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NOTE

Diaminobutyricibacter tongyongensis gen. nov., sp. nov. and *Homoserinibacter gongjuensis* gen. nov., sp. nov. Belong to the Family *Microbacteriaceae*§

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Two bacterial strains, KIS66-7^T and 5GH26-15^T, were isolated from soil samples collected in the South Korean cities of Tongyong and Gongju, respectively. Both strains were aerobic, Gram-stain-positive, mesophilic, flagellated, and rod-shaped. A phylogenetic analysis revealed that both strains belonged to the family *Microbacteriaceae* of the phylum *Actinobacteria*. The 16S rRNA gene sequence of strain KIS66-7^T had the highest similarities with those of *Labedella gwakjiensis* KSW2-17^T (97.3%), *Cryobacterium psychrophilum* DSM 4854^T (97.2%), *Leifsonia lichenia* 2Sb^T (97.2%), *Leifsonia naganoensis* JCM 10592^T (97.0%), and *Cryobacterium mesophilum* MSL-15^T (97.0%). Strain 5GH26-15^T showed the highest sequence similarities with *Leifsonia psychrotolerans* LI1^T (97.4%) and *Schumannella luteola* KHIA^T (97.1%). The 16S rRNA gene sequence from KIS66-7^T exhibited 96.4% similarity with that from 5GH26-15^T. Strain KIS66-7^T contained a B2γ type peptidoglycan structure with D-DAB as the diamino acid; MK-13, MK-12, and MK-14 as the respiratory quinones; ai-$C_{15:0}$, ai-$C_{17:0}$, and i-$C_{16:0}$ as the major cellular fatty acids; and diphosphatidylglycerol, phatidylglycerol, and glycolipids as the predominant polar lipids. Strain 5GH26-15^T had a B2β type peptidoglycan structure with D-DAB as the diamino acid; MK-14 and MK-13 as the respiratory quinones; ai-$C_{15:0}$, i-$C_{16:0}$, and ai-$C_{17:0}$ as the major cellular fatty acids; and diphosphatidylglycerol, phatidylglycerol, and glycolipids as the predominant polar lipids. Both strains had low DNA-DNA hybridization values (<40%) with closely related taxa. Based on our polyphasic taxonomic characterization, we propose that strains KIS66-7^T and 5GH26-15^T represent novel genera and species, for which we propose the names *Diaminobutyricibacter tongyongensis* gen. nov., sp. nov. (type strain KIS66-7^T =KACC 15515^T =NBRC 108724^T) and *Homoserinibacter gongjuensis* gen. nov., sp. nov. (type strain 5GH26-15^T =KACC 15524^T =NBRC 108755^T) within the family *Microbacteriaceae*.

***Keywords*:** *Diaminobutyricibacter tongyongensis*, *Homoserinibacter gongjuensis*, *Microbacteriaceae*, new genus

The family *Microbacteriaceae* was first proposed by Park *et al.* (1993) and then emended by Stackebrandt *et al.* (1997). Presently, 41 valid genera have been reported within the family *Microbacteriaceae* (http://www.bacterio.cict.fr/classifgenerafamilies.html). Several new genera, including *Alpinimonas*, *Compostimonas*, *Diaminobutyricimonas*, *Homoserinimonas*, *Lysinimonas*, *Naasia*, and *Pontimonas*, which were isolated from air, soil, spent mushroom compost, seawater, and alpine silt, have been reported as new members of the family *Microbacteriaceae* (Kim *et al.*, 2012c, 2012d; Jang *et al.*, 2012, 2013a, 2013b; Schumann *et al.*, 2012; Weon *et al.*, 2013).

We isolated several bacterial strains in the course of investigating the culturable bacterial community in soil samples collected from uncultivated soil at Daemaemuldo in the city of Tongyong and greenhouse soil in Gongju, South Korea. The soil samples were serially diluted, spread on R2A (Difco, USA) medium and incubated for 1 week. We sequenced the 16S rRNA gene sequences in several colony-forming isolates. Among them, strains KIS66-7^T and 5GH26-15^T were identified as members of the family *Microbacteriaceae*.

For phenotypic characterization, cultures were grown at 28°C for 3 days in R2A base medium. The assimilation of various substrates, enzyme activities, and other physiological properties were tested in duplicate with commercial API 20NE, API ID 32GN, and API ZYM test strips (bioMérieux, France) according to the manufacturer's protocols. The API ZYM test strips were checked after 4 h, while the API 20NE and API ID 32GN test strips were checked after 10 days of incubation. The hydrolysis of casein, chitin, hypoxanthine, starch, tyrosine, and xanthine was examined on R2A plates containing 5% (w/v) milk powder, 1% (w/v) chitin, 0.5% (w/v) hypoxanthine, 1% (w/v) starch, 0.1% (w/v) tyrosine, and 0.5% (w/v) xanthine, respectively. CM-cellulose and Tween

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80 degradation was examined using R2A supplemented with 1% (w/v) of each substrate (Smibert and Krieg, 1994). DNase activity was determined using DNase test agar (Difco). Growth under anaerobic conditions was examined after incubation using the BBL GasPak Anaerobic System (Difco) for 14 days at 28°C on R2A agar. Catalase and oxidase activity was examined by bubble production in 3% (v/v) hydrogen peroxide solution and 1% (w/v) tetramethyl-*p*-phenylenediamine (bioMérieux, France), respectively. Cell morphology and the presence of flagella were observed by electron microscopy (LEO model 912AB; Leo Electron Microscopy Inc., USA) in the exponential phase of growth. A Difco Gram staining kit was used for testing the Gram reaction. The pH range for growth was tested using R2A broth medium. The pH was adjusted prior to sterilization to a value of 4–10 (at intervals of 1.0 pH unit) using appropriate biological buffers (Breznak and Costilow, 1994). The growth temperature range was assessed at 4, 10, 15, 20, 25, 20, 35, 37, 40, and 45°C. To investigate tolerance to NaCl, R2A broth was prepared with the NaCl concentration adjusted to 0–5% (w/v) (at 1% intervals). Both strains were aerobic, Gram-positive, monotrichous, and rod-shaped (Supplementary data Fig. S1). Strain KIS66-7^T was catalase- and oxidase-negative under aerobic conditions, tolerated 2% NaCl (w/v), and grew at 15–37°C (optimum, 28–30°C) with a pH range of 4.0–10.0 (optimum, pH 7.0). Growth was observed on nutrient agar (NA), R2A, and trypticase soy agar (TSA), but not on ISP medium 2 or MacConkey agar (all from Difco). Strain 5GH26-15^T was catalase-negative and oxidase-positive, tolerated 2% NaCl (w/v), and grew at 15–40°C (optimum, 28–30°C) and a pH of 5.0–9.0 (optimum, 7.0). Growth was observed on R2A and TSA agar, but not on ISP medium 2, NA, or MacConkey agar. The physiological, biochemical, and morphological characteristics of strains KIS66-7^T and 5GH26-15^T are provided in the genus and species descriptions, and in Tables 1 and 2.

Table 1. Comparison of the differential characteristics of strains KIS66-7^T and 5GH26-15^T

Strains: 1, *Diaminobutyricibacter tongyongensis* KIS66-7^T; 2, *Homoserinibacter gongjuensis* 5GH26-15^T. Both strains were positive for esculin hydrolysis and *β*-galactosidase, but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, and gelatin hydrolysis. Both strains assimilated D-glucose, D-mannitol, D-maltose, and L-rhamnose, but not D-mannose, *N*-acetylglucosamine, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, phenylacetic acid, inositol, itaconic acid, suberic acid, sodium malonate, sodium acetate, lactic acid, L-alanine, potassium 5-ketogluconate, 3-hydroxybenzoic acid, L-serine, salicin, D-sorbitol, propionic acid, valeric acid, L-histidine, potassium 2-ketogluconate, 3-hydroxybutyric acid, 4-hydroxybenzoic acid, or L-proline. Both strains were positive for esterase (C4), esterase lipase (C8), leucine arylamidase, cystine arylamidase, acid phosphatase, naphthol-AS-BI-phosphohydrolase, *α*-glucosidase, *β*-glucosidase, *N*-acetyl-*β*-glucosaminidase, and *α*-mannosidase, but negative for lipase (C14), trypsin, *α*-chymotrypsin, *β*-glucuronidase, and *α*-fucosidase. +, Positive; -, negative.

Characteristics	1	2
Oxidase	-	+
Hydrolysis of:		
Tyrosine	+	-
Starch	+	-
pH range for growth	4.0–10.0	5.0–9.0
Growth on nutrient agar	+	-
Assimilation:		
L-Arabinose	-	+
D-Ribose	-	+
D-Saccharose	+	-
Glycogen	-	+
D-Melibiose	-	+
L-Fucose	-	+
Enzymatic activity of:		
Alkaline phosphatase	+	-
Valine arylamidase	-	+
α-Galactosidase	+	-
β-Galactosidase	-	+
Fatty acids:		
iso-$C_{14:0}$	0.6	1.8
iso-$C_{15:0}$	5.7	0.7
anteiso-$C_{15:0}$	42.3	38.5
$C_{16:0}$	1.1	3.2
iso-$C_{16:0}$	22.7	35.7
iso-$C_{17:0}$	2.0	-
anteiso-$C_{17:0}$	25.4	19.2

The 16S rRNA genes of strains KIS66-7^T and 5GH26-15^T were amplified using the universal primers 9F and 1512R (Weisburg *et al.*, 1991) and sequenced by Genotec (Korea). The sequences obtained (1466 bp for strain KIS66-7^T and 1468 bp for strain 5GH26-15^T) were compared with other sequences in the EzTaxon-e server (http://eztaxon-e.ezbiocloud.net; Kim *et al.*, 2012b). The 16S rRNA gene sequences of strain KIS66-7^T, 5GH26-15^T and their associated species were aligned using the integrated SINA alignment tool from the ARB-silva website (Pruesse *et al.*, 2007). Phylogenetic trees based on the aligned sequences and evolutionary analyses were constructed using mega version 5 (Tamura *et al.*, 2011) with three algorithms, neighbor-joining (Saitou and Nei, 1987), maximum parsimony (Kluge and Farris, 1969), and maximum-likelihood (Felsenstein, 1981), based on 1000 randomly chosen bootstrap replications. Strain KIS66-7^T showed >97.0% sequence similarity to *Labedella gwakjiensis* KSW2-17^T (97.3%), *Cryobacterium psychrophilum* DSM 4854^T (97.2%), and *Leifsonia lichenia* 2Sb^T (97.2%), whereas strain 5GH26-15^T showed >97.0% sequence similarity to *Leifsonia psychrotolerans* LI1^T (97.4%) and *Schumannella luteola* KHIA^T (97.1%). The phylogenetic tree showed that both strains were members of the family *Microbacteriaceae*. According to the neighbor-joining tree analysis, strain KIS66-7^T was clustered with the genera *Cryobacterium* and *Klugiella*, while strain 5GH26-15^T was grouped with the genera *Agrococcus*, *Leifsonia*, *Microterricola*, and *Phycicola* (Fig. 1). Although these topologies were not highly supported due to the low bootstrap values, both strains were considered to be new members of the family *Microbacteriaceae* in light of the sequence similarities and overall tree topologies among the members of the family *Microbacteriaceae*.

For the analysis of whole-cell fatty acids, strains KIS66-7^T and 5GH26-15^T were grown for 3 days at 28°C in R2A to the exponential stage. The cells were then saponified, the fatty acids were methylated and extracted, and the fatty acid methyl esters were determined using the protocols described by Sasser (1990). The fatty acid methyl esters were identified and quantified using the TSBA 6 database (version 6.10) of the Sherlock Microbial Identification System (MIDI).

Table 2. Differential characteristics of KIS66-7^{T}, 5GH26-15^{T}, and closely related genera in the family *Microbacteriaceae*

Taxa: 1, *Diaminobutyricibacter*; 2, *Homoserinibacter*; 3, *Agrococcus* (Groth *et al.*, 1996; Wieser *et al.*, 1999; Zlamala *et al.*, 2002; Mayilraj *et al.*, 2006; Bora *et al.*, 2007; Lee, 2008; Behrendt *et al.*, 2008; Zhang *et al.*, 2010; Dhanjal *et al.*, 2011); 4, *Cryobacterium* (Suzuki *et al.*, 1997; Zhang *et al.*, 2007; Dastager *et al.*, 2008a; Reddy *et al.*, 2010; Liu *et al.*, 2013); 5, *Herbiconiux* (Qiu *et al.*, 2007; Behrendt *et al.*, 2011; Kim *et al.*, 2012a); 6, *Klugiella* (Cook *et al.*, 2008); 7, *Labedella* (Lee, 2007); 8, *Leifsonia* (Leifson, 1962; Davis *et al.*, 1984; Suzuki *et al.*, 1999; Evtushenko *et al.*, 2000; Reddy *et al.*, 2003; An and Yokota, 2007; Qiu *et al.*, 2007; Dastager *et al.*, 2008b; Pindi *et al.*, 2009; An *et al.*, 2009, 2010; Madhaiyan *et al.*, 2010; Ganzert *et al.*, 2011); 9, *Microterricola* (Matsumoto *et al.*, 2008); 10, *Phycicola* (Lee *et al.*, 2008); 11, *Schumannella* (An *et al.*, 2008). +, Positive; -, negative; NA, not available; V, variable; C, cream; LP, light pink; O, orange; P, pink; Re, red; W, white; Y, yellow; R, rod; CO, coccus; F, filament; DAB, 2,4-diaminobutyric acid; Lys, lysine; Orn, ornithine; DPG, diphosphatidylglycerol; PA, phosphatidic acid; PC, phosphatidylcholine; PE, phosphatidylethanolamine; PG, phosphatidylglycerol; PI, phosphatidylinositol; UGL, unknown glycolipid; UL, unknown lipid; UPL, unknown phospholipid.

Characteristics	1	2	3	4	5	6	7	8	9	10	11
Species no.	1	1	9	8	4	1	1	13	1	1	1
Source	Soil	Soil	Air, cheese, glacier ice, phyllosphere, soil, wall paintings	Glacier, soil	Phyllosphere, tissue	Hindgut of *Tipula abdominalis* larvae	Seaweed	Glacier, soil, water	Soil	Sea water	Lichen
Colony color	W	W	C, O, P, W, Y	LP, P, Y	W, Y	Y	Y	RE, W, Y	Y	W, Y	Y
Morphology	R	R	R,CO	R	R	R	R	R,F	R	R,CO	R
Motility	+	+	-	V	-	-	-	V	+	+	-
Temperature for growth (optimum)	15–37 (28)	15–40 (28)	10–40 (18–33)	0–28 (9–28)	4–37 (21–30)	4–30 (28)	10–37 (25–30)	-6–42 (15–30)	10–38 (15–30)	4–30 (25)	8–35 (NA)
Diamino acid	DAB	DAB	DAB	DAB	DAB	Lys	Orn	DAB	DAB	DAB	DAB
Peptidoglycan type	B2γ	B2β	B, B2γ	B2γ	B2γ	NA	NA	B,B2γ	NA	B	NA
Major menaquinones	13, 12, 14	14, 13	11, 12, 10, 9	8, 9, 10, 11, 12	11, 10	12, 11	10, 11	11, 12, 10, 9	12	11	11, 10
Polar lipids	DPG, PG, UGL	DPG, PG, UGL	PG, DPG, UGL, UL, UPL	PG, DPG, UL, UGL	DPG, PG, UPL, UGL	NA	PG, DPG	DPG, PG, UGL, PE, UL, PA	NA	DPG, PC, PG, PI	NA
Major fatty acids	ai-$C_{15:0}$, ai-$C_{17:0}$, i-$C_{16:0}$	ai-$C_{15:0}$, i-$C_{16:0}$, ai-$C_{17:0}$	ai-$C_{15:0}$, i-$C_{16:0}$, ai-$C_{17:0}$, i-$C_{15:0}$, $C_{16:0}$, $C_{17:0}$	ai-$C_{15:0}$, ai-$C_{15:1}$, i-$C_{15:0}$, ai-$C_{17:0}$, i-$C_{16:0}$	ai-$C_{15:0}$, ai-$C_{17:0}$, cyclohexyl-$C_{17:0}$, i-$C_{16:0}$	ai-$C_{15:0}$, ai-$C_{17:0}$, i-$C_{16:0}$	ai-$C_{15:0}$, i-$C_{16:0}$, ai-$C_{17:0}$	ai-$C_{15:0}$, ai-$C_{17:0}$, i-$C_{16:0}$	ai-$C_{15:0}$, ai-$C_{17:0}$	ai-$C_{15:0}$, ai-$C_{17:0}$	ai-$C_{15:0}$, i-$C_{16:0}$

Menaquinones and polar lipids were extracted and analyzed according to the method of Minnikin *et al.* (1984). Mycolic acids were extracted and analyzed as described by Minnikin *et al.* (1980). For the analysis of peptidoglycan structure, strains KIS66-7^{T} and 5GH26-15^{T} were grown in shaking flasks containing liquid NBRC medium 802 [1.0% polypeptone (Wako Pure Chemical Industries Ltd., Japan), 0.2% yeast extract, and 0.1% $MgSO_4 \cdot 7H_2O$; pH 7.0] on a rotary shaker for 72 h at 28°C. Cell wall samples were prepared from approximately 1 g of wet cells by mechanical disruption with an ultrasonic oscillator and glass beads. The cell walls were separated from unbroken cells by differential centrifugation in distilled water and further purified in boiling 4% SDS (100°C, 40 min) followed by several washings with distilled water. The molar ratios of the amino acids in the cell wall hydrolysates (4 M HCl, 16 h) were determined using the method of Hamada *et al.* (2010). The amino acid isomers in the cell wall hydrolysates were examined by the method of Nozawa *et al.* (2007) using liquid chromatography-mass spectrometry (model LCMS-2020; Shimadzu Corp., Japan). Both KIS66-7^{T} and 5GH26-15^{T} contained anteiso-$C_{15:0}$, iso-$C_{16:0}$, and anteiso-$C_{17:0}$ as the dominant fatty acids (Table 1). The menaquinones of strain KIS66-7^{T} consisted of MK-13 (44%), MK-12 (40%), and MK-14 (16%), whereas those of strain 5GH26-15^{T} consisted of MK-14 (64%), MK-13 (24%), MK-12 (9%), and MK-11 (3%). Diphosphatidylglycerol, phosphatidylglycerol, and unknown glycolipids appeared as the major polar lipids in both strains (Supplementary data Fig. S2); no mycolic acids were found in these strains. The peptidoglycan in strain KIS66-7^{T} contained alanine (Ala), glutamic acid (Glu), glycine (Gly), and 2,4-diaminobutyric acid (DAB) at a molar ratio of 0.5:1.0:1.2:1.2. An enantiomer analysis showed the presence of D-Ala, D-Glu, Gly, D-DAB, and L-DAB. On the other hand, the peptidoglycan in strain 5GH26-15^{T} contained Ala, Glu, Gly, homoserine (Hsr), and DAB at a molar ratio of 0.8:1.0:1.0:0.4:0.8. In addition, the enantiomer analysis revealed the presence of D-Ala, D-Glu, Gly, L-Hsr, and D-DAB. These results suggest that the peptidoglycan type in strain KIS66-7^{T} was B1γ with D-DAB as the diagnostic diamino acid in the interpeptide bridge and L-DAB at position 3 in the peptide subunit, while the peptidoglycan type in strain 5GH26-15^{T} was B1β with D-DAB as the diagnostic diamino acid in the interpeptide bridge and L-Hsr at position 3 in the peptide subunit (Schleifer and Kandler, 1972).

To measure the DNA-DNA hybridization values and DNA G+C content, genomic DNA was extracted and purified as described by Ausubel *et al.* (1987), and DNA-DNA hybridization was conducted in triplicate as described by Seldin and Dubnau (1985). Probe labeling was performed using a nonradioactive DIG High Prime DNA Labeling and Detection Starter Kit II (Roche Molecular Biochemicals, USA), and the hybridized DNA was visualized using a DIG Luminescent Detection Kit (Roche Molecular Biochemicals, Germany). DNA-DNA relatedness was quantified with a

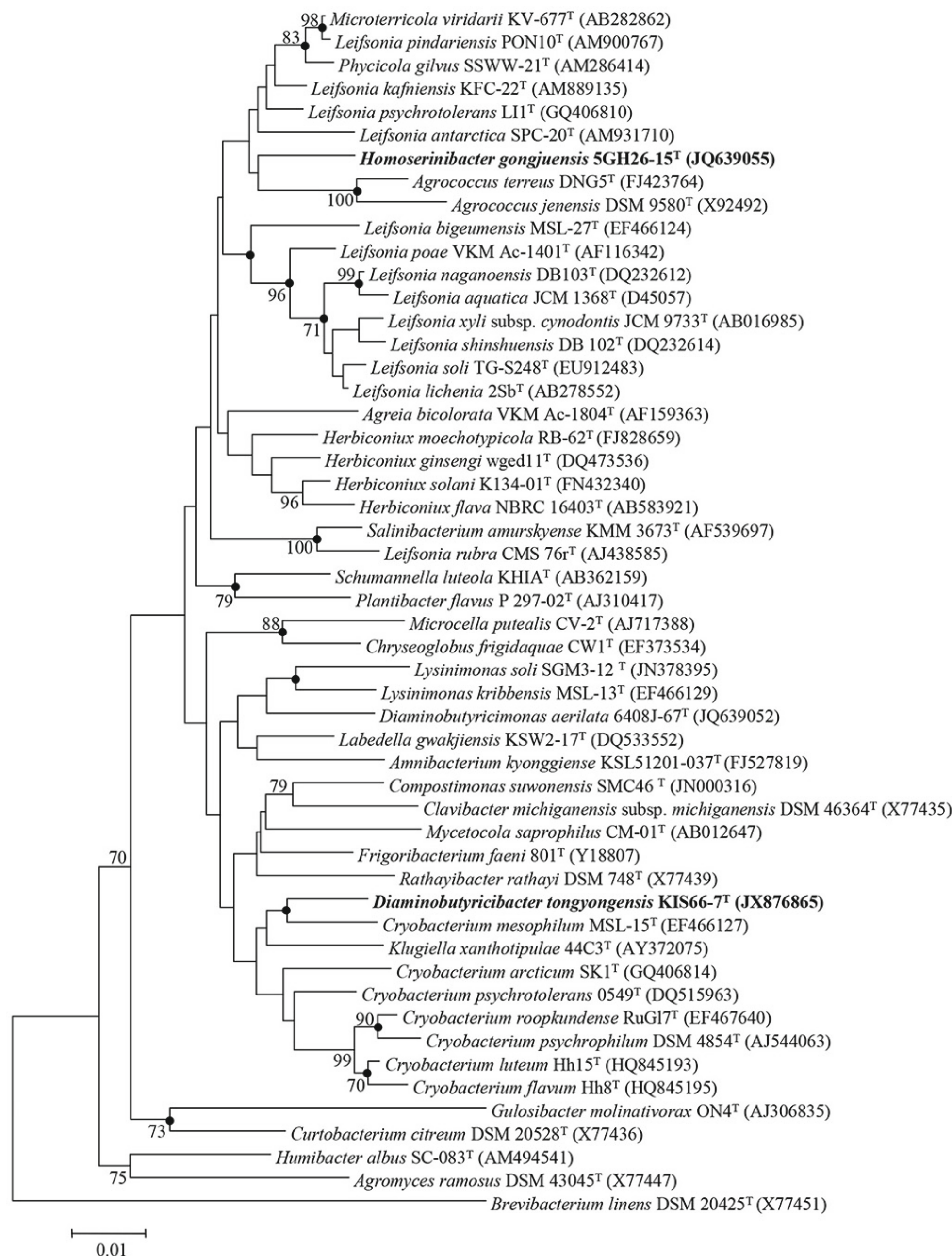

Fig. 1. Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences, showing the relationship between KIS66-7^{T}, 5GH26-15^{T}, and related taxa within the family *Microbacteriaceae*. Bootstrap values >70% (based on 1000 replicates) are shown at branching points. Dots indicate that the corresponding branches were also recovered in the maximum-parsimony and maximum-likelihood trees. Bar, 0.01 substitutions per nucleotide.

densitometer (Bio-Rad, USA). The G+C content was determined by the fluorometric method (Gonzalez and Saiz-Jimenez, 2002) using SYBR Green I and a real-time polymerase chain reaction thermocycler (Bio-Rad). DNA-DNA hybridization of strain KIS66-7^{T} with *Labedella gwakjiensis* KACC 14984^{T}, *Cryobacterium psychrophilum* KACC 14511^{T}, and *Leifsonia lichenia* KACC 15539^{T} resulted in hybridization values of 32±2% (reciprocal value, 29±4%), 28±4%, and 31±5%, respectively, while the hybridization values of strain 5GH26-15^{T} with *Leifsonia psychrotolerans* KACC 15592^{T} and *Schumannella luteola* KACC 15538^{T} were 33±4% (reciprocal value, 27±2%) and 33±3%, respectively. The genomic DNA G+C content of strain KIS66-7^{T} was 61.4% while that of strain 5GH26-15^{T} was 69.3 mol%.

Based on our sequence and phylogenetic analyses of the 16S rRNA gene, strain KIS66-7^{T} was closely related to *Cryobacterium* and *Klugiella*. The differences in some features such as motility, temperature range for growth, peptidoglycan structure, and menaquinones could be used to distinguish this strain from phylogenetically related taxa (Table 2). Strain 5GH26-15^{T} was phylogenetically clustered with the genera *Agrococcus*, *Leifsonia*, *Microterricola*, and *Phycicola*. However, this strain could be differentiated from these genera on the basis of motility, peptidoglycan structure, menaquinones, polar lipids, and major fatty acids (Table 2). The differences in chemotaxonomic properties such as menaquinone com-

position and peptidoglycan structure provide evidence to support the proposal of two new genera within the family *Microbacteriaceae*.

Description of *Diaminobutyricibacter* gen. nov.

Diaminobutyricibacter (Di.a.mi.no.bu.ty.ri.ci.bac'ter. N.L. n. *acidum diaminobutyricum*, DAB; N.L. masc. n. *bacter*, a rod; N.L. masc. n. *Diaminobutyricibacter*, a rod with DAB-containing peptidoglycan).

Diaminobutyricibacter gen. nov. is a Gram-positive, aerobic, monotrichous, non-spore-forming rod-shaped, catalase- and oxidase-negative bacterium. The predominant menaquinones are MK-13, MK-12, and MK-14. The polar lipids are comprised of diphosphatidylglycerol, phosphatidylglycerol, and unknown glycolipids. The cellular fatty acid profile is characterized by the predominance of anteiso-$C_{15:0}$, iso-$C_{16:0}$, and anteiso-$C_{17:0}$. The peptidoglycan type is B1γ with D-DAB as the diagnostic diamino acid in the interpeptide bridge and L-DAB at position 3 of the peptide subunit. Mycolic acid is absent. Phylogenetically, the genus is in the family *Microbacteriaceae*. The type species is *Diaminobutyricibacter tongyongensis* sp. nov.

Description of *D. tongyongensis* sp. nov.

Diaminobutyricibacter tongyongensis (tong.yong.en'sis. N.L. masc. adj. *tongyongensis* refers to the Tongyong region where the type strain was isolated).

Diaminobutyricibacter tongyongensis sp. nov. displays the following characteristics in addition to the general morphological and chemotaxonomic characteristics given in the genus description. The cells are rods that measure 0.4–0.5 × 1.2–1.9 μm after incubation for 3 days at 28°C on R2A agar. The colonies on R2A agar are white, round, and convex. It grows on NA, R2A, and TSA, but not on ISP medium 2 or MacConkey agar. It grow at 15–37°C (optimum, 28–30°C) and pH 4.0–10.0 (optimum, pH 7.0) and tolerates up to 2% NaCl. It hydrolyzes tyrosine and starch, but not casein, cellulose, chitin, DNA, hypoxanthine, Tween 80, or xanthine. It is positive for esculin hydrolysis and β-galactosidase, but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, and gelatin hydrolysis (API 20NE test strips). It assimilates D-glucose, D-mannitol, L-rhamnose, and D-saccharose, but not L-arabinose, D-mannose, *N*-acetylglucosamine, D-maltose, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, phenylacetic acid, D-ribose, inositol, itaconic acid, suberic acid, sodium malonate, sodium acetate, lactic acid, L-alanine, potassium 5-ketogluconate, glycogen, 3-hydroxybenzoic acid, L-serine, salicin, D-melibiose, L-fucose, D-sorbitol, propionic acid, valeric acid, L-histidine, potassium 2-ketogluconate, 3-hydroxybutyric acid, 4-hydroxybenzoic acid, or L-proline (API 20NE and API ID 32GN test strips). It displays positive activities for alkaline phosphatase, esterase (C4), esterase lipase (C8), leucine arylamidase, cystine arylamidase, acid phosphatase, naphthol-AS-BI-phosphohydrolase, *α*-galactosidase, *α*-glucosidase, *β*-glucosidase, *N*-acetyl-*β*-glucosaminidase, and *α*-mannosidase, but negative activities for lipase (C14), valine arylamidase, trypsin, *α*-chymotrypsin, *β*-galactosidase, *β*-glucuronidase, and *α*-fucosidase (API ZYM test strips). The genomic DNA G+C content of the type strain is 61.4 mol%.

Strain KIS66-7^T (=KACC 15515^T =NBRC 108724^T) was isolated from a soil sample collected at Daemaemuldo in the city of Tongyong, South Korea.

Description of *Homoserinibacter* gen. nov.

Homoserinibacter (Ho.mo.se.ri.ni.bac'ter. N.L. n. *homoserinum*, Hsr; N.L. masc. n. *bacter*, a rod; N.L. masc. n. *Homoserinibacter* [Hsr rod] refers to the presence of Hsr in the cell wall).

Homoserinibacter gen. nov. is a Gram-positive, aerobic, monotrichous, non-spore-forming rod-shaped, catalase-negative, and oxidase-positive bacterium. The predominant menaquinones are MK-14 and MK-13. Its polar lipids are diphosphatidylglycerol, phosphatidylglycerol, and unknown glycolipids. The cellular fatty acid profile is characterized by the predominance of anteiso-$C_{15:0}$, iso-$C_{16:0}$, and anteiso-$C_{17:0}$. The peptidoglycan type is B1*β* with D-DAB as the diagnostic diamino acid in the interpeptide bridge and L-Hsr at position 3 of the peptide subunit. Mycolic acid is absent. Phylogenetically, the genus is a member of the family *Microbacteriaceae*. The type species is *Homoserinibacter gongjuensis* sp. nov.

Description of *H. gongjuensis* sp. nov.

Homoserinibacter gongjuensis (gong,ju,en'sis. N.L. masc. adj. *Gongjuensis* refers to Gongju city where the type strain was isolated).

Homoserinibacter gongjuensis sp. nov. displays the following characteristics in addition to the general morphological and chemotaxonomic characteristics given in the genus description. The cells are rods that measure 0.4–0.5 × 1.1–1.8 μm after 3 days of incubation at 28°C on R2A agar. The colonies on R2A agar are white, irregular, and flat. It grows on R2A and TSA, but not on ISP medium 2, NA, or MacConkey agar. It grows at 15–40°C (optimum, 28–30°C), pH 5.0–9.0 (optimum, pH 7.0), and tolerates up to 2% NaCl. It does not hydrolyze casein, cellulose, chitin, DNA, hypoxanthine, starch, Tween 80, tyrosine, or xanthine. It is positive for esculin hydrolysis and β-galactosidase, but negative for nitrate reduction, indole production, glucose fermentation, arginine dihydrolase, urease, and gelatin hydrolysis (API 20NE test strips). It assimilates D-glucose, L-arabinose, D-mannitol, D-maltose, L-rhamnose, D-ribose, glycogen, D-melibiose, and L-fucose, but not D-mannose, *N*-acetylglucosamine, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate, phenylacetic acid, inositol, D-saccharose, itaconic acid, suberic acid, sodium malonate, sodium acetate, lactic acid, L-alanine, potassium 5-ketogluconate, 3-hydroxybenzoic acid, L-serine, salicin, D-sorbitol, propionic acid, valeric acid, L-histidine, potassium 2-ketogluconate, 3-hydroxybutyric acid, 4-hydroxybenzoic acid, or L-proline (API 20NE and API ID 32GN test strips). It shows positive activities for esterase (C4), esterase lipase (C8), leucine arylamidase, valine arylamidase, cystine arylamidase, acid phosphatase, naphthol-AS-BI-phosphohydrolase, *β*-galactosidase, *α*-glucosidase, *β*-glucosidase, *N*-acetyl-*β*-glucosaminidase, and *α*-mannosidase, but negative activities for alkaline phos-

phatase, lipase (C14), trypsin, α-chymotrypsin, α-galactosidase, β-glucuronidase, and α-fucosidase (API ZYM test strips). The genomic DNA G+C content of the type strain is 69.3 mol%.

The type strain 5GH26-15^T (=KACC 15524^T =NBRC 108755^T) was isolated from greenhouse soil in Gongju, South Korea.

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