and filamentous shaped. Colonies are filamentous, umbonate, and mud yellow colored after incubation for 5 days on TSA at 30°C. In the API 20NE system, positive for esculin hydrolysis, β-galactosidase activity, and oxidase activity; but negative for nitrate reduction, indole production, glucose acidification, arginine dihydrolase, urease activity, gelatin hydrolysis. 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 are not utilized as sole carbon sources. Strain MMS16-UL617 (=NIBR BAC000498612) was isolated from a soil sample in Ulleung-gun, Gyeongsangbuk-do, Republic of Korea.

Description of *Bacillus gobiensis* CAU 11110

Cells are Gram-staining-positive, non-flagellated, and rod shaped. Colonies are convex, entire, and cream colored after incubation for 3 days on MA at 37°C. In the API 20NE system, positive for nitrate reduction, glucose acidification, esculin hydrolysis, gelatin hydrolysis, β-galactosidase activity; but negative for indole production, arginine dihydrolase, urease activity, and oxidase activity. D-Glucose, L-arabinose, D-mannose, D-mannitol, D-maltose, and potassium gluconate are utilized as sole carbon sources; while *N*-acetyl-D-glucosamine, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid are not. Strain CAU 11110 (=NIBR BAC000498489) was isolated from a soil sample in Jeju-si, Jeju-do, Republic of Korea.

Description of *Metabacillus malikii* LM3308

Cells are Gram-staining-positive, flagellated, and rod shaped. Colonies are circular, convex, entire, and white colored after incubation for 3 days on MA at 37°C. In the API 20NE system, positive for nitrate reduction, indole production, esculin hydrolysis, and β-galactosidase activity; but negative for glucose acidification, arginine dihydrolase, urease activity, gelatin hydrolysis, and oxidase activity. Potassium gluconate is utilized as a sole carbon source; while 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 are not. Strain LM3308 (=NIBR BAC000501180) was isolated from a gut sample of Swinhoe's pheasant in Gwacheon-si, Gyeonggi-do, Republic of Korea.

Description of *Jeotgalibaca arthritidis* PTS2502

Cells are Gram-staining-positive, non-flagellated, and rod shaped. Colonies are circular, raised, and cream colored after incubation for 2 days on TSA at 30°C. In the API 20NE system, positive for nitrate reduction and β-galactosidase activity; but negative for indole production, glucose acidification, arginine dihydrolase, urease activity, esculin hydrolysis, gelatin hydrolysis, and oxidase activity. 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 are not utilized as sole carbon sources. Strain PTS2502 (=NIBRBAC000498383) was isolated from feces in Gwacheon-si, Gyeonggi-do, Republic of Korea.

Description of *Lactobacillus apis* HY_M_2_4

Cells are Gram-staining-positive, flagellated, and, rod shaped. Colonies are circular, raised, entire, and white colored after incubation for 2 days on MRS at 25°C. In the API 20NE system, positive for nitrate reduction; but negative for indole production, glucose acidification, arginine dihydrolase, urease activity, esculin hydrolysis, gelatin hydrolysis, β-galactosidase activity, and oxidase activity. 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 are not utilized as sole carbon sources. Strain HY_M_2_4 (=NIBRBAC000002176) was isolated from a gut sample of an insect in Dongdaemun-gu, Seoul, Republic of Korea.

Description of *Algoriphagus sanaruensis* KYW691

Cells are Gram-staining-negative, non-flagellated, and rod shaped. Colonies are opaque, round, smooth, convex, and red colored after incubation for 3 days on MA at 25°C. In the API 20NE system, negative for nitrate reduction, indole production, glucose acidification, arginine dihydrolase, urease activity, esculin hydrolysis, gelatin hydrolysis, β-galactosidase activity, and oxidase activity. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-ace-

tyl-D-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid are not utilized as sole carbon sources. Strain KYW691 (=NIBRBAC000002267) was isolated from a seawater sample in Gwangyang-si, Jeollanam-do, Republic of Korea.

Description of *Arenibacter aquaticus* CAU 1462

Cells are Gram-staining-negative, non-flagellated, and rod shaped. Colonies are circular, convex, smooth, and cream colored after incubation for 2 days on MA at 30°C. In the API 20NE system, positive for oxidase activity; but negative for nitrate reduction, indole production, glucose acidification, arginine dihydrolase, urease activity, esculin hydrolysis, gelatin hydrolysis, and β-galactosidase activity. D-Glucose, L-arabinose, and D-mannose are utilized as sole carbon sources, while D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid are not. Strain CAU 1462 (=NIBRBAC000501258) was isolated from a marine sand sample in Busan, Republic of Korea.

Description of *Flavobacterium plurextorum* RSG-18

Cells are Gram-staining-negative, non-flagellated, and rod shaped. Colonies are radial, convex, and yellow colored after incubation for 3 days on R2A at 20°C. In the API 20NE system, positive for nitrate reduction, glucose acidification, esculin hydrolysis, β-galactosidase activity, and oxidase activity; but negative for indole production, arginine dihydrolase, urease activity, and gelatin hydrolysis. D-Glucose, L-arabinose, D-mannose, *N*-acetyl-D-glucosamine, and D-maltose are utilized as sole carbon sources; while D-mannitol, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid are not. Strain RSG-18 (=NIBRBAC000002469) was isolated from a gut of *Sebastes schlegeli* in Gwacheon-si, Gyeonggi-do, Republic of Korea.

Description of *Flavobacterium endophyticum* WW92

Cells are Gram-staining-negative, non-flagellated, and rod shaped. Colonies are opaque, round, smooth, and light yellow colored after incubation for 3 days on R2A at 25°C. In the API 20NE system, positive for esculin hydrolysis and gelatin hydrolysis; but negative for nitrate reduction, indole production, glucose acidification, arginine dihydrolase, urease activity, β-galactosidase activity, and oxidase activity. 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 are not utilized as sole carbon sources. Strain WW92 (=NIBRBAC000002550) was isolated from a freshwater sample in Changnyeong-gun, Gyeongsangnam-do, Republic of Korea.

Description of *Lacinutrix venerupis* KYW850

Cells are Gram-staining-negative, non-flagellated, and rod shaped. Colonies are opaque, round, smooth, convex, and yellow colored after incubation for 2 days on MA at 25°C. In the API 20NE system, negative for nitrate reduction, indole production, glucose acidification, arginine dihydrolase, urease activity, esculin hydrolysis, gelatin hydrolysis, β-galactosidase activity, and oxidase activity. 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 are not utilized as sole carbon sources. Strain KYW850 (=NIBRBAC000002269) was isolated from a seawater sample in Gwangyang-si, Jeollanam-do, Republic of Korea.

Description of *Mesonia oceanica* IMCC25659

Cells are Gram-staining-negative, non-flagellated, and rod shaped. Colonies are circular, convex, entire, and yellow colored after incubation for 3 days on MA at 20°C. In the API 20NE system, positive for oxidase activity; but negative for nitrate reduction, indole production, glucose acidification, arginine dihydrolase, urease activity, esculin hydrolysis, gelatin hydrolysis, and β-galactosidase activity. D-Mannose, D-maltose, and malic acid are utilized as sole carbon sources; while D-glucose, L-arabinose, D-mannitol, *N*-acetyl-D-glucosamine, potassium gluconate, capric acid, adipic acid, trisodium citrate, and phenylacetic acid are not. Strain IMCC25659 (=NIBRBAC000498556) was isolated from a plant root in Junggu, Incheon, Republic of Korea.

Description of *Chryseobacterium subflavum* BSSK-MA29

Cells are Gram-staining-negative, non-flagellated, and oval shaped. Colonies are circular, raised, glistening, and vivid yellow colored after incubation for 5 days on MA at 25°C. In the API 20NE system, positive for arginine dihydrolase, urease activity, esculin hydrolysis, gelatin hydrolysis, and β-galactosidase activity; but negative for nitrate reduction, indole production, glucose acidification, and oxidase activity. 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 are not utilized as sole carbon sources. Strain BSSK-MA29 (=NIBRBAC000506377) was isolated from a tidal flat sample in Boryeong-si, Chungcheongnam-do, Republic of Korea.

Description of *Chryseobacterium aquaeductus* JPSW-R7

Cells are Gram-staining-negative, non-flagellated, and rod shaped. Colonies are circular, convex, glistening, and light yellow colored after incubation for 3 days on R2A at 25°C. In the API 20NE system, positive for esculin hydrolysis and gelatin hydrolysis; but negative for nitrate reduction, indole production, glucose acidification, arginine dihydrolase, urease activity, β-galactosidase activity, and oxidase activity. 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 are not utilized as sole carbon sources. Strain JPSW-R7 (=NIBRBAC000509638) was isolated from a seawater sample in Buan-gun, Jeollabuk-do, Republic of Korea.

Description of *Pedobacter schmidteae* BY5

Cells are Gram-staining-negative, non-flagellated, and rod shaped. Colonies are circular, raised, entire, and yellow colored after incubation for 2 days on R2A at 30°C. In the API 20NE system, positive for nitrate reduction, esculin hydrolysis, gelatin hydrolysis, and β-galactosidase activity; but negative for indole production, glucose acidification, arginine dihydrolase, urease activity, and oxidase activity. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, and D-maltose are utilized as sole carbon sources; while potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid are not. Strain BY5 (=NIBRBAC000497881) was isolated from a soil sample in Gyeongsangbuk-do, Republic of Korea.

Description of *Cohaesibacter intestini* CAU 1516

Cells are Gram-staining-negative, flagellated, and rod shaped. Colonies are circular, convex, smooth, opaque, and cream colored after incubation for 3 days on MA at 30°C. In the API 20NE system, positive for esculin hydrolysis and β-galactosidase activity; but negative for nitrate reduction, indole production, glucose acidification, arginine dihydrolase, urease activity, gelatin hydrolysis, and oxidase activity. 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 are not utilized as sole carbon sources. Strain CAU 1516 (=NIBRBAC000502383) was isolated from a tidal flat sample in Busan, Republic of Korea.

Description of *Litorivita pollutaquae* G7-2

Cells are Gram-staining-negative, non-flagellated, and rod shaped. Colonies are circular, raised, entire, and pale yellow colored after incubation for 2 days on MA at 25°C. In the API 20NE system, positive for nitrate reduction and esculin hydrolysis; but negative for indole production, glucose acidification, arginine dihydrolase, urease activity, gelatin hydrolysis, β-galactosidase activity, and oxidase activity. 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 are not utilized as sole carbon sources. Strain G7-2 (=NIBRBAC000002485) was isolated from a tidal flat sample in Taean-gun, Chungcheongnam-do, Republic of Korea.

Description of *Sinirhodobacter huangdaonensis* SJ5-2

Cells are Gram-staining-negative, non-flagellated, and rod shaped. Colonies are circular, convex, smooth, glistening, and pink colored after incubation for 2 days on TSA at 30°C. In the API 20NE system, positive for nitrate reduction, glucose acidification, urease activity, esculin hydrolysis, gelatin hydrolysis, β-galactosidase activity, and oxidase activity; but negative for indole production and arginine dihydrolase. D-Glucose, L-arabinose, D-maltose, trisodium citrate and phenylacetic acid are utilized as sole carbon sources; while D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, potassium gluconate, capric acid, adipic acid, and malic acid are not. Strain SJ5-2 (=NIBRBAC000502467) was isolated from a sludge sample in Suwon-si, Gyeonggi-do, Republic of Korea.

Description of *Sinirhodobacter huangdaonensis* H1Y

Cells are Gram-staining-negative, non-flagellated, and rod or oval shaped. Colonies are circular, raised, entire, glistening, and white colored after incubation for 3 days on R2A at 30°C. In the API 20NE system, positive for urease activity, esculin hydrolysis and gelatin hydrolysis; but negative for nitrate reduction, indole production, glucose acidification, arginine dihydrolase, β-galactosidase activity, and oxidase activity. 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 are not utilized as sole carbon sources. Strain H1Y (=NIBRBAC000498408) was isolated from a sludge sample in Busan, Republic of Korea.

Description of *Thioclava sediminum* 6-2

Cells are Gram-staining-negative, flagellated, and rod shaped. Colonies are circular, raised, entire, and pale yellow colored after incubation for 3 days on MA at 25°C. In the API 20NE system, positive for nitrate reduction, urease activity, esculin hydrolysis, and β-galactosidase

activity; but negative for indole production, glucose acidification, arginine dihydrolase, gelatin hydrolysis, and oxidase activity. Malic acid is utilized as a sole carbon source; while D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, trisodium citrate, and phenylacetic acid are not. Strain 6-2 (=NIBRBAC 000002501) was isolated from a tidal flat sample in Taean-gun, Chungcheongnam-do, Republic of Korea.

Description of *Shimia thalassica* CAU 1190

Cells are Gram-staining-negative, non-flagellated, and rod shaped. Colonies are circular, convex, and cream colored after incubation for 3 days on MA at 30°C. In the API 20NE system, positive for arginine dihydrolase, urease activity and esculin hydrolysis; but negative for nitrate reduction, indole production, glucose acidification, gelatin hydrolysis, β-galactosidase activity, and oxidase activity. 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 are not utilized as sole carbon sources. Strain CAU 1190 (=NIBRBAC000498495) was isolated from a soil sample in Jeju-si, Jeju-do, Republic of Korea.

Description of *Oceanibaculum nanhaiense* Gri0127

Cells are Gram-staining-negative, flagellated, and rod shaped. Colonies are circular, convex, smooth, and cream colored after incubation for 3 days on MA at 30°C. In the API 20NE system, positive for nitrate reduction and urease activity; but negative for indole production, glucose acidification, arginine dihydrolase, esculin hydrolysis, gelatin hydrolysis, β-galactosidase activity, and oxidase activity. 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 are not utilized as sole carbon sources. Strain Gri0127 (=NIBRBAC000502472) was isolated from an algae of seawater in Taean-gun, Chungcheongnam-do, Republic of Korea.

Description of *Croceicoccus pelagius* J2

Cells are Gram-staining-negative, non-flagellated, and coccoid shaped. Colonies are opaque, round, smooth, convex, and light yellow colored after incubation for 3 days on MA at 25°C. In the API 20NE system, negative for nitrate reduction, indole production, glucose acidification, arginine dihydrolase, urease activity, esculin hydrolysis, gelatin hydrolysis, β-galactosidase activity, and oxidase activity. 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 are not utilized as sole carbon sources. Strain J2 (=NIBRBAC000002260) was isolated from a seawater sample in Gwangyang-si, Jeollanam-do, Republic of Korea.

Description of *Novosphingobium ovatum* CAU 1464

Cells are Gram-staining-negative, flagellated, and rod shaped. Colonies are circular, convex, smooth, opaque, and yellow colored after incubation for 3 days on R2A at 30°C. In the API 20NE system, positive for esculin hydrolysis and oxidase activity; but negative for nitrate reduction, indole production, glucose acidification, arginine dihydrolase, urease activity, gelatin hydrolysis, and β-galactosidase activity. D-Glucose, L-arabinose, and D-maltose are utilized as sole carbon sources; while D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid are not. Strain CAU 1464 (=NIBRBAC000501261) was isolated from a dead mine water sample in Gyeonggi-do, Republic of Korea.

Description of *Vitreoscilla massiliensis* NSG-13

Cells are Gram-staining-negative, non-flagellated, and rod shaped. Colonies are radial, convex, and cream colored after incubation for 3 days on NA at 20°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, and β-galactosidase activity. Capric acid is utilized as a sole carbon source; while D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, potassium gluconate, adipic acid, malic acid, trisodium citrate, and phenylacetic acid are not. Strain NSG-13 (=NIBRBAC000002465) was isolated from a gut sample of *Sebastes schlegeli* in Gwacheon-si, Gyeonggi-do, Republic of Korea.

Description of *Rheinheimera coerulea* SyP7R

Cells are Gram-staining-negative, flagellated, and rod shaped. Colonies are circular and ivory colored after incubation for 3 days on R2A at 30°C. In the API 20NE system, positive for nitrate reduction and esculin hydrolysis; but negative for indole production, glucose acidification, arginine dihydrolase, urease activity, gelatin hydrolysis, β-galactosidase activity, and oxidase activity. 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 are not utilized as sole carbon sources. Strain SyP7R (=NIBRBAC000502479) was isolated from an algae of seawater in Gyeongsangbuk-do, Republic of Korea.

Description of *Microbulbifer okhotskensis* TATF-M118

Cells are Gram-staining-negative, non-flagellated, and rod shaped. Colonies are circular, convex, glistening, and pale orange colored after incubation for 3 days on MA at 25°C. In the API 20NE system, positive for nitrate reduction, esculin hydrolysis and gelatin hydrolysis; but negative for indole production, glucose acidification, arginine dihydrolase, urease activity, β-galactosidase activity, and oxidase activity. 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 are not utilized as sole carbon sources. Strain TATF-M118 (=NIBRBAC 000508890) was isolated from a tidal flat sample in Taean-gun, Chungcheongnam-do, Republic of Korea.

Description of *Rahnella inusitata* RSG-8

Cells are Gram-staining-negative, non-flagellated, and rod shaped. Colonies are circular, convex, and white colored after incubation for 3 days on R2A at 20°C. In the API 20NE system, positive for nitrate reduction, glucose acidification, esculin hydrolysis, gelatin hydrolysis, and β-galactosidase activity; but negative for indole production, arginine dihydrolase, urease activity, and oxidase activity. D-Glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, potassium gluconate, malic acid, and trisodium citrate are utilized as sole carbon sources, while capric acid, adipic acid, and phenylacetic acid are not. Strain RSG-8 (=NIBR BAC000002468) was isolated from a gut sample of *Sebastes schlegeli* in Gwacheon-si, Gyeonggi-do, Republic of Korea.

***Description of Dyella halodurans* CAU 1486**

Cells are Gram-staining-negative, non-flagellated, and rod shaped. Colonies are circular, convex, smooth, and yellow colored after incubation for 3 days on GYE at 30°C. In the API 20NE system, positive for nitrate reduction and arginine dihydrolase; but negative for indole production, glucose acidification, urease activity, esculin hydrolysis, gelatin hydrolysis, β-galactosidase activity, and oxidase activity, D-glucose is utilized as a sole carbon source; while 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 are not. Strain CAU 1486 (=NIBR BAC000502380) was isolated from a tidal flat sample in Yeosu-si, Jeollanam-do, Republic of Korea.

Description of *Halomonas litopenaei* BSW10-2

Cells are Gram-staining-negative, non-flagellated, and rod shaped. Colonies are circular, raised, entire, and pale yellow colored after incubation for 2 days on MA at 25°C. In the API 20NE system, positive for esculin hydrolysis, β-galactosidase activity, and oxidase activity; but negative for nitrate reduction, indole production, glucose acidification, arginine dihydrolase, urease activity, and gelatin hydrolysis. 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 are not utilized as sole carbon sources. Strain BSW10-2 (=NIBRBAC000002768) was isolated from a tidal flat sample in Taean-gun, Chungcheongnam-do, Republic of Korea.

Description of *Nitrincola schmidtii* KA17

Cells are Gram-staining-negative, non-flagellated, and rod shaped. Colonies are opaque, round, smooth, convex, and white colored after incubation for 3 days on MA at 25°C. In the API 20NE system, negative for nitrate reduction, indole production, glucose acidification, arginine dihydrolase, urease activity, esculin hydrolysis, gelatin hydrolysis, β-galactosidase activity, and oxidase activity. 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 are utilized as sole carbon sources. Strain KA17 (=NIBRBAC000002263) was isolated from a seawater sample in Gwangyang-si, Jeollanam-do, Republic of Korea.

Description of *Spartinivicinus ruber* CAU 1596

Cells are Gram-staining-negative, flagellated, and rod shaped. Colonies are circular, convex, rough, opaque, and cream colored after incubation for 3 days on MA at 30°C. In the API 20NE system, positive for esculin hydrolysis and gelatin hydrolysis; but negative for nitrate reduction, indole production, glucose acidification, arginine dihydrolase, urease activity, β-galactosidase activity, and oxidase activity. 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 are not utilized as sole carbon sources. Strain CAU 1596 (=NIBRBAC000503246) was isolated from a marine sand sample in Jeju-si, Jeju-do, Republic of Korea.

Description of *Marinobacter shengliensis* subsp. *alexandrii* SAG5

Cells are Gram-staining-negative, flagellated, and rod shaped. Colonies are circular, raised, entire, and pale yellow colored after incubation for 2 days on MA at 30°C. In the API 20NE system, negative for nitrate reduction, indole production, glucose acidification, arginine dihydro-

lase, urease activity, esculin hydrolysis, gelatin hydrolysis, β-galactosidase activity, and oxidase activity. D-Glucose is utilized as a sole carbon source, but 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 are not. Strain SAG5 (=NIBRBAC000497878) was isolated from an algae of seawater in Taean-gun, Chungcheongnam-do, Republic of Korea.

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