

## Report of seven unrecorded bacterial species in Korea belonging to the family *Acetobacteraceae*

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Several genera belonging to the family *Acetobacteraceae* were generally considered to be acetic acid bacteria (AAB) which produce acetic acid from alcohols using an oxidation pathway. Some species of the family *Acetobacteraceae* have been of interest to the industry due to their capability to produce vinegar. In 2018–2020, several bacterial strains were isolated from plants, fruits and vinegar in various regions of the Republic of Korea. Based on the 16S rRNA gene sequences, seven species classified into the family *Acetobacteraceae* were found to be ones unrecorded in the Republic of Korea, including two *Asaia* species, one *Gluconacetobacter* species, three *Gluconobacter* species and one *Komagataeibacter* species. As a result, we report *Asaia lannensis* AF11C3 (= KACC 22050) isolated from plant *Chrysanthemum zawadskii*, *Asaia platycodi* AF15C2 (= KACC 22051) isolated from plant *Isodon inflexus*, *Gluconacetobacter liquefaciens* C23-3 (= KACC 22064) isolated from fruit of *Pyrus pyrifolia*, *Gluconobacter cerinus* BGF2-R2 (= KACC 22053) isolated from fruit of *Prunus armeniaca*, *Gluconobacter kondonii* FR39A4 (= KACC 22388) isolated from persimmon fruit, *Gluconobacter thailandicus* FR36C4 (= KACC 22057) isolated from fruit of *Pseudocarya sinensis* and *Komagataeibacter melaceti* SPV-2 (= KACC 22058) isolated from potato vinegar.

Keywords: acetic acid bacteria, *Acetobacteraceae*, unrecorded species

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### INTRODUCTION

The family *Acetobacteraceae*, proposed by Gillis & De Ley (1980), belongs to the class *Alphaproteobacteria*. At the time of writing, this family *Acetobacteraceae* comprised 47 validly published names represented by *Acetobacter* as the type genus (<https://lpsn.dsmz.de/>). It is taxonomically characterized as Gram-negative or Gram-variable, ellipsoidal to rod-shaped cells with an obligate aerobic metabolism with oxygen as the terminal electron acceptor. Acetic acid bacteria (AAB) are defined as bacteria that convert alcohols to organic acids, mainly acetic acid, through an oxidation pathway (Wang *et al.*, 2015). The production of acetic acid by AAB is very important in the vinegar industry (Sengun and Karabivikli, 2011). Many members of the family *Acetobacteraceae* are regarded as AAB and are widely distributed in various environments rich in carbohydrates, acids and alcohol (Crotti *et al.*, 2010). The genera within the family *Aceto-*

*bacteraceae* have been isolated from a variety of environments including soil (Margesin and Zhang, 2013), plants (Ramírez-Bahena *et al.*, 2013), purified water (Eder *et al.*, 2015), a marine cyanobacterial mat (Yurkov *et al.*, 1994), a soda lake (Boldareva *et al.*, 2009), hot springs (Dong *et al.*, 2014), blood (Han *et al.*, 2003), insect gut (Li *et al.*, 2015), acidic habitats (Muhadesi *et al.*, 2019) and alcohol-containing habitats (Takemura *et al.*, 1993). Recently, we reported eight unrecorded *Acetobacter* species in Korea (Heo *et al.*, 2022), various AAB species have been found to be distributed in the Republic of Korea, from this study. Here we present the taxonomic properties of seven unrecorded AAB species of the genera *Asaia*, *Gluconacetobacter*, *Gluconobacter* and *Komagataeibacter*, isolated from diverse environments.

### MATERIALS AND METHODS

Samples for isolation of bacteria including fruits, plants

and vinegars were diluted in 0.85% NaCl (w/v) solution, respectively. After serial dilution, the aliquots of the diluted samples were spread onto AAB medium [2.5% (w/v) D-mannitol, 0.5% (w/v) yeast extract, 0.3% (w/v) peptone, 0.2% (w/v) bromocresol purple and 1.5% (w/v) agar] (Heo *et al.*, 2022) and incubated at 28°C for 3–5 days. Colonies with yellow zone were selected and then subcultured on the YPM medium [0.5% (w/v) yeast extract, 0.3% (w/v) peptone, 2.5% (w/v) D-mannitol and 1.5% (w/v) agar] to obtain pure cultures. All strains were deposited at the Korean Agricultural Culture Collection (KACC). The designated strain IDs, isolation sources and identification results are summarized in Table 1. All cultured strains were maintained in glycerol suspension (15%, v/v) at –80°C.

The 16S rRNA gene sequencing of the strains pure-cultured by the above procedure was conducted by Genotech. The 16S rRNA gene sequences of the type strains of the *Acetobacteraceae* species were obtained from NCBI database (<https://www.ncbi.nlm.nih.gov/genbank/>). Phylogenetic trees were reconstructed with three different algorithms, neighbor-joining (NJ) (Saitou and Nei, 1987), maximum-likelihood (ML) (Felsenstein, 1981) and maximum-parsimony (MP) (Fitch, 1971), in MEGA X (Kumar *et al.*, 2018). Evolutionary distance matrices for the NJ and ML analyses were evaluated using Kimura 2-parameter model. Bootstrap analyses with 1,000 times were carried out for stability evaluation of tree topology (Felsenstein, 1985). Cell morphology was observed by a phase-contrast microscope (AX10; Carl Zeiss) and a transmission electron microscope (TEM; LEO 912AB; LEO Electron) after being grown on YPM medium at 28°C for 3 days. Gram staining was tested using a Gram staining kit (Sigma), according to the manufacturer's instructions. Catalase and oxidase tests were conducted by bubbling in 3% (v/v) hydrogen peroxide solution (bioMérieux) and change of color in 1% (w/v) tetramethyl-*p*-phenylenediamine, respectively. Additional biochemical properties, including substrate assimilation and acid production from various carbohydrates, were tested using API 20NE and API 50CH test kits (bioMérieux) were used according to the manufacturer's recommendations.

## RESULTS AND DISCUSSION

According to the 16S rRNA gene sequence analysis, seven strains were identified as unrecorded *Acetobacteraceae* species in the Republic of Korea (Table 1). Most of the AAB isolated, particularly from 20 different commercial vinegars, were identified as *Acetobacter pasteurianus*, which is a microorganism generally recognized as safe (GRAS). The phylogenetic tree for the isolated strains and type strains of the *Acetobacteraceae* species is presented in Figure 1. Cellular morphology and the pres-

**Table 1.** The taxonomic affiliations of isolated strains belonging to the family *Acetobacteraceae*.

Genus	Strain code	KACC <sup>a</sup> ID	Identification	Similarity (%)	Isolation source	Location	Culture conditions
<i>Asaia</i>	AF11C3	22050	<i>Asaia lannensis</i>	100	plant of <i>Chrysanthemum zawadskii</i>	Jeongeup-si, Jeollabuk-do	YPM <sup>b</sup> medium, 28°C, 3 days
	AF15C2	22051	<i>Asaia platycodi</i>	99.7	plant of <i>Isodon inflexus</i>	Jeongeup-si, Jeollabuk-do	
<i>Gluconacetobacter</i>	C23-3	22064	<i>Gluconacetobacter liquefaciens</i>	99.7	Fruit of <i>Pyrus pyrifolia</i>	Naju-si, Jeollanam-do	
	BGF2-R2	22053	<i>Gluconobacter cerinus</i>	99.9	Fruit of <i>Prunus armeniaca</i>	Suwon-si, Gyeonggi-do	
<i>Gluconobacter</i>	FR39 A4	22388	<i>Gluconobacter kondonii</i>	99.9	Persimmon fruit	Cheongdo-gun, Gyeongsangbuk-do	
	FR36C4	22057	<i>Gluconobacter thailandicus</i>	100	Fruit of <i>Pseudocarya sinensis</i>	Jeonju-si, Jeollabuk-do	
<i>Komagataeibacter</i>	SPV-2	22058	<i>Komagataeibacter melaceti</i>	99.9	Potato vinegar	Haenam-gun, Jeollanam-do	

<sup>a</sup>Korean Agricultural Culture Collection (KACC).

<sup>b</sup>YPM agar medium containing yeast extract 0.5% (w/v), peptone 0.3% (w/v), D-mannitol 2.5% (w/v) and agar 1.5% (w/v).

ence of flagella, which were examined by transmission electron microscope, are presented in Figure 2. Seven *Acetobacteraceae* species are coccoid rod- or rod-shaped. Flagellum or flagella are present only in strains AF15C2, BGF2-R2 and FR36C4, depending on species. All strains were reactive for specific substrates including D-glucose on the API assimilation test while the genus *Acetobacter* strains were not responsive on the test (Heo *et al.*, 2022). The differential phenotypic characteristics among seven species are listed in Table 2. The detailed description of each of *Acetobacteraceae* strain is described below.

### **Description of *Asaia lannensis* AF11C3 (= KACC 22050)**

Cells are Gram-stain-negative, non-flagellated, non-pigmented and rod shaped (0.8–1.0  $\mu\text{m}$   $\times$  1.4–2.3  $\mu\text{m}$ ) after three days incubation on YPM medium at 28°C. Colonies are round, raised and brownish beige colored with a diameter of 1.0 mm. Catalase-positive and oxidase-negative. Positive for glucose fermentation and aesculin hydrolysis; but negative for nitrate reduction, indole production, arginine dihydrolase, urease and gelatin hydrolysis. According to API 20 NE test results, it assimilates D-glucose, L-arabinose, D-mannose, D-mannitol and potassium gluconate; but does not assimilate *N*-acetylglucosamine, D-maltose, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. According to API 50CH test results, acid is produced from glycerol, erythritol, L-arabinose, D-ribose, D-xylose, D-adonitol, D-galactose, D-glucose, D-fructose, D-mannose, L-sorbose, L-rhamnose, dulcitol, inositol, D-mannitol, D-sorbitol, *N*-acetylglucosamine, D-melibiose, xylitol, gentiobiose, D-lyxose, D-tagatose, D-fucose, L-fucose, D-arabitol and L-arabitol; but not produced from D-arabinose, L-xylose, methyl- $\beta$ -D-xylopyranoside, methyl- $\alpha$ -D-mannopyranoside, methyl- $\alpha$ -D-glucopyranoside, amygdalin, arbutin, esculin ferric citrate, salicin, D-cellobiose, D-maltose, D-lactose, D-saccharose, D-trehalose, inulin, D-melezitose, D-raffinose, amidon, glycogen, D-turanose, potassium gluconate, potassium 2-ketogluconate and potassium 5-ketogluconate. Strain AF11C3 (=KACC 22050) was isolated from plant *Chrysanthemum zawadskii* sampled at Jeongeup-si, Jeollabuk-do. The GenBank accession number for the 16S rRNA gene sequence of strain AF11C3 is ON746592.

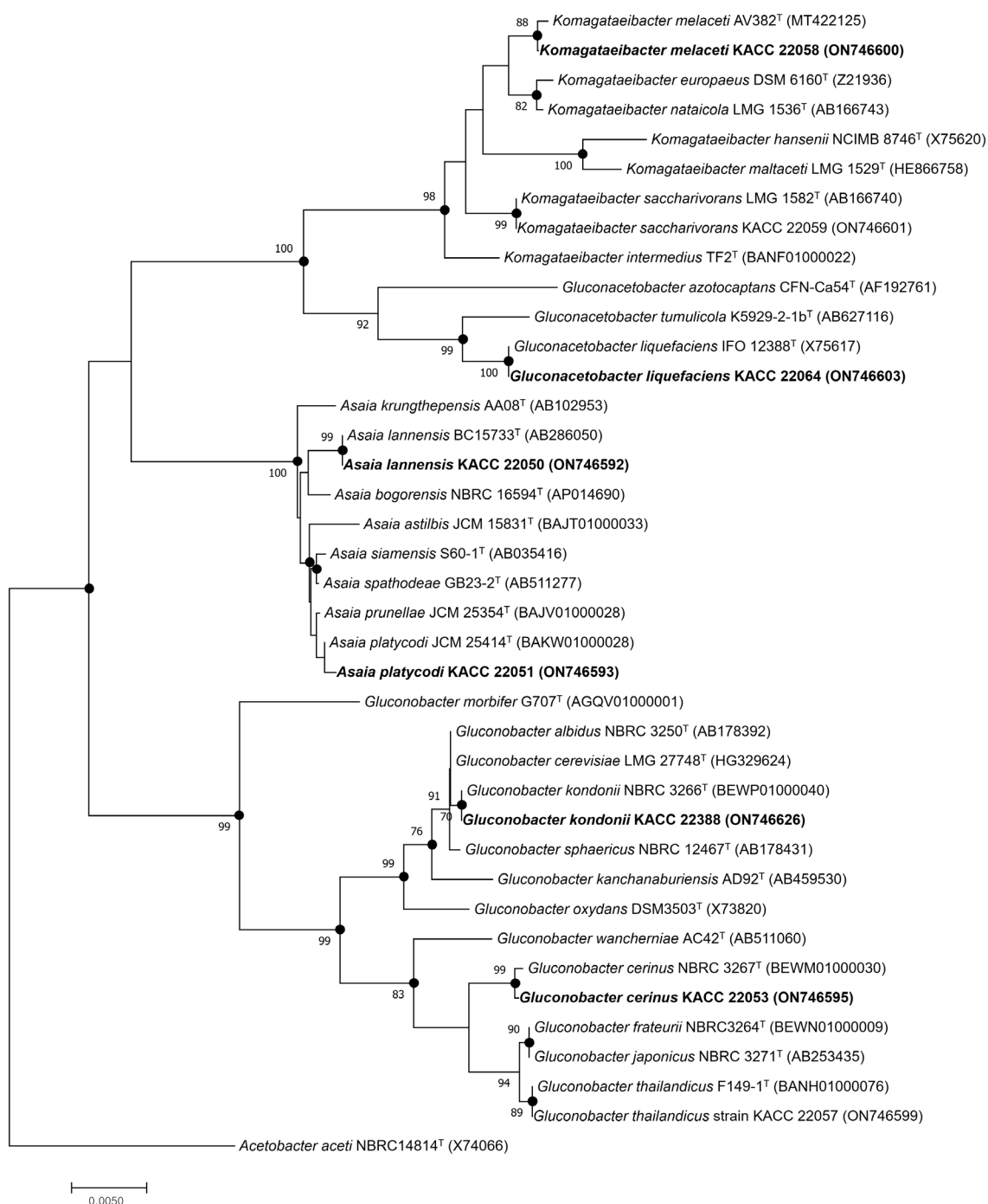
### **Description of *Asaia platycodi* AF15C2 (= KACC 22051)**

Cells are Gram-stain-negative, flagellated, non-pigmented and rod (0.9–1.1  $\mu\text{m}$   $\times$  1.6–2.2  $\mu\text{m}$ ) after three days incubation on YPM medium at 28°C. Colonies are round, raised and brownish beige colored with a diameter of 1.0 mm. Catalase-positive and oxidase-negative. Posi-

tive for glucose fermentation and aesculin hydrolysis, but negative for nitrate reduction, indole production, arginine dihydrolase, urease and gelatin hydrolysis. According to API 20 NE test results, it assimilates D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetylglucosamine and potassium gluconate, but does not assimilate D-maltose, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. According to API 50CH test results, acid is produced from glycerol, erythritol, D-arabinose, L-arabinose, D-ribose, D-xylose, L-xylose, D-adonitol, D-galactose, D-glucose, D-fructose, D-mannose, L-sorbose, inositol, D-melibiose, D-saccharose, D-raffinose, xylitol, gentiobiose, D-lyxose, D-tagatose, D-fucose, L-fucose, D-arabitol and L-arabitol, but not produced from methyl- $\beta$ -D-xylopyranoside, L-rhamnose, dulcitol, D-mannitol, D-sorbitol, methyl- $\alpha$ -D-mannopyranoside, methyl- $\alpha$ -D-glucopyranoside, *N*-acetylglucosamine, amygdalin, arbutin, esculin ferric citrate, salicin, D-cellobiose, D-maltose, D-lactose, D-trehalose, inulin, D-melezitose, amidon, glycogen, D-turanose, potassium gluconate, potassium 2-ketogluconate and potassium 5-ketogluconate. Strain AF15C2 (=KACC 22051) was isolated from plant of *Isodon inflexus* sampled from Jeongeup-si, Jeollabuk-do. The GenBank accession number for the 16S rRNA gene sequence of strain AF15C2 is ON746593.

### **Description of *Gluconacetobacter liquefaciens* C23-3 (= KACC 22064)**

Cells are Gram-stain-negative, non-flagellated, non-pigmented, and rod (0.9–1.0  $\mu\text{m}$   $\times$  1.6–2.3  $\mu\text{m}$ ) after three days incubation on YPM medium at 28°C. Colonies are round, raised and brownish beige colored with a diameter of 0.3 mm. Catalase-positive and oxidase-negative. Positive for glucose fermentation and aesculin hydrolysis, but negative for nitrate reduction, indole production, arginine dihydrolase, urease and gelatin hydrolysis. According to API 20 NE test results, it assimilates D-glucose and potassium gluconate; but does not assimilate L-arabinose, D-mannose, D-mannitol, *N*-acetylglucosamine, D-maltose, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. According to API 50CH test results, acid is produced from L-arabinose, D-ribose, D-xylose, D-galactose, D-glucose, D-fructose, D-mannose, D-melibiose, D-lyxose and D-fucose; but not produced from glycerol, erythritol, D-arabinose, L-xylose, D-adonitol, methyl- $\beta$ -D-xylopyranoside, L-sorbose, L-rhamnose, dulcitol, inositol, D-mannitol, D-sorbitol, methyl- $\alpha$ -D-mannopyranoside, methyl- $\alpha$ -D-glucopyranoside, *N*-acetylglucosamine, amygdalin, arbutin, esculin ferric citrate, salicin, D-cellobiose, D-maltose, D-lactose, D-saccharose, D-trehalose, inulin, D-melezitose, D-raffinose, amidon, glycogen, xylitol, gentiobiose, D-turanose, D-tagatose, L-fucose, D-arabitol, L-arabitol, potassium gluconate, potassium

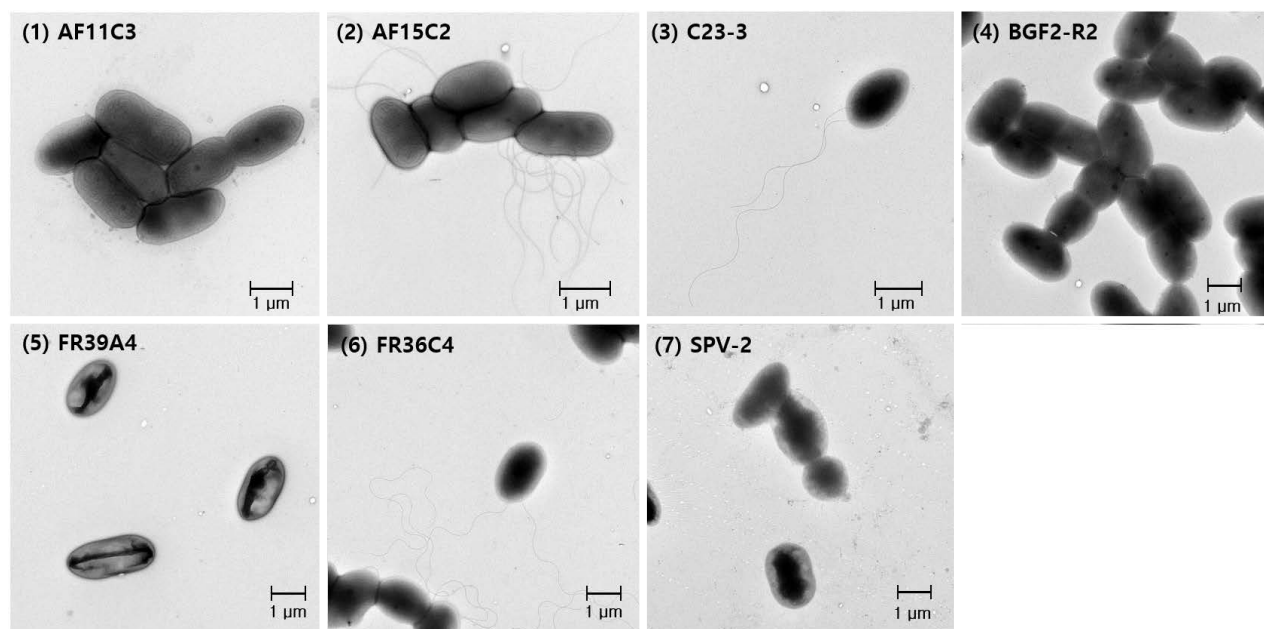


**Fig. 1.** Neighbor-joining phylogenetic tree showing the phylogenetic relationships of strains reported in this study and related species of *Acetobacteraceae*, based on 16S rRNA gene sequences. Numbers on nodes correspond to bootstrap values for branches (1,000 replicates); only values over 70% are shown. Filled circles indicate the corresponding nodes that were also recovered in trees constructed using the maximum-likelihood and maximum-parsimony algorithms. Scale bar, 0.005 substitutions per nucleotide.

2-ketogluconate and potassium 5-ketogluconate. Strain C23-3 (= KACC 22064) was isolated from fruit of *Pyrus pyrifolia* sampled from Naju-si, Jeollanam-do. The GenBank accession number for the 16S rRNA gene sequence of strain C23-3 is ON746603.

#### Description of *Gluconobacter cerinus* BGF2-R2 (= KACC 22053)

Cells are Gram-stain-negative, flagellated, non-pigmented and rod shaped (0.7–0.9  $\mu\text{m}$   $\times$  1.6–2.3  $\mu\text{m}$ ) after



**Fig. 2.** Transmission electron micrographs of the *Acetobacteraceae* strains. Strains: 1, *Asaia lannensis* AF11C3; 2, *Asaia platycodi* AF15C2; 3, *Gluconacetobacter liquefaciens* C23-3; 4, *Gluconobacter cerinus* BGF2-R2; 5, *Gluconobacter kondonii* FR39A4; 6, *Gluconobacter thailandicus* FR36C4; 7, *Komagataeibacter melaceti* SPV-2.

three days incubation on YPM medium at 28°C. Colonies are round, raised and brownish beige colored with a diameter of 1.0 mm. Catalase-positive and oxidase-negative. Positive for glucose fermentation and aesculin hydrolysis; but negative for nitrate reduction, indole production, arginine dihydrolase, urease and gelatin hydrolysis. According to API 20 NE test results, it assimilates D-glucose and D-mannitol; but does not assimilate L-arabinose, D-mannose, *N*-acetylglucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. According to API 50CH test results, acid is produced from glycerol, erythritol, D-arabinose, L-arabinose, D-ribose, D-xylose, L-xylose, D-adonitol, D-galactose, D-glucose, D-fructose, D-mannose, inositol, D-mannitol, D-sorbitol, D-melibiose, D-saccharose, gentiobiose, D-lyxose, D-fucose, D-arabitol and potassium 5-ketogluconate; but not produced from methyl- $\beta$ -D-xylopyranoside, L-sorbose, L-rhamnose, dulcitol, methyl- $\alpha$ -D-mannopyranoside, methyl- $\alpha$ -D-glucopyranoside, *N*-acetylglucosamine, amygdalin, arbutin, esculin ferric citrate, salicin, D-cellobiose, D-maltose, D-lactose, D-trehalose, inulin, D-melezitose, D-raffinose, amidon, glycogen, xylitol, D-turanose, D-tagatose, L-fucose, L-arabitol, potassium gluconate and potassium 2-ketogluconate. Strain BGF2-R2 (= KACC 22053) was isolated from fruit of *Prunus armeniaca* sampled from Suwon-si, Gyeonggi-do. The GenBank accession number for the 16S rRNA gene sequence of strain BGF2-R2 is ON746595.

#### Description of *Gluconobacter kondonii* FR39A4 (= KACC 22388)

Cells are Gram-stain-negative, non-flagellated, non-pigmented, and rod shaped (1.0–1.1  $\mu\text{m} \times 1.6$ –2.2  $\mu\text{m}$ ) after three days incubation on YPM medium at 28°C. Colonies are round, raised and brownish beige colored with a diameter of 0.8 mm. Catalase-positive and oxidase-negative. Positive for glucose fermentation and aesculin hydrolysis; but negative for nitrate reduction, indole production, arginine dihydrolase, urease and gelatin hydrolysis. According to API 20 NE test results, it assimilates D-glucose; but does not assimilate L-arabinose, D-mannose, D-mannitol, *N*-acetylglucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. According to API 50CH test results, acid is produced from glycerol, erythritol, L-arabinose, D-ribose, D-xylose, D-galactose, D-glucose, D-fructose, D-mannose, D-melibiose, gentiobiose, D-lyxose, D-fucose and potassium 5-ketogluconate; but not produced from D-arabinose, L-xylose, D-adonitol, methyl- $\beta$ -D-xylopyranoside, L-sorbose, L-rhamnose, dulcitol, inositol, D-mannitol, D-sorbitol, methyl- $\alpha$ -D-mannopyranoside, methyl- $\alpha$ -D-glucopyranoside, *N*-acetylglucosamine, amygdalin, arbutin, esculin ferric citrate, salicin, D-cellobiose, D-maltose, D-lactose, D-saccharose, D-trehalose, inulin, D-melezitose, D-raffinose, amidon, glycogen, xylitol, D-turanose, D-tagatose, L-fucose, D-arabitol, L-arabitol, potassium gluconate and potassium 2-ketogluconate. Strain

**Table 2.** Differential phenotypic characteristics among the isolated strains classified into the family.

Characteristics	1	2	3	4	5	6	7
Cell Shape	R	R	R	R	R	R	R or C
Cell size ( $\mu\text{m}$ )	0.8–1.0 $\times$ 1.4–2.3	0.9–1.1 $\times$ 1.6–2.2	0.9–1.0 $\times$ 1.6–2.3	0.7–0.9 $\times$ 1.6–2.3	1.0–1.1 $\times$ 1.6–2.2	0.9–1.1 $\times$ 1.5–2.4	1.0–1.5 $\times$ 1.4–3.0
Flagellum	Absent	Present	Present	Absent	Absent	Present	Absent
Glucose fermentation	+	+	+	+	+	+	-
Assimilation							
L-Arabinose	+	+	-	-	-	-	-
D-Mannose	+	+	-	-	-	-	-
D-Mannitol	+	+	-	+	-	+	-
N-Acetylglucosamine	-	+	-	-	-	-	-
Potassium gluconate	+	+	+	-	-	-	-
Acid production							
Glycerol	+	+	-	+	+	+	-
Erythritol	+	+	-	+	+	+	-
D-Arabinose	-	+	-	+	-	+	-
L-Xylose	-	+	-	+	-	-	-
D-Adonitol	+	+	-	+	-	-	-
D-Fructose	+	+	+	+	+	-	-
L-Sorbose	+	+	-	-	-	-	-
L-Rhamnose	+	-	-	-	-	-	-
Dulcitol	+	-	-	-	-	-	-
Inositol	+	+	-	+	-	-	-
D-Mannitol	+	-	-	+	-	-	-
D-Sorbitol	+	-	-	+	-	-	-
N-Acetylglucosamine	+	-	-	-	-	-	-
D-Saccharose	-	+	-	+	-	+	+
D-Trehalose	-	-	-	-	-	-	+
D-Raffinose	-	+	-	-	-	-	+
Xylitol	+	+	-	-	-	-	-
Gentiobiose	+	+	-	+	+	+	+
D-Lyxose	+	+	+	+	+	+	-
D-Tagatose	+	+	-	-	-	-	-
L-Fucose	+	+	-	-	-	-	-
D-Arabitol	+	+	-	+	-	-	-
L-Arabitol	+	+	-	-	-	-	-
Potassium 5-ketogluconate	-	-	-	+	+	+	+

Strain: 1, *Asaia lannensis* AF11C3 (=KACC 22050); 2, *Asaia platycodi* AF15C2 (=KACC 22051); 3, *Gluconacetobacter liquefaciens* C23-3 (=KACC 22064); 4, *Gluconobacter cerinus* BGF2-R2 (=KACC 22053); 5, *Gluconobacter kondonii* FR39A4 (=KACC 22388); 6, *Gluconobacter thailandicus* FR36C4 (=KACC 22057); 7, *Komagataeibacter melaceti* SPV-2 (=KACC 22058). All strains are positive for catalase and aesculin hydrolysis, but negative for Gram-staining, oxidase, nitrate reduction, indole production, arginine dihydrolase, urease and gelatine hydrolysis. R, rod; C, cocci; +, Positive; -, negative.

FR39A4 (=KACC 22388) was isolated from persimmon fruit sampled from Cheongdo-gun, Gyeongsangbuk-do. The GenBank accession number for the 16S rRNA gene sequence of strain FR39A4 is ON746626.

#### Description of *Gluconobacter thailandicus* FR36C4 (=KACC 22057)

Cells are Gram-stain-negative, flagellated, non-pig-

mented and rod shaped (0.9–1.1  $\mu\text{m} \times$  1.5–2.4  $\mu\text{m}$ ) after three days incubation on YPM medium at 28°C. Colonies are round, raised and brownish beige colored with a diameter of 1.0 mm. Catalase-positive and oxidase-negative. Positive for glucose fermentation and aesculin hydrolysis; but negative for nitrate reduction, indole production, arginine dihydrolase, urease and gelatin hydrolysis. According to API 20 NE test results, it assimilates D-glucose and D-mannitol; but does not assimilate L-arabinose,

D-mannose, *N*-acetylglucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. According to API 50CH test results, acid is produced from glycerol, erythritol, D-arabinose, L-arabinose, D-ribose, D-xylose, D-galactose, D-glucose, D-mannose, D-melibiose, D-saccharose, gentiobiose, D-lyxose, D-fucose and potassium 5-ketogluconate; but not produced from L-xylose, D-adonitol, methyl- $\beta$ -D-xylopyranoside, D-fructose, L-sorbose, L-rhamnose, dulcitol, inositol, D-mannitol, D-sorbitol, methyl- $\alpha$ -D-mannopyranoside, methyl- $\alpha$ -D-glucopyranoside, *N*-acetylglucosamine, amygdalin, arbutin, esculin ferric citrate, salicin, D-cellobiose, D-maltose, D-lactose, D-trehalose, inulin, D-melezitose, D-raffinose, amidon, glycogen, xylitol, D-turanose, D-tagatose, L-fucose, D-arabitol, L-arabitol, potassium gluconate and potassium 2-ketogluconate. Strain FR36C4 (=KACC 22057) was isolated from fruit of *Pseudocystodonia sinensis* sampled from Jeonju-si, Jeollabuk-do. The GenBank accession number for the 16S rRNA gene sequence of strain FR36C4 is ON746599.

#### Description of *Komagataeibacter melaceti* SPV-2 (= KACC 22058)

Cells are Gram-stain-negative, non-flagellated, non-pigmented, and rod or coccus shaped (1.0–1.5  $\mu\text{m}$   $\times$  1.4–3.0  $\mu\text{m}$ ) after three days incubation on YPM medium at 28°C. Colonies are round, raised and brownish beige colored with a diameter less than 0.1 mm. Catalase-positive and oxidase-negative. Positive for aesculin hydrolysis; but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease and gelatin hydrolysis. According to API 20 NE test results, it assimilates D-glucose; but does not assimilate L-arabinose, D-mannose, D-mannitol, *N*-acetylglucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. According to API 50CH test results, acid is produced from L-arabinose, D-ribose, D-xylose, D-galactose, D-glucose, D-mannose, D-melibiose, D-saccharose, D-trehalose, D-raffinose, gentiobiose, D-fucose and potassium 5-ketogluconate; but not produced from glycerol, erythritol, D-arabinose, L-xylose, D-adonitol, methyl- $\beta$ -D-xylopyranoside, D-fructose, L-sorbose, L-rhamnose, dulcitol, inositol, D-mannitol, D-sorbitol, methyl- $\alpha$ -D-mannopyranoside, methyl- $\alpha$ -D-glucopyranoside, *N*-acetylglucosamine, amygdalin, arbutin, esculin ferric citrate, salicin, D-cellobiose, D-maltose, D-lactose, inulin, D-melezitose, amidon, glycogen, xylitol, D-turanose, D-lyxose, D-tagatose, L-fucose, D-arabitol, L-arabitol, potassium gluconate and potassium 2-ketogluconate. Strain SPV-2 (=KACC 22058) was isolated from potato vinegar sampled from Haenam-gun, Jeollanam-do. The GenBank accession number for the 16S rRNA gene sequence of strain SPV-2 is ON746600.

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