

A report of 11 unrecorded bacterial species in Korea isolated in 2017

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Eleven bacterial strains 17SD2_15, 17Sr1_23, 17SD2_13, 17Sr1_31, 17gy_18, 16B15D, 16B02D, 16B04G, 16B01D, 17U4-2 and 17J28-10 assigned to the phylum *Proteobacteria* were isolated from soil samples collected from Seoul Women's University, in South Korea. The *Belnapia* species, strain 17SD2_15 was cocci-shaped and pink-colored. The *Methylobacterium* species, strain 17Sr1_23, 17SD2_13, 17Sr1_31, and 16B15D were short rod-shaped and pink-colored. The *Microvirga* species, strain 17gy_18, and 16B02D were short rod-shaped and pink-colored. The *Oxalicibacterium* species, strain 16B04G was short rod-shaped and pink-colored. The *Sphingomonas* species, strain 16B01D was short rod-shaped and yellow-colored. The *Variovorax* species, strain 17U4-2 was cocci-shaped and yellow-colored. The *Paracoccus* species, 17J28-10 was cocci-shaped and orange-colored. Phylogenetic analysis based on 16S rRNA gene sequence showed that strains 17SD2_15, 17Sr1_23, 17SD2_13, 17Sr1_31, 17gy_18, 16B15D, 16B02D, 16B04G, 16B01D, 17U4-2 and 17J28-10 were most closely related to *Belnapia soli* (with 99.9% similarity), *Methylobacterium gregans* (99.1%), *Methylobacterium isbiliense* (99.6%), *Methylobacterium oxalidis* (99.9%), *Microvirga aerilata* (98.7%), *Methylobacterium aerolatum* (99.0%), *Microvirga vignae* (100.0%), *Noviherbaspirillum canariense* (100.0%), *Sphingomonas desiccabilis* (100.0%), *Variovorax humicola* (99.6%), and *Paracoccus acridae* (99.1%), respectively. This is the first report of these eleven species in Korea.

Keywords: 16S rRNA, bacterial diversity, *Proteobacteria*, unreported species

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DOI:10.12651/JSR.2018.7.2.135

INTRODUCTION

In 2017, eleven unreported species were isolated from diverse soil samples collected in Korea. The current report focuses on the description of eleven unreported bacterial species belonging to phylum *Proteobacteria* that have not officially reported in Korea.

Six bacterial strains 17Sr1_23, 17SD2_13, 17Sr1_31, 17gy_18, 16B15D and 16B02D belong to the family *Methylobacteriaceae*. The family *Methylobacteriaceae* is one of the large family of *Alphaproteobacteria* (Garrity *et al.*, 2005a; Kelly *et al.*, 2014) and at present contains three genera, *Methylobacterium*, *Microvirga* and *Meganema* (<http://www.bacterio.net/>). The genus *Methylobacterium* is one of the largest genus containing 44 validated species. They are facultative methylotrophs able to grow on methanol and other one-carbon compounds as sources

of energy and carbon (Gallego *et al.*, 2005; Konovalova *et al.*, 2007; Cao *et al.*, 2011). The family *Methylobacteriaceae* are pink-pigmented and contain ubiquinone Q-10. The eight species of *Microvirga* and the single species of *Meganema* are not methylotrophic (Kanso and Patel 2003; Weon *et al.*, 2010; Ardley *et al.*, 2012).

Remaining five Strains 17SD2_15, 16B04G, 16B01D, 17U4-2 and 17J28-10 belonged to the family *Acetobacteraceae*, *Oxalobacteraceae*, *Sphingomonadaceae*, *Comamonadaceae*, and *Rhodobacteraceae*, respectively. *Acetobacteraceae* are included in the order *Rhodospirillales* and 32 genera are validly published (<http://www.bacterio.net/-classifphyla.html#rhodospirillales>). The genera in the family *Acetobacteraceae* are basically classified into two groups, an acetous group and an acidophilic group, in the light of application, ecology, and phylogeny (Komagata *et al.*, 2014).

Table 1. 16S rRNA gene sequence similarity, isolation source, medium, and incubation conditions of unrecorded strains.

Strain ID	Most closely related species	Similarity (%)	Isolation source	Medium	Incubation conditions
17SD2_15	<i>Belnapia soli</i>	99.9	Soil	R2A	25°C, 3d
17Sr1_23	<i>Methylobacterium gregans</i>	99.1	Soil	R2A	25°C, 3d
17SD2_13	<i>Methylobacterium isbiliense</i>	99.6	Soil	R2A	25°C, 3d
17Sr1_31	<i>Methylobacterium oxalidis</i>	99.9	Soil	R2A	25°C, 3d
17gy_18	<i>Microvirga aerilata</i>	98.7	Soil	R2A	25°C, 3d
16B15D	<i>Methylobacterium aerolatum</i>	99.0	Soil	R2A	25°C, 3d
16B02D	<i>Microvirga vignae</i>	100.0	Soil	R2A	25°C, 3d
16B04G	<i>Oxalicibacterium flavum</i>	100.0	Soil	R2A	25°C, 3d
16B01D	<i>Sphingomonas desiccabilis</i>	100.0	Soil	R2A	25°C, 3d
17U4-2	<i>Variovorax humicola</i>	99.6	Soil	R2A	25°C, 3d
17J28-10	<i>Paracoccus acridae</i>	99.1	Soil	R2A	25°C, 3d

The family *Oxalobacteraceae* which contains the 13 genera (Xu *et al.*, 2005) is belonged to the order *Burkholderiales*. The family *Sphingomonadaceae* was proposed based on the 16S rRNA gene sequence phylogeny and the presence of 2'-hydroxymyristol dihydrosphingosine 1-glucuronic acid (SGL-1) as major sphingoglycolipid in the cellular lipids (Kosako *et al.*, 2000). *Sphingomonadaceae* is belonged to the order *Sphingomonadales* which contains the 18 genera at the time of writing (<http://www.bacterio.net/-classifphylo.html#sphingomonadaceae>). The *Sphingomonadaceae* family was proposed based on the 16S rRNA gene sequence phylogeny and the presence of 2'-hydroxymyristol dihydrosphingosine 1-glucuronic acid (SGL-1) as major sphingoglycolipid in the cellular lipids (Kosako *et al.* 2000).

The family *Comamonadaceae* is one of the biggest family belonging to the order *Burkholderiales* in which contains 37 genera (<http://www.bacterio.net/-classifphylo.html#comamonadaceae>). These genera form a phylogenetic cluster based on 16S rRNA gene sequence similarity of 93-97% yet, have a diverse phenotypic characteristic that includes aerobic organotrophs, anaerobic denitrifiers, Fe³⁺-reducing bacteria, hydrogen oxidizers, photoautotrophic and photoheterotrophic bacteria, and fermentative bacteria (Willems *et al.*, 1991).

The family *Rhodobacteraceae* are basically, aquatic bacteria that frequently thrive in marine environments. They include mainly aerobic photo- and chemoheterotrophs but also purple non-sulfur bacteria which perform photosynthesis in anaerobic environments. They are deeply involved in sulfur and carbon biogeochemical cycling and symbiosis with aquatic micro- and macroorganisms (Garrity *et al.*, 2005b).

MATERIAL AND METHODS

Different soil samples were collected and suspended

in distilled water and serially diluted. The 100 µL of the aliquot was inoculated onto R2A agar and incubated at 25°C for 3 days. The designated strain IDs, isolation sources, growth media, and incubation conditions are summarized in Table 1. All strains were purified as single colonies and stored as 20% glycerol suspension at -80°C as well as freeze-dried ampoules.

The colony morphology and cell size of the strains were observed by transmission electron microscopy (LI BRA 120, Carl Zeiss) using cells grown for 3 days at 25°C on R2A agar. Transmission electron micrograph of the strains are shown in Fig. 1. Gram reaction was performed following the classic Gram procedure described by Doetsch (1981). Biochemical characteristics were tested by using Biolog Microstation with GEN III microplate system. A single colony was selected and emulsified into 'inoculating fluid A' (Biolog) for subsequent inoculation on to the Microplate test plate (Biolog). More fastidious organisms, including capnophilic strains, were cultured on alternative media, according to the manufacturer's instructions, and inocula were prepared to a specified transmittance using a turbidimeter, as specified in the user guide. For each isolate, 100 µL of the cell suspension was inoculated into each well of the microplate, using a multichannel pipette and incubated at 37°C for 24 h, according to growth characteristics. Microplates were read in the MicroStation semi-automated reader after 24 h and results interpreted by the identification system's software (GEN III database, version 5.2.1). Whereas the system which indicates that the isolates could not be identified after 20 h and required further incubation. Such isolates were re-incubated and re-read between 3 and 6 h later (Wragg *et al.*, 2014). Genomic DNA was extracted and 16S rRNA gene was amplified by PCR with 9F and 1492R universal bacterial primers (Weisburg *et al.*, 1991). The 16SrRNA gene sequences of the closely related strains were obtained from EzTaxon-e (<http://eztaxon-e.ezbiocloud.net>) (Kim *et al.*, 2012) and edited

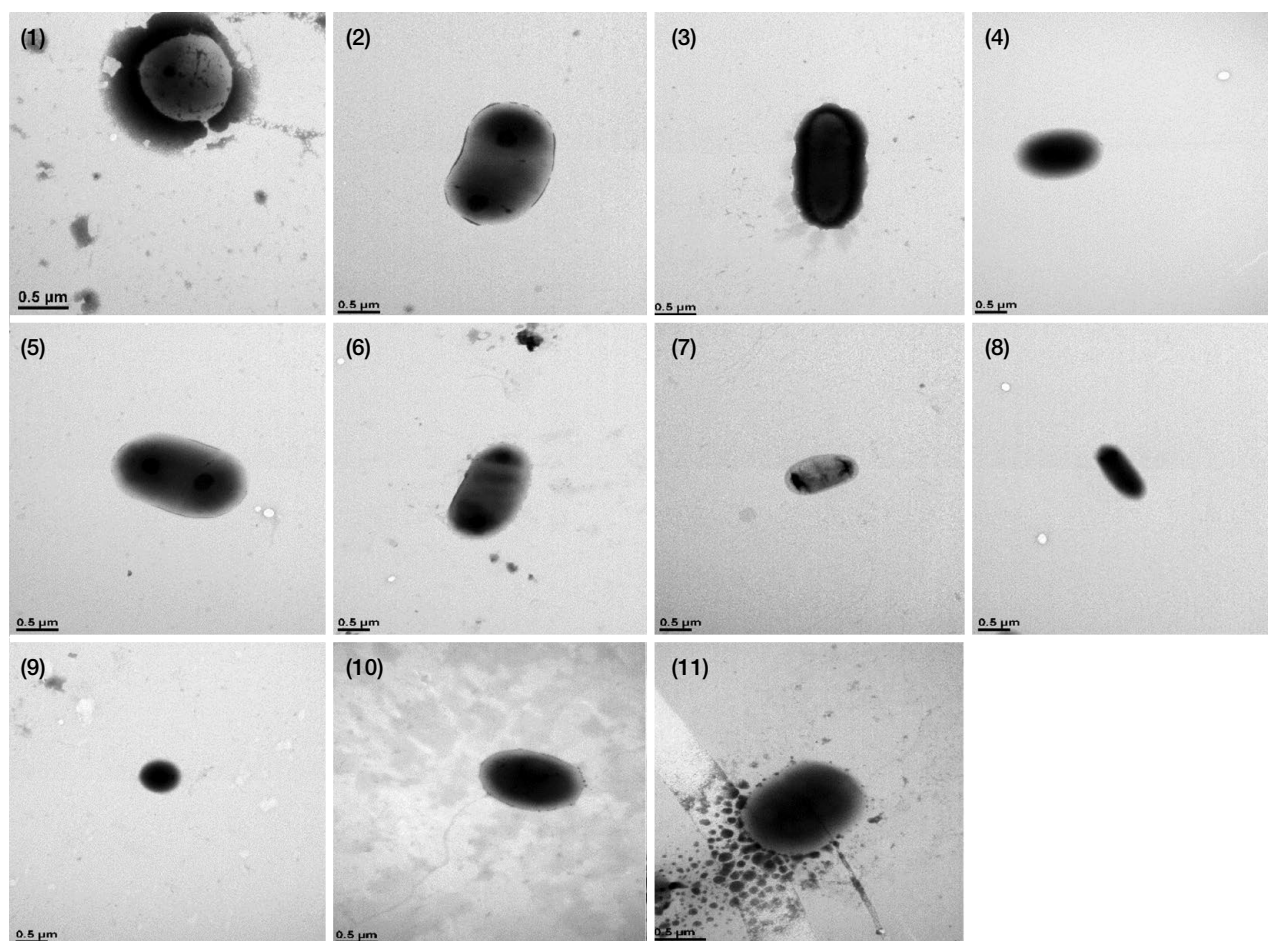


Fig. 1. Transmission electron micrographs of the strains isolated in this study. Strains: 1, 17SD2_15; 2, 17Sr1_23; 3, 17SD2_13; 4, 17Sr1_31; 5, 17gy_18; 6, 16B15D; 7, 16B02D; 8, 16B04G; 9, 16B01D; 10, 17U4-2; 11, 17J28-10.

using the BioEdit program (Hall, 1999). Multiple alignments were performed with the MUSCL program (Edgar, 2004). Using the two-parameter model (Kimura, 1983) calculated the evolutionary distances. Phylogenetic trees were constructed using the neighbor-joining (Saitou and Nei, 1987) in the MEGA5 program (Tamura, 2011) with bootstrap values based on 1,000 replications (Felsenstein, 1985).

RESULTS AND DISCUSSION

Based on 16S rRNA gene sequence similarity, 11 of previously unreported bacterial species were identified. The taxonomic composition and identification results are summarized in Table 1. The 11 strains were assigned to the family *Acetobacteraceae* (1 strain), *Methylobacteriaceae* (6 strain), *Oxalobacteraceae* (1 strain), and *Sphingomonadaceae* (1 strain), *Comamonadaceae* (1 strain), *Rhodobacteraceae* (1 strain) of the phylum *Proteobacteria*. At the generic level, the strains belong to 7

different genera: *Belnapia* (1 species), *Methylobacterium* (4 species), *Microvirga* (2 species), *Sphingomonas* (1 species), *Oxalicibacterium* (1 species), *Variovorax* (1 species), and *Paracoccus* (1 species). The identification of the isolates based on sequence similarity was supported by the phylogenetic trees. The neighbor-joining trees show the close relationship of the isolates and type strains of validly published species (Fig. 1). The detailed morphological and physiological characteristics are given in the strain descriptions.

As an outcome of this study, the diversity of radiation-resistant bacterial species is not reported previously in Korean ecosystems was discovered. The 11 isolates were identified as unreported species, and their phenotypic characteristics were examined through polyphasic study. Accordingly, the following 11 species are unreported species in Korea.

Description of *Belnapia soli* 17SD2_15

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

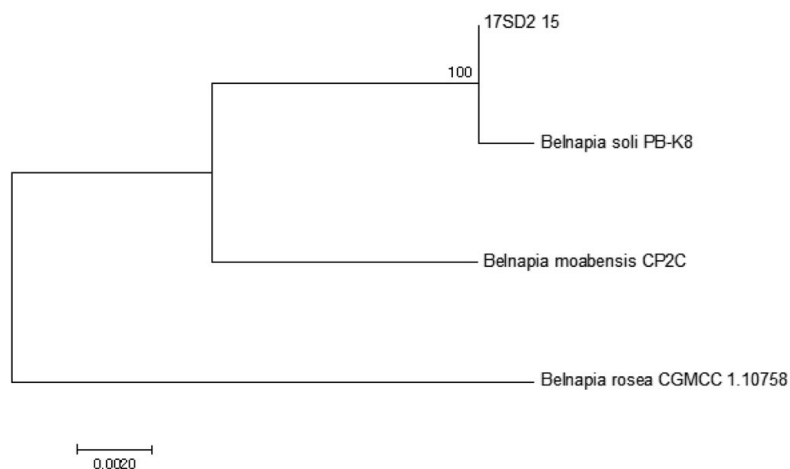


Fig. 2. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences shows the relationship between the strains isolated in this study and their relatives of the genus *Belnapia*. Bootstrap values (>70%) are shown above nodes for the neighbor-joining methods. Bar: 0.01 and 0.02 substitutions per nucleotide position, respectively.

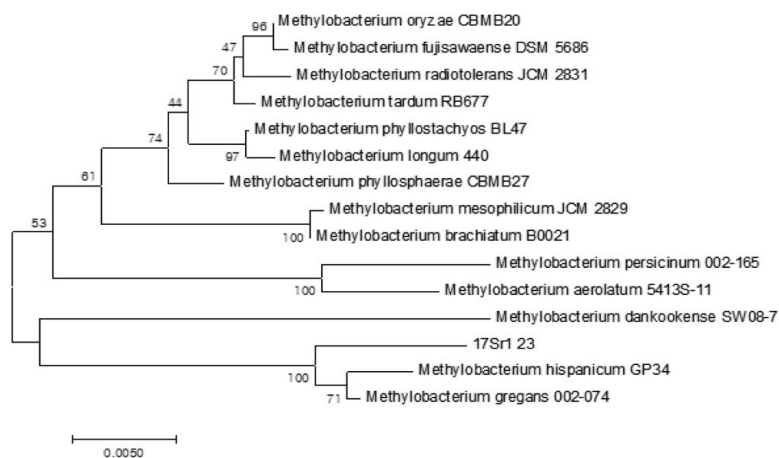


Fig. 3. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences shows the relationship between the strains isolated in this study and their relatives of the genus *Methylobacterium*. Bootstrap values (>70%) are shown above nodes for the neighbor-joining methods. Bar: 0.01 and 0.02 substitutions per nucleotide position, respectively.

coccus-shaped. Colonies are pale pinkish-colored after 3 days of incubation on R2A at 25°C. In the BIOLOG GEN III, D-glucuronic acid was utilized as a sole carbon source. But acetoacetic acid, *N*-acetyl-D-mannosamine, L-alanine, L-arginine, L-aspartic acid, D-cellobiose, dextrin, D-fructose, D-fructose 6-PO₄, L-galactonic acid lactone, D-galactose, D-galacturonic acid, gelatin, gentiobiose, D-gluconic acid, α -D-glucose, glucuronamide, L-glutamic acid, inosine, α -keto-glutaric acid, L-malic acid, D-maltose, D-mannitol, D-mannose, D-melibiose, β -methyl-D-glucoside, 3-methyl glucose, myo-inositol, pectin, propionic acid, glycyl-L-proline, L-pyroglytamic acid, quinic acid, D-raffinose, L-rhamnose, L-serine, stachyose, sucrose, D-trehalose, D-turanose, acetic

acid, *N*-acetyl-D-galactosamine, *N*-acetyl-neuraminic acid, *N*-acetyl-D-glucosamine, γ -amino-butyric acid, D-arabitol, D-aspartic acid, bromo-succinic acid, citric acid, formic acid, D-fucose, L-fucose, D-glucose-6-PO₄, glycerol, L-histidine, α -hydroxybutyric acid, β -hydroxy-D, L-butyric acid, *p*-hydroxy-phenylacetic acid, α -keto-butyric acid, L-lactic acid, D-lactic acid methyl ester, α -D-lactose, D-malic acid, methyl pyruvate, mucic acid, D-saccharic acid, D-salicin, D-serine, D-sorbitol, and tween 40 were not utilized. In sensitivity tests, the tetrazolium redox dye was reduced at pH 6 but not at 1% NaCl, 1% sodium lactate, 4% NaCl, 8% NaCl, guanidine HCl, lithium chloride, pH 6, potassium tellurite, D-serine, sodium butyrate, aztreonam, fusidic acid,

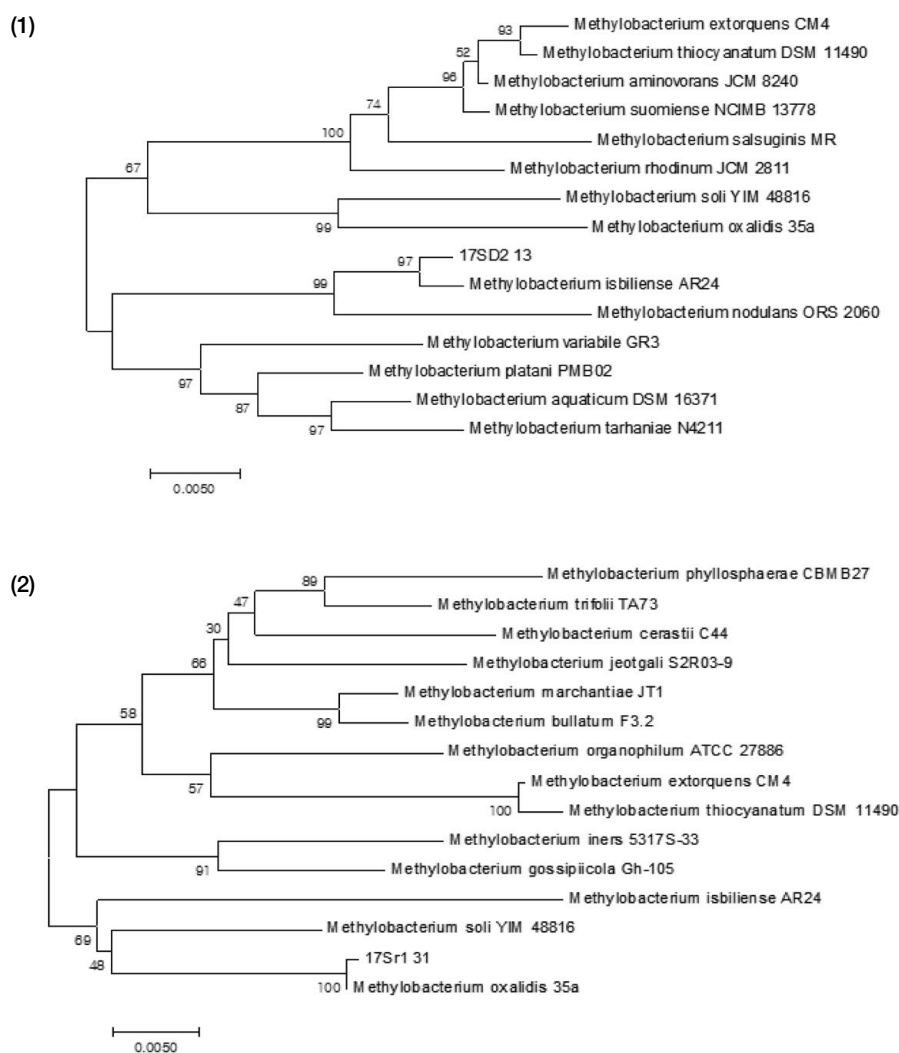


Fig. 4. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences shows the relationship between the strains isolated in this study and their relatives of the genus *Methylobacterium* (1), (2). Bootstrap values (>70%) are shown above nodes for the neighbor-joining methods. Bar: 0.01 and 0.02 substitutions per nucleotide position, respectively.

lincomycin, minocycline, nalidixic acid, niaproof 4, pH 5, rifamycin SV, sodium bromate, tetrazolium blue, troleandomycin, and vancomycin.

In API 20NE system, positive for arginine dihydrolase and urease. Negative for nitrate reduction, indole production, glucose fermentation, esculin hydrolysis, gelatin hydrolysis, and β -galactosidase. Uses D-glucose, potassium gluconate, adipic acid, malic acid, and trisodium citrate but not L-arabinose, D-mannose, D-mannitol, *N*-acetyl-glucosamine, capric acid, D-maltose, and phenyl acetic acid as carbon sources.

In API 32GN system, positive for itaconic acid, suberic acid, sodium malonate, sodium acetate, lactic acid, L-serine, propionic acid, capric acid, potassium 2-ketogluconate, 3-hydroxybutyric acid, 4-hydroxybenzoic acid, and L-proline. Negative for L-rhamnose, *N*-acetyl-glucos-

amine, D-ribose, inositol, D-saccharose (sucrose), D-maltose, L-alanine, potassium 5-ketogluconate, glycogen, 3-hydroxybenzoic acid, D-mannitol, D-glucose, salicin, D-melibiose, D-fucose, D-sorbitol, L-arabinose, valeric acid, trisodium citrate, and L-histidine. Strain 17SD2_15 (= NIBRBAC000500510) was isolated from a soil sample.

Description of *Methylobacterium gregans* 17Sr1_23

Cells are Gram-stain-negative, non-flagellated, and short rod-shaped. Colonies are pink-colored after 3 days of incubation on R2A at 25°C. In the BIOLOG GEN III, D-glucuronic acid and formic acid is utilized as a sole carbon source. But acetoacetic acid, *N*-acetyl-D-mannosamine, L-alanine, L-arginine, L-aspartic acid, D-cel-

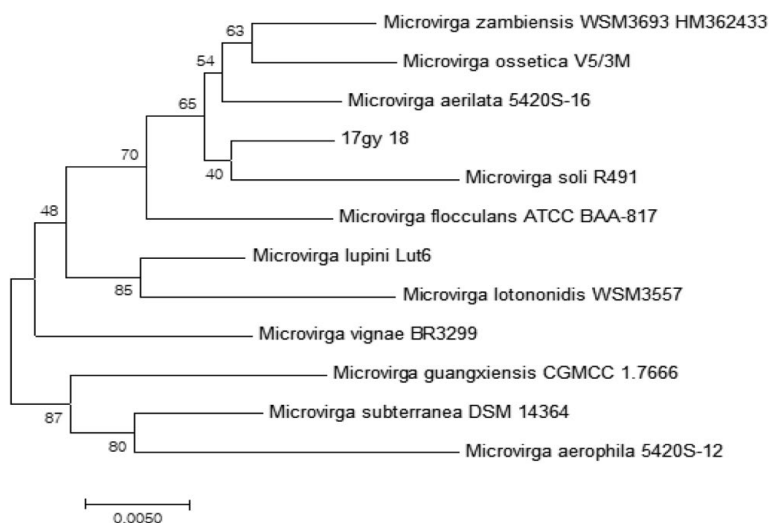


Fig. 5. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences shows the relationship between the strains isolated in this study and their relatives of the genus *Microvirga*. Bootstrap values (>70%) are shown above nodes for the neighbor-joining methods. Bar: 0.01 and 0.02 substitutions per nucleotide position, respectively.

lobiose, dextrin, D-fructose, D-fructose 6-PO₄, L-galactonic acid lactone, D-galactose, D-galacturonic acid, gelatin, gentiobiose, D-gluconic acid, α -D-glucose, glucuronamide, L-glutamic acid, inosine, α -keto-glutaric acid, L-malic acid, D-maltose, D-mannitol, D-mannose, D-melibiose, β -methyl-D-glucoside, 3-methyl glucose, myo-inositol, pectin, propionic acid, glycyl-L-proline, L-pyroglytamic acid, quinic acid, D-raffinose, L-rhamnose, L-serine, stachyose, sucrose, D-trehalose, D-turanose acetic acid, *N*-acetyl-D-galactosamine, *N*-acetyl-neuraminic acid, *N*-acetyl-D-glucosamine, γ -amino-butyric acid, D-arabitol, D-aspartic acid, bromo-succinic acid, citric acid, D-fucose, L-fucose, D-glucose-6-PO₄, glycerol, L-histidine, α -hydroxybutyric acid, β -hydroxy-D,L-butyric acid, *p*-hydroxy-phenylacetic acid, α -keto-butyric acid, L-lactic acid, D-lactic acid methyl ester, α -D-lactose, D-malic acid, methyl pyruvate, mucic acid, D-saccharic acid, D-salicin, D-serine, D-sorbitol, and tween 40 were not utilized. In sensitivity tests, the tetrazolium redox dye is reduced in the presence of lincomycin, vancomycin, tetrazolium blue, nalidixic acid, potassium tellurite, and aztreonam; but not in the presence of 1% NaCl, 1% sodium lactate, 4% NaCl, 8% NaCl, guanidine HCl, lithium chloride, pH 6, D-serine, sodium butyrate, tetrazolium violet fusidic acid, minocycline, niaproof 4, pH 5, rifamycin SV, sodium bromate, and troleandomycin.

In API 20NE system, positive for the reduction of nitrates (NO₃) to nitrogen (N₂), arginine dihydrolase, urease, esculin hydrolysis, β -galactosidase, D-mannose, and D-maltose. Negative for the reduction of nitrates (NO₃) to nitrite (NO₂⁻), indole production on tryptophan, glucose

fermentation, gelatin hydrolysis, D-glucose, L-arabinose, D-mannitol, *N*-acetyl-D-glucosamine, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, and phenylacetic acid.

In API 32GN system, positive for itaconic acid, suberic acid, lactic acid, L-alanine, propionic acid, trisodium citrate, and 3-hydroxybutyric acid. Negative for L-rhamnose, *N*-acetyl-glucosamine, D-ribose, inositol, D-saccharose (sucrose), D-maltose, sodium malonate, sodium acetate, potassium 5-ketogluconate, glycogen, 3-hydroxybenzoic acid, L-serine, D-mannitol, D-glucose, salicin, D-melibiose, D-fucose, D-sorbitol, L-arabinose, capric acid, valeric acid, L-histidine, potassium 2-ketogluconate, 4-hydroxybenzoic acid, and L-proline. Strain 17Sr1_23 (=NIBRBAC000500515) was isolated from a soil sample.

Description of *Methylobacterium isbiliense* 17SD2_13

Cells are Gram-stain-negative, non-flagellated, and short rod-shaped. Colonies are pink-colored after 3 days of incubation on R2A at 25°C. In the BIOLOG GEN III acetoacetic acid, *N*-acetyl-D-mannosamine, L-alanine, L-arginine, L-aspartic acid, D-cellobiose, dextrin, D-fructose, D-fructose 6-PO₄, L-galactonic acid lactone, D-galactose, D-galacturonic acid, gelatin, gentiobiose, D-gluconic acid, α -D-glucose, glucuronamide, D-gluconic acid, L-glutamic acid, inosine, α -keto-glutaric acid, L-malic acid, D-maltose, D-mannitol, D-mannose, D-melibiose, β -methyl-D-glucoside, 3-methyl glucose, myo-inositol, pectin, propionic acid, glycyl-L-proline, L-pyroglytamic acid, quinic acid, D-raffinose, L-rham-

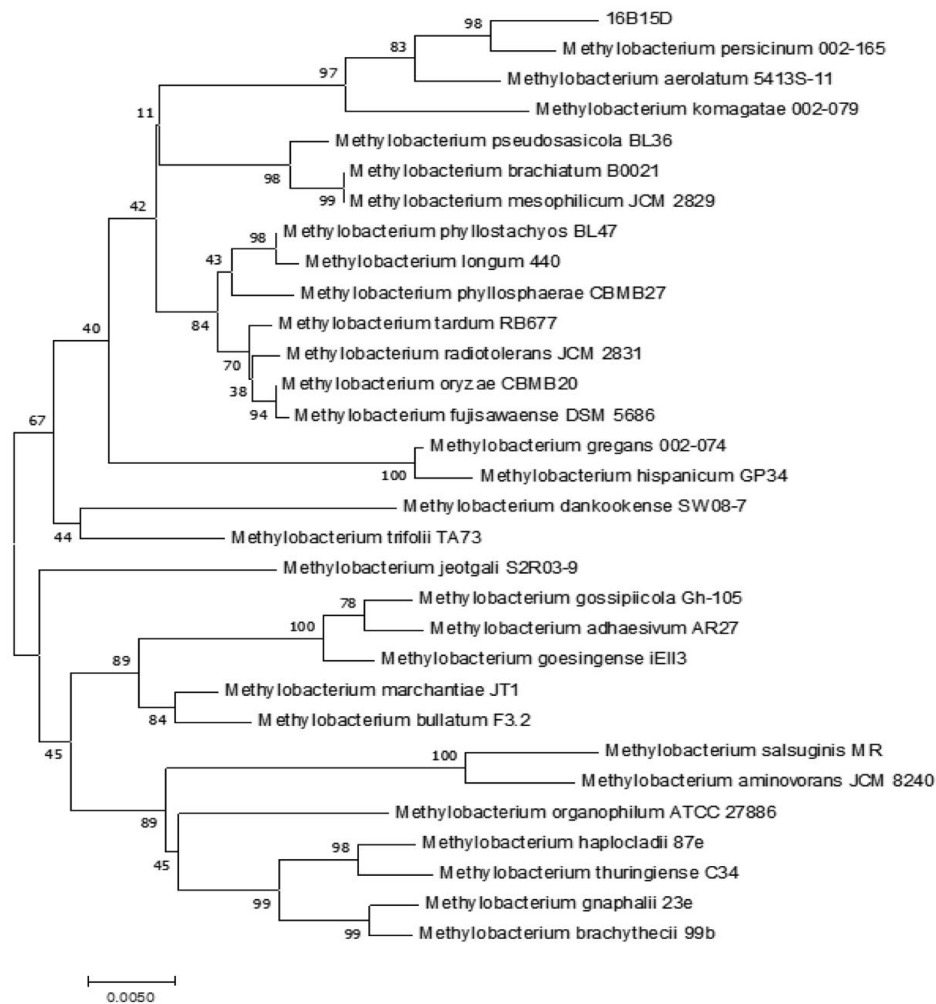


Fig. 6. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences shows the relationship between the strains isolated in this study and their relatives of the genus *Methylobacterium*. Bootstrap values (>70%) are shown above nodes for the neighbor-joining methods. Bar: 0.01 and 0.02 substitutions per nucleotide position, respectively.

nose, L-serine, stachyose, sucrose, D-trehalose, D-turanose, acetic acid, *N*-acetyl-D-galactosamine, *N*-acetyl-neuraminic acid, *N*-acetyl-D-glucosamine, γ -amino-butyric acid, D-arabitol, D-aspartic acid, bromo-succinic acid, citric acid, formic acid, D-fucose, L-fucose, D-glucose-6-PO₄, glycerol, L-histidine, α -hydroxybutyric acid, β -hydroxy-D, L-butyric acid, *p*-hydroxy-phenylacetic acid, α -keto-butyric acid, L-lactic acid, D-lactic acid methyl ester, α -D-lactose, D-malic acid, methyl pyruvate, mucic acid, D-saccharic acid, D-salicin, D-serine, D-sorbitol, and tween 40 were not utilized. In sensitivity tests, the tetrazolium redox dye is reduced in the presence of tetrazolium violet, tetrazolium blue, and aztreonam; but not in the presence of 1% NaCl, 1% sodium lactate, 4% NaCl, 8% NaCl, guanidine HCl, lithium chloride, pH 6, potassium tellurite, D-serine, sodium butyrate, fusidic acid, lincomycin, minocycline, nalidix-

ic acid, niaproof 4, pH 5, rifamycin SV, sodium bromate, troleandomycin, and vancomycin.

In API 20NE system, positive for the reduction of nitrates (NO₃) to nitrite (NO₂⁻), arginine dihydrolase, urease, esculin hydrolysis, β -galactosidase, D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, potassium gluconate, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Weak positive for gelatin hydrolysis. Negative for the reduction of nitrates (NO₃) to nitrogen (N₂), indole production on tryptophan, glucose fermentation, and capric acid.

In API 32GN system, positive for L-rhamnose, D-ribose, itaconic acid, suberic acid, sodium malonate, sodium acetate, lactic acid, potassium 2-ketogluconate, 3-hydroxybutyric acid, L-serine, D-glucose, L-arabinose, propionic acid, capric acid, valeric acid, trisodium citrate,

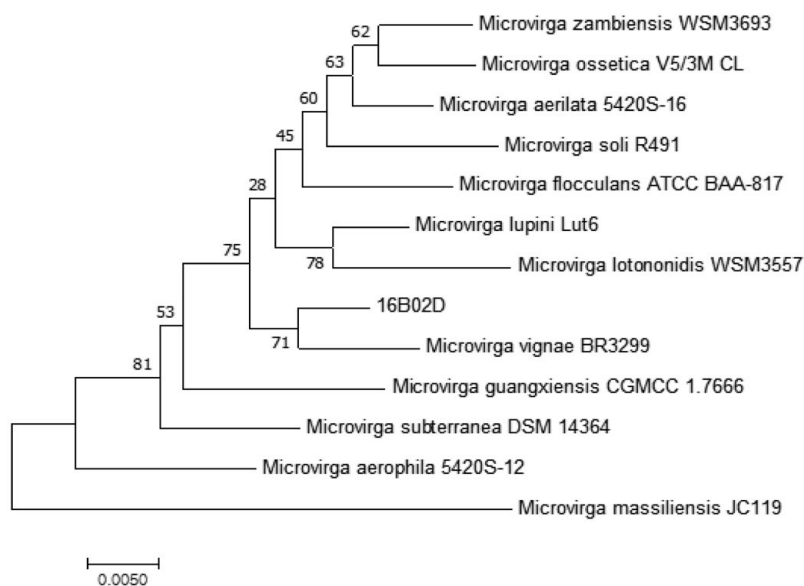


Fig. 7. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences shows the relationship between the strains isolated in this study and their relatives of the genus *Microvirga*. Bootstrap values (>70%) are shown above nodes for the neighbor-joining methods. Bar: 0.01 and 0.02 substitutions per nucleotide position, respectively.

4-hydroxybenzoic acid, L-proline, and 3-hydroxybenzoic acid. Negative for *N*-acetyl-glucosamine, inositol, D-saccharose (sucrose), D-maltose, L-alanine, potassium 5-ketogluconate, glycogen, L-serine, D-mannitol, salicin, D-melibiose, D-fucose, D-sorbitol, and L-histidine. Strain 17SD2_13 (= NIBRBAC000500516) was isolated from a soil sample.

Description of *Methylobacterium oxalidis* 17Sr1_31

Cells are Gram-stain-negative, non-flagellated, and short rod-shaped. Colonies are orange-colored after 3 days of incubation on R2A at 25°C. In the BIOLOG GEN III, L-malic acid and acetic acid is utilized as a sole carbon source. But acetoacetic acid, *N*-acetyl-D-mannosamine, L-alanine, L-arginine, L-aspartic acid, D-cellobiose, dextrin, D-fructose, D-fructose 6-PO₄, L-galactonic acid lactone, D-galactose, D-galacturonic acid, gelatin, gentiobiose, D-gluconic acid, α -D-glucose, glucuronamide, D-glucuronic acid, L-glutamic acid, inosine, α -keto-glutaric acid, D-maltose, D-mannitol, D-mannose, D-melibiose, β -methyl-D-glucoside, 3-methyl glucose, myo-inositol, pectin, propionic acid, glycyl-L-proline, L-pyroglutamic acid, quinic acid, D-raffinose, L-rhamnose, L-serine, stachyose, sucrose, D-trehalose, D-turanose, *N*-acetyl-D-galactosamine, *N*-acetyl-neuraminic acid, *N*-acetyl-D-glucosamine, γ -amino-butyric acid, D-arabitol, D-aspartic acid, bromo-succinic acid, citric acid, formic acid, D-fucose, L-fucose, D-glucose-6-PO₄, glycerol, L-histidine, α -hydroxybutyric acid, β -hy-

droxy-D, L-butyric acid, *p*-hydroxy-phenylacetic acid, α -keto-butyric acid, L-lactic acid, D-lactic acid methyl ester, α -D-lactose, D-malic acid, methyl pyruvate, mucic acid, D-saccharic acid, D-salicin, D-serine, D-sorbitol, and tween 40 were not utilized. In sensitivity tests, the tetrazolium redox dye is reduced in the presence of lincomycin, tetrazolium blue, aztreonam; but not in the presence of 1% NaCl, 1% sodium lactate, 4% NaCl, 8% NaCl, guanidine HCl, lithium chloride, pH 6, potassium tellurite, D-serine, sodium butyrate, tetrazolium violet fusidic acid, minocycline, nalidixic acid, niaproof 4, pH 5, rifamycin SV, sodium bromate, troleandomycin, and vancomycin.

In API 20NE system, positive for the reduction of nitrates (NO₃) to nitrite (NO₂⁻), arginine dihydrolase, urease, esculin hydrolysis, gelatin hydrolysis, β -galactosidase, D-glucose, L-arabinose, D-mannose, D-mannitol *N*-acetyl-D-glucosamine, D-maltose, potassium gluconate, adipic acid, malic acid, and trisodium citrate. Weak positive for phenylacetic acid. Negative for the reduction of nitrates (NO₃) to nitrogen (N₂), indole production on tryptophan, glucose fermentation, and capric acid.

In API 32GN system, positive for D-mannitol, D-glucose, D-sorbitol, valeric acid, and 3-hydroxybutyric acid. Negative for L-rhamnose, *N*-acetyl-glucosamine, D-ribose, inositol, D-saccharose (sucrose), D-maltose, itaconic acid, suberic acid, sodium malonate, sodium acetate, lactic acid, L-alanine, potassium 5-ketogluconate, glycogen, 3-hydroxybenzoic acid, L-serine, salicin, D-melibiose, D-fucose, L-arabinose, propionic acid, capric acid,

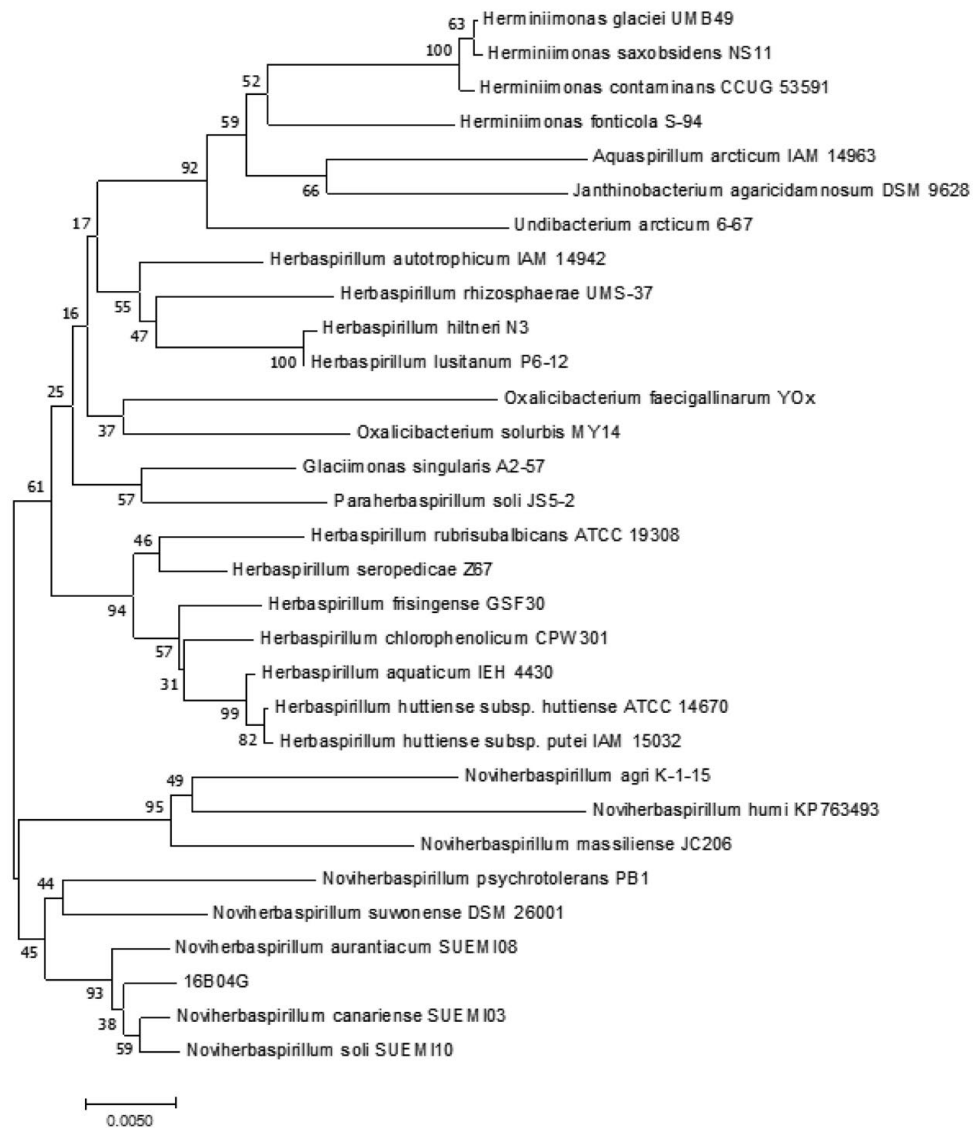


Fig. 8. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences shows the relationship between the strains isolated in this study and their relatives of the genus *Novisherbaspirillum*. Bootstrap values (>70%) are shown above nodes for the neighbor-joining methods. Bar: 0.01 and 0.02 substitutions per nucleotide position, respectively.

valeric acid, trisodium citrate, L-histidine, potassium 2-ketogluconate, 3-hydroxybutyric acid, L-serine, 4-hydroxybenzoic acid, and L-proline. Strain 17Sr1_31 (=NI BRBAC000500517) was isolated from a soil sample.

Description of *Microvirga aerilata* 17gy_18

Cells are Gram-stain-negative, non-flagellated, and short rod-shaped. Colonies are pink-colored after 3 days of incubation on R2A at 25°C. In the BIOLOG GEN III, acetoacetic acid, *N*-acetyl-D-mannosamine, L-alanine, L-arginine, L-aspartic acid, D-cellobiose, dextrin, D-fructose, D-fructose 6-PO₄, L-galactonic acid lactone,

D-galactose, D-galacturonic acid, gelatin, gentiobiose, D-gluconic acid, α -D-glucose, glucuronamide, D-glucuronic acid, L-glutamic acid, inosine, α -keto-glutaric acid, L-malic acid, D-maltose, D-mannitol, D-mannose, D-melibiose, β -methyl-D-glucoside, 3-methyl glucose, myo-inositol, pectin, propionic acid, glycyl-L-proline, L-pyroglutamic acid, quinic acid, D-raffinose, L-rhamnose, L-serine, stachyose, sucrose, D-trehalose, D-turanose acetic acid, *N*-acetyl-D-galactosamine, *N*-acetyl-neuraminic acid, *N*-acetyl-D-glucosamine, γ -amino-butyric acid, D-arabitol, D-aspartic acid, bromo-succinic acid, citric acid, formic acid, D-fucose, L-fucose, D-glucose-6-PO₄, glycerol, L-histidine, α -hydroxybu-

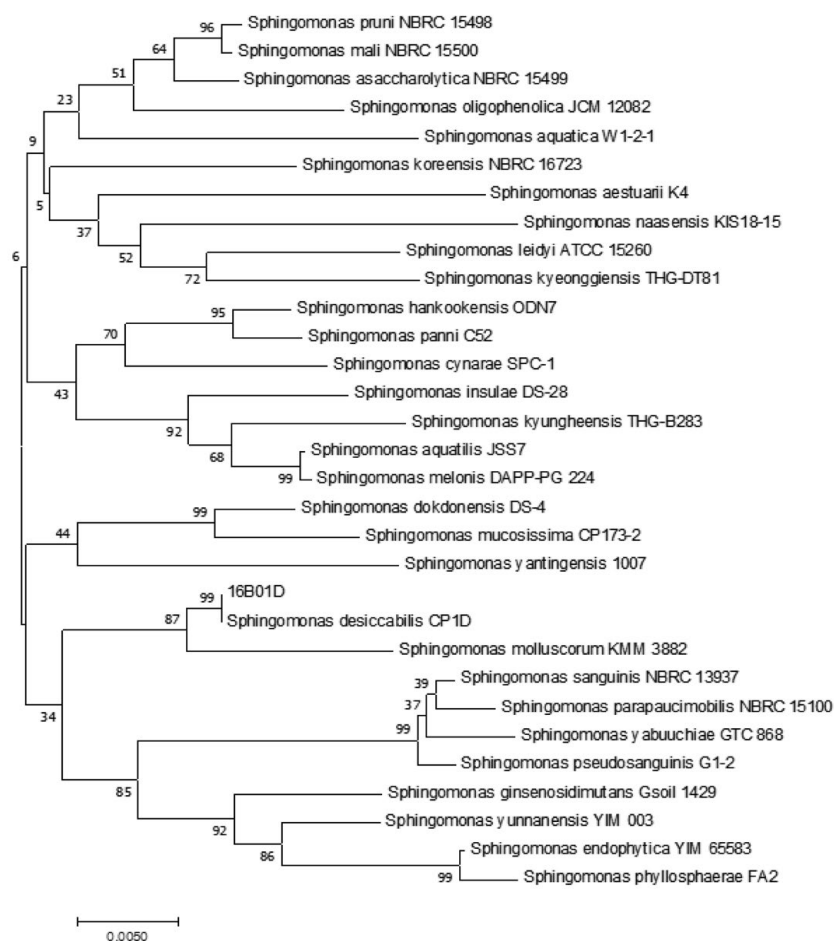


Fig. 9. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences shows the relationship between the strains isolated in this study and their relatives of the genus *Sphingomonas*. Bootstrap values (>70%) are shown above nodes for the neighbor-joining methods. Bar: 0.01 and 0.02 substitutions per nucleotide position, respectively.

tyric acid, β -hydroxy-D, L-butyric acid, *p*-hydroxy-phenylacetic acid, α -keto-butyric acid, L-lactic acid, D-lactic acid methyl ester, α -D-lactose, D-malic acid, methyl pyruvate, mucic acid, D-saccharic acid, D-salicin, D-serine, D-sorbitol, and tween 40 were not utilized. In sensitivity tests, the tetrazolium redox dye is reduced in the presence of tetrazolium violet; but not in the presence of 1% NaCl, 1% sodium lactate, 4% NaCl, 8% NaCl, guanidine HCl, lithium chloride, pH 6, potassium tellurite, D-serine, sodium butyrate, aztreonam, fusidic acid, lincomycin, minocycline, nalidixic acid, niaproof 4, pH 5, rifamycin SV, sodium bromate, tetrazolium blue, troleandomycin, and vancomycin.

In API 20NE system, positive for the reduction of nitrates (NO_3) to nitrite (NO_2^-), urease, esculin hydrolysis, D-glucose, L-arabinose, D-mannose, *N*-acetyl-D-glucosamine, adipic acid, phenylacetic acid, potassium 2-ketogluconate, and 3-hydroxybutyric acid. Negative for the reduction of nitrates (NO_3) to nitrogen (N_2), indole pro-

duction on tryptophan, glucose fermentation, arginine dihydrolase, gelatin hydrolysis, β -galactosidase, D-mannitol, D-maltose, potassium gluconate, capric acid, malic acid, trisodium citrate.

In API 32GN system, positive for *N*-acetyl-glucosamine, D-saccharose (sucrose), itaconic acid, sodium malonate, lactic acid, D-glucose, D-fucose, and L-arabinose. Negative for L-rhamnose, D-ribose, inositol, D-maltose, suberic acid, L-alanine, potassium 5-ketogluconate, glycogen, 3-hydroxybenzoic acid, L-serine, D-mannitol, sodium acetate, salicin, D-melibiose, D-sorbitol, propionic acid, capric acid, valeric acid, trisodium citrate, L-histidine, 4-hydroxybenzoic acid, and L-proline. Strain 17gy_18 (=NIBRBAC000500518) was isolated from a soil sample.

Description of *Methylobacterium aerolatum* 16B15D

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

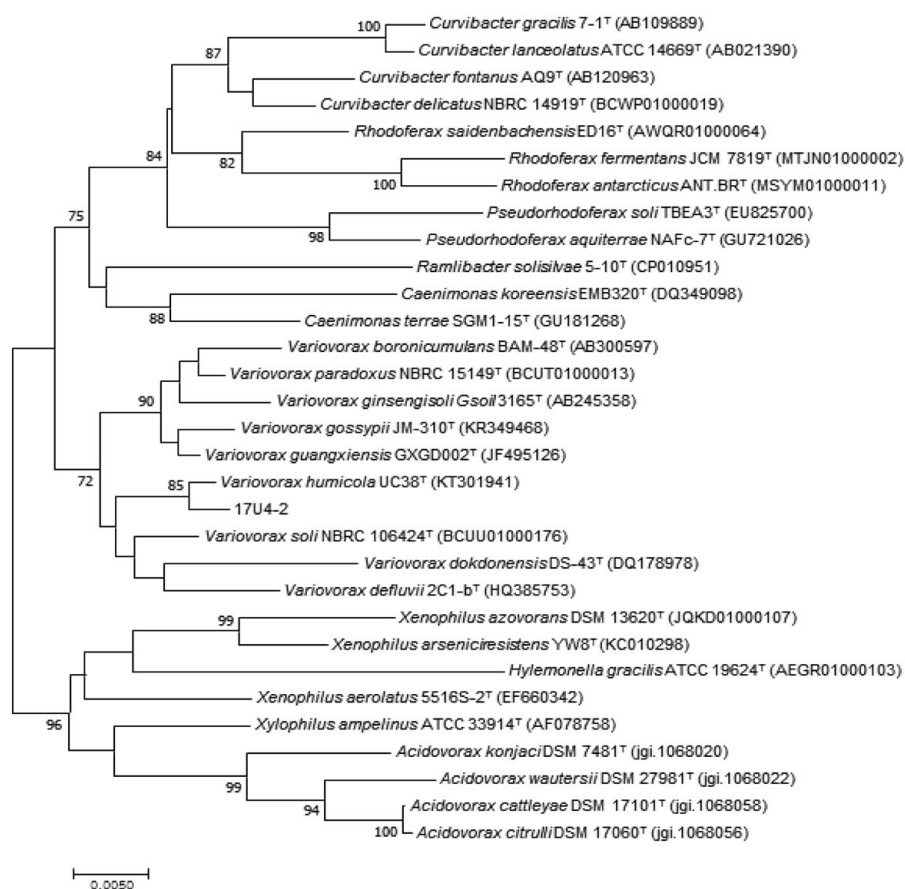


Fig. 10. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences shows the relationship between the strains isolated in this study and their relatives of the genus *Variovorax*. Bootstrap values (>70%) are shown above nodes for the neighbor-joining methods. Bar: 0.01 and 0.02 substitutions per nucleotide position, respectively.

short rod-shaped. Colonies are pink-colored after 3 days of incubation on R2A at 25°C. In the BIOLOG GEN III, acetoacetic acid, *N*-acetyl-D-mannosamine, L-alanine, L-arginine, L-aspartic acid, D-cellobiose, dextrin, D-fructose, D-fructose 6-PO₄, L-galactonic acid lactone, D-galactose, D-galacturonic acid, gelatin, gentiobiose, D-gluconic acid, α -D-glucose, glucuronamide, D-gluconic acid, L-glutamic acid, inosine, α -keto-glutaric acid, L-malic acid, D-maltose, D-mannitol, D-mannose, D-melibiose, β -methyl-D-glucoside, 3-methyl glucose, myo-inositol, pectin, propionic acid, glycyl-L-proline, L-pyroglutamic acid, quinic acid, D-raffinose, L-rhamnose, L-serine, stachyose, sucrose, D-trehalose, D-turanose acetic acid, *N*-acetyl-D-galactosamine, *N*-acetyl-neuraminic acid, *N*-acetyl-D-glucosamine, γ -amino-butyric acid, D-arabitol, D-aspartic acid, bromo-succinic acid, citric acid, formic acid, D-fucose, L-fucose, D-glucose-6-PO₄, glycerol, L-histidine, α -hydroxybutyric acid, β -hydroxy-D, L-butyric acid, *p*-hydroxy-phenylacetic acid, α -keto-butyric acid, L-lactic acid, D-lactic acid methyl ester, α -D-lactose, D-malic

acid, methyl pyruvate, mucic acid, D-saccharic acid, D-salicin, D-serine, D-sorbitol, and tween 40 were not utilized. In sensitivity tests, the tetrazolium redox dye is reduced in the presence tetrazolium violet; but not in the presence of 1% NaCl, 1% sodium lactate, 4% NaCl, 8% NaCl, guanidine HCl, lithium chloride, pH 6, potassium tellurite, D-serine, sodium butyrate, aztreonam, fusidic acid, lincomycin, minocycline, nalidixic acid, niaproof 4, pH 5, rifamycin SV, sodium bromate, tetrazolium blue, troleandomycin, and vancomycin.

In API 20NE system, positive for the reduction of nitrates (NO₃) to nitrite (NO₂⁻), arginine dihydrolase, urease, D-glucose, L-arabinose, D-mannose, D-mannitol, D-maltose, potassium gluconate, adipic acid, and malic acid. Weak positive for trisodium citrate. Negative for the reduction of nitrates (NO₃) to nitrogen (N₂), indole production on tryptophan, glucose fermentation, esculin hydrolysis, gelatin hydrolysis, β -galactosidase, *N*-acetyl-D-glucosamine, capric acid, and phenylacetic acid.

In API 32GN system, positive for D-ribose, itaconic acid, D-glucose, and L-arabinose. Negative for L-rham-

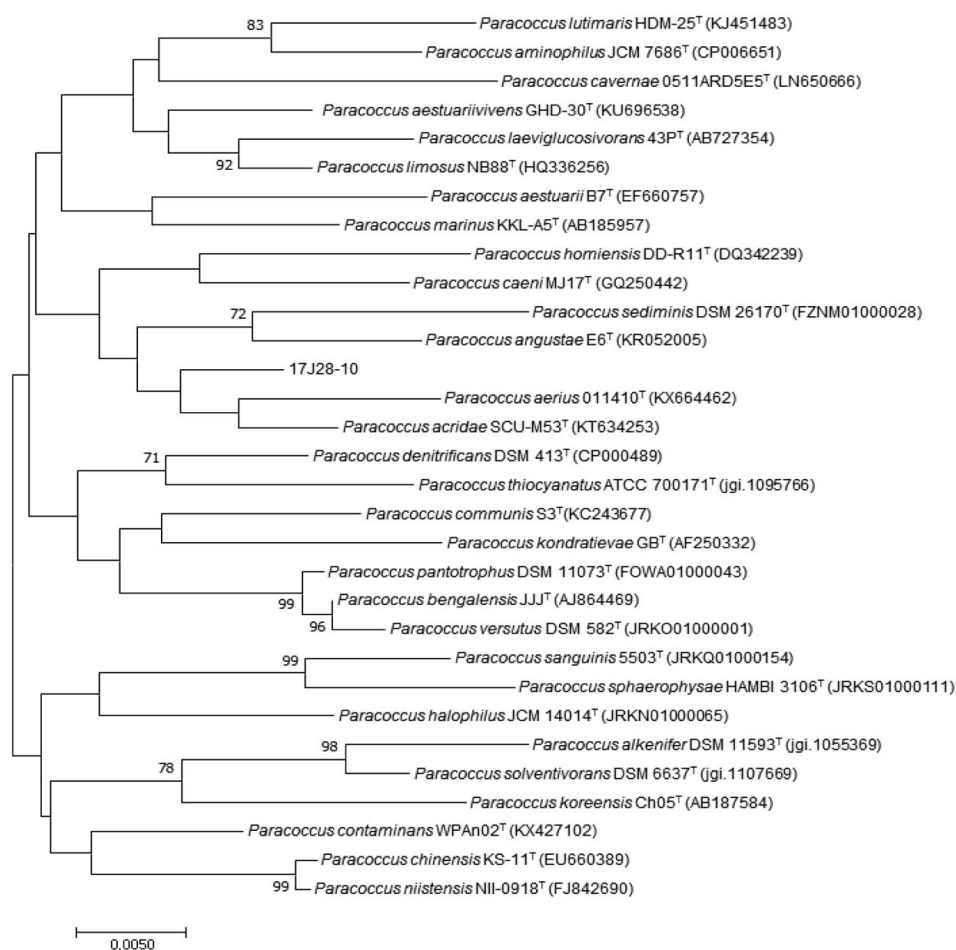


Fig. 11. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences shows the relationship between the strains isolated in this study and their relatives of the genus *Paracoccus*. Bootstrap values (> 70%) are shown above nodes for the neighbor-joining methods. Bar: 0.01 and 0.02 substitutions per nucleotide position, respectively.

nose, inositol, *N*-acetyl-glucosamine, D-saccharose (sucrose), D-maltose, suberic acid, sodium malonate, sodium acetate, lactic acid, L-alanine, potassium 5-ketogluconate, glycogen, 3-hydroxybenzoic acid, L-serine, D-mannitol, salicin, D-melibiose, D-fucose, D-sorbitol, propionic acid, capric acid, valeric acid, trisodium citrate, L-histidine, potassium 2-ketogluconate, 3-hydroxybutyric acid, L-serine, 4-hydroxybenzoic acid, and L-proline. Strain 16B15D (= NIBRBAC000500519) was isolated from a soil sample.

Description of *Microvirga vignae* 16B02D

Cells are Gram-stain-negative, non-flagellated, and short rod-shaped. Colonies are pink-colored after 3 days of incubation on R2A at 25°C. In the BIOLOG GEN III, acetoacetic acid, *N*-acetyl-D-mannosamine, L-alanine, L-arginine, L-aspartic acid, D-cellobiose, dextrin, D-fructose, D-fructose 6-PO₄, L-galactonic acid lactone,

D-galactose, D-galacturonic acid, gelatin, gentiobiose, D-gluconic acid, α -D-glucose, glucuronamide, D-gluconic acid, L-glutamic acid, inosine, α -keto-glutaric acid, L-malic acid, D-maltose, D-mannitol, D-mannose, D-melibiose, β -methyl-D-glucoside, 3-methyl glucose, myo-inositol, pectin, propionic acid, glycyl-L-proline, L-pyroglutamic acid, quinic acid, D-raffinose, L-rhamnose, L-serine, stachyose, sucrose, D-trehalose, D-turanose acetic acid, *N*-acetyl-D-galactosamine, *N*-acetyl-neuraminic acid, *N*-acetyl-D-glucosamine, γ -amino-butyric acid, D-arabitol, D-aspartic acid, bromo-succinic acid, citric acid, formic acid, D-fucose, L-fucose, D-glucose-6-PO₄, glycerol, L-histidine, α -hydroxybutyric acid, β -hydroxy-D, L-butyric acid, *p*-hydroxy-phenylacetic acid, α -keto-butyric acid, L-lactic acid, D-lactic acid methyl ester, α -D-lactose, D-malic acid, methyl pyruvate, mucic acid, D-saccharic acid, D-salicin, D-serine, D-sorbitol, and tween 40 were not utilized. In sensitivity tests, the tetrazolium redox dye is

reduced in the presence tetrazolium violet; but not in the presence of 1% NaCl, 1% sodium lactate, 4% NaCl, 8% NaCl, guanidine HCl, lithium chloride, pH 6, potassium tellurite, D-serine, sodium butyrate, aztreonam, fusidic acid, lincomycin, minocycline, nalidixic acid, niaproof 4, pH 5, rifamycin SV, sodium bromate, tetrazolium blue, troleandomycin, and vancomycin.

In API 20NE system, positive for arginine dihydrolase, urease, β -galactosidase, D-glucose, L-arabinose, D-mannose, malic acid, and trisodium citrate. Weak positive for D-mannitol. Negative for the reduction of nitrates (NO_3) to nitrite (NO_2^-), reduction of nitrates (NO_3) to nitrogen (N_2), indole production on tryptophan, glucose fermentation, esculin hydrolysis, gelatin hydrolysis, *N*-acetyl-D-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, and phenylacetic acid.

In API 32GN system, positive for *N*-acetyl-glucosamine, inositol, L-alanine, D-mannitol, D-glucose, salicin, D-sorbitol, L-arabinose, propionic acid, potassium 2-ketogluconate, 4-hydroxybenzoic acid, and L-proline. Negative for L-rhamnose, D-ribose, D-saccharose (sucrose), D-maltose, itaconic acid, suberic acid, sodium malonate, sodium acetate, lactic acid, potassium 5-ketogluconate, glycogen, 3-hydroxybenzoic acid, L-serine, D-melibiose, D-fucose, capric acid, valeric acid, trisodium citrate, L-histidine, and 3-hydroxybutyric acid. Strain 16B02D (=NIBRBAC000500520) was isolated from a soil sample.

Description of *Oxalicibacterium flavum* 16B04G

Cells are Gram-stain-negative and short rod-shaped. Colonies are pink-colored after 3 days of incubation on R2A at 25°C. In the BIOLOG GEN III, acetoacetic acid, *N*-acetyl-D-mannosamine, L-aspartic acid, D-cellobiose, dextrin, D-fructose, D-fructose 6- PO_4 , L-galactonic acid lactone, D-galactose, D-galacturonic acid, gentiobiose, D-gluconic acid, α -D-glucose, D-glucuronic acid, L-glutamic acid, α -keto-glutaric acid, L-malic acid, D-maltose, D-mannitol, D-mannose, β -methyl-D-glucoside, 3-methyl glucose, myo-inositol, pectin, propionic acid, glycyl-L-proline, L-pyroglutamic acid, L-rhamnose, L-serine, stachyose, sucrose, D-trehalose, D-turanose, acetic acid, *N*-acetyl-neuraminic acid, *N*-acetyl-D-glucosamine, γ -amino-butyric acid, D-arabitol, D-aspartic acid, bromo-succinic acid, citric acid, formic acid, D-fucose, L-fucose, D-glucose-6- PO_4 , glycerol, L-histidine, α -hydroxybutyric acid, β -hydroxy-D,L-butyric acid, *p*-hydroxy-phenylacetic acid, α -keto-butyric acid, L-lactic acid, D-lactic acid methyl ester, α -D-lactose, D-malic acid, methyl pyruvate, mucic acid, D-saccharic acid, D-sorbitol, tween 40 are utilized as sole carbon source. But D-raffinose, D-melibiose, D-salicin, *N*-acetyl-D-galactosamine, inosine, D-serine, L-alanine, L-arginine,

glucuronamide, and quinic acid were not utilized. In sensitivity tests, the tetrazolium redox dye is reduced in the presence of 1% NaCl, 1% sodium lactate, 4% NaCl, lithium chloride, pH 6, potassium tellurite, D-serine, sodium butyrate, aztreonam, nalidixic acid, niaproof 4, sodium bromate; but not in the presence of pH 5, 8% NaCl, fusidic acid, troleandomycin, rifamycin SV, minocycline, gelatin, lincomycin, guanidine HCl, vancomycin tetrazolium violet, tetrazolium blue.

In API 20NE system, positive for arginine dihydrolase, urease, esculin hydrolysis, D-glucose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, adipic acid, malic acid, trisodium citrate, and potassium gluconate. Negative for the reduction of nitrates (NO_3) to nitrite (NO_2^-), reduction of nitrates (NO_3) to nitrogen (N_2), indole production on tryptophan, glucose fermentation, gelatin hydrolysis, β -galactosidase, L-arabinose, D-maltose, capric acid, and phenylacetic acid.

In API 32GN system, positive for D-ribose, inositol, D-saccharose (sucrose), *N*-acetyl-glucosamine, suberic acid, lactic acid, D-mannitol, D-glucose, salicin, L-arabinose, and 4-hydroxybenzoic acid. Negative for L-rhamnose, D-maltose, itaconic acid, sodium malonate, sodium acetate, L-alanine, potassium 5-ketogluconate, glycogen, 3-hydroxybenzoic acid, L-serine, D-melibiose, D-fucose, D-sorbitol, propionic acid, capric acid, valeric acid, trisodium citrate, L-histidine, potassium 2-ketogluconate, 3-hydroxybutyric acid, and L-proline. Strain 16B04G (=NIBRBAC000500521) was isolated from a soil sample.

Description of *Sphingomonas desiccabilis* 16B01D

Cells are Gram-stain-negative and short rod-shaped. Colonies are yellow-colored after 3 days of incubation on R2A at 25°C. In the BIOLOG GEN III, dextrin, D-maltose, D-trehalose, D-cellobiose, gentiobiose, sucrose, D-turanose, D-raffinose, α -D-lactose, D-melibiose, β -methyl-D-glucoside, D-salicin, D-mannose, D-galactose, D-galacturonic acid, and D-glucuronic acid were utilized as a sole carbon source. But acetoacetic acid, *N*-acetyl-D-mannosamine, L-alanine, L-arginine, L-aspartic acid, D-fructose, D-fructose 6- PO_4 , L-galactonic acid lactone, gelatin, D-gluconic acid, α -D-glucose, glucuronamide, L-glutamic acid, inosine, α -keto-glutaric acid, L-malic acid, D-mannitol, 3-methyl glucose, myo-inositol, pectin, propionic acid, glycyl-L-proline, L-pyroglutamic acid, quinic acid, L-rhamnose, L-serine, stachyose, acetic acid, *N*-acetyl-D-galactosamine, *N*-acetyl-neuraminic acid, *N*-acetyl-D-glucosamine, γ -amino-butyric acid, D-arabitol, D-aspartic acid, bromo-succinic acid, citric acid, formic acid, D-fucose, L-fucose, D-glucose-6- PO_4 , glycerol, L-histidine, α -hydroxybutyric acid, β -hydroxy-D, L-butyric acid, *p*-hydroxy-pheny-

lactic acid, α -keto-butyric acid, L-lactic acid, D-lactic acid methyl ester, D-malic acid, methyl pyruvate, mucic acid, D-saccharic acid, D-serine, D-sorbitol, and tween 40 were not utilized. In sensitivity tests, the tetrazolium redox dye is reduced at pH 6 but not at pH 5; the dye is reduced in the presence of pH 6, 1% NaCl, 1% sodium lactate, rifamycin SV, tetrazolium blue; but not in the presence of sodium lactate, 4% NaCl, 8% NaCl, guanidine HCl, lithium chloride, potassium tellurite, D-serine, sodium butyrate, tetrazolium violet aztreonam, fusidic acid, lincomycin, minocycline, nalidixic acid, niaproof 4, pH 5, sodium bromate, troleandomycin, and vancomycin.

In API 20NE system, positive for of arginine dihydro-lase, urease, esculin hydrolysis, β -galactosidase, D-glucose, L-arabinose, D-mannose, *N*-acetyl-D-glucosamine, and D-maltose. Weak positive for D-mannitol, potassium gluconate, adipic acid, malic acid, and trisodium citrate. Negative for the reduction of nitrates (NO₃) to nitrite (NO₂⁻), reduction of nitrates (NO₃) to nitrogen (N₂), indole production on tryptophan, glucose fermentation, gelatin hydrolysis, capric acid, and phenylacetic acid.

In API 32GN system, positive for *N*-acetyl-glucosamine, D-saccharose (sucrose), D-maltose, suberic acid, sodium malonate, sodium acetate, lactic acid, L-alanine, potassium 5-ketogluconate, glycogen, 3-hydroxybenzoic acid, L-serine, D-glucose, salicin, D-melibiose, D-sorbitol, L-arabinose, valeric acid, trisodium citrate, L-histidine, potassium 2-ketogluconate, 3-hydroxybutyric acid, 4-hydroxybenzoic acid, and L-proline. Negative for L-rhamnose, D-ribose, inositol, itaconic acid, D-mannitol, D-fucose, propionic acid, and capric acid. Strain 16B01D (=NIBRBAC000500522) was isolated from a soil sample.

Description of *Variovorax humicola* 17U4-2

Cells are Gram-stain-positive and short rod-shaped. Colonies are yellow-colored after 3 days of incubation on R2A at 25°C. In the BIOLOG GEN III, D-maltose, D-trehalose, D-cellobiose, gentiobiose, sucrose, D-turanose, stachyose, D-raffinose, D-melibiose, β -D-glucoside, D-salicin, neuraminic acid, α -D-glucose, D-fructose, D-mannitol, glycerol, L-histidine, D-gluconic acid, and L-malic acid were utilized as sole carbon source. But dextrin, α -D-lactose, *N*-glucosamine, β -mannosamin, *N*-galactosamin, D-mannose, D-galactose, 6-methyl-glucose, D-fucose, L-fucose, L-rhamnose, inosine, D-sorbitol, D-arabitol, myo-inositol, D-glucose, D-fructose, D-aspartic acid, D-serine, gelatin, glycyl-L-proline, L-alanine, L-arginine, L-aspartic acid, L-glutamic acid, pyroglutamic acid, L-serine, pectin, galacturonic acid, L-galactonic lactone, D-glucuronic acid, glucuronamide, mucic acid, quinic acid, D-saccharic acid, phenylacetic

acid, methyl pyruvate, D-lactic acid, L-lactic acid, citric acid, α -glutaric acid, D-malic acid, succinic acid, tween 40, γ -butyric acid, α -butyric acid, β -butyric acid, acetoacetic acid, propionic acid, acetic acid, and formic acid were not utilized. In sensitivity tests, the tetrazolium redox dye is reduced at pH 6 but not at pH 5; the dye is reduced in the presence of 1% NaCl, 4% NaCl, sodium lactate, D-serine, tetrazolium violet, nalidixic acid, lithium chloride, potassium tellurite, aztreonam, and sodium butyrate; but not in the presence of 8% NaCl, fusidic acid, troleandomycin, rifamycin SV, minocycline, lincomycin, guanidine HCl, niaproof 4, vancomycin, tetrazolium blue, and sodium bromate.

In API 20NE system, positive for of reduction of nitrates (NO₃) to nitrogen (N₂), arginine dihydro-lase, urease, esculin hydrolysis, β -galactosidase, D-glucose, L-arabinose, D-mannose, D-mannitol, *N*-acetyl-D-glucosamine, D-maltose, potassium gluconate, adipic acid, malic acid, trisodium citrate, and phenylacetic acid. Negative for reduction of nitrates (NO₃) to nitrite (NO₂⁻), indole production on tryptophan, glucose fermentation, gelatin hydrolysis, and capric acid.

In API 32GN system, positive for L-rhamnose, *N*-acetyl-glucosamine, D-ribose, D-saccharose (sucrose), D-maltose, suberic acid, sodium acetate, lactic acid, L-alanine, potassium 5-ketogluconate, 3-hydroxybenzoic acid, D-mannitol, D-glucose, salicin, D-melibiose, D-sorbitol, L-arabinose, propionic acid, valeric acid, L-histidine, potassium 2-ketogluconate, 3-hydroxybutyric acid, 4-hydroxybenzoic acid, and L-proline. Negative for inositol, itaconic acid, sodium malonate, glycogen, L-serine, D-fucose, capric acid, and trisodium citrate. Strain 17U4-2 (=NIBRBAC000500500) was isolated from a soil sample.

Description of *Paracoccus acridae* 17J28-10

Cells are Gram-stain-negative and cocci-shaped. Colonies are orange-colored after 3 days of incubation on R2A at 25°C. In the BIOLOG GEN III, L-alanine, pyroglutamic acid, L-lactic acid, L-malic acid, acetoacetic acid, and acetic acid is utilized as sole carbon source. But D-maltose, D-trehalose, D-cellobiose, gentiobiose, sucrose, D-turanose, stachyose, D-raffinose, D-melibiose, β -D-glucoside, D-salicin, neuraminic acid, α -D-glucose, D-fructose, D-mannitol, glycerol, L-histidine, D-gluconic acid, dextrin, α -D-lactose, *N*-glucosamine, β -mannosamin, *N*-galactosamin, D-mannose, D-galactose, 6-methyl-glucose, D-fucose, L-fucose, L-rhamnose, inosine, D-sorbitol, D-arabitol, myo-inositol, D-glucose, D-fructose, D-aspartic acid, D-serine, gelatin, glycyl-L-proline, L-arginine, L-aspartic acid, L-glutamic acid, L-serine, pectin, galacturonic acid, L-galactonic lactone, D-glucuronic acid, glucuronamide, mu-

cic acid, uinic acid, D-saccharic acid, phenylacetic acid, methyl pyruvate, D-lactic acid, citric acid, α -glutaric acid, D-malic acid, succinic acid, tween40, γ -butyric acid, α -butyric acid, β -butyric acid, propionic acid, and formic acid were not utilized. In sensitivity tests, the tetrazolium redox dye is reduced in the presence of pH 6, 1% NaCl, sodium lactate, and lithium chloride; but not in the presence of pH 5, 4% NaCl, 8% NaCl, fusidic acid, D-serine, troleandomycin, rifamycin SV, minocycline, lincomycin, guanidine HCl, niaproof 4, vancomycin, tetrazolium violet, tetrazolium Blue, nalidixic acid, potassium tellurite, aztreonam, sodium butyrate, and sodium bromate.

In API 20NE system, positive for of reduction of nitrates (NO₃) to nitrogen (N₂), arginine dihydrolase, urease, D-glucose, L-arabinose, D-mannose, D-mannitol, and phenylacetic acid. Negative for reduction of nitrates (NO₃) to nitrite (NO₂⁻), indole production on tryptophan, glucose fermentation, esculin hydrolysis, gelatin hydrolysis, β -galactosidase, *N*-acetyl-D-glucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, and trisodium citrate.

In API 32GN system, positive for L-rhamnose, D-ribose, inositol, lactic acid, L-alanine, potassium 5-ketogluconate, 3-hydroxybenzoic acid, L-serine, D-mannitol, D-glucose, salicin, D-sorbitol, propionic acid, L-histidine, 3-hydroxybutyric acid, 4-hydroxybenzoic acid, and L-proline. Negative for *N*-acetyl-glucosamine, D-saccharose (sucrose), D-maltose, itaconic acid, suberic acid, sodium malonate, sodium acetate, glycogen, D-melibiose, D-fucose, L-arabinose, capric acid, valeric acid, trisodium citrate, and potassium 2-ketogluconate. Strain 17J28-10 (=NIBRBAC000500501) was isolated from a soil sample.

ACKNOWLEDGMENTS

This work was supported by a research grant from Seoul Women's University (2018) and by a grant from the National Institute of Biological Resources (NIBR), funded by the Ministry of Environment (MOE) of the Republic of Korea (NIBR201701107).

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Submitted: March 8, 2018

Revised: April 14, 2018

Accepted: May 14, 2018