

# Twenty-five unrecorded bacterial species of the Republic of Korea belonging to the phylum *Actinomycetota* discovered during surveys in 2021

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We isolated and identified 25 unrecorded bacterial species belonging to the phylum *Actinomycetota* found in the Republic of Korea. Sequence comparison of 16S rRNA was performed using the NCBI BLAST and EzBioCloud database to identify 25 species, which had a 16S rRNA gene sequence similarity of >98.8% and were allocated as unrecorded species in the Republic of Korea. Among the 25 unrecorded bacterial strains, *Streptomyces* was the most common with nine species, followed by *Leifsonia* with two species. *Isoptricola*, *Nocardioides*, *Dermaococcus*, *Sinomonas*, *Patulibacter*, *Marmoricola*, *Allobranchiibius*, *Aldersonia*, *Actinokineospora*, *Agromyces*, *Aeromicrobium*, *Cellulomonas*, and *Gordonia* with one species each were also found. Twenty-five unrecorded species were excavated in various environments, such as tidal flats, ferns, soil, pine cones, moss, mud, wetlands, and plants. These isolates were characterized on the basis of their phylogenetic, biochemical properties, and morphological data, and species descriptions were provided.

Keywords: 16S rRNA gene, *Actinomycetota*, phylogenetic analysis, polyphasic approach, unrecorded species

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## INTRODUCTION

*Actinomycetota*, one of the major phyla in the domain Bacteria, is characterized by a high G + C content and Gram-positive staining (Ludwig *et al.*, 2012). Many *Actinomycetota* members have a mycelial lifestyle and are characterized by complex differentiation (Barka *et al.*, 2016). At the time of writing this manuscript, *Actinomycetota* comprises six classes with validly published names based on their 16S rRNA gene sequences (<https://lpsn.dsmz.de/phylum/actinomycetota>): *Acidimicrobiia*, *Actinomycetes*, *Coriobacteriia*, *Nitriliruptora*, *Rubrobacteria*, and *Thermoleophilina*. It is also known as the largest group of prokaryotes (Bhatti *et al.*, 2017). *Actinomycetota* includes strains that produce useful secondary products, such as antibiotics, anticancer drugs, and antivirals (Silva

*et al.*, 2020). Since this phylum is a source of novel natural bioactive substances, identifying strains and understanding their phylogenetic relationships are of great industrial importance (Anandan *et al.*, 2016). For instance, *Streptomyces* species are known producers of many natural products such as caboxamycin B, anthracycline antibiotic daunorubicin, streptovaricin, and metatricycloene (Jeong *et al.*, 2006; Hohmann *et al.*, 2009; Lucas *et al.*, 2013; Iqbal *et al.*, 2016; Liu *et al.*, 2017; Sarmiento-Vizcaíno *et al.*, 2022). They inhabit various places, such as soil, ocean, and plants, and they account for more than 70–80% of secondary metabolites (Manivasagan *et al.*, 2014). Therefore, studies on *Actinomycetota* can help address concerns on resistant pathogens and serve as a basis for discovering new drugs for diseases. In this study, we reported and described 25 unreported species that belonged

to *Actinomycetota* and were isolated from various environmental sources in the Republic of Korea in 2021.

## MATERIALS AND METHODS

Twenty-five bacterial strains were collected from diverse environmental samples, such as soil, wetland, plant, and pine cone. Each sample was processed apart; spread on Reasoner's 2A agar (R2A; MB cell), marine agar 2216 (MA; MB cell), glucose yeast extract agar (GYEA; MB cell) plates, and incubated at 25–30°C for 3–5 days (Table 1). The strain no. NIBR ID, 16S rRNA gene sequence similarity, and incubation conditions are summarized in Table 1. All purified strains supplemented with glycerol (25% v/v) in the optimal medium were stored at –80°C, and additionally, lyophilized ampoules were prepared and stored. Cell morphology was observed using a transmission electron microscope or a scanning electron microscope. Gram reaction was determined using the non-staining KOH lysis method (3% KOH; Bucks, 1982). Biochemical features were tested using API 20NE (BioMérieux) in accordance with the manufacturer's instructions.

The 16S rRNA gene was amplified using the universal bacterial primer sets 518F (5'-CCA GCA GCC GCG GTA ATA C-3') and 805R (3'-GAC TAC CAG GGT ATC TAA TC-5'; Chhetri *et al.*, 2021). The 16S rRNA gene sequences were contrasted with the sequences of bacterial type strains listed in the EzBioCloud database (<http://ezbiocloud.net>; Yoon *et al.*, 2017). Phylogenetic placements were designed using neighbor-joining (NJ; Saitou and Nei, 1987), maximum likelihood (ML; Guindon and Gascuel, 2003), and maximum parsimony (MP; Fitch, 1971) methods by using MEGA X software (Kumar *et al.*, 2018). ML and NJ were used to construct phylogenetic trees via bootstrap analysis with 1000 replications following Kimura's two-parameter method (Felsenstein, 1985). A min-mini heuristic was applied to the MP to compare with the NJ and ML phylogenetic trees.

## RESULTS AND DISCUSSION

Twenty-five bacterial strains were isolated (Table 1). They represented 21 unrecorded species belonging to 17 genera in 13 families in the Republic of Korea. Nine species were assigned to *Streptomycetaceae*, while three species each were assigned to *Nocardioidaceae* and *Microbacteriaceae*. Two species each were assigned to *Derma-coccaceae*. One species was assigned to each of the following families: *Promicromonosporaceae*, *Micrococca-ceae*, *Patulibacteraceae*, *Pseudonocardiaceae*, *Thermo-monosporaceae*, *Cellulomonadaceae*, and *Gordoniaceae*. At the genus level, *Streptomyces* (nine species) was pre-

dominant. *Leifsonia* had two species, and each of the remaining genera had single species (Table 1). The phylogenetic relationship between isolated strains and closely related species is shown in Fig. 1, and the transmission electron microscopy images of the isolates are presented in Fig. 2. The detailed descriptions of each unrecorded species are given below.

### Description of *Isoptericola halotolerans* 14MAJJD-20

Cells are Gram-stain-positive, non-flagellated, and ovoid or rod shaped. When grown on MA plates at 25°C for 5 days, colonies are light greenish yellow, circular, glistening, and slightly convex. In the API 20NE test, the cells showed positive results for nitrate reaction; esculin, gelatin, and  $\beta$ -galactosidase hydrolysis; and D-glucose, L-arabinose, D-mannose, D-mannitol, D-maltose, and potassium glutamate assimilation. Conversely, they had negative results for indole production; D-glucose fermentation; arginine and urea hydrolysis; and *N*-acetyl- $\beta$ -glucosamine, caprate, adipate, malate, trisodium citrate, and phenylacetic acid assimilation. Strain 14MAJJD-20 (NIBRBAC 000508916) was isolated from a tidal flat sample in Jangheung-eup, Jeollanam-do, Republic of Korea. The Gen Bank accession number of the 16S rRNA gene sequence of strain 14MAJJD-20 is OR226650.

### Description of *Nocardioides oleivorans* HMF4597

Cells are Gram-stain-positive, non-flagellated, and irregular rod shaped. When grown on R2A plates at 30°C for 3 days, colonies are pale yellow, circular, convex, and smooth. In the API 20NE test, the cells showed positive results for esculin, gelatin; and  $\beta$ -galactosidase hydrolysis, D-glucose, D-mannitol, D-mannose, *N*-acetyl- $\beta$ -glucosamine, D-maltose, potassium glutamate, malate, and phenylacetic acid assimilation. Conversely, they had negative results for nitrate reaction; indole production; D-glucose fermentation; arginine and urea hydrolysis; D-glucose fermentation; and caprate, L-arabinose, adipate, and trisodium citrate assimilation. Strain HMF4597 (NIBRBAC 000508751) was isolated from bracken on Jirisan Mountain, Jeollanam-do, Republic of Korea. The GenBank accession number of the 16S rRNA gene sequence of strain HMF4597 is OL347553.

### Description of *Derma-coccus abyssi* HMG2333

Cells are Gram-stain-positive, non-flagellated, and coccoid shaped. When grown on R2A plates at 30°C for 3 days, colonies are yellow, convex, circular, and smooth. In the API 20NE test, the cells showed positive results for gelatin hydrolysis; and D-glucose, D-maltose, potassium glutamate, and malate assimilation. Conversely, they had negative results for nitrate reaction; arginine, urea,

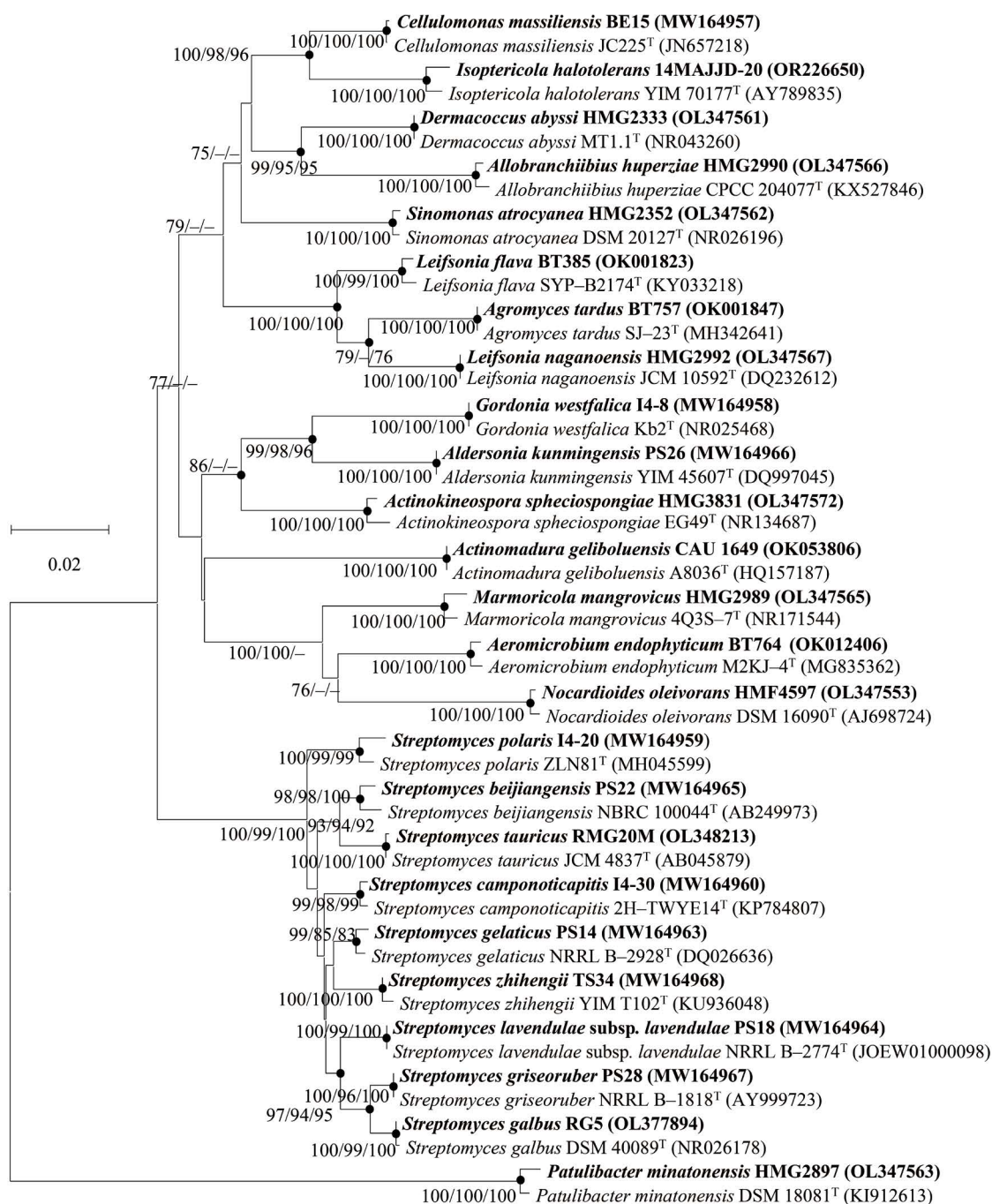
**Table 1.** List of isolated strains belonging to the phylum Actinomycetota and their taxonomic affiliations.

Affiliation	Strain ID	NIBR <sup>a</sup> ID	Identification	Similarity (%)	Isolation source	Location of collecting sample (GPS)	Medium <sup>b</sup>	Culture conditions
<i>Promicromonosporaceae</i>	14MAJJD-20	NIBRBAC000508916	<i>Isosperitcola halotolerans</i>	99.13	Tidal flat	Jangheung, Jeollanam-do (34°36'49.2"N 127°00'41.7"E)	MA	25°C, 5 days
<i>Cellulomonadaceae</i>	BE15	NIBRBAC000508776	<i>Cellulomonas massiliensis</i>	99.79	Wetland	Gangdong-gu, Seoul (37°34'02.2"N 127°08'59.1"E)	R2A	30°C, 3 days
<i>Dermacoccaceae</i>	HMG2333	NIBRBAC000508759	<i>Dermacoccus abyssii</i>	99.86	Soil	Hankuk University of Foreign Studies, Gyeonggi-do (37°20'19.4"N 127°15'58.0"E)	R2A	30°C, 3 days
	HMG2990	NIBRBAC000508764	<i>Allobranchiobius huperziae</i>	99.52	Pine cone	Hankuk University of Foreign Studies, Gyeonggi-do (37°20'19.8"N 127°16'20.4"E)	R2A	30°C, 3 days
	BT757	NIBRBAC000508877	<i>Agromyces tardus</i>	100	Soil	Jocheon-eup, Jeju-do (33°26'05"N 126°41'20"E)	R2A	25°C, 3 days
<i>Microbacteriaceae</i>	HMG2992	NIBRBAC000508765	<i>Leifsonia naganoensis</i>	100	Pine cone	Hankuk University of Foreign Studies, Gyeonggi-do (37°20'19.8"N 127°16'20.4"E)	R2A	30°C, 3 days
	BT385	NIBRBAC000508869	<i>Leifsonia flava</i>	98.82	Soil	Gyeongju-si, Gyeongsangbuk-do (35°48'39.3"N 129°18'36.8"E)	R2A	25°C, 3 days
<i>Micrococcaceae</i>	HMG2352	NIBRBAC000508760	<i>Sinomonas atrocyanea</i>	99.65	Soil	Hankuk University of Foreign Studies, Gyeonggi-do (37°20'19.4"N 127°15'58.0"E)	R2A	30°C, 3 days
<i>Gordoniaceae</i>	I4-8	NIBRBAC000508777	<i>Gordonia wesfalica</i>	100	Wetland	Gangdong-gu, Seoul (37°34'02.2"N 127°08'59.1"E)	R2A	30°C, 3 days
<i>Nocardiaceae</i>	PS26	NIBRBAC000508785	<i>Aldersonia kunningensis</i>	100	Wetland	Gangdong-gu, Seoul (37°34'02.2"N 127°08'59.1"E)	R2A	30°C, 3 days
	HMF4597	NIBRBAC000508751	<i>Nocardioides oleivorans</i>	99.65	Bracken	Sandong-myeon, Jeollanam-do (35°18'19.2"N 127°30'41.3"E)	R2A	30°C, 3 days
<i>Nocardioideae</i>	HMG2989	NIBRBAC000508763	<i>Marmoricola mangrovicus</i>	99.1	Pine cone	Hankuk University of Foreign Studies, Gyeonggi-do (37°20'19.8"N 127°16'20.4"E)	R2A	30°C, 3 days
	BT764	NIBRBAC000508880	<i>Aeromicrobium endophyticum</i>	99.58	Soil	Jocheon-eup, Jeju-do (33°26'05"N 126°41'20"E)	R2A	25°C, 3 days
<i>Pseudonocardiaceae</i>	HMG3831	NIBRBAC000508770	<i>Actinokineospora sphectospongiae</i>	99.03	Moss	Sangdang-gu, Chungcheongbuk-do (36°37'39.3"N 127°40'14.7"E)	R2A	30°C, 3 days
<i>Pattulibacteraceae</i>	HMG2897	NIBRBAC000508761	<i>Pattulibacter minatonensis</i>	99.04	Pine cone	Jununjin beach, Gangwon-do (37°54'31.0"N 128°49'15.0"E)	R2A	30°C, 3 days

Table 1. Continued.

Affiliation	Strain ID	NIBR <sup>a</sup> ID	Identification	Similarity (%)	Isolation source	Location of collecting sample (GPS)	Medium <sup>b</sup>	Culture conditions
	I4-20	NIBRBAC000508778	<i>Streptomyces polaris</i>	99.03	Wetland	Gangdong-gu, Seoul (37°34'02.2"N 127°08'59.1"E)	R2A	30°C, 3 days
	I4-30	NIBRBAC000508779	<i>Streptomyces camponotocapitis</i>	99.65	Wetland	Gangdong-gu, Seoul (37°34'02.2"N 127°08'59.1"E)	R2A	30°C, 3 days
	PS14	NIBRBAC000508782	<i>Streptomyces gelaticus</i>	99.59	Wetland	Gangdong-gu, Seoul (37°34'02.2"N 127°08'59.1"E)	R2A	30°C, 3 days
	PS18	NIBRBAC000508783	<i>Streptomyces lavendulae</i> subsp. <i>lavendulae</i>	100	Wetland	Gangdong-gu, Seoul (37°34'02.2"N 127°08'59.1"E)	R2A	30°C, 3 days
<i>Streptomycetaceae</i>	PS22	NIBRBAC000508784	<i>Streptomyces beijiagensis</i>	99.03	Wetland	Gangdong-gu, Seoul (37°34'02.2"N 127°08'59.1"E)	R2A	30°C, 3 days
	PS28	NIBRBAC000508786	<i>Streptomyces griseoruber</i>	100	Wetland	Gangdong-gu, Seoul (37°34'02.2"N 127°08'59.1"E)	R2A	30°C, 3 days
	TS34	NIBRBAC000508787	<i>Streptomyces zihhengii</i>	99.79	Wetland	Gangdong-gu, Seoul (37°34'02.2"N 127°08'59.1"E)	R2A	30°C, 3 days
	RMG20M	NIBRBAC000508930	<i>Streptomyces tauricus</i>	99.93	Soil	Siheung-si, Gyeonggi-do (37°23'01.8"N 126°47'02.7"E)	R2A	28°C, 3 days
	RG5	NIBRBAC000508932	<i>Streptomyces galbus</i>	99.93	Plant	Ilсандong-gu, Gyeonggi-do (37°40'26.4"N 126°48'20.88"E)	R2A	30°C, 3 days
<i>Thermomonosporaceae</i>	CAU 1649	NIBRBAC000508831	<i>Actinomadura getiboluensis</i>	100	Mud	Samsan-myeon, Incheon (37°39'09.6"N 126°19'49.6"E)	GYEA	30°C, 3-5 days

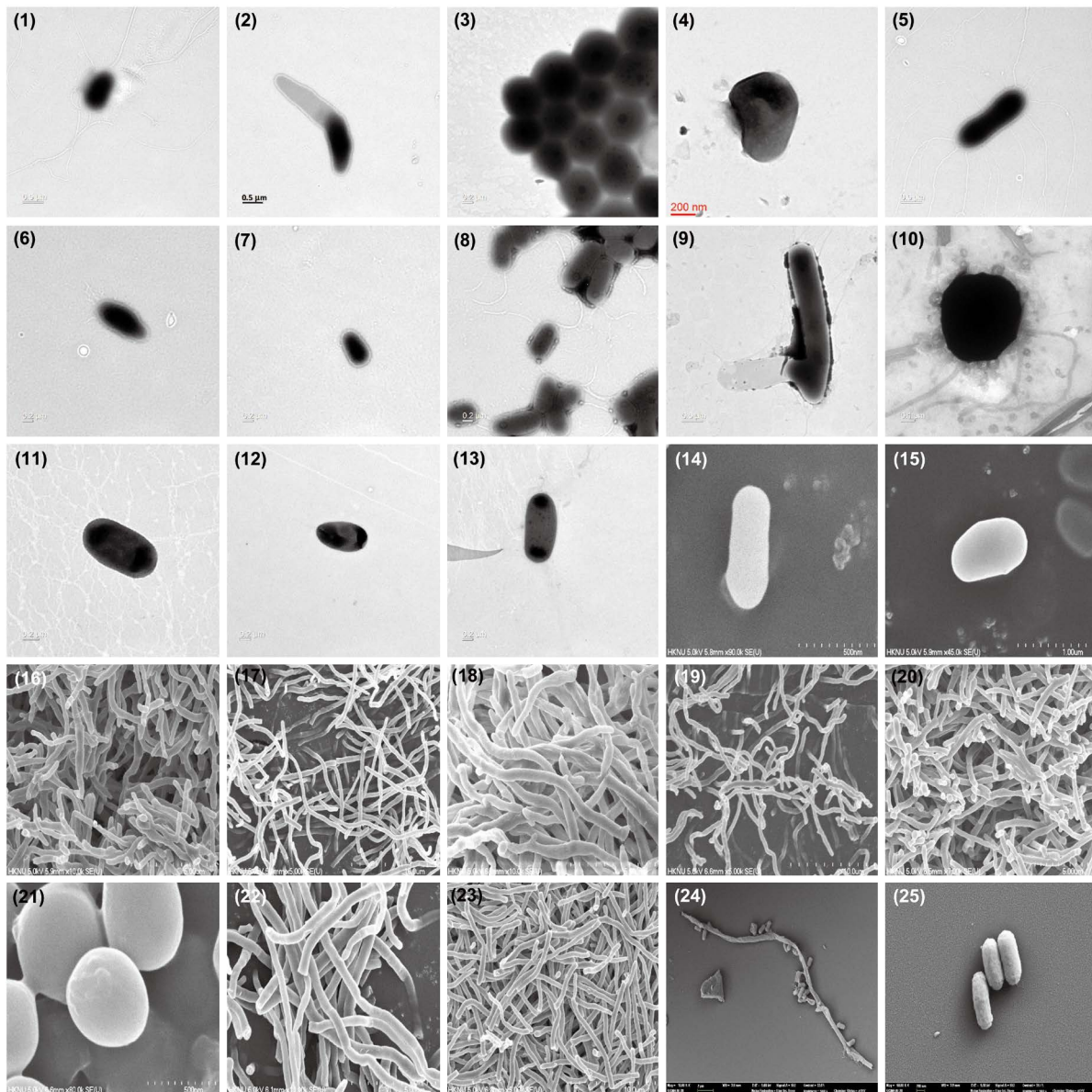
<sup>a</sup>National Institute of Biological Resources.<sup>b</sup>MA, marine agar; R2A, Reasoner's 2A agar; GYEA, glucose yeast extract agar



**Fig. 1.** Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences showing the relationships between 25 strains isolated and their closely related species from the orders Cellulomonadales, Dermatophilales, Microbacteriales, Micrococcales, Propionibacteriales, Pseudonocardiales, Solirubrobacterales, Streptomycetales, and Streptosporangiales of the phylum Actinomycetota. Dots indicate that the nodes also recovered in the maximum-likelihood and maximum-parsimony trees, and bootstrap values > 70% (NJ/ML/MP) are shown at branching points. Bar, 0.02 substitutions per nucleotide position.

esculin, and  $\beta$ -galactosidase hydrolysis; indole production; D-glucose fermentation; and L-arabinose, N-acetyl- $\beta$ -glucosamine, D-mannose, D-mannitol, caprate, adipate, trisodium citrate, and phenylacetic acid assimilation. Strain HMG2333 (NIBRBAC000508759) was isolated from soil

at Hankuk University of Foreign Studies, Yongin-si, Republic of Korea. The GenBank accession number of the 16S rRNA gene sequence of strain HMG2333 is OL347561.



**Fig. 2.** Transmission electron micrographs of scanning electron micrographs of cells of the strains isolated in the study. Strains: 1, 14MAJJD-20; 2, HMF4597; 3, HMG2333; 4, HMG2352; 5, HMG2897; 6, HMG2989; 7, HMG2990; 8, HMG2992; 9, HMG3831; 10, CAU 1649; 11, BT757; 12, BT385; 13, BT764; 14, BE15; 15, I4-8; 16, I4-10; 17, I4-30; 18, PS14; 19, PS18; 20, PS22; 21, PS26; 22, PS28; 23, TS34; 24, RMG20M; 25, RG5.

#### Description of *Sinomonas atrocyanea* HMG2352

Cells are Gram-stain-positive, motile with flagella, and rod shaped. When grown on R2A plates at 30°C for 3 days, colonies are pale yellow, circular, convex, and smooth. In the API 20NE test, the cells showed positive results for nitrate reaction; urea, esculin, gelatin, and  $\beta$ -galactosidase hydrolysis; and D-glucose, D-mannose, D-mannitol, N-acetyl- $\beta$ -glucosamine, D-maltose, potassium glutamate, caprate, malate, trisodium citrate, and phenylacetic acid assimilation. Conversely, they had negative results for indole production, D-glucose fermentation; arginine hydro-

lysis; and L-arabinose and adipate assimilation. Strain HMG2352 (NIBRBAC000508760) was isolated from soil at Hankuk University of Foreign Studies, Cheoin-gu, Yongin-si, Republic of Korea. The GenBank accession number of the 16S rRNA gene sequence of strain HMG2352 is OL347562.

#### Description of *Patulibacter minatonensis* HMG2897

Cells are Gram-stain-positive, motile with flagella, and rod shaped. When grown on R2A plates at 30°C for 3 days, colonies are white, circular, convex, and smooth. In

the API 20NE test, the cells showed positive results for gelatin hydrolysis and D-glucose and D-mannose assimilation. Conversely, they had negative results for nitrate reaction; indole production; D-glucose fermentation; arginine, urea, esculin, and  $\beta$ -galactosidase hydrolysis; and L-arabinose, D-mannitol, *N*-acetyl- $\beta$ -glucosamine, D-maltose, potassium glutamate, caprate, adipate, malate, trisodium citrate, and phenylacetic acid assimilation. Strain HMG2897 (NIBRBAC000508761) was isolated from a pine cone at Jumunjin Beach, Gangneung-si, Republic of Korea. The GenBank accession number of the 16S rRNA gene sequence of strain HMG2897 is OL347563.

#### **Description of *Marmoricola mangrovicus* HMG2989**

Cells are Gram-stain-positive, non-flagellated, and rod shaped. When grown on R2A plates at 30°C for 3 days, colonies are cream colored, circular, convex, and smooth. In the API 20NE test, the cells showed positive results for gelatin hydrolysis; and D-glucose, D-mannose, L-arabinose, D-mannitol, *N*-acetyl- $\beta$ -glucosamine, potassium glutamate, and phenylacetic acid assimilation. Conversely, they had negative results for nitrate reaction; indole production; D-glucose fermentation; arginine, urea, esculin, and  $\beta$ -galactosidase hydrolysis; and D-maltose, caprate, adipate, malate, and trisodium citrate assimilation. Strain HMG2989 (NIBRBAC000508763) was isolated from a pine cone at Hankuk University of Foreign Studies, Cheoin-gu, Yongin-si, Republic of Korea. The GenBank accession number of the 16S rRNA gene sequence of strain HMG 2989 is OL347565.

#### **Description of *Allobranchiobius huperziae* HMG2990**

Cells are Gram-stain-positive, non-flagellated, and rod shaped. When grown on R2A plates at 30°C for 3 days, colonies are yellow, circular, convex, and smooth. In the API 20NE test, the cells showed positive results for urea and gelatin hydrolysis and D-glucose, D-mannose, D-mannitol, and D-maltose assimilation. Conversely, they had negative results for nitrate reaction; indole production; D-glucose fermentation; arginine, esculin, and  $\beta$ -galactosidase hydrolysis; and L-arabinose, *N*-acetyl- $\beta$ -glucosamine, potassium glutamate, caprate, adipate, malate, trisodium citrate, and phenylacetic acid assimilation. Strain HMG 2990 (NIBRBAC000508764) was isolated from a pine cone at Hankuk University of Foreign Studies, Cheoin-gu, Yongin-si, Republic of Korea. The GenBank accession number of the 16S rRNA gene sequence of strain HMG 2990 is OL347566.

#### **Description of *Leifsonia naganoensis* HMG2992**

Cells are Gram-stain-positive, motile with flagella, and rod shaped. When grown on R2A plates at 30°C for 3 days, colonies are cream colored, circular, convex, and

smooth. In the API 20NE test, the cells showed positive results for the fermentation of D-glucose; hydrolysis of esculin and  $\beta$ -galactosidase; assimilation of D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl- $\beta$ -glucosamine, D-maltose, potassium glutamate, and trisodium citrate. Conversely, they had negative results for the nitrate reaction; production of indole; hydrolysis of arginine, urea, and gelatin; assimilation of caprate, adipate, malate, and phenylacetic acid. Strain HMG2992 (NIBRBAC000508765) was isolated from the pine cone, at Hankuk University of Foreign Studies, Cheoin-gu, Yongin-si, Republic of Korea. The GenBank accession number of the 16S rRNA gene sequence of strain HMG2992 is OL347567.

#### **Description of *Actinokineospora spheciospongiae* HMG3831**

Cells are Gram-stain-positive, non-flagellated, and rod shaped arthrospores. When grown on R2A plates at 30°C for 3 days, colonies are white, circular, umbonate, and mycelium penetrated. In the API 20NE test, the cells showed positive results for the hydrolysis of urea, esculin, and gelatin; and the assimilation of D-glucose, D-mannitol, D-maltose, malate, and phenylacetic acid. Conversely, they had negative results for nitrate reaction; indole production; D-glucose fermentation; arginine and  $\beta$ -galactosidase hydrolysis; and L-arabinose, D-mannose, *N*-acetyl- $\beta$ -glucosamine, caprate, adipate, potassium glutamate, and trisodium citrate assimilation. Strain HMG3831 (NIBRBAC000508770) was isolated from a moss on Midongsan Mountain, Sangdang-gu, Cheongju-si, Republic of Korea. The GenBank accession number of the 16S rRNA gene sequence of strain HMG3831 is OL347572.

#### **Description of *Actinomadura geliboluensis* CAU 1649**

Cells are Gram-stain-positive, non-flagellated, and rod shaped. When grown on GYE agar plates at 30°C for 3–5 days, colonies are white, circular, entire, convex, rough, and translucent. In the API 20NE test, the cells showed positive results for the hydrolysis of esculin; and the assimilation of D-glucose, *N*-acetyl- $\beta$ -glucosamine, D-maltose, potassium glutamate, and adipate. Conversely, they had negative results for nitrate reaction; indole production; D-glucose fermentation; arginine, urea, gelatin, and  $\beta$ -galactosidase hydrolysis; and L-arabinose, D-mannose, D-mannitol, caprate, malate, trisodium citrate, and phenylacetic acid assimilation. Strain CAU 1649 (NIBRBAC000508831) was isolated from mud in Seokmodo Island, Ganghwa-gun, Incheon, Republic of Korea. The GenBank accession number of the 16S rRNA gene sequence of strain CAU 1649 is OK053806.

#### **Description of *Agromyces tardus* BT757**

Cells are Gram-stain-positive, non-flagellated, and rod

shaped. When grown on R2A plates at 25°C for 3 days, colonies are yellow, circular, convex, and glistening. In the API 20NE test, the cells showed positive results for esculin and  $\beta$ -galactosidase hydrolysis. Conversely, they had negative results for nitrate reaction; indole production; D-glucose fermentation; arginine, urea, and gelatin hydrolysis; and D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl- $\beta$ -glucosamine, D-maltose, potassium glutamate, caprate, adipate, malate, trisodium citrate, and phenylacetic acid assimilation. Strain BT757 (NIBRBAC000508877) was isolated from soil in Jeju-si, Jeju-do, Republic of Korea. The GenBank accession number of the 16S rRNA gene sequence of strain BT757 is OK001847.

#### **Description of *Leifsonia flava* BT385**

Cells are Gram-stain-positive, non-flagellated, and rod shaped. When grown on R2A plates at 25°C for 3 days, colonies are yellow and smooth. In the API 20NE test, the cells showed positive results for esculin and  $\beta$ -galactosidase hydrolysis. Conversely, they had negative results for nitrate reaction; indole production; D-glucose fermentation; arginine, urea, and gelatin hydrolysis; D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl- $\beta$ -glucosamine, D-maltose, potassium glutamate, caprate, adipate, malate, trisodium citrate, and phenylacetic acid assimilation. Strain BT385 (NIBRBAC000508869) was isolated from soil at Gyeongju National Park, Gyeongju-si, Republic of Korea. The GenBank accession number of the 16S rRNA gene sequence of strain BT385 is OK001823.

#### **Description of *Aeromicrobium endophyticum* BT764**

Cells are Gram-stain-positive, non-flagellated, and rod shaped. When grown on R2A plates at 25°C for 3 days, colonies are white, circular, convex, and glistening. In the API 20NE test, the cells showed positive results for indole production and esculin hydrolysis. Conversely, they had negative results for nitrate reaction; D-glucose fermentation; arginine, urea, gelatin, and  $\beta$ -galactosidase hydrolysis; and D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl- $\beta$ -glucosamine, D-maltose, potassium glutamate, caprate, adipate, malate, trisodium citrate, and phenylacetic acid assimilation. Strain BT764 (NIBRBAC000508880) was isolated from soil in Jeju-si, Jeju-do, Republic of Korea. The GenBank accession number of the 16S rRNA gene sequence of strain BT764 is OK012406.

#### **Description of *Cellulomonas massiliensis* BE15**

Cells are Gram-stain-positive, aerobic, non-flagellated, and rod shaped. When grown on R2A plates at 30°C for 3 days, colonies are pale yellow, round, entire, and raised. In the API 20NE test, the cells showed positive results for nitrate reaction; D-glucose fermentation; esculin and  $\beta$ -gal-

actosidase hydrolysis; and D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl- $\beta$ -glucosamine, D-maltose, and potassium glutamate assimilation. Conversely, they had negative results for indole production; arginine, urea, and gelatin hydrolysis; and caprate, adipate, malate, trisodium citrate, and phenylacetic acid assimilation. Strain BF15 (NIBRBAC000508776) was isolated from Godeok Waterfront Ecological Park, Republic of Korea. The GenBank accession number of the 16S rRNA gene sequence of strain BE15 is MW164957.

#### **Description of *Gordonia westfalica* I4-8**

Cells are Gram-stain-positive, aerobic, non-flagellated, and rod shaped. When grown on R2A plates at 30°C for 3 days, colonies are pale orange, round, entire, and convex. In the API 20NE test, the cells showed positive results for the hydrolysis of urea; and the assimilation of D-mannitol, malate, and trisodium citrate. Conversely, they had negative results for nitrate reaction; indole production; D-glucose fermentation; arginine, esculin, gelatin, and  $\beta$ -galactosidase hydrolysis; and D-glucose, L-arabinose, D-mannose, *N*-acetyl- $\beta$ -glucosamine, D-maltose, potassium glutamate, caprate, adipate, and phenylacetic acid assimilation. Strain I4-8 (NIBRBAC000508777) was isolated from Godeok Waterfront Ecological Park, Republic of Korea. The GenBank accession number of the 16S rRNA gene sequence of strain I4-8 is MW164958.

#### **Description of *Streptomyces polaris* I4-20**

Cells are Gram-stain-positive, aerobic, non-flagellated, and rod shaped. When grown on R2A plates at 30°C for 3 days, colonies are white, filamentous, and umbonate. In the API 20NE test, the cells showed positive results for the hydrolysis of esculin; and the assimilation of D-glucose, D-mannose, D-mannitol, *N*-acetyl- $\beta$ -glucosamine, and potassium glutamate. Conversely, they had negative results for nitrate reaction; indole production; D-glucose fermentation; arginine, urea, gelatin, and  $\beta$ -galactosidase hydrolysis; and L-arabinose, D-maltose, caprate, adipate, malate, trisodium citrate, and phenylacetic acid assimilation. Strain I4-10 (NIBRBAC000508778) was isolated from Godeok Waterfront Ecological Park, Republic of Korea. The GenBank accession number of the 16S rRNA gene sequence of strain I4-20 is MW164959.

#### **Description of *Streptomyces camponoticapitis* I4-30**

Cells are Gram-stain-positive, aerobic, non-flagellated, and rod shaped. When grown on R2A plates at 30°C for 3 days, colonies are white, filamentous, and umbonate. In the API 20NE test, the cells showed positive results for the hydrolysis of esculin and  $\beta$ -galactosidase; and the assimilation of D-glucose, D-mannose, D-mannitol, *N*-acetyl-



$\beta$ -glucosamine, potassium glutamate, and malate. Conversely, they had negative results for nitrate reaction; indole production; arginine, urea, and gelatin hydrolysis; and L-arabinose, D-maltose, caprate, adipate, trisodium citrate, and phenylacetic acid assimilation. Strain I4-30 (= NIBR BAC000508779) was isolated from a Godeok Waterfront Ecological Park, Republic of Korea. The GenBank accession number of the 16S rRNA gene sequence of strain I4-30 is MW164960.

#### Description of *Streptomyces gelaticus* PS14

Cells are Gram-stain-positive, aerobic, non-flagellated, and rod shaped. When grown on R2A plates at 30°C for 3 days, colonies are gray, filamentous, and umbonate. In the API 20NE test, the cells showed positive results for nitrate reaction; urea, esculin, and  $\beta$ -galactosidase hydrolysis; and D-glucose, D-mannose, N-acetyl- $\beta$ -glucosamine, D-maltose, potassium glutamate, and malate assimilation. Conversely, they had negative results for indole production; D-glucose fermentation; arginine and gelatin hydrolysis; and L-arabinose, D-mannitol, caprate, adipate, trisodium citrate, and phenylacetic acid assimilation. Strain PS14 (NIBRBAC000508782) was isolated from Godeok Waterfront Ecological Park, Republic of Korea. The GenBank accession number of the 16S rRNA gene sequence of strain PS14 is MW164963.

#### Description of *Streptomyces lavendulae* subsp. *lavendulae* PS18

Cells are Gram-stain-positive and aerobic. When grown on R2A plates at 30°C for 3 days, colonies are white and branched, and they form an aerial mycelium. In the API 20NE system, the cells showed positive results for the hydrolysis of esculin; assimilation of D-glucose, N-acetyl- $\beta$ -glucosamine, potassium glutamate, and malate. Conversely, they had negative results for nitrate reaction; indole production; D-glucose fermentation; arginine, urea, gelatin, and  $\beta$ -galactosidase hydrolysis; and L-arabinose, D-mannose, D-mannitol, D-maltose, caprate, adipate, trisodium citrate, and phenylacetic acid assimilation. Strain PS18 (= NIBRBAC000508783) was isolated from a wetland in Seoul, Republic of Korea. The GenBank accession number of the 16S rRNA gene sequence of strain PS18 is MW164964.

#### Description of *Streptomyces beijiagensis* PS22

Cells are Gram-stain-positive and aerobic. When grown on R2A plates at 30°C for 3 days, colonies are gray and branched, and they form an aerial mycelium. In the API 20NE system, the cells showed positive results for nitrate reaction; urea, esculin, and  $\beta$ -galactosidase hydrolysis; and D-glucose, L-arabinose, D-mannose, N-acetyl- $\beta$ -glucos-

amine, D-maltose, potassium glutamate, adipate, malate, and trisodium citrate assimilation. Conversely, they had negative results for indole production; D-glucose fermentation; arginine and gelatin hydrolysis; and D-mannitol, caprate, and phenylacetic acid assimilation. PS22 (= NIBR BAC000508784) was isolated from a wetland in Seoul, Republic of Korea. The GenBank accession number of the 16S rRNA gene sequence of strain PS22 is MW164965.

#### Description of *Aldersonia kunmingensis* PS26

Cells are Gram-stain-positive, aerobic, and non-flagellated. When grown on R2A plates at 30°C for 3 days, colonies are white, coccus shaped, round, entire, and flat. In the API 20NE system, the cells showed positive results for nitrate reaction and D-glucose, D-mannose, D-mannitol, N-acetyl- $\beta$ -glucosamine, potassium glutamate, adipate, malate, and phenylacetic acid assimilation. Conversely, they had negative results for indole production; D-glucose fermentation; arginine, urea, esculin, gelatin, and  $\beta$ -galactosidase hydrolysis; and L-arabinose, D-maltose, caprate, and trisodium citrate assimilation. Strain PS26 (= NIBR BAC000508785) was isolated from a wetland in Seoul, Republic of Korea. The GenBank accession number of the 16S rRNA gene sequence of strain PS26 is MW164966.

#### Description of *Streptomyces griseoruber* PS28

Cells are Gram-stain-positive and aerobic. When grown on R2A plates at 30°C for 3 days, colonies are gray and branched, and they form an aerial mycelium. In the API 20 NE system, the cells showed positive results for the hydrolysis of esculin and  $\beta$ -galactosidase; and the assimilation of D-glucose, L-arabinose, D-mannose, D-mannitol, N-acetyl- $\beta$ -glucosamine, D-maltose, potassium glutamate, adipate, malate, trisodium citrate, and phenylacetic acid. Conversely, they had negative results for nitrate reaction; indole production; D-glucose fermentation; arginine, urea, and gelatin hydrolysis; and caprate assimilation. Strain PS28 (= NIBRBAC000508786) was isolated from a wetland in Seoul, Republic of Korea. The GenBank accession number of the 16S rRNA gene sequence of strain PS28 is MW164967.

#### Description of *Streptomyces zhihengii* TS34

Cells are Gram-stain-positive and aerobic. When grown on R2A plates at 30°C for 3 days, colonies are gray colored, branched, and form aerial mycelium (Huang *et al.*, 2016). In the API 20NE system, the cells showed positive results for nitrate reaction; esculin, gelatin, and  $\beta$ -galactosidase hydrolysis; and D-glucose, L-arabinose, D-mannose, N-acetyl- $\beta$ -glucosamine, D-maltose, potassium glutamate, adipate, malate, and trisodium citrate assimilation. Conversely, they had negative results for indole production;

D-glucose fermentation; arginine and urea hydrolysis; and D-mannitol, caprate, and phenylacetic acid assimilation. Strain TS34 (= NIBRBAC00050878) was isolated from a wetland in Seoul, Republic of Korea. The GenBank accession number of the 16S rRNA gene sequence of strain TS34 is MW164968.

#### Description of *Streptomyces tauricus* RMG20M

Cells are Gram-stain-positive, aerobic, and rod shaped. When grown on R2A plates at 28°C for 3 days, colonies are white, circular, and opaque, and they form brown mycelium. In the API 20NE test, the cells showed positive results for the hydrolysis of urea and  $\beta$ -galactosidase; and the assimilation of D-glucose, L-arabinose, D-mannose, D-mannitol, N-acetyl- $\beta$ -glucosamine, D-maltose, potassium glutamate, and malate. Conversely, they had negative results for nitrate reaction; indole production; D-glucose fermentation; arginine, esculin, and gelatin hydrolysis; caprate, adipate, trisodium citrate, and phenylacetic acid assimilation. Strain RMG20M (= NIBRBAC000508930) was isolated from soil in Sihung-si, Republic of Korea. The GenBank accession number of the 16S rRNA gene sequence of strain RMG20M is OL348213.

#### Description of *Streptomyces galbus* RG5

Cells are Gram-stain-positive, aerobic, and rod shaped. When grown on R2A plates at 30°C for 3 days, colonies are white, circular, and opaque, and they form mycelium. In the API 20NE test, the cells showed positive results for the hydrolysis of esculin and  $\beta$ -galactosidase; and the assimilation of D-glucose, adipate, and malate. Conversely, they had negative results for nitrate reaction; indole production; D-glucose fermentation; arginine, urea, and gelatin hydrolysis; and L-arabinose, D-mannose, D-mannitol, N-acetyl- $\beta$ -glucosamine, D-maltose, potassium glutamate, caprate, trisodium citrate, and phenylacetic acid assimilation. Strain RG5 (= NIBRBAC000508932) was isolated from a plant in Gayang-si, Korea. The GenBank accession number of the 16S rRNA gene sequence of strain RG5 is OL377894.

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