

## A report of 22 unrecorded bacterial species in Korea in the phyla *Bacteroidetes* and *Rhodothermaeota*

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A total of 22 bacterial strains belonging to the phylum Bacteroidetes were isolated primarily from aquatic environments such as seawater, freshwater, lagoon and tidal flat. One of these 22 strains was isolated from ginseng soil. Phylogenetic analyses based on 16S rRNA gene sequences revealed that 21 strains showed the high sequence similarities ( $\geq 98.7\%$ ) to the closest type strains and formed robust phylogenetic clades with closely related species in the phylum Bacteroidetes. One strain, which had been previously classified as *Balneola vulgaris* in the phylum Bacteroidetes, was identified as a member of the newly described phylum Rhodothermaeota. These strains had not been previously reported in Korea. Here, we report 21 species of 13 genera in the phylum Bacteroidetes and one species in the phylum Rhodothermaeota which were not reported in Korea. Morphological, biochemical, and physiological characteristics, isolation sources, and NIBR deposit numbers are described in the species descriptions.

Keywords: Bacteroidetes, indigenous Korean prokaryotic species, Rhodothermaeota, unreported species

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### INTRODUCTION

Members of the phylum *Bacteroidetes*, which was originally defined as a monophyletic branch encompassing the genera *Cytophaga*, *Flavobacterium* and *Bacteroides* (CFB), are generally described to be Gram-staining-negative, non-spore-forming and rod-shaped bacteria (Woese *et al.*, 1990). Due to their importance in environmental and gut microbiology, they have been extensively studied and hence the number of species names in the nomenclature has doubled in the past several years. Therefore, a phylogeny of *Bacteroidetes* has recently been revised using multilocus sequence analysis (Munoz *et al.*, 2016). As a result of these efforts, seven new taxa within *Bacteroidetes* and one new phylum, *Rhodothermaeota* phyl. nov., were proposed. The members of *Bacteroidetes* are widely distributed in various environments, includ-

ing soil, sediments, sea water, and animal gut and skin (Thomas *et al.*, 2011). Some members are known as opportunistic pathogens.

In this study, bacterial strains belonging to the phyla *Bacteroidetes* and *Rhodothermaeota* were isolated from various environments (seawater, freshwater, tidal flat, wet land, lagoon and ginseng soil) during the investigation of indigenous bacterial species in Korea by the research program supported by NIBR (National Institute of Biological Resource) in 2015. As a result, 22 strains are proposed as unrecorded species of Korea.

### MATERIALS AND METHODS

A total of 22 bacterial strains assigned to the phylum *Bacteroidetes* were isolated from various environmental

samples. Treatment of environmental samples and bacterial isolation were done independently in several laboratories. Pure cultures of isolated bacteria were grown on various media including R2A agar (BD), marine agar (MA; BD) and tryptic soy agar (TSA; BD) at 15–30°C for 2–3 days, depending on strains. The designated strain ID, isolation source, culture media and incubation conditions are summarized in Table 1. All pure cultures were maintained in 10–20% glycerol suspension at –80°C and lyophilized ampoules.

Cellular morphology and cell size were examined using either transmission electron microscope (TEM) or scanning electron microscope (SEM). Gram staining was performed using a Gram staining kit (Sigma) according to the standard procedures. Biochemical characteristics were tested using API 20NE galleries (bioMérieux) according to the manufacturer's instructions. Bacterial DNA extraction, PCR amplification and sequencing of 16S rRNA genes were performed using the standard procedures as described elsewhere (Lee and Cha, 2016). The 16S rRNA gene sequences were compared with those of the type strains of validly published bacterial species collected from the EzTazon-e server (Kim *et al.*, 2012). Multiple alignments of the 16S rRNA gene sequences of the isolates and those of the related type strains were carried out using the Clustal\_X program (Thompson *et al.*, 1997) for the phylogenetic analysis. Phylogenetic trees were reconstructed by maximum-likelihood (ML) (Felsenstein, 1981) and neighbour-joining (NJ) (Saitou and Nei, 1987) algorithms using MEGA7 software (Kumar *et al.*, 2016). The best substitution model for the ML tree was determined by a model test in the software. Both tree topologies were evaluated based on bootstrap analysis of 1000 datasets (Felsenstein, 1985).

## RESULTS AND DISCUSSION

Twenty-one strains were classified into three orders in three classes in the phylum *Bacteroidetes*; two strains in the order *Cytophagales*, five strains in the order *Sphingobacteriales*, and 14 strains in the order *Flavobacteriales*. These strains were Gram-negative and rod-shaped bacteria except for strain CH1, which had a coccoid shape (Fig. 1). In the order *Cytophagales*, one strain was assigned to the genus *Algoriphagus* in the family *Cyclobacteriaceae* and another strain belonged to the genus *Arcicella* in the family *Cytophagaceae* (Fig. 2). In the order *Sphingobacteriales*, two strains belonged to the family *Chitinophagaceae* and three strains belonged to the family *Sphingobacteriaceae* (Fig. 3). Fourteen strains were assigned to the family *Flavobacteriaceae* in the order *Flavobacteriales* (Fig. 4).

Strain IMCC12361, which showed a 16S rRNA gene

sequence similarity of 100% with *Balneola vulgaris* DSM 17893<sup>T</sup>, was previously classified as a member of *Bacteroidetes*. Since a recent revision of a *Bacteroidetes* phylogeny proposed the new phylum *Rhodothermaeota* (Munoz *et al.*, 2016), the family *Balneolaceae*, to which *Balneola vulgaris* belongs, is now separated from *Bacteroidetes* and classified as a member of the newly described phylum *Rhodothermaeota* (Fig. 5). Here, we report 22 bacterial species belonging to the phyla *Bacteroidetes* and *Rhodothermaeota* which were unrecorded in Korea. Colony size, morphology, and physiological characteristics of these strains are presented in the species description section.

Figs. 2, 3, 4, and 5 show the phylogenetic assignment of 22 strains into 22 species in the phylum *Bacteroidetes* and *Rhodothermaeota*. These strains belonged to *Balneola vulgaris* (Urios *et al.*, 2006), *Algoriphagus aquatilis* (Liu *et al.*, 2009), *Arcicella aurantiaca* (Sheu *et al.*, 2010), *Chryseobacterium carnis* (Holmes *et al.*, 2013), *C. chaponense* (Kämpfer *et al.*, 2011), *C. gambrini* (Herzog *et al.*, 2008), *C. lactis* (Holmes *et al.*, 2013), *C. piscium* (de Beer *et al.*, 2006), *C. indologenes* (Montero-Calasanz *et al.*, 2013), *Croceibacter atlanticus* (Cho and Giovannoni, 2003), *Elizabethkingia anopheles* (Kämpfer *et al.*, 2011), *Flavobacterium araucanum* (Kämpfer *et al.*, 2012), *F. sinopsychrotolerans* (Xu *et al.*, 2011), *F. aquatile* (Sheu *et al.*, 2013), *F. succinicans* (Bernardet *et al.*, 1996), *Lutimonas saemankumensis* (Yoon *et al.*, 2008), *Maribacter spongiicola* (Jackson *et al.*, 2015), *Nonlabens xylanidelens* (apos *et al.*, 2006), *Lacibacter daecheungensis* (Jin *et al.*, 2013), *Sediminibacterium ginsengisoli* (Kim *et al.*, 2013), *Mucilaginibacter koreensis* (Park *et al.*, 2014), *Pedobacter alluvionis* (Gordon *et al.*, 2009), *P. luteus* (Oh *et al.*, 2013).

### Description of *Balneola vulgaris* IMCC12361

Cells are Gram-staining-negative, non-flagellated and rod-shaped (1.6 µm long, 0.4 µm wide). Colonies are circular, convex, opaque and red-colored after 3 days of incubation on MA at 15°C. Negative reactions are obtained for indole production, glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis and gelatinase in API 20NE. Does not utilize L-arabinose, N-acetyl-glucosamine, capric acid, trisodium citrate, and phenylacetic acid. Strain IMCC12361 (=NIBRBA 0000114858) was isolated from a sea water sample, East sea, Sokcho, Korea.

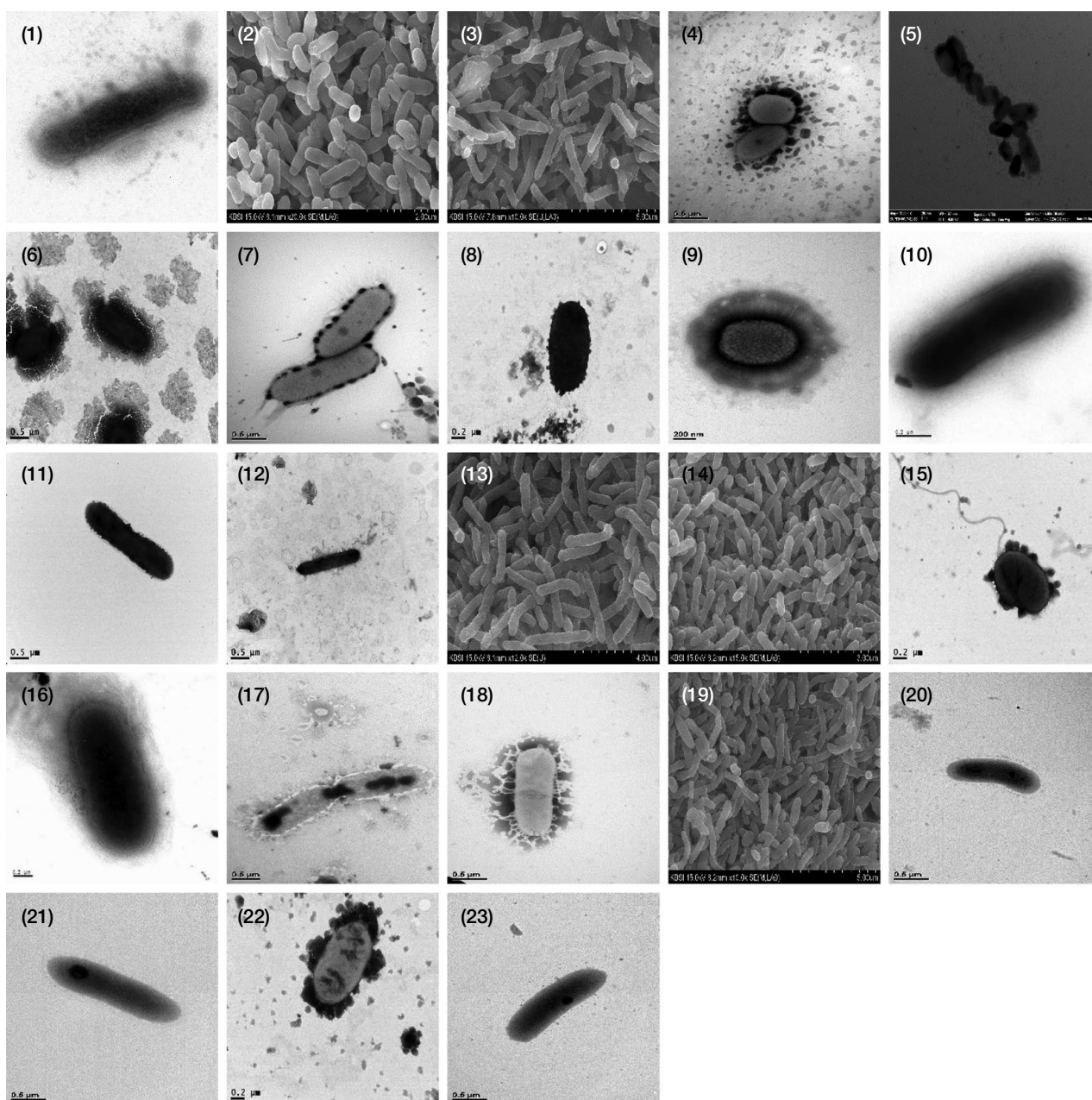
### Description of *Algoriphagus aquatilis* WS57

Cells are Gram-staining-negative, non-flagellated and rod-shaped (0.7 µm long, 0.2 µm wide). Colonies are round, circular, convex and red-pink-colored after 3 days of incubation on R2A at 25°C. Negative reactions

**Table 1.** Summary of strains belonging to the phyla *Bacteroidetes* and *Rhodothermaeota* and their taxonomic affiliations.

Phylum	Order	Genus	Strain ID	NIBR ID	Most closely related species	Similarity (%)	Isolation source	Medium	Incubation conditions	
<i>Rhodothermaeota</i>	<i>Balneolales</i>	<i>Balneola</i>	IMCC12361	NIBRBA0000114858	<i>Balneola vulgaris</i>	100	Seawater	MA	15°C, 3d	
			WS57	NIBRBA0000115012	<i>Algoriphagus aquatilis</i>	99.7	Fresh water	R2A	25°C, 3d	
	<i>Cytophagales</i>	<i>Arcticella</i>		WS16	NIBRBA0000115013	<i>Arcticella aurantica</i>	99.8	Fresh water	R2A	25°C, 3d
			<i>Chryseobacterium</i>	CHI	NIBRBA0000114884	<i>Chryseobacterium carnis</i>	99.6	Tidal flat	R2A	30°C, 3d
		<i>Chryseobacterium</i>	CWF4	NIBRBA0000114786	<i>Chryseobacterium gambrii</i>	100	Fresh water	R2A	25°C, 2d	
		<i>Chryseobacterium</i>	HMF2732	NIBRBA0000115000	<i>Chryseobacterium lactis</i>	99.0	Lagoon	R2A	30°C, 2d	
		<i>Chryseobacterium</i>	GOF5	NIBRBA0000114771	<i>Chryseobacterium piscium</i>	99.7	Fresh water	R2A	25°C, 2d	
		<i>Chryseobacterium</i>	NK 6Y-4-4	NIBRBA0000114871	<i>Chryseobacterium indologenes</i>	99.2	Ginseng soil	R2A	30°C, 2d	
		<i>Croceibacter</i>	IMCC12433	NIBRBA0000114868	<i>Croceibacter atlanticus</i>	100	Seawater	MA	15°C, 3d	
		<i>Flavobacteriales</i>	<i>Elizabethkingia</i>	<i>Elizabethkingia</i>	142-9	NIBRBA0000114764	<i>Elizabethkingia anophelis</i>	99.6	Fresh water	TSA
<i>Flavobacterium</i>	WA3			NIBRBA0000114767	<i>Flavobacterium araucanum</i>	98.8	Fresh water	R2A	25°C, 2d	
<i>Flavobacterium</i>	WM121		NIBRBA0000115033	<i>Flavobacterium sinopsychrotolerans</i>	99.7	Fresh water	R2A	25°C, 3d		
<i>Flavobacterium</i>	WW93		NIBRBA0000115032	<i>Flavobacterium aquatile</i>	99.2	Fresh water	R2A	25°C, 3d		
<i>Flavobacterium</i>	SRY 13		NIBRBA0000114776	<i>Flavobacterium succinicans</i>	99.4	Fresh water	R2A	25°C, 3d		
<i>Lutimonas</i>	IMCC12447		NIBRBA0000114869	<i>Lutimonas saemankumensis</i>	99.4	Seawater	MA	15°C, 3d		
<i>Maribacter</i>	HMF2263		NIBRBA0000114992	<i>Maribacter aquivivus</i>	99.3	Lagoon	MA	25°C, 3d		
<i>Nonlabens</i>	HMF2264		NIBRBA0000114993	<i>Nonlabens xylanidelens</i>	99.0	Fresh water	MA	25°C, 3d		
<i>Bacteroidetes</i>	<i>Lacibacter</i>		<i>Lacibacter</i>	WS72	NIBRBA0000115017	<i>Lacibacter daechungensis</i>	99.7	Fresh water	R2A	25°C, 3d
			<i>Sediminibacterium</i>	HME7508	NIBRBA0000114981	<i>Sediminibacterium ginsengisoli</i>	99.8	Fresh water	R2A	30°C, 3d
	<i>Sphingobacteriales</i>	<i>Mucilaginibacter</i>	HME8677	NIBRBA0000114986	<i>Mucilaginibacter koreensis</i>	100	Fresh water	R2A	30°C, 3d	
		<i>Pedobacter</i>	WB5	NIBRBA0000114769	<i>Pedobacter alluvionis</i>	99.9	Fresh water	R2A	25°C, 2d	
	<i>Pedobacter</i>	HME8461	NIBRBA0000114984	<i>Pedobacter luteus</i>	99.6	Fresh water	R2A	30°C, 3d		

MA, marine agar; TSA, tryptic soy agar

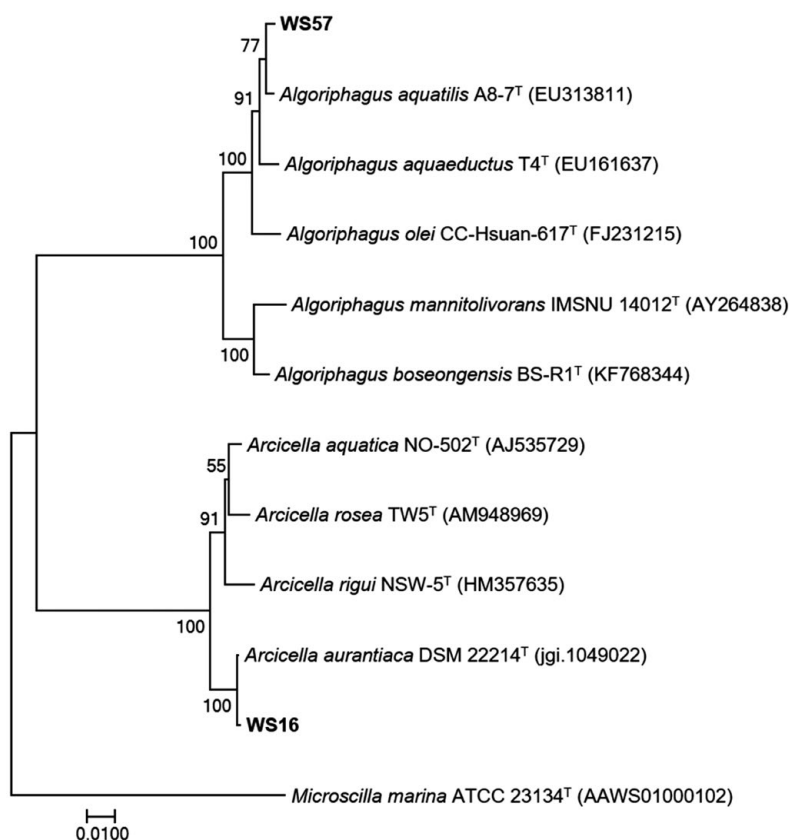


**Fig. 1.** Transmission electron micrographs or scanning electron micrographs of cells of the strains isolated in this study. Strains: 1. IMCC12361; 2. WS57; 3. WS16; 4. CH1; 5. SCR0201; 6. CWF4; 7. HMF2732; 8. GOF5; 9. NK 6Y-4-4; 10. IMCC12433; 11. 142-9; 12. WA3; 13. WM121; 14. WW93; 15. SRY13; 16. IMCC12447; 17. HMF2263; 18. HMF2264; 19. WS72; 20. HME7508; 21. HME8677; 22. WB5; 23. HME8461.

are obtained for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease and gelatinase in API 20NE. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, N-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Strain WS57 (=NIBRBA0000115012) was isolated from a swamp sample, Upo wetland, Changnyeong, Korea.

#### **Description of *Arcicella aurantiaca* WS16**

Cells are Gram-staining-negative, non-flagellated and rod-shaped (2.2  $\mu\text{m}$  long, 0.4  $\mu\text{m}$  wide). Colonies are round, circular, convex and orange-colored after 3 days of incubation on R2A at 25°C. Negative reactions are obtained for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase and urease in



**Fig. 2.** Neighbor-joining phylogenetic tree, based on 16S rRNA gene sequences, showing the relationship between the strains isolated in this study and their relatives of the order *Cytophagales*. Numbers at the nodes are levels of bootstrap value (%) based on 1000 replicated datasets; only values above 50% are shown. *Microscilla marina* ATCC 23134<sup>T</sup> (AAWS01000102) was used as an outgroup. Bar, 0.01 substitutions per nucleotide position.

API 20NE. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, N-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. Strain WS16 (=NIBRBA0000115013) was isolated from a freshwater sample, Upo wetland, Changnyeong, Korea.

#### Description of *Chryseobacterium carnis* CH1

Cells are Gram-staining-negative, non-flagellated and coccus-shaped (0.7 µm long, 0.4 µm wide). Colonies are circular, entire, raised and yellow-colored after 2 days of incubation on R2A at 30°C. Negative reactions are obtained for glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis and β-galactosidase in API 20NE. Does not utilize D-mannose, N-acetyl-glucosamine, capric acid and phenylacetic acid. Strain CH1 (=NIBRBA0000114884) was isolated from a tidal flat sample, Ganghwa, Incheon, Korea.

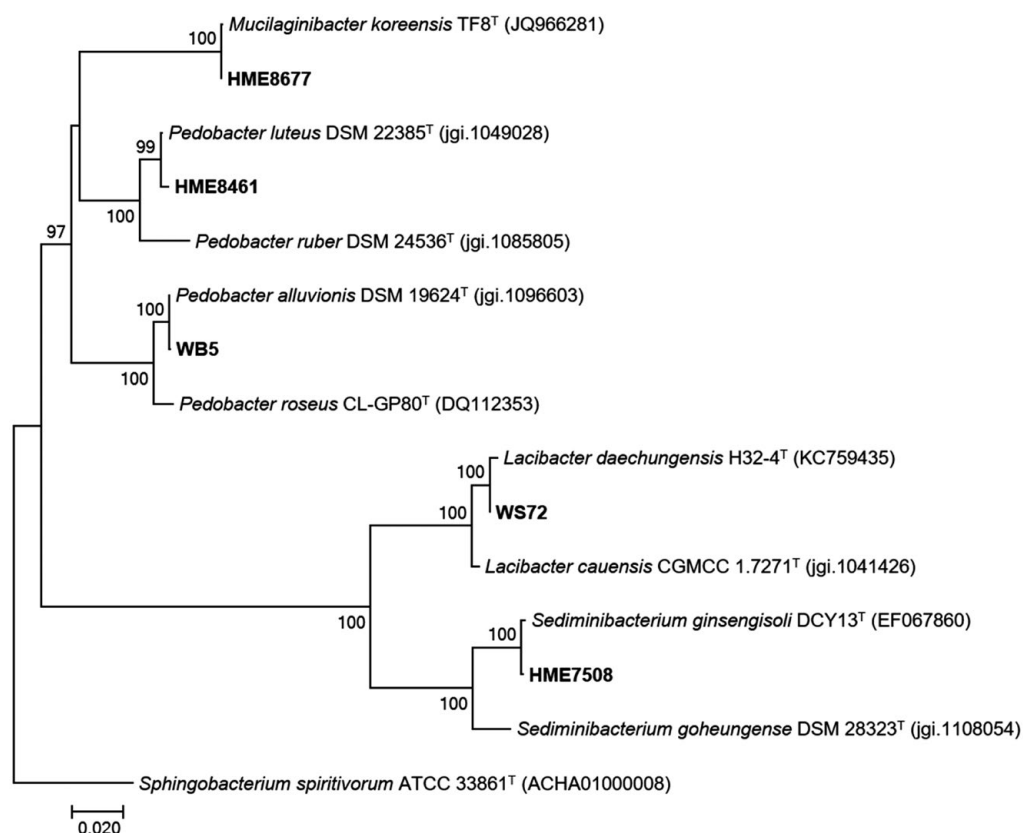
#### Description of *Chryseobacterium gambrini* CWF4

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

rod-shaped (2.5 µm long, 1.3 µm wide). Colonies are circular, entire, raised and yellow-colored after 2 days of incubation on R2A at 25°C. Negative reactions are obtained for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease and β-galactosidase in API 20NE. Does not utilize L-arabinose, D-mannitol, N-acetyl-glucosamine, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. Strain CWF4 (=NIBRBA0000114786) was isolated from a freshwater sample, Chonbuk national university fountain, Jeonju, Korea.

#### Description of *Chryseobacterium lactis* HMF2732

Cells are Gram-staining-negative, non-flagellated and rod-shaped (1.6 µm long, 0.4 µm wide). Colonies are circular, entire, convex and yellow-colored after 2 days of incubation on R2A at 30°C. Negative reactions are obtained for nitrate reduction, glucose fermentation, arginine dihydrolase and urease in API 20NE. Does not utilize L-arabinose, D-mannitol, N-acetyl-glucosamine, potassium gluconate, capric acid and trisodium citrate.



**Fig. 3.** Neighbor-joining phylogenetic tree, based on 16S rRNA gene sequences, showing the relationship between the strains isolated in this study and their relatives of the order *Sphingobacteriales*. Numbers at the nodes are levels of bootstrap value (%) based on 1000 replicated datasets; only values above 50% are shown. *Sphingobacterium spiritivorum* ATCC 33861<sup>T</sup> (ACHA01000008) was used as an out-group. Bar, 0.02 substitutions per nucleotide position.

Strain HMF2732 (= NIBRBA0000115000) was isolated from a lagoon sample, lagoon, Gangneung, Korea.

#### Description of *Chryseobacterium piscium* GOF5

Cells are Gram-staining-negative, non-flagellated and rod-shaped (1.3  $\mu\text{m}$  long, 0.6  $\mu\text{m}$  wide). Colonies are circular, entire, raised and yellow-colored after 2 days of incubation on R2A at 25°C. Negative reactions are obtained for indole production, glucose fermentation, arginine dihydrolase and  $\beta$ -galactosidase in API 20NE. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, N-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. Strain GOF5 (= NIBRBA 0000114771) was isolated from a freshwater sample, *Acer pictum* subsp. *mono* water, Jangseong, Korea.

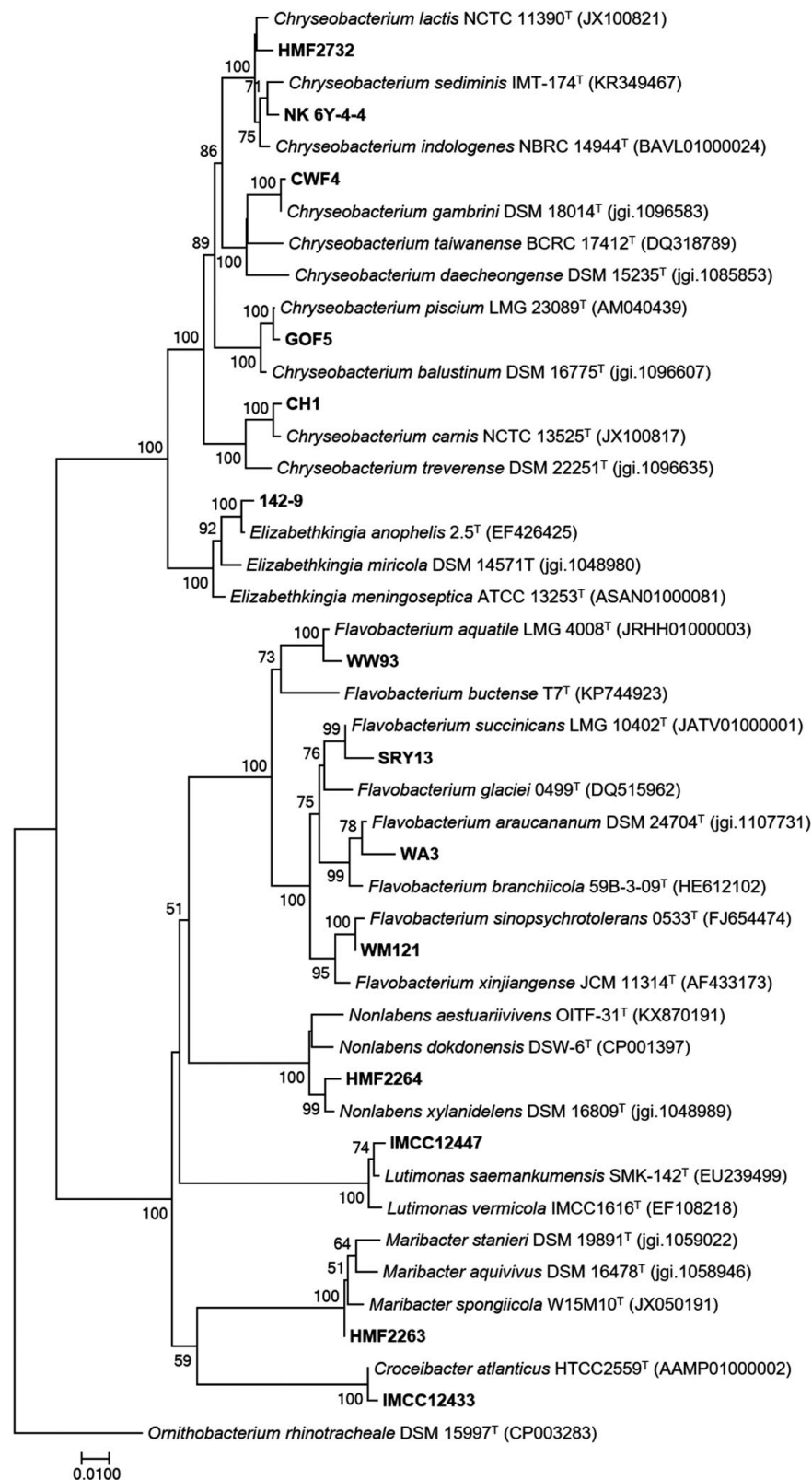
#### Description of *Chryseobacterium indologenes* NK 6Y-4-4

Cells are Gram-staining-negative, non-flagellated and rod-shaped (0.7  $\mu\text{m}$  long, 0.4  $\mu\text{m}$  wide). Colonies are cir-

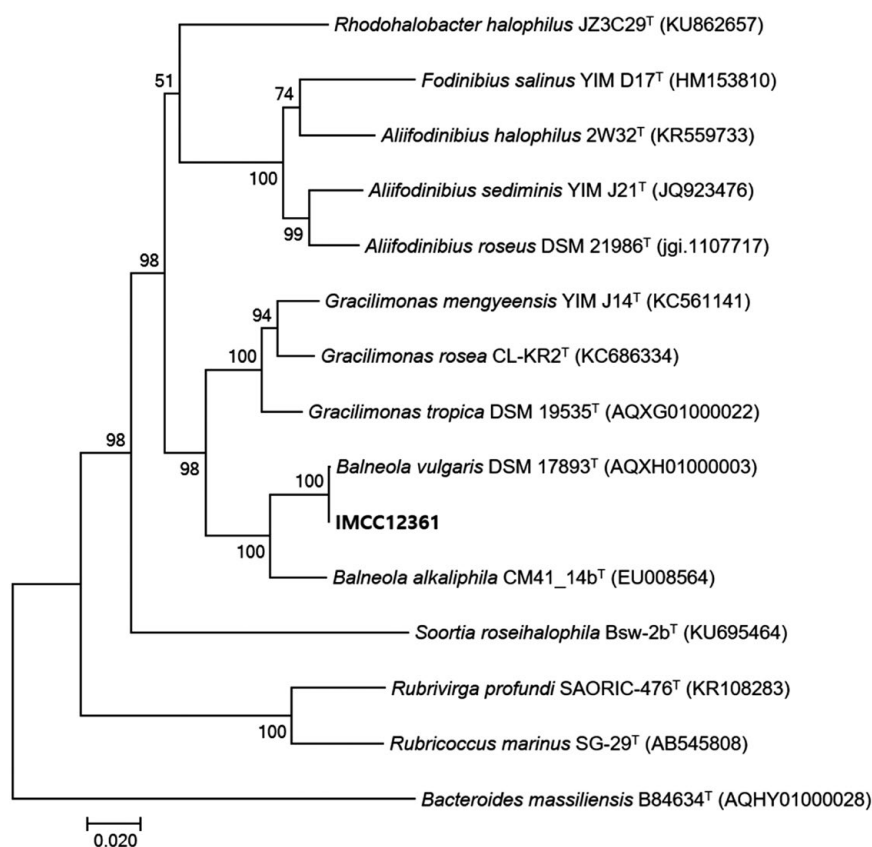
cular, entire smooth, convex and yellow-colored after 2 days of incubation on R2A at 30°C. Negative reactions are obtained for nitrate reduction, indole production, glucose fermentation and arginine dihydrolase in API 20NE. Does not utilize capric acid. Strain NK 6Y-4-4 (= NIBRBA0000114871) was isolated from a Ginseng field sample, Anseong, Korea.

#### Description of *Croceibacter atlanticus* IMCC12433

Cells are Gram-staining-negative, non-flagellated and rod-shaped (2.6  $\mu\text{m}$  long, 0.8  $\mu\text{m}$  wide). Colonies are circular, convex, smooth and yellow-colored after 3 days of incubation on MA at 15°C. Negative reactions are obtained for indole production, glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis, gelatinase and  $\beta$ -galactosidase in API 20NE. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, N-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. Strain IMCC12433 (= NIBRBA 0000114868) was isolated from a sea water sample, East



**Fig. 4.** Neighbor-joining phylogenetic tree, based on 16S rRNA gene sequences, showing the relationship between the strains isolated in this study and their relatives of the order *Flavobacteriales*. Numbers at the nodes are levels of bootstrap value (%) based on 1000 replicated datasets; only values above 50% are shown. *Ornithobacterium rhinotracheale* DSM 15997<sup>T</sup> (CP003283) was used as an outgroup. Bar, 0.02 substitutions per nucleotide position.



**Fig. 5.** Neighbor-joining phylogenetic tree, based on 16S rRNA gene sequences, showing the relationship between the strains isolated in this study and their relatives of the phylum *Rhodothermaeota*. Numbers at the nodes are levels of bootstrap value (%) based on 1000 replicated datasets; only values above 50% are shown. *Bacteroides massiliensis* B84634<sup>T</sup> (AQHY01000028) was used as an outgroup. Bar, 0.02 substitutions per nucleotide position.

sea, Sokcho, Korea.

#### Description of *Elizabethkingia anophelis* 142-9

Cells are Gram-staining-negative, non-flagellated and rod-shaped (2.9 µm long, 0.6 µm wide). Colonies are circular, entire, raised and yellow-colored after 2 days of incubation on TSA at 25°C. Negative reactions are obtained for indole production, glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis and gelatinase in API 20NE. Does not utilize L-arabinose, D-mannose, D-mannitol, N-acetyl-glucosamine, potassium gluconate, capric acid, adipic acid, trisodium citrate and phenylacetic acid. Strain 142-9 (=NIBRBA 0000114764) was isolated from a freshwater sample, Juwang mountain, Cheongsong, Korea.

#### Description of *Flavobacterium araucanum* WA3

Cells are Gram-staining-negative, non-flagellated and rod-shaped (1.7 µm long, 0.3 µm wide). Colonies are circular, entire, raised and yellow-colored after 2 days of

incubation on R2A at 25°C. Negative reactions are obtained for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase and urease in API 20NE. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, N-acetyl-glucosamine, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. Strain WA3 (=NIBRBA 0000114767) was isolated from a freshwater sample, Jeonjucheon, Jeonju, Korea.

#### Description of *Flavobacterium sinopsychrotolerans* WM121

Cells are Gram-staining-negative, non-flagellated and rod-shaped (2.2 µm long, 0.5 µm wide). Colonies are circular, convex, smooth and yellow-colored after 3 days of incubation on R2A at 25°C. Negative reactions are obtained for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis, gelatinase and β-galactosidase in API 20NE. Does not utilize L-arabinose, D-mannose, D-mannitol,



*N*-acetyl-glucosamine, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. Strain WM121 (=NIBRBA0000115033) was isolated from a freshwater sample, Upo wetland, Changnyeong, Korea.

#### **Description of *Flavobacterium aquatile* WW93**

Cells are Gram-staining-negative, non-flagellated and rod-shaped (1.5 µm long, 0.6 µm wide). Colonies are circular, convex, smooth and yellow-colored after 3 days of incubation on R2A at 25°C. Negative reactions are obtained for indole production, glucose fermentation, arginine dihydrolase, urease, esculin hydrolysis and β-galactosidase in API 20NE. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. Strain WW93 (=NIBRBA0000115032) was isolated from a freshwater sample, Upo wetland, Changnyeong, Korea.

#### **Description of *Flavobacterium succinicans* SRY13**

Cells are Gram-staining-negative, flagellated and rod-shaped (1.0 µm long, 0.6 µm wide). Colonies are circular, entire, raised and yellow-colored after 2 days of incubation on R2A at 25°C. Negative reactions are obtained for indole production, glucose fermentation, arginine dihydrolase, urease and gelatinase in API 20NE. Does not utilize L-arabinose, D-mannitol, *N*-acetyl-glucosamine, potassium gluconate, capric acid, malic acid, trisodium citrate and phenylacetic acid. Strain SRY13 (=NIBRBA0000114776) was isolated from a freshwater sample, gut of *Coreoleuciscus splendidus*, Jeonju, Korea.

#### **Description of *Lutimonas saemankumensis* IMCC12447**

Cells are Gram-staining-negative, non-flagellated and rod-shaped (2.3 µm long, 0.9 µm wide). Colonies are circular, convex, smooth and yellow-colored after 3 days of incubation on MA at 15°C. Negative reactions are obtained for indole production, glucose fermentation, arginine dihydrolase and urease in API 20NE. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. Strain IMCC12447 (=NIBRBA0000114869) was isolated from a seawater sample, East sea, Sokcho, Korea.

#### **Description of *Maribacter spongiicola* HMF2263**

Cells are Gram-staining-negative, non-flagellated and rod-shaped (1.3 µm long, 0.4 µm wide). Colonies are

circular, convex, entire and yellow-colored after 3 days of incubation on MA at 25°C. Negative reactions are obtained for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease and gelatinase in API 20NE. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. Strain HMF2263 (=NIBRBA0000114992) was isolated from a lagoon sample, lagoon, Gangneung, Korea.

#### **Description of *Nonlabens xylanidelens* HMF2264**

Cells are Gram-staining-negative, non-flagellated and rod-shaped (1.3 µm long, 0.5 µm wide). Colonies are circular, entire, convex and orange-colored after 3 days of incubation on MA at 25°C. Negative reactions are obtained for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease and β-galactosidase in API 20NE. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. Strain HMF2264 (=NIBRBA0000114993) was isolated from a freshwater sample, Yongin, Korea.

#### **Description of *Lacibacter daechungensis* WS72**

Cells are Gram-staining-negative, non-flagellated and rod-shaped (2.8 µm long, 0.5 µm wide). Colonies are circular, convex, smooth and orange-colored after 3 days of incubation on R2A at 25°C. Negative reactions are obtained for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase and urease in API 20NE. Does not utilize D-mannose, D-mannitol, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. Strain WS72 (=NIBRBA0000115017) was isolated from a freshwater sample, Upo wetland, Changnyeong, Korea.

#### **Description of *Sediminibacterium ginsengisoli* HME7508**

Cells are Gram-staining-negative, non-flagellated and rod-shaped (1.3 µm long, 0.3 µm wide). Colonies are circular, convex, entire and orange-colored after 3 days of incubation on R2A at 30°C. Negative reactions are obtained for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease and gelatinase in API 20NE. Does not utilize capric acid. Strain HME7508 (=NIBRBA0000114981) was isolated from a freshwater sample, Yongin, Korea.

#### **Description of *Mucilagibacter koreensis* HME8677**

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

rod-shaped (2.1 µm long, 0.5 µm wide). Colonies are circular, convex, entire and pale pink-colored after 3 days of incubation on R2A at 30°C. Negative reactions are obtained for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease and gelatinase in API 20NE. Does not utilize L-arabinose, D-mannitol, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. Strain HME8677 (=NIBRBA0000114986) was isolated from a freshwater sample, Soyangho lake, Chuncheon, Korea.

#### Description of *Pedobacter alluvionis* WB5

Cells are Gram-staining-negative, non-flagellated and rod-shaped (1.3 µm long, 0.6 µm wide). Colonies are circular, entire, raised and white-colored after 2 days of incubation on R2A at 25°C. Negative reactions are obtained for indole production, glucose fermentation, arginine dihydrolase, urease and gelatinase in API 20NE. Does not utilize D-glucose, L-arabinose, D-mannose, D-mannitol, N-acetyl-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. Strain WB5 (=NIBRBA0000114769) was isolated from a freshwater sample, Jeonjucheon, Jeonju, Korea.

#### Description of *Pedobacter luteus* HME8461

Cells are Gram-staining-negative, non-flagellated and rod-shaped (1.7 µm long, 0.5 µm wide). Colonies are circular, convex, entire and red-colored after 3 days of incubation on R2A at 30°C. Negative reactions are obtained for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease and gelatinase in API 20NE. Does not utilize L-arabinose, D-mannitol, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. Strain HME8461 (=NIBRBA0000114984) was isolated from a freshwater sample, Yangpyeong, Korea.

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### REFERENCES

Bernardet, J.-F., P. Segers, M. Vancanneyt, F. Berthe, K. Kersters and P. Vandamme. 1996. Cutting a Gordian Knot:

- Emended Classification and Description of the Genus *Flavobacterium*, Emended Description of the Family *Flavobacteriaceae*, and Proposal of *Flavobacterium hydatis* nom. nov. (Basonym, *Cytophaga aquatilis* Strohl and Tait 1978). *International Journal of Systematic and Evolutionary Microbiology* 46:128-148.
- Cho, J.C. and S.J. Giovannoni. 2003. *Croceibacter atlanticus* gen. nov., sp. nov., a novel marine bacterium in the family Flavobacteriaceae. *Systematic and Applied Microbiology* 26:76-83.
- de Beer, H., C.J. Hugo, P.J. Jooste, M. Vancanneyt, T. Coenye and P. Vandamme. 2006. *Chryseobacterium piscium* sp. nov., isolated from fish of the South Atlantic Ocean off South Africa. *International Journal of Systematic and Evolutionary Microbiology* 56:1317-1322.
- Felsenstein, J. 1981. Evolutionary trees from DNA sequences: a maximum likelihood approach. *Journal of Molecular Evolution* 17:368-376.
- Felsenstein, J. 1985. Confidence limits on phylogenies: an approach using the bootstrap. *Evolution* 39:783-791.
- Gordon, N.S., A. Valenzuela, S.M. Adams, P.W. Ramsey, J.L. Pollock, W.E. Holben and J.E. Gannon. 2009. *Pedobacter nyackensis* sp. nov., *Pedobacter alluvionis* sp. nov. and *Pedobacter borealis* sp. nov., isolated from Montana flood-plain sediment and forest soil. *International Journal of Systematic and Evolutionary Microbiology* 59:1720-1726.
- Herzog, P., I. Winkler, D. Wolking, P. Kämpfer and A. Lipski. 2008. *Chryseobacterium ureilyticum* sp. nov., *Chryseobacterium gambrini* sp. nov., *Chryseobacterium pallidum* sp. nov. and *Chryseobacterium molle* sp. nov., isolated from beer-bottling plants. *International Journal of Systematic and Evolutionary Microbiology* 58:26-33.
- Holmes, B., A.G. Steigerwalt and A.C. Nicholson. 2013. DNA-DNA hybridization study of strains of *Chryseobacterium*, *Elizabethkingia* and *Empedobacter* and of other usually indole-producing non-fermenters of CDC groups IIc, IIe, IIh and III, mostly from human clinical sources, and proposals of *Chryseobacterium bernardetii* sp. nov., *Chryseobacterium carnis* sp. nov., *Chryseobacterium lactis* sp. nov., *Chryseobacterium nakagawai* sp. nov. and *Chryseobacterium taklimakanense* comb. nov. *International Journal of Systematic and Evolutionary Microbiology* 63:4639-4662.
- Jackson, S.A., J. Kennedy, J.P. Morrissey, F. O'Gara and A.D.W. Dobson. 2015. *Maribacter spongiicola* sp. nov. and *Maribacter vaceletii* sp. nov., isolated from marine sponges, and emended description of the genus *Maribacter*. *International Journal of Systematic and Evolutionary Microbiology* 65:2097-2103.
- Jin, L., S.-Y. Shin, H.-G. Lee, C.-Y. Ahn and H.-M. Oh. 2013. *Lacibacter daechungensis* sp. nov., isolated from deep freshwater of a reservoir. *International Journal of*

- Systematic and Evolutionary Microbiology 63:4519-4523.
- Kämpfer, P., H. Matthews, S.P. Glaeser, K. Martin, N. Lodders and I. Faye. 2011. *Elizabethkingia anophelis* sp. nov., isolated from the midgut of the mosquito *Anopheles gambiae*. International Journal of Systematic and Evolutionary Microbiology 61:2670-2675.
- Kämpfer, P., K. Fallschissel and R. Avendaño-Herrera. 2011. *Chryseobacterium chaponense* sp. nov., isolated from farmed Atlantic salmon (*Salmo salar*). International Journal of Systematic and Evolutionary Microbiology 61:497-501.
- Kämpfer, P., N. Lodders, K. Martin and R. Avendaño-Herrera. 2012. *Flavobacterium chilense* sp. nov. and *Flavobacterium araucanum* sp. nov., isolated from farmed salmonid fish. International Journal of Systematic and Evolutionary Microbiology 62:1402-1408.
- Kim, O.S., Y.J. Cho, K. Lee, S.H. Yoon, M. Kim, H. Na, S.C. Park, Y.S. Jeon, J.H. Lee, H. Yi, S. Won and J. Chun. 2012. Introducing EzTaxon-e: a prokaryotic 16S rRNA gene sequence database with phylotypes that represent uncultured species. International Journal of Systematic and Evolutionary Microbiology 62:716-721.
- Kim, Y.-J., N.-L. Nguyen, H.-Y. Weon and D.-C. Yang. 2013. *Sediminibacterium ginsengisoli* sp. nov., isolated from soil of a ginseng field, and emended descriptions of the genus *Sediminibacterium* and of *Sediminibacterium salmoneum*. International Journal of Systematic and Evolutionary Microbiology 63:905-912.
- Kumar, S., G. Stecher and K. Tamura. 2016. MEGA7: molecular evolutionary genetics analysis version 7.0 for bigger datasets. Molecular Biology and Evolution 33:1870-1874.
- Lee, D.H. and C.J. Cha. 2016. *Flaviumibacter sediminis* sp. nov., isolated from tidal flat sediment. International Journal of Systematic and Evolutionary Microbiology 66:1-5.
- Liu, Y., H. Li, J.-T. Jiang, Y.-H. Liu, X.-F. Song, C.-J. Xu and Z.-P. Liu. 2009. *Algoriphagus aquatilis* sp. nov., isolated from a freshwater lake. International Journal of Systematic and Evolutionary Microbiology 59:1759-1763.
- Montero-Calasanz, M. d. C., M. Göker, M. Rohde, C. Spröer, P. Schumann, H.-J. Busse, M. Schmid, B.J. Tindall, H.-P. Klenk and M. Camacho. 2013. *Chryseobacterium hispalense* sp. nov., a plant-growth-promoting bacterium isolated from a rainwater pond in an olive plant nursery, and emended descriptions of *Chryseobacterium defluvii*, *Chryseobacterium indologenes*, *Chryseobacterium wanjuense* and *Chryseobacterium gregarium*. International Journal of Systematic and Evolutionary Microbiology 63:4386-4395.
- Munoz, R., R. Rosselló-Móra and R. Amann. 2016. Revised phylogeny of *Bacteroidetes* and proposal of sixteen new taxa and two new combinations including *Rhodothermaeota* phyl. nov. Systematic and Applied Microbiology 39:281-296.
- O'Sullivan, L.A., J. Rinna, G. Humphreys, A.J. Weightman and J.C. Fry. 2006. Culturable phylogenetic diversity of the phylum 'Bacteroidetes' from river epilithon and coastal water and description of novel members of the family Flavobacteriaceae: *Epilithonimonas tenax* gen. nov., sp. nov. and *Persicivirga xylanidelens* gen. nov., sp. nov. International Journal of Systematic and Evolutionary Microbiology 56:169-180.
- Oh, H.-W., B.-C. Kim, D.-S. Park, W.-J. Jeong, H. Kim, K.H. Lee and S.U. Kim. 2013. *Pedobacter luteus* sp. nov., isolated from soil. International Journal of Systematic and Evolutionary Microbiology 63:1304-1310.
- Park, C.S., K. Han and T.-Y. Ahn. 2014. *Mucilaginibacter koreensis* sp. nov., isolated from leaf mould. International Journal of Systematic and Evolutionary Microbiology 64:2274-2279.
- Saitou, N. and M. Nei. 1987. The neighbor-joining method: a new method for reconstructing phylogenetic trees. Molecular Biology and Evolution 4:406-425.
- Sheu, S.-Y., C.-S. Yang, M.-H. Chen, A.B. Arun, C.-C. Young and W.-M. Chen. 2010. *Arcicella aurantiaca* sp. nov., isolated from stream water. International Journal of Systematic and Evolutionary Microbiology 60:2979-2983.
- Sheu, S.-Y., C.-S. Yang and W.-M. Chen. 2013. *Flavobacterium squillarum* sp. nov., isolated from a freshwater shrimp culture pond, and emended descriptions of *Flavobacterium haorani*, *Flavobacterium cauense*, *Flavobacterium terrae* and *Flavobacterium aquatile*. International Journal of Systematic and Evolutionary Microbiology 63:2239-2247.
- Thomas, F., J.H. Hehemann, E. Rebuffet, M. Czjzek and G. Michel. 2011. Environmental and Gut *Bacteroidetes*: The Food Connection. Frontiers in Microbiology 2:93.
- Thompson, J.D., T.J. Gibson, F. Plewniak, F. Jeanmougin and D.G. Higgins. 1997. The CLUSTAL\_X windows interface: flexible strategies for multiple sequence alignment aided by quality analysis tools. Nucleic Acids Research 25:4876-4882.
- Urios, L., H. Agogué, F. Lesongeur, E. Stackebrandt and P. Lebaron. 2006. *Balneola vulgaris* gen. nov., sp. nov., a member of the phylum Bacteroidetes from the north-western Mediterranean Sea. International Journal of Systematic and Evolutionary Microbiology 56:1883-1887.
- Woese, C.R., D. Yang, L. Mandelco and K.O. Stetter. 1990. The flexibacter-flavobacter connection. Systematic and Applied Microbiology 13:161-165.
- Xu, M., Y. Xin, J. Tian, K. Dong, Y. Yu, J. Zhang, H. Liu and Y. Zhou. 2011. *Flavobacterium sinopsychrotolerans* sp. nov., isolated from a glacier. International Journal of

Systematic and Evolutionary Microbiology 61:20-24.  
Yoon, J.-H., S.-J. Kang, Y.-T. Jung and T.-K. Oh. 2008.  
*Aestuariicola saemankumensis* gen. nov., sp. nov., a  
member of the family Flavobacteriaceae, isolated from  
tidal flat sediment. International Journal of Systematic

and Evolutionary Microbiology 58:2126-2131.

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