A report of 18 unrecorded prokaryotic species isolated from the feces of an Oriental stork (*Ciconia boyciana*), and from the intestinal tracts of a cobitid fish (*Kichulchoia multifasciata*) and a Korean splendid dace (*Coreoleuciscus splendidus*)

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The animal gut is filled with highly diverse microbes associated with host metabolism, physiology, and pathology. However, numerous animal gut microbes have not been cultured or reported. We isolated various bacterial species using culture-dependent approaches during a comprehensive investigation of endangered endemic vertebrate species in the Republic of Korea. A total of 18 unrecorded bacterial species were isolated from the feces of an Oriental stork (*Ciconia boyciana*), and from the intestinal tracts of a cobitid fish (*Kichulchoia multifasciata*) and a Korean splendid dace (*Coreoleuciscus splendidus*). Based on a phylogenetic analysis of 16S rRNA gene sequences, we discovered species belonging to the phyla Actinobacteria (eight species), Firmicutes (seven species), Proteobacteria (two species), and Bacteroidetes (one species). Based on their high 16S rRNA gene sequence similarities (>98.7%) and formation of monophyletic clades with type species, each species was classified into an independent and predefined bacterial species. Gram-stain reaction, colony and cell morphology, basic biochemical characteristics, isolation source, and NIBR IDs for each species are described in the species description section.

Keywords: 16S rRNA gene sequences, phylogenetic analysis, unreported bacterial species

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INTRODUCTION

Numerous studies have revealed a pivotal role of the gut microbial community in host metabolism, physiology, and pathology (Tremaroli and Bäckhed, 2012). Symbiotic bacteria help metabolize indigestible nutrients, protect hosts from opportunistic pathogens (Hooper and Gordon, 2001), help regulate inflammation and (Round and Mazmanian, 2009) insulin sensitivity, and even affect the progression of neurological disorders (Wu *et al.*, 2017). There is even speculation that the activity and composition of gut microbiota are related to all pathological or physiological conditions (Cani, 2017). Given the importance of the gut microbiota, they have been called 'a forgotten organ' (O'Hara and Shanahan, 2006).

Next-generation sequencing (NGS) technologies and bioinformatics analysis tools have undergone remarkable advances and offer alternative methods to investigate uncultured or even unculturable bacterial species. Nevertheless, marker gene-based, culture-independent approaches such as NGS cannot provide metabolic functional information of bacterial species (Shigematsu *et al.*, 2009). In addition to NGS and bioinformatics analysis tools, culture-dependent approaches, including isolation and cultivation, can be used to obtain a comprehensive understanding of the complex biochemical characteristics and physiology of the isolated bacterial species. However, many microbes have not been cultured under laboratory conditions (Dave *et al.*, 2012; Fodor *et al.*, 2012; Nayfach *et al.*, 2019).

In 2018, we collected the feces of an Oriental stork (*Ciconia boyciana*) and the intestinal tracts of a cobitid fish (*Kichulchoia multifasciata*) and a Korean splendid dace (*Coreoleuciscus splendidus*). These vertebrate species are endemic to the Republic of Korea (Choe *et al.*, 2016; Kim and Park, 2017). We isolated a number of

bacterial species from these indigenous samples, including 18 unreported bacterial species in the Republic of Korea. We present the detailed descriptions of these 18 bacterial species belonging to the phyla Actinobacteria, Firmicutes, Proteobacteria, and Bacteroidetes.

MATERIALS AND METHODS

Strain isolation and characterization

The feces of *C. boyciana* were collected at the Seoul Grand Park Zoo (N $37^{\circ}25'22.3'' \to 127^{\circ}1'17.8''$). Intestinal tracts of *K. multifasciata* and *C. splendidus* were collected from streams in Gimcheon-si, Gyeongsangbuk-do (N $36^{\circ}05'54.9'' \to 128^{\circ}07'32.1''$), and Gapyeong-gun, Gyeonggi-do (N $37^{\circ}51'55.3'' \to 127^{\circ}21'00.9''$), Republic of Korea, respectively. All feces and intestinal samples were homogenized in sterile phosphate buffered saline and serially diluted. Samples were spread onto three different culture media (marine agar, tryptic soy agar, and Reasoner's 2A agar; BD Difco) and incubated at 10° C and 30° C. We repeated several sub-cultivations using the streak-plating method to obtain pure isolates.

Analysis of 16S rRNA genes

Genomic DNA was extracted using an UltraClean Microbial DNA Isolation Kit (MoBio) and prepared as described previously (Lee *et al.*, 2019). Extracted DNA was amplified using a PCR premix (iNtron Biotechnology) and two universal bacteria-specific primers, Bac 27F (5'-AGAGTTTGATCCTGGCTCAG-3') and Bac 1492R (5'-GGYTACCTTGTTACGACTT-3') (Lane, 1991). Near-full-length 16S rRNA genes were sequenced using a PRISM 3730xl DNA analyzer (Applied Biosystem) and the sequence fragments were assembled using SeqMan 5.0 program (DNASTAR). The genomic DNA G + C content was determined using high-performance liquid chromatography (Mesbah *et al.*, 1989). The most closely related taxa were determined by comparing to bacterial type strains from the EzBioCloud database (Yoon *et al.*, 2017).

Phylogenetic analysis

The 16S rRNA gene sequences of the isolates were aligned to closely related species using CLUSTAL W software (Thompson *et al.*, 1994). To determine the phylogenetic position of the isolates, phylogenetic consensus trees were constructed using MEGA version 7 (Kumar *et al.*, 2016) with neighbor-joining (NJ) (Saitou and Nei, 1987), maximum-likelihood (ML) (Felsenstein, 1981), and maximum-parsimony (MP) (Kluge and Farris, 1969) tree-construction algorithms. To confirm the robustness of the phylogenetic trees, 1000 bootstrap replicates were performed.

Morphological and Biochemical analysis

We observed cells under a LIBRA 120 transmission electron microscope (Carl Zeiss) to describe morphological characteristics. Gram-stain reactions were evaluated using a Gram staining kit (bioMerieux). For biochemical analysis, 71 carbon source utilization assays were performed using Biolog GEN III MicroPlate system (BiOLOG) (dextrin, D-maltose, D-trehalose, D-cellobiose, gentiobiose, sucrose, D-turanose, stachyose, D-raffinose, α -D-lactose, D-melibiose, β -methyl-D-glucoside, D-salicin, N-acetyl-D-glucosamine, N-acetyl- β -D-mannosamine, N-acetyl-D-galactosamine, N-acetylneuraminic acid, α -D-glucose, D-mannose, D-fructose, D-galactose, 3-methyl glucose, D-fucose, L-fucose, L-rhamnose, inosine, D-sorbitol, D-mannitol, D-arabitol, myo-inositol, glycerol, D-glucose-6-PO4, D-fructose-6-PO4, D-aspartic acid, gelatin, glycyl-L-proline, L-alanine, L-arginine, L-aspartic acid, L-glutamic acid, L-histidine, L-pyroglutamic acid, L-serine, pectin, D-galacturonic acid, L-galactonic acid lactone, D-gluconic acid, D-glucuronic acid, glucuronamide, mucin acid, quinic acid, D-saccharic acid, p-hydroxy-phenylacetic acid, methyl pyruvate, D-lactic acid methyl ester, L-lactic acid, citric acid, α -keto-glutaric acid, D-malic acid, L-malic acid, bromo-succinic acid, Tween 40, γ -amino-butyric acid, α -hydroxy-butyric acid, β -hydroxy-D,L-butyric acid, α -keto-butyric acid, acetoacetic acid, propionic acid, acetic acid, and formic acid) and 23 chemical sensitivity assays (pH 6, pH 5, 1% NaCl, 4% NaCl, 8% NaCl, 1% sodium lactate, fusidic acid, D-serine, troleandomycin, rifamycin SV, minocycline, lincomycin, guanidine HCl, niaproof 4, vancomycin, tetrazolium violet, tetrazolium blue, nalidixic acid, lithium chloride, potassium tellurite, aztreonam, sodium butyrate, and sodium bromate).

RESULTS AND DISCUSSION

Based on the phylogenetic analyses using 16S rRNA gene sequences, 18 strains (designated H11M7, H11M9, H23M10, H21T1, H13T1, H43T7, H21T20, H23M25, H23M9, S13R1, H13R26, H11M5, H11M15, H11R12, H21T7, H11R21, M13M1, and H23T21) were assigned to the phyla Actinobacteria, Firmicutes, Proteobacteria, and Bacteroidetes. The isolated strains were confirmed as chemoheterotrophic, and rod or coccoid-shaped bacteria (Fig. 1). Detailed morphological and biochemical properties of these isolated strains are described in the description section.

Strains assigned to the phylum Actinobacteria

Phylogenetic consensus tree concluded that eight strains (H11M7, H11M9, H23M10, H21T1, H13T1, H43T7,



Fig. 1. Transmission electron micrographs of the strains isolated in this study. The arrows indicate flagella. Strains: 1, H11M7; 2, H11M9; 3, H23M10; 4, H21T1; 5, H13T1; 6, H43T7; 7, H21T20; 8, H23M25; 9, H23M9; 10, S13R1; 11, H13R26; 12, H11M5; 13, H11M15; 14, H11R12; 15, H21T7; 16, H11R21; 17, M13M1; 18, H23T21.

H21T20, and H23M25) were all assigned to the class Actinobacteria. Strains H11M7, H11M9, H23M10, H21T1, H13T1, and H43T7 were assigned to the order Micrococcales, and strains H21T20 and H23M25 were assigned to the order Corynebacteriales (Fig. 2). The most closely related strains were Glutamicibacter protophormiae DSM 20168^T (X80745; 100%) for H11M7, *Glutamicibacter creatinolyticus* JCM 19049^T (D88211; 99.6%) for H11M9, Microbacterium keratanolyticum IFO 13309^T (AB004717; 99.8%) H23M10, Microbacterium hydrocarbonoxydans NBRC 103074^T (AJ698726; 99.9%) for H21T1, Janibacter limosus DSM 11140^T (Y08539; 100%) H13T1, Jonesia denitrificans DSM 20603^T (NR 074806; 100%) H43T7, Corynebacterium casei LMG S-19264^T (AF267152; 99%) for H21T20, and *Dietzia aurantiaca* CCUG 35676^T (FR821260;

99.9%) for H23M25 (Table 1).

These strains were all Gram-stain positive and rodshaped bacteria, except for strain H13T1 that was coccoid-shaped (Fig. 1).

Strains assigned to the phylum Firmicutes

Phylogenetic analysis using 16S rRNA gene sequences revealed that seven strains (H23M9, S13R1, H13R26, H11M5, H11M15, H11R12, and H21T7) were all assigned to the class *Bacilli*. Strain H21T7 was assigned to the order *Lactobacillales* and the other strains were assigned to the order *Bacillales* (Fig. 3). The most phylogenetically related species to strains were *Jeotgalicoccus aerolatus* MPA-33^T (GU295939; 99.9%) for H23 M9, *Bacillus pacificus* EB422^T (KJ812450; 100%) for

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					Strain		Accession	Most closely related speci	es Si	milarity	
Phylum	Class	Order	Family	Genus	Ð	NIBR ID	number	Closest type strain	Accession number	(%)	Isolation source
Actinobacteria	Actinobacteria	Micrococcales	Micrococcaceae	Glutamicibacter	HIIM7	NIBRBAC000502712	MK253322	Glutamicibacter protophormiae	X80745	100	Oriental stork (Ciconia boyciana)
Actinobacteria	Actinobacteria	Micrococcales	Micrococcaceae	Glutamicibacter	H11M9	NIBRBAC000502713	MK253323	Glutamicibacter creatinolyticus	D88211	99.93	Oriental stork (<i>Ciconia boyciana</i>)
Actinobacteria	Actinobacteria	Micrococcales	Microbacteriaceae	Microbacterium	H23M10	NIBRBAC000502706	MK253315	Microbacterium keratanolyticum	AB004717	<i>91.</i> 79	Oriental stork (<i>Ciconia boyciana</i>)
Actinobacteria	Actinobacteria	Micrococcales	Microbacteriaceae	Microbacterium	H21T1	NIBRBAC000502717	MK253327	Microbacterium hydrocarbonoxydans	AJ698726	99.93	Oriental stork (<i>Ciconia boyciana</i>)
Actinobacteria	Actinobacteria	Micrococcales	Intrasporangiaceae	Janibacter	H13T1	NIBRBAC000502707	MK253316	Janibacter limosus	Y08539	100	Oriental stork (Ciconia boyciana)
Actinobacteria	Actinobacteria	Micrococcales	Jonesiaceae	Jonesia	H43T7	NIBRBAC000502709	MK253318	Jonesia denitrificans	NR_074806	100	Oriental stork (<i>Ciconia boyciana</i>)
Actinobacteria	Actinobacteria	Corynebacteriales	Corynebacteriaceae	Corynebacterium	H21T20	NIBRBAC000502718	MK253328	Corynebacterium casei	AF267152	99.86	Oriental stork (Ciconia boyciana)
Actinobacteria	Actinobacteria	Corynebacteriales	Dietziaceae	Dietzia	H23M25	NIBRBAC000502710	MK253319	Dietzia aurantiaca	FR821260	99.85	Oriental stork (Ciconia boyciana)
Firmicutes	Bacilli	Bacillales	Staphylococcaceae	Jeotgalicoccus	H23M9	NIBRBAC000502705	MK253314	Jeotgalicoccus aerolatus	GU295939	100	Oriental stork (Ciconia boyciana)
Firmicutes	Bacilli	Bacillales	Bacillaceae	Bacillus	SI3RI	NIBRBAC000502725	MT055843	Bacillus pacificus	KJ812450	100	Korean splendid dace (Coreoleuciscus splendidus)
Firmicutes	Bacilli	Bacillales	Planococcaceae	Kurthia	H13R26	NIBRBAC000502708	MK253317	Kurthia zopfii	AB271740	100	Oriental stork (Ciconia boyciana)
Firmicutes	Bacilli	Bacillales	Staphylococcaceae	Staphylococcus	H11M5	NIBRBAC000502711	MK253321	Staphylococcus xylosus	NR_113350	100	Oriental stork (Ciconia boyciana)
Firmicutes	Bacilli	Bacillales	Staphylococcaceae	Staphylococcus	H11M15	NIBRBAC000502714	MK253324	Staphylococcus equorum subsp. equorum	AB009939	100	Oriental stork (Ciconia boyciana)
Firmicutes	Bacilli	Bacillales	Staphylococcaceae	Staphylococcus	HIIR12	NIBRBAC000502715	MK253325	Staphylococcus succinus subsp. casei	AJ320272	100	Oriental stork (Ciconia boyciana)
Firmicutes	Bacilli	Lactobacillales	Enterococcaceae	Emterococcus	H21T7	NIBRBAC000502719	MK253329	Enterococcus aquimarinus	AJ877015	<i>91.7</i> 9	Oriental stork (Ciconia boyciana)
Proteobacteria	Gammaproteobacteria	Pseudomonadales	Moraxellaceae	Psychrobacter	H11R21	NIBRBAC000502716	MK253326	Psychrobacter ciconiae	KM486054	100	Oriental stork (Ciconia boyciana)
Proteobacteria	Gammaproteobacteria	Alteromonadales	Shewanellaceae	Shewanella	M13M1	NIBRBAC000502722	MK253332	Shewanella xiamenensis	FJ589031	99.43	Cobitid fish (Kichulchoia multifasciata)
Bacteroidetes	Sphingobacteriia	Sphingobacteriales	Sphingobacteriaceae	Sphingobacterium	H23T21	NIBRBAC000502721	MK253331	Sphingobacterium mizutaii	NR_118144	100	Oriental stork (Ciconia boyciana)

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Fig. 2. Phylogenetic tree based on 16S rRNA gene sequence comparisons, showing the relationship between the eight strains belonging to the phylum Actinobacteria isolated in this study and the notable type species from each genus. The tree was reconstructed using neighbor joining (NJ), maximum likelihood (ML), and maximum parsimony (MP) algorithms. Filled diamonds indicate corresponding branches present in the phylogenetic tree generated using the three different tree construction methods. Numbers at the nodes represent bootstrap values of more than 70% are shown, based on 1000 replicates (NJ/MP/ML). *Akkermansia muciniphila* ATCC BAA-835^T (NR_074436.1) was used as the outgroup. The bar indicates 0.02 accumulated substitutions per nucleotide.

S13R1, *Kurthia zopfii* NBRC 101529^T (AB271740; 100%) for H13R26, *Staphylococcus xylosus* CCM 2738^T (NR_113350; 100%) for H11M5, *Staphylococcus equorum* subsp. *equorum* ATCC 43958^T (AB009939; 100%) for H11M15, *Staphylococcus succinus* subsp. *casei* SB72^T (AJ320272; 100%) for H11R12, and *Enterococcus aquimarinus* DSM 17690^T (AJ877015; 99.6%) for H21T7 (Table 1).

These strains were all Gram-stain positive and rodshaped bacteria, except for strains H11M15, H11R12, and H21T7 that were coccoid-shaped (Fig. 1).

Strains assigned to the phylum Proteobacteria

Phylogenetic tree showed that strains H11R21, and M13M1 were assigned to the class *Gammaproteobac*teria. Strain H11R21 and M13M1 were members of the order *Pseudomonadales* and *Alteromonadales*, respectively (Fig. 4). The most closely related taxa of strain H11R21 was *Psychrobacter ciconiae* 176/10^T (KM4860 54; 100%) and of M13M1 was *Shewanella xiamenensis* S4^T (FJ589031; 99.4%) (Table 1).

Both strains were Gram-stain negative and rod-shaped (Fig. 1).

Strains assigned to the phylum Bacteroidetes

Strain H23T21 was assigned to the class *Flavobac*teria and the order *Flavobacteriales* (Fig. 5). The most closely related species to strain H23T21 was *Sphingobacterium mizutaii* ATCC 33299^T (NR_118144; 100%) (Table 1).

This strain was Gram-stain negative and rod-shaped (Fig. 1).

Description of Glutamicibacter protophormiae H11M7

Cells are Gram-stain positive, non-flagellated, and rodshaped. Colonies are circular, raised, entire, and white colored after 2 days of incubation on MA at 10°C. Positive for *N*-acetyl neuraminic acid, L-fucose, sodium lactate, L-glutamic acid, L-pyroglutamic acid, guanidine HCl, tetrazolium blue, L-lactic acid, citric acid, α keto-glutaric acid, L-malic acid, bromo-succinic acid, nalidixic acid, lithium chloride, potassium tellurite, aztreonam, sodium butyrate, and sodium bromate in Biolog GEN III; but negative for dextrin, D-maltose, D-trehalose, D-cellobiose, gentiobiose, sucrose, D-turanose, stachyose, D-raffinose, α -D-lactose, D-melibiose, β -methyl-D-glucoside, D-salicin, *N*-acetyl-D-glucos-



Fig. 3. Phylogenetic tree based on 16S rRNA gene sequence comparisons, showing the relationship between the seven strains belonging to the phylum Firmicutes isolated in this study and the notable type species from each genus. The tree was reconstructed using neighbor joining (NJ), maximum likelihood (ML), and maximum parsimony (MP) algorithms. Filled diamonds indicate corresponding branches present in the phylogenetic tree generated using the three different tree construction methods. Numbers at the nodes represent bootstrap values of more than 70% are shown, based on 1000 replicates (NJ/MP/ML). *Limnochorda pilosa* HC45^T (AP014924) was used as the outgroup. The bar indicates 0.02 accumulated substitutions per nucleotide.

amine, N-acetyl- β -D-mannosamine, N-acetyl-D-galactosamine, α -D-glucose, D-mannose, D-fructose, D-galactose, 3-methyl glucose, D-fucose, L-rhamnose, inosine, D-sorbitol, D-mannitol, D-arabitol, myo-inositol, glycerol, D-glucose, D-fructose-6-PO4, D-aspartic acid, D-serine, troleandomycin, gelatin, L-arginine, L-aspartic acid, L-histidine, L-serine, lincomycin, pectin, D-galacturonic acid, L-galactonic acid lactone, D-gluconic acid, D-glucuronic acid, glucuronamide, mucin acid, quinic acid, D-saccharic acid, vancomycin, p-hydroxy-phenylacetic acid, methyl pyruvate, D-lactic acid, D-malic acid, Tween 40, γ -amino-butyric acid, β -hydroxy-D,L-butyric acid, α -hydroxy-butyric acid, α -keto-butyric acid, acetoacetic acid, propionic acid, acetic acid, formic acid, pH 5, 8% NaCl, fusidic acid, rifamycin SV, minocycline, niaproof 4, and tetrazolium violet.

Strain H11M7 (=NIBRBAC000502712) was isolated from the feces of a stork (*Ciconia boyciana*) from Seoul Grand Park Zoo, Gwacheon-si, Gyeonggi-do, Korea. The DNA G+C content of the type strain is 31.9 mol%.

Description of Glutamicibacter creatinolyticus H11M9

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

rod-shaped. Colonies are circular, raised, entire, and yellow-colored after 2 days of incubation on MA at 10°C. Positive for dextrin, gentiobiose, sucrose, D-turanose, stachyose, α -D-lactose, D-melibiose, β -methyl-D-glucoside, D-salicin, N-acetyl-D-glucosamine, N-acetyl- β -Dmannosamine, N-acetyl-D-galactosamine, N-acetylneuraminic acid, α -D-glucose, D-mannose, D-fructose, D-galactose, 3-methyl glucose, D-fucose, L-fucose, L-rhamnose, inosine, sodium lactate, fusidic acid, D-serine, D-sorbitol, D-mannitol, D-arabitol, myo-inositol, glycerol, D-glucose, D-aspartic acid, D-fructose-6-PO4, troleandomycin, rifamycin SV, glycyl-L-proline, L-alanine, L-arginine, L-aspartic acid, L-glutamic acid, L-histidine, L-pyroglutamic acid, L-serine, lincomycin, guanidine HCl, pectin, D-galacturonic acid, L-galactonic acid lactone, D-gluconic acid, D-glucuronic acid, glucuronamide, mucin acid, quinic acid, D-saccharic acid, vancomycin, tetrazolium violet, tetrazolium blue, methyl pyruvate, D-lactic acid, L-lactic acid, citric acid, α -keto-glutaric acid, D-malic acid, L-malic acid, bromo-succinic acid, nalidixic acid, lithium chloride, α -hydroxy-butyric acid, α -keto-butyric acid, acetoacetic acid, acetic acid, aztreonam, sodium butyrate, and sodium bromate in Biolog GEN III; but negative for D-maltose, D-trehalose,



Fig. 4. Phylogenetic tree based on 16S rRNA gene sequence comparisons, showing the relationship between the two strains belonging to the phylum Proteobacteria isolated in this study and the notable type species from each family. The tree was reconstructed using neighbor joining (NJ), maximum likelihood (ML), and maximum parsimony (MP) algorithms. Filled diamonds indicate corresponding branches present in the phylogenetic tree generated using the three different tree construction methods. Numbers at the nodes represent bootstrap values of more than 70% are shown, based on 1000 replicates (NJ/MP/ML). *Bacteroides fragilis* NCTC 9343^T (NR_074784.2) was used as the outgroup. The bar indicates 0.05 accumulated substitutions per nucleotide.

D-raffinose, gelatin, p-hydroxy-phenylacetic acid, pH 5, minocycline, niaproof 4, potassium tellurite, Tween 40, γ -amino-butyric acid, β -hydroxy-D,L-butyric acid, propionic acid, and formic acid.

Strain H11M9 (=NIBRBAC000502713) was isolated from the feces of a stork (*Ciconia boyciana*) from Seoul Grand Park Zoo, Gwacheon-si, Gyeonggi-do, Korea. The DNA G+C content of the type strain is 63.8 mol%.

Description of *Microbacterium keratanolyticum* H23M10

Cells are Gram-stain positive, non-flagellated, and rod-shaped. Colonies are circular, raised, entire, and yellow colored after 2 days of incubation on MA at 25°C. Positive for dextrin, D-maltose, D-trehalose, D-cellobiose, gentiobiose, sucrose, D-turanose, α -D-lactose, D-melibiose, β -methyl-D-glucoside, D-salicin, N-acetyl-D-glucosamine, N-acetyl- β -D-mannosamine, N-acetylneuraminic acid, α -D-glucose, D-mannose, D-fructose, D-galactose, 3-methyl glucose, D-fucose, L-fucose, L-rhamnose, inosine, sodium lactate, fusidic acid, D-sorbitol, D-mannitol, D-arabitol, myo-inositol, glycerol, D-glucose, D-fructose-

6-PO4, D-serine, gelatin, glycyl-L-proline, L-alanine, L-arginine, L-aspartic acid, L-glutamic acid, L-histidine, L-pyroglutamic acid, L-serine, guanidine HCl, pectin, D-gluconic acid, D-saccharic acid, tetrazolium blue, p-hydroxy-phenylacetic acid, methyl pyruvate, D-lactic acid, L-lactic acid, citric acid, α -keto-glutaric acid, D-malic acid, L-malic acid, nalidixic acid, lithium chloride, potassium tellurite, Tween 40, α -hydroxy-butyric acid, α -keto-butyric acid, acetoacetic acid, propionic acid, acetic acid, aztreonam, sodium butyrate, and sodium bromate in Biolog GEN III; but negative for stachyose, D-raffinose, N-acetyl-D-galactosamine, D-aspartic acid, troleandomycin, lincomycin, D-galacturonic acid, L-galactonic acid lactone, D-glucuronic acid, glucuronamide, mucin acid, quinic acid, vancomycin, bromo-succinic acid, γ -amino-butyric acid, β -hydroxy-D,L-butyric acid, formic acid, pH 5, 8% NaCl, rifamycin SV, minocycline, and niaproof 4.

Strain H23M10 (=NIBRBAC000502706) was isolated from the feces of a stork (*Ciconia boyciana*) from Seoul Grand Park Zoo, Gwacheon-si, Gyeonggi-do, Korea. The DNA G + C content of the type strain is 67.3 mol%.



Fig. 5. Phylogenetic tree based on 16S rRNA gene sequence comparisons, showing the relationship between strain H23T21 and the notable type species from the family *Sphingobacteriaceae*. The tree was reconstructed using neighbor joining (NJ), maximum likelihood (ML), and maximum parsimony (MP) algorithms. Filled diamonds indicate corresponding branches present in the phylogenetic tree generated using the three different tree construction methods. Numbers at the nodes represent bootstrap values of more than 70% are shown, based on 1000 replicates (NJ/MP/ML). *Filobacterium rodentium* SMR-C^T (LC055729) was used as the outgroup. The bar indicates 0.05 accumulated substitutions per nucleotide.

Description of *Microbacterium hydrocarbonoxydans* H21T1

Cells are Gram-stain positive, flagellated, and rodshaped. Colonies are circular, raised, entire, and whitecolored after 2 days of incubation on TSA at 25°C. Positive for dextrin, D-maltose, D-trehalose, D-cellobiose, gentiobiose, sucrose, D-turanose, stachyose, D-raffinose, α -D-lactose, D-melibiose, β -methyl-D-glucoside, D-salicin, N-acetyl-D-glucosamine, N-acetyl- β -D-mannosamine, N-acetyl-D-galactosamine, N-acetylneuraminic acid, α -D-glucose, D-mannose, D-fructose, D-galactose, 3-methyl glucose, D-fucose, L-fucose, L-rhamnose, inosine, sodium lactate, fusidic acid, D-sorbitol, D-mannitol, D-arabitol, myo-inositol, glycerol, D-glucose, D-fructose-6-PO4, D-aspartic acid, D-serine, troleandomycin, rifamycin SV, gelatin, glycyl-L-proline, L-alanine, L-arginine, L-aspartic acid, L-glutamic acid, L-histidine, L-pyroglutamic acid, L-serine, lincomycin, guanidine HCl, pectin, D-galacturonic acid, L-galactonic acid lactone, D-gluconic acid, D-glucuronic acid, glucuronamide, mucin acid, quinic acid. D-saccharic acid, vancomvcin, tetrazolium violet, tetrazolium blue, p-hydroxy-phenylacetic acid, methyl pyruvate, D-lactic acid, L-lactic acid, citric acid, α -keto-glutaric acid, D-malic acid, L-malic acid, bromo-succinic acid, nalidixic acid, lithium chloride, potassium tellurite, Tween 40, γ -amino-butyric acid, β -hydroxy-D,L-butyric acid, α -hydroxy-butyric acid, α -keto-butyric acid, acetoacetic acid, propionic acid, acetic acid, aztreonam, sodium butyrate, and sodium bromate in Biolog GEN III; but negative for formic acid, pH 5, minocycline, and niaproof 4.

Strain H21T1 (=NIBRBAC000502717) was isolated from the feces of a stork (*Ciconia boyciana*) from Seoul Grand Park Zoo, Gwacheon-si, Gyeonggi-do, Korea. The DNAG+C content of the type strain is 66.5 mol%.

Description of Janibacter limosus H13T1

Cells are Gram-stain positive, non-flagellated, and coccoid-shaped. Colonies are circular, raised, entire, and cream colored after 2 days of incubation on TSA at 10°C. Positive for D-maltose, D-trehalose, gentiobiose, sucrose, D-turanose, N-acetyl-D-glucosamine, α -D-glucose, sodium lactate, rifamycin SV, D-gluconic acid, tetrazolium blue, L-malic acid, nalidixic acid, lithium chloride,

Tween 40, β -hydroxy-D,L-butyric acid, α -hydroxy-butyric acid, α -keto-butyric acid, propionic acid, acetic acid, aztreonam, and sodium butyrate in Biolog GEN III; but negative for dextrin, D-cellobiose, stachyose, D-raffinose, α -D-lactose, D-melibiose, β -methyl-D-glucoside, D-salicin, N-acetyl- β -D-mannosamine, N-acetyl-D-galactosamine, N-acetylneuraminic acid, D-mannose, D-fructose, D-galactose, 3-methyl glucose, D-fucose, L-fucose, L-rhamnose, inosine, D-sorbitol, D-mannitol, D-arabitol, myo-inositol, glycerol, D-glucose, D-fructose-6-PO4, D-aspartic acid, D-serine, troleandomycin, gelatin, glycyl-L-proline, L-alanine, L-arginine, L-aspartic acid, L-glutamic acid, L-histidine, L-pyroglutamic acid, L-serine, lincomycin, D-galacturonic acid, L-galactonic acid lactone, D-glucuronic acid, glucuronamide, mucin acid, quinic acid, D-saccharic acid, vancomycin, p-hydroxy-phenylacetic acid, methyl pyruvate, D-lactic acid, L-lactic acid, citric acid, α -keto-glutaric acid, D-malic acid, bromo-succinic acid, γ -amino-butyric acid, acetoacetic acid, formic acid, pH 5, 8% NaCl, fusidic acid, minocycline, guanidine HCl, niaproof 4, tetrazolium violet, potassium tellurite, and sodium bromate.

Strain H13T1 (=NIBRBAC000502707) was isolated from the feces of a stork (*Ciconia boyciana*) from Seoul Grand Park Zoo, Gwacheon-si, Gyeonggi-do, Korea. The DNA G+C content of the type strain is 68.7 mol%.

Description of Jonesia denitrificans H43T7

Cells are Gram-stain positive, flagellated, and rodshaped. Colonies are circular, raised, entire, and white colored after 2 days of incubation on TSA at 30°C. Positive for dextrin, D-maltose, D-trehalose, D-cellobiose, gentiobiose, sucrose, D-raffinose, D-turanose, α -D-lactose, D-melibiose, D-salicin, N-acetyl-D-glucosamine, α -D-glucose, D-mannose, D-fructose, D-galactose, inosine, sodium lactate, fusidic acid, D-sorbitol, glycerol, D-fructose-6-PO4, troleandomycin, minocycline, lincomycin, guanidine HCl, pectin, D-gluconic acid, D-glucuronic acid, glucuronamide, mucin acid, vancomycin, tetrazolium violet, tetrazolium blue, methyl pyruvate, nalidixic acid, lithium chloride, potassium tellurite, α -hydroxy-butyric acid, α -keto-butyric acid, acetoacetic acid, acetic acid, aztreonam, and sodium butyrate in Biolog GEN III; but negative for stachyose, β -methyl-D-glucoside, N-acetyl- β -D-mannosamine, N-acetyl-D-galactosamine, N-acetylneuraminic acid, 3-methyl glucose, D-fucose, L-fucose, L-rhamnose, D-mannitol, D-arabitol, myo-inositol, D-glucose, D-aspartic acid, D-serine, gelatin, glycyl-L-proline, L-alanine, L-arginine, L-aspartic acid, L-glutamic acid, L-histidine, L-pyroglutamic acid, L-serine, D-galacturonic acid, L-galactonic acid lactone, quinic acid, D-saccharic acid, p-hydroxy-phenylacetic acid, D-lactic acid, L-lactic acid, citric acid, α -keto-glutaric acid, D-malic acid, L-malic acid, bromo-succinic acid, Tween 40, γ -amino-butyric acid, β -hydroxy-D,L-butyric acid, propionic acid, formic acid, pH 5, rifamycin SV, niaproof 4, and sodium bromate.

Strain H43T7 (=NIBRBAC000502709) was isolated from the feces of a stork (*Ciconia boyciana*) from Seoul Grand Park Zoo, Gwacheon-si, Gyeonggi-do, Korea. The DNAG+C content of the type strain is 57.9 mol%.

Description of Corynebacterium casei H21T20

Cells are Gram-stain positive, flagellated, and rodshaped. Colonies are circular, raised, entire, and yellow-colored after 2 days of incubation on TSA at 25°C. Positive for dextrin, D-trehalose, D-cellobiose, gentiobiose, sucrose, D-turanose, stachyose, D-raffinose, α -D-lactose, D-melibiose, β -methyl-D-glucoside, D-salicin, *N*-acetyl-D-glucosamine, *N*-acetyl- β -D-mannosamine, N-acetyl-D-galactosamine, N-acetylneuraminic acid, α -D-glucose, D-mannose, D-fructose, D-galactose, 3-methyl glucose, D-fucose, L-fucose, L-rhamnose, inosine, sodium lactate, fusidic acid, D-serine, D-mannitol, D-arabitol, myo-inositol, glycerol, D-glucose, D-fructose-6-PO4, D-aspartic acid, troleandomycin, rifamycin SV, minocycline, gelatin, glycyl-L-proline, L-alanine, L-arginine, L-aspartic acid, L-glutamic acid, L-histidine, L-pyroglutamic acid, L-serine, lincomycin, guanidine HCl, D-galacturonic acid, L-galactonic acid lactone, D-gluconic acid, D-glucuronic acid, glucuronamide, mucin acid, quinic acid, D-saccharic acid, vancomycin, tetrazolium violet, tetrazolium blue, p-hydroxy-phenylacetic acid, methyl pyruvate, D-lactic acid, L-lactic acid, citric acid, α -keto-glutaric acid, D-malic acid, L-malic acid, bromo-succinic acid, nalidixic acid, lithium chloride, potassium tellurite, Tween 40, γ -amino-butyric acid, α -hydroxy-butyric acid, α -keto-butyric acid, β -hydroxy-D,L-butyric acid, acetoacetic acid, propionic acid, acetic acid, formic acid, aztreonam, sodium butyrate, and sodium bromate in Biolog GEN III; but negative for D-maltose, D-sorbitol, pectin, pH 5, and niaproof 4.

Strain H21T20 (= NIBRBAC000502718) was isolated from the feces of a stork (*Ciconia boyciana*) from Seoul Grand Park Zoo, Gwacheon-si, Gyeonggi-do, Korea. The DNA G+C content of the type strain is 61.9 mol%.

Description of Dietzia aurantiaca H23M25

Cells are Gram-stain positive, non-flagellated, and rodshaped. Colonies are circular, raised, entire, and cream colored after 2 days of incubation on MA at 25°C. Positive for D-trehalose, D-fructose, sodium lactate, D-serine, tetrazolium blue, nalidixic acid, lithium chloride, potassium tellurite, Tween 40, β -hydroxy-D,L-butyric acid, acetoacetic acid, propionic acid, and acetic acid in Biolog GEN III; but negative for dextrin, D-maltose, D-cellobiose, gentiobiose, sucrose, D-turanose, stachyose, D-raffinose, α -D-lactose, D-melibiose, β -methyl-D-glucoside, D-salicin, N-acetyl-D-glucosamine, N-acetyl- β -D-mannosamine, N-acetyl-D-galactosamine, N-acetylneuraminic acid, α -D-glucose, D-mannose, D-galactose, 3-methyl glucose, D-fucose, L-fucose, L-rhamnose, inosine, D-sorbitol, D-mannitol, D-arabitol, myo-inositol, glycerol, D-glucose, D-fructose-6-PO4, D-aspartic acid, troleandomycin, gelatin, glycyl-L-proline, L-alanine, L-arginine, L-aspartic acid, L-glutamic acid, L-histidine, L-pyroglutamic acid, L-serine, lincomycin, pectin, D-galacturonic acid, L-galactonic acid lactone, D-gluconic acid, D-glucuronic acid, glucuronamide, mucin acid, quinic acid, D-saccharic acid, vancomycin, p-hydroxy-phenylacetic acid, methyl pyruvate, D-lactic acid, L-lactic acid, citric acid, α -keto-glutaric acid, D-malic acid, L-malic acid, bromo-succinic acid, γ -amino-butyric acid, α -hydroxy-butyric acid, α -keto-butyric acid, formic acid, aztreonam, pH 5, fusidic acid, rifamycin SV, minocycline, guanidine HCl, niaproof 4, tetrazolium violet, sodium butyrate, and sodium bromate.

Strain H23M25 (=NIBRBAC000502710) was isolated from the feces of a stork (*Ciconia boyciana*) from Seoul Grand Park Zoo, Gwacheon-si, Gyeonggi-do, Korea. The DNA G + C content of the type strain is 67.9 mol%.

Description of Jeotgalicoccus aerolatus H23M9

Cells are Gram-stain positive, non-flagellated, and rodshaped. Colonies are circular, raised, entire, and cream colored after 2 days of incubation on MA at 25°C. Positive for D-cellobiose, gentiobiose, β -methyl-D-glucoside, D-salicin, N-acetyl-D-glucosamine, N-acetyl- β -D-mannosamine, N-acetyl-D-galactosamine, N-acetylneuraminic acid, α -D-glucose, D-fucose, L-fucose, sodium lactate, D-sorbitol, D-arabitol, D-aspartic acid, troleandomycin, minocycline, L-glutamic acid, L-histidine, glucuronamide, tetrazolium violet, tetrazolium blue, α -keto-glutaric acid, D-malic acid, nalidixic acid, lithium chloride, potassium tellurite, acetoacetic acid, acetic acid, aztreonam, and sodium butyrate in Biolog GEN III; but negative for dextrin, D-maltose, D-trehalose, sucrose, D-turanose, stachyose, D-raffinose, α -D-lactose, D-melibiose, D-mannose, D-fructose, D-galactose, 3-methyl glucose, L-rhamnose, inosine, D-mannitol, myo-inositol, glycerol, D-glucose, D-fructose-6-PO4, D-serine, gelatin, glycyl-L-proline, L-alanine, L-arginine, L-aspartic acid, L-pyroglutamic acid, L-serine, lincomycin, pectin, D-galacturonic acid, L-galactonic acid lactone, D-gluconic acid, D-glucuronic acid, mucin acid, quinic acid, D-saccharic acid, vancomycin, p-hydroxy-phenylacetic acid, methyl pyruvate, D-lactic acid, L-lactic acid, citric acid, L-malic acid, bromo-succinic acid, Tween 40, γ -amino-butyric acid, β -hydroxy-D,L-butyric acid, α -hydroxy-butyric acid, α -keto-butyric acid, formic acid, pH 5, fusidic acid, rifamycin SV, guanidine

HC, niaproof 4, and sodium bromate.

Strain H23M9 (=NIBRBAC000502705) was isolated from the feces of a stork (*Ciconia boyciana*) from Seoul Grand Park Zoo, Gwacheon-si, Gyeonggi-do, Korea. The DNAG+C content of the type strain is 39.7 mol%.

Description of Bacillus pacificus S13R1

Cells are Gram-stain positive, flagellated, and rodshaped. Colonies are circular, raised, entire, and white colored after 2 days of incubation on R2A at 10°C. Positive for sodium lactate, D-fructose, rifamycin SV, gelatin, glycyl-L-proline, guanidine HCl, tetrazolium blue, potassium tellurite, acetoacetic acid, propionic acid, aztreonam, and sodium butyrate in Biolog GEN III; but negative for dextrin, D-maltose, D-trehalose, D-cellobiose, gentiobiose, sucrose, D-turanose, stachyose, D-raffinose, α -D-lactose, D-melibiose, β -methyl-D-glucoside, D-salicin, N-acetyl-D-glucosamine, N-acetyl- β -D-mannosamine, N-acetyl-D-galactosamine, N-acetylneuraminic acid, α -D-glucose, D-mannose, D-fructose-6-PO4, D-galactose, 3-methyl glucose, D-fucose, L-fucose, L-rhamnose, inosine, D-sorbitol, D-mannitol, D-arabitol, myo-inositol, glycerol, D-glucose, D-aspartic acid, D-serine, troleandomycin, L-alanine, L-arginine, L-aspartic acid, L-glutamic acid, L-histidine, L-pyroglutamic acid, L-serine, lincomycin, pectin, D-galacturonic acid, L-galactonic acid lactone, D-gluconic acid, D-glucuronic acid, glucuronamide, mucin acid, quinic acid, D-saccharic acid, vancomycin, p-hydroxy-phenylacetic acid, methyl pyruvate, D-lactic acid, L-lactic acid, citric acid, α -keto-glutaric acid, D-malic acid, L-malic acid, bromo-succinic acid, nalidixic acid, Tween 40, γ -amino-butyric acid, β -hydroxy-D,L-butyric acid, α -hydroxy-butyric acid, α -keto-butyric acid, acetic acid, formic acid, pH 5, 4% NaCl, 8% NaCl, fusidic acid, minocycline, niaproof 4, tetrazolium violet, lithium chloride, and sodium bromate.

Strain S13R1 (=NIBRBAC000502725) was isolated from the intestinal tract of a Korean splendid dace (*Coreoleuciscus splendidus*) from Gapyeong-gun, Gyeonggi-do, Korea. The DNA G+C content of the type strain is 43.6 mol%.

Description of Kurthia zopfii H13R26

Cells are Gram-stain positive, flagellated, and rodshaped. Colonies are circular, raised, entire, and cream colored after 2 days of incubation on TSA at 10°C. Positive for sodium lactate, L-glutamic acid, guanidine HCl, tetrazolium blue, L-lactic acid, nalidixic acid, lithium chloride, potassium tellurite, acetoacetic acid, acetic acid, formic acid, aztreonam, and sodium butyrate in Biolog GEN III; but negative for dextrin, D-maltose, D-trehalose, D-cellobiose, gentiobiose, sucrose, D-turanose, stachyose, D-raffinose, α -D-lactose, D-melibiose, β -methyl-D-gluco-

side, D-salicin, N-acetyl-D-glucosamine, N-acetyl- β -Dmannosamine, N-acetyl-D-galactosamine, N-acetylneuraminic acid, α -D-glucose, D-mannose, D-fructose, D-galactose, 3-methyl glucose, D-fucose, L-fucose, L-rhamnose, inosine, D-sorbitol, D-mannitol, D-arabitol, myo-inositol, glycerol, D-glucose, D-fructose-6-PO4, D-aspartic acid, D-serine, troleandomycin, gelatin, glycyl-L-proline, L-alanine, L-arginine, L-aspartic acid, L-histidine, L-pyroglutamic acid, L-serine, lincomycin, pectin, D-galacturonic acid, L-galactonic acid lactone, D-gluconic acid, D-glucuronic acid, glucuronamide, mucin acid, quinic acid, D-saccharic acid, vancomycin, p-hydroxy-phenylacetic acid, methyl pyruvate, D-lactic acid, citric acid, α -keto-glutaric acid, D-malic acid, L-malic acid, bromo-succinic acid, Tween 40, γ -amino-butyric acid, β -hydroxy-D,L-butyric acid, α -hydroxy-butyric acid, α -keto-butyric acid, propionic acid, pH 5, 4% NaCl, 8% NaCl, fusidic acid, rifamycin SV, minocycline, niaproof 4, tetrazolium violet, and sodium bromate.

Strain H13R26 (=NIBRBAC000502708) was isolated from the feces of a stork (*Ciconia boyciana*) from Seoul Grand Park Zoo, Gwacheon-si, Gyeonggi-do, Korea. The DNA G + C content of the type strain is 36.9 mol%.

Description of Staphylococcus xylosus H11M5

Cells are Gram-stain positive, non-flagellated, rodshaped, motile, and spore forming. Colonies are circular, raised, entire, and white colored after 2 days of incubation on MA at 10°C. Positive for dextrin, D-maltose, D-trehalose, D-cellobiose, gentiobiose, sucrose, D-turanose, stachyose, D-raffinose, α -D-lactose, D-melibiose, β -methyl-D-glucoside, D-salicin, N-acetyl-D-glucosamine, *N*-acetyl- β -D-mannosamine, *N*-acetyl-D-galactosamine, *N*-acetylneuraminic acid, α -D-glucose, D-mannose, D-fructose, D-galactose, 3-methyl glucose, D-fucose, L-fucose, L-rhamnose, inosine, sodium lactate, fusidic acid, D-serine, D-sorbitol, D-mannitol, D-arabitol, myo-inositol, glycerol, D-glucose, D-fructose-6-PO4, D-aspartic acid, gelatin, glycyl-L-proline, L-alanine, L-arginine, L-aspartic acid, L-glutamic acid, L-histidine, L-pyroglutamic acid, L-serine, lincomycin, guanidine HCl, pectin, D-galacturonic acid, L-galactonic acid lactone, D-gluconic acid, D-glucuronic acid, glucuronamide, mucin acid, quinic acid, D-saccharic acid, vancomycin, tetrazolium violet, tetrazolium blue, methyl pyruvate, D-lactic acid, L-lactic acid, citric acid, α -keto-glutaric acid, D-malic acid, L-malic acid, bromo-succinic acid, nalidixic acid, lithium chloride, potassium tellurite, Tween 40, β -hydroxy-D,L-butyric acid, α -hydroxy-butyric acid, α -keto-butyric acid, acetoacetic acid, propionic acid, acetic acid, formic acid, aztreonam, sodium butyrate, and sodium bromate in Biolog GEN III; but negative for stachyose, p-hydroxy-phenylacetic acid, γ -amino-butyric acid, minocycline, and niaproof 4.

Strain H11M5 (=NIBRBAC000502711) was isolated from the feces of a stork (*Ciconia boyciana*) from Seoul Grand Park Zoo, Gwacheon-si, Gyeonggi-do, Korea. The DNAG+C content of the type strain is 31.9 mol%.

Description of *Staphylococcus equorum* subsp. *equorum* H11M15

Cells are Gram-stain positive, flagellated, and coccoid-shaped. Colonies are circular, raised, entire, and cream-colored after 2 days of incubation on MA at 10°C. Positive for dextrin, D-maltose, D-trehalose, D-cellobiose, gentiobiose, sucrose, D-turanose, stachyose, D-raffinose, α -D-lactose, D-melibiose, β -methyl-D-glucoside, D-salicin, N-acetyl-D-glucosamine, N-acetyl- β -D-mannosamine, N-acetyl-D-galactosamine, N-acetylneuraminic acid, α -D-glucose, D-mannose, D-fructose, D-galactose, 3-methyl glucose, D-fucose, L-fucose, L-rhamnose, inosine, sodium lactate, fusidic acid, D-sorbitol, D-mannitol, D-arabitol, myo-inositol, glycerol, D-glucose, D-fructose-6-PO4, D-aspartic acid, D-serine, troleandomycin, rifamycin SV, gelatin, glycyl-L-proline, L-alanine, L-arginine, L-aspartic acid, L-glutamic acid, L-histidine, L-pyroglutamic acid, L-serine, lincomycin, guanidine HCl, pectin, D-galacturonic acid, L-galactonic acid lactone, D-gluconic acid, D-glucuronic acid, glucuronamide, mucin acid, quinic acid, D-saccharic acid, vancomycin, tetrazolium violet, tetrazolium blue, methyl pyruvate, D-lactic acid, L-lactic acid, citric acid, α -keto-glutaric acid, D-malic acid, L-malic acid, bromo-succinic acid, nalidixic acid, lithium chloride, potassium tellurite, Tween 40, γ -amino-butyric acid, β -hydroxy-D,L-butyric acid, α -hydroxy-butyric acid, α -keto-butyric acid, acetoacetic acid, propionic acid, acetic acid, aztreonam, sodium butyrate and sodium bromate in Biolog GEN III; but negative for p-hydroxy-phenylacetic acid, pH 5, minocycline, and niaproof 4.

Strain H11M15 (= NIBRBAC000502714) was isolated from the feces of a stork (*Ciconia boyciana*) from Seoul Grand Park Zoo, Gwacheon-si, Gyeonggi-do, Korea. The DNAG+C content of the type strain is 33.2 mol%.

Description of *Staphylococcus succinus* subsp. *casei* H11R12

Cells are Gram-stain positive, non-flagellated, and coccoid-shaped. Colonies are circular, raised, entire, and white-colored after 2 days of incubation on R2A at 10°C. Positive for dextrin, D-maltose, D-trehalose, D-cellobiose, gentiobiose, sucrose, D-turanose, D-raffinose, α -D-lactose, D-melibiose, β -methyl-D-glucoside, D-salicin, N-acetyl-D-glucosamine, N-acetylneuraminic acid, α -D-glucose, D-mannose, D-fructose, D-galactose, 3-methyl glucose, D-fucose, L-fucose, L-rhamnose, sodium lactate, D-serine, D-sorbitol, D-mannitol, D-arabitol, myo-inositol, glycerol, D-glucose, D-fructose-6-PO4, D-aspartic acid, gelatin, glycyl-L-proline, L-alanine, L-arginine, L-aspartic acid, L-glutamic acid, L-histidine, L-pyroglutamic acid, L-serine, guanidine HCl, pectin, D-galacturonic acid, L-galactonic acid lactone, D-gluconic acid, D-glucuronic acid, glucuronamide, mucin acid, quinic acid, D-saccharic acid, tetrazolium blue, methyl pyruvate, D-lactic acid, L-lactic acid, citric acid, α -keto-glutaric acid, D-malic acid, L-malic acid, bromo-succinic acid, nalidixic acid, lithium chloride, potassium tellurite, Tween 40, γ -amino-butyric acid, β -hydroxy-D,L-butyric acid, α -hydroxy-butyric acid, α -keto-butyric acid, acetoacetic acid, propionic acid, acetic acid, formic acid, aztreonam, sodium butyrate, and sodium bromate in Biolog GEN III; but negative for stachyose, N-acetyl- β -D-mannosamine, N-acetyl-D-galactosamine, inosine, troleandomycin, lincomycin, vancomycin, p-hydroxy-phenylacetic acid, fusidic acid, rifamycin SV, minocycline, niaproof 4, and tetrazolium violet.

Strain H11R12 (= NIBRBAC000502715) was isolated from the feces of a stork (*Ciconia boyciana*) from Seoul Grand Park Zoo, Gwacheon-si, Gyeonggi-do, Korea. The DNA G+C content of the type strain is 32.7 mol%.

Description of Enterococcus aquimarinus H21T7

Cells are Gram-stain positive, non-flagellated, and coccoid-shaped. Colonies are circular, raised, entire, and cream-colored after 2 days of incubation on TSA at 25°C. Positive for dextrin, sucrose, α -D-lactose, D-melibiose, β -methyl-D-glucoside, D-salicin, N-acetyl-D-glucosamine, *N*-acetyl- β -D-mannosamine, *N*-acetyl-D-galactosamine, *N*-acetylneuraminic acid, α -D-glucose, D-mannose, D-fructose, D-galactose, 3-methyl glucose, D-fucose, L-fucose, L-rhamnose, inosine, sodium lactate, fusidic acid, D-serine, D-mannitol, D-arabitol, myo-inositol, glycerol, D-glucose, D-fructose-6-PO4, D-aspartic acid, troleandomycin, rifamycin SV, minocycline, glycyl-L-proline, L-alanine, L-arginine, L-aspartic acid, L-glutamic acid, L-histidine, L-pyroglutamic acid, L-serine, lincomycin, guanidine HCl, pectin, D-galacturonic acid, L-galactonic acid lactone, D-gluconic acid, D-glucuronic acid, glucuronamide, mucin acid, quinic acid, D-saccharic acid, vancomycin, tetrazolium violet, tetrazolium blue, methyl pyruvate, D-lactic acid, L-lactic acid, citric acid, α -keto-glutaric acid, D-malic acid, L-malic acid, bromo-succinic acid, nalidixic acid, lithium chloride, potassium tellurite, aztreonam, sodium butyrate, and sodium bromate in Biolog GEN III; but negative for D-maltose, D-trehalose, D-cellobiose, gentiobiose, D-turanose, stachyose, D-raffinose, D-sorbitol, gelatin, p-hydroxy-phenylacetic acid, Tween 40, γ -amino-butyric acid, β -hydroxy-D,L-butyric acid, α -hydroxy-butyric acid, α -keto-butyric acid, acetoacetic acid, propionic acid, acetic acid, formic acid, and niaproof 4.

Strain H21T7 (=NIBRBAC000502719) was isolated

from the feces of a stork (*Ciconia boyciana*) from Seoul Grand Park Zoo, Gwacheon-si, Gyeonggi-do, Korea. The DNAG+C content of the type strain is 39.4 mol%.

Description of Psychrobacter ciconiae H11R21

Cells are Gram-stain positive, flagellated, and rodshaped. Colonies are circular, raised, entire, and white-colored after 2 days of incubation on MA at 10°C. Positive for sodium lactate, L-glutamic acid, L-histidine, L-pyroglutamic acid, L-serine, lincomycin, tetrazolium violet, L-lactic acid, α -keto-glutaric acid, lithium chloride, β -hydroxy-D,L-butyric acid, propionic acid, acetic acid, and sodium bromate in Biolog GEN III; but negative for dextrin, D-maltose, D-trehalose, D-cellobiose, gentiobiose, sucrose, D-turanose, stachyose, D-raffinose, α -D-lactose, D-melibiose, β -methyl-D-glucoside, D-salicin, N-acetyl-D-glucosamine, N-acetyl- β -D-mannosamine, N-acetyl-D-galactosamine, N-acetylneuraminic acid, α -D-glucose, D-mannose, D-fructose, D-galactose, 3-methyl glucose, D-fucose, L-fucose, L-rhamnose, inosine, D-sorbitol, D-mannitol, D-arabitol, myo-inositol, glycerol, D-glucose, D-fructose-6-PO4, D-aspartic acid, D-serine, troleandomycin, gelatin, glycyl-L-proline, L-alanine, L-arginine, L-aspartic acid, pectin, D-galacturonic acid, L-galactonic acid lactone, D-glucuronic acid, glucuronamide, quinic acid, D-saccharic acid, vancomycin, p-hydroxy-phenylacetic acid, methyl pyruvate, D-lactic acid, citric acid, D-malic acid, L-malic acid, bromo-succinic acid, nalidixic acid, Tween 40, γ -amino-butyric acid, α -hydroxy-butyric acid, α -keto-butyric acid, acetoacetic acid, formic acid, aztreonam, pH 5, 8% NaCl, fusidic acid, rifamycin SV, minocycline, guanidine HCl, niaproof 4, and sodium butyrate.

Strain H11R21 (= NIBRBAC000502716) was isolated from the feces of a stork (*Ciconia boyciana*) from Seoul Grand Park Zoo, Gwacheon-si, Gyeonggi-do, Korea. The DNAG+C content of the type strain is 44.7 mol%.

Description of Shewanella xiamenensis M13M1

Cells are Gram-stain positive, non-flagellated, and rod-shaped. Colonies are circular, raised, entire, and cream-colored after 2 days of incubation on MA at 10°C. Positive for dextrin, D-mannose, D-maltose, gentiobiose, sucrose, D-melibiose, N-acetyl- β -D-mannosamine, D-fructose, D-galactose, 3-methyl glucose, D-fucose, L-fucose, L-rhamnose, inosine, sodium lactate, fusidic acid, D-fructose-6-PO4, troleandomycin, glycyl-L-proline, L-glutamic acid, lincomycin, guanidine HCl, niaproof 4, pectin, D-galacturonic acid, L-galactonic acid lactone, D-glucuronic acid, glucuronamide, vancomycin, tetrazolium violet, tetrazolium blue, methyl pyruvate, D-lactic acid, L-lactic acid, L-malic acid, lithium chloride, potassium tellurite, acetoacetic acid, acetic acid, and aztreonam in Biolog GEN III; but negative for D-trehalose, D-cellobiose, D-turanose, stachyose, D-raffinose, α -D-lactose, β -methyl-D-glucoside, D-salicin, *N*-acetyl-D-galactosamine, *N*-acetylneuraminic acid, α -D-glucose, D-sorbitol, D-mannitol, D-arabitol, myo-inositol, glycerol, D-glucose, D-aspartic acid, D-serine, gelatin, L-alanine, L-arginine, L-aspartic acid, L-histidine, L-pyroglutamic acid, L-serine, D-gluconic acid, mucin acid, quinic acid, D-saccharic acid, p-hydroxy-phenylacetic acid, citric acid, α -keto-glutaric acid, D-malic acid, bromo-succinic acid, nalidixic acid, Tween 40, γ -amino-butyric acid, β -hydroxy-D,L-butyric acid, α -hydroxy-butyric acid, α -keto-butyric acid, propionic acid, formic acid, pH 5, 4% NaCl, 8% NaCl, rifamycin SV, minocycline, sodium butyrate, *N*-acetyl-D-glucosamine, and sodium bromate.

Strain M13M1 (= NIBRBAC000502722) was isolated from the intestinal tract of a cobitid fish (*Niwaella multi-fasciata*) from Gimcheon-si, Gyeongsangbuk-do, Korea. The DNAG+C content of the type strain is 42.7 mol%.

Description of Sphingobacterium mizutaii H23T21

Cells are Gram-stain positive, non-flagellated, and rod-shaped. Colonies are circular, raised, entire, and cream-colored after 2 days of incubation on TSA at 25°C. Positive for dextrin, gentiobiose, D-raffinose, α -D-lactose, D-melibiose, β -methyl-D-glucoside, D-salicin, N-acetyl-D-glucosamine, N-acetyl-D-galactosamine, N-acetylneuraminic acid, α -D-glucose, D-mannose, D-fructose, D-galactose, 3-methyl glucose, D-fucose, L-fucose, L-rhamnose, inosine, sodium lactate, fusidic acid, p-sorbitol, D-mannitol, D-arabitol, myo-inositol, glycerol, D-glucose, D-fructose-6-PO4, D-aspartic acid, troleandomycin, rifamycin SV, gelatin, glycyl-L-proline, L-alanine, L-arginine, L-aspartic acid, L-glutamic acid, L-histidine, L-pyroglutamic acid, L-serine, lincomycin, guanidine HCl, pectin, D-galacturonic acid, L-galactonic acid lactone, D-gluconic acid, D-glucuronic acid, glucuronamide, mucin acid, quinic acid, D-saccharic acid, vancomycin, tetrazolium violet, tetrazolium blue, p-hydroxy-phenylacetic acid, methyl pyruvate, D-lactic acid, L-lactic acid, citric acid, α -keto-glutaric acid, D-malic acid, L-malic acid, bromo-succinic acid, nalidixic acid, lithium chloride, acetoacetic acid, acetic acid, aztreonam, sodium butyrate, and sodium bromate in Biolog GEN III; but negative for N-acetyl- β -D-mannosamine, D-serine, L-arginine, D-gluconic acid, mucin acid, γ -amino-butyric acid, β -hydroxy-D,L-butyric acid, α -hydroxy-butyric acid, α -keto-butyric acid, propionic acid, formic acid, pH 5, 8% NaCl, rifamycin SV, minocycline, niaproof 4, and potassium tellurite.

Strain H23T21 (=NIBRBAC000502721) was isolated from the feces of a stork (*Ciconia boyciana*) from Seoul Grand Park Zoo, Gwacheon-si, Gyeonggi-do, Korea. The DNAG+C content of the type strain is 64.1 mol%.

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