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Sphingobacterium bambusae sp. nov., Isolated from Soil of Bamboo Plantation

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A Gram-negative, non-motile, non-spore-forming bacterial strain designated IBFC2009^T was isolated from soil of a bamboo plantation. The strain could grow at 11°C~39°C, pH 6.0~9.0, and in the presence of 0~5% NaCl. Based on 16S rRNA gene sequence analysis, Strain IBFC2009^T belonged to the genus *Sphingobacterium* and showed the highest sequence similarity of 94.6% (*S. composti* T5-12^T) with the type strains within the genus. The major fatty acids were summed feature 3 (iso-$C_{15:0}$ 2-OH and/or $C_{16:1}$ *ω7c*, 34.4%), iso-$C_{15:0}$ (22.4%), $C_{16:0}$ 3-OH (15.2%), and iso-$C_{17:0}$ 3-OH (12.8%). The G+C content of the genomic DNA was 41.0 mol%. According to the phenotypic and genotypic characteristics, Strain IBFC2009^T should represent a novel species of the genus *Sphingobacterium*, for which the name *Sphingobacterium bambusae* sp. nov. is proposed. The type strain is IBFC2009^T (=CCTCC AB 209162^T =KCTC 22814^T).

***Keywords*:** *Sphingobacterium bambusae* sp. nov., novel bacterium, taxonomy

The genus *Sphingobacterium* was created by Yabuuchi *et al.* (1983), which includes *Sphingobacterium multivorum*, *S. spiritivorum*, and *S. mizutae*. To date, nine other species have been described: *S. antarcticum* (Shivaji *et al.*, 1992), *S. faecium* and *S. thalpophilum* (Takeuchi and Yokota, 1992), *S. daejeonense* (Kim *et al.*, 2006), *S. composti* (Ten *et al.*, 2006), *S. composti* (Yoo *et al.*, 2007), *S. siyangense* (Liu *et al.*, 2008), *S. kitahiroshimense* (Matsuyama *et al.*, 2008), and *S. anhuiense* (Wei *et al.*, 2008). There were two different *S. composti* with validly published names. *S. composti* T5-12^T was described by Ten *et al.* (2006) one year before the *S. composti* 4M24^T of Yoo *et al*. (2007) The name *S. composti* 4M24^T was then considered illegitimate and thus changed. Two other previously described species, *S. heparinum* and *S. piscium*, were reclassified in the genus *Pedobacter* (Steyn *et al.*, 1998). *Sphingobacterium* species have been isolated from soil (Shivaji *et al.*, 1992; Matsuyama *et al.*, 2008), clinical specimens (Holmes *et al.*, 1982; Yabuuchi *et al.*, 1983), and compost (Ten *et al.*, 2006; Yoo *et al.*, 2007).

In this study, we isolated Strain IBFC2009^T from the soil of a bamboo plantation. Its phenotypic and chemotaxonomic characteristics were examined and a phylogenetic analysis was carried out. The results suggest that Strain IBFC2009^T represents a novel species of the genus *Sphingobacterium*, for which the name *Sphingobacterium bambusae* sp. nov. is proposed.

Materials and Methods

Isolation and culture of the bacterial strain

Strain IBFC2009^T was originally isolated from the soil of a bamboo plantation, which was collected from Hangzhou, China. The soil sample (5 g) was thoroughly shaken (250 rpm, 30°C) in 200 ml sterile water for 10 min. The suspension, following serial dilution, was spread onto Nutrient Agar (NA, Sinopharm Chemical Reagent Co., Ltd, China) plates (g/L): 10.0 peptone, 3.0 beef extract, 5.0 NaCl, and 20 agar. The plates were incubated at 31°C for 2 d. Single colonies on the plates were purified by transferring them onto fresh plates and subsequent reincubation. Strain IBFC 2009^T was one of the isolates that appeared on the NA plates in aerobic conditions. The strain was cultured routinely on nutrient broth medium (NB) at 31°C and maintained as a glycerol suspension (20%, w/v) at -70°C.

Phenotypic and biochemical characteristics

IBFC2009^T was grown for 2 d on NA plates at 31°C, and cell morphology was observed under Olympus light microscope (Olympus Corporation, Japan) at a magnification of ×1,000, an atomic force microscope Nano-Scope IIIa (SPA 400, Seiko Inc & Multimode SPM, Digital Instruments, Co. Ltd) at ×20,000 and an electron microscope JEOL-1230 (JEOL Ltd., Japan) at ×60,000. Growth was assessed at 4, 10, 11, 16, 30, 31, 32, 33, 34, 37, 39, 40, 42, and 45°C, at pH 4, 5, 6, 7, 8, 9, and 10 in the presence of 0, 0.5, 1, 1.5, 2, 3, 4, 5, 6, 7, 9, and 11% NaCl. Bacterial concentration was measured at 550 nm using a spectrophotometer (UV-755B; Shanghai Precision & Scientific Instrument Co., Ltd., China).

For single-carbon-source assimilation study, a defined liquid medium containing basal salts was used (g/L): 0.5 K_2HPO_4, 0.5 NaH_2PO_4, 2.0 $(NH_4)_2SO_4$, 0.2 $MgSO_4$, and 0.1 $CaCl_2$. Filter-sterilized carbohydrate, alcohol, amino acid, or organic acids were added to the medium, and final concentration was adjusted to 0.5%. After one to three serial culture transferring sessions to the fresh medium, the strain, which still grew in the medium, was identified as positive character.

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For the studies of acid production from carbohydrates and oxidative fermentation from glucose, a defined liquid medium containing basal salts was used (g/L): 2.0 peptone, 5.0 NaCl, 0.2 K_2HPO_4, 10.0 glucose, 6.0 agar, and 0.03 bromothymol blue, at pH 7.0~7.2. After stab culture for about 2 d, the strain that caused the medium to turn yellow was identified as positive character (Dong and Cai, 2001).

Oxidase activity was tested by determining the oxidation of 1% (w/v) tetramethyl-p-phenylenediamine, and catalase activity was evaluated by determining the production of oxygen bubbles in a 5% (v/v) aqueous hydrogen peroxide solution (Dong and Cai, 2001; Cappuccino and Sherman, 2002). Nitrate reduction, indole, H_2S production, methyl red, and Voges-Proskauer reaction, were investigated as described by Dong and Cai (2001). Gram staining, endospore-forming features, hydrolysis of CM-cellulose, DNA, gelatin, starch, Tween 80, urease, and aesculin were tested as described by Gerhardt *et al.* (1994).

16S rRNA gene sequencing and phylogenetic analysis

For the extraction of genomic DNA from IBFC2009^T, 5 ml of exponential phase cultures were centrifuged for 2 min at 10,000 rpm. The cell pellet was resuspended in 200 μl 100 mM (pH 7.4) Tris-EDTA (TE) buffer containing 400 μg/ml lysozyme and incubated at 55°C for 5 min. The genomic DNA was then extracted using UNIQ-10 Column Bacteria Genomic DNA Extraction kit (Shanghai Sangon, China) according to the manufacturer's instruction.

The 50 μl reaction mixture for PCR of 16S rRNA gene contained 0.5 μM each of the forward and reverse primers, 1× PCR buffer, 50 ng of DNA, and other ingredients in TaKaRa 16S rDNA Bacterial Identification PCR kit (Dalian TaKaRa, China). The cycling conditions were as follows: 5 min at 95°C for pre-denaturation, followed by 0.5 min at 94°C for denaturation, 1 min at 52°C for annealing, 1 min at 72°C for extension for 30 cycles, and, finally, preservation at 72°C for 10 min. Purification and sequencing were carried out by Dalian TaKaRa Co., Ltd. using the dideoxy chain termination method with 3730 XL DNA sequencer (Applied Biosystems, USA).

For phylogenetic analyses, the 16S rRNA gene sequences of the type strains of *Sphingobacterium* species (and some *Pedobacter* species, serving as an out-group) were used. The 16S rRNA gene sequences were aligned using the CLUSTAL X program (Thompson *et al.*, 1997). A phylogenetic tree was constructed using the neighbor-joining method (Saitou and Nei, 1987) and the maximum-parsimony method (Fitch, 1972) in the MEGA3 program (Kumar *et al.*, 2004), with bootstrap values based on 1,000 replications (Felsenstein, 1985).

Analysis of cellular fatty acids and determination of G+C content

Cellular fatty acids were analyzed in organisms grown on NA at 31°C for 48 h. The cellular fatty acids were saponified, methylated, and extracted according to the protocol of the Sherlock Microbial Identification System (MIDI, 1999). The cellular fatty acids were analyzed by gas chromatography (Hewlett-Packard 6890) with the Microbial Identification software package (Sasser, 1990), workstation (HP Chemstation ver. A 5.01), and chromatographic column Ultra-2 (Agilent).

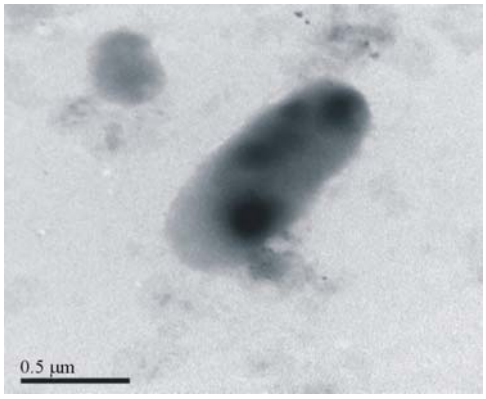

Fig. 1. Transmission electron micrograph of cell of Strain IBFC 2009^T after growth on NA for 2 d at 31°C. Bar, 0.5 μm. Magnification, ×60,000.

The genomic DNA was extracted and purified; the DNA G+C content was determined by a spectrophotometer with a thermal controller (DU800; Beckman Coulter, Inc., USA) according to absorbance during the thermal denaturalization of genomic DNA (Marmur and Doty, 1962; Dong and Cai, 2001).

Results

Phenotypic and biochemical characteristics

Microscopically, the cells of IBFC2009^T appeared to be short rods, 1.2~2.5 μm in length and 0.5~0.8 μm in diameter (Fig. 1 and 2). The cells were Gram-negative and did not produce spores during incubation. After 2 d incubation at 31°C on NA, colonies were 1.0 to 2.0 mm in diameter, circular in shape, smooth, convex, glossy, and yellow in color. They were able to grow at a range of 11°C to 39°C. The

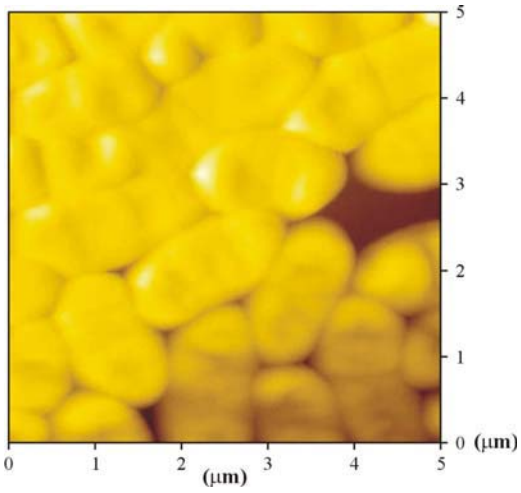

Fig. 2. Transmission atomic force micrograph of cell of Strain IBFC2009^T after growth on NA for 2 d at 31°C. Bar, 1.0 μm. Magnification, ×20,000.

Table 1. Differential phenotypic characteristics of Strain IBFC2009^T and other type strains of *Sphingobacterium* species
Strains: 1, IBFC2009^T; 2, *S. composti* 4M24^T; 3, *S. composti* T5-12^T; 4, *S. kitahiroshimense* 10C^T (Matsuyama *et al.*, 2008); 5, *S. siyangense* SY1^T (Liu *et al.*, 2008); 6, *S. daejeonense* TR6-04^T (Kim *et al.*, 2006); 7, *S. spiritivorum* NBRC 14948^T; 8, *S. multivorum* NBRC 14947^T; 9, *S. mizutaii* ATCC 33299^T; 10, *S. thalpophilum* NBRC 14963^T; 11, *S. faecium* NBRC 15299^T [data in Columns 7~11 are from Takeuchi and Yokota (1992) and Steyn *et al.* (1998)]; 12, *S. antarcticum* MTCC 675^T (Shivaji *et al.*, 1992); 13, *S. anhuiense* CW 186^T (Wei *et al.*, 2008). +, Positive; -, negative; V, variable; ND, no data available.

Characteristic	1[a]	2[a]	3[a]	4	5	6	7	8	9	10	11	12	13
Growth at:													
5°C	-	-	-	+	+	-	-	-	-	-	+	+	+
42°C	-	+	+	-	+	+	-	-	-	+	-	-	-
Hydrolysis of:													
DNA	-	-	+	-	+	-	+	+	+	-	+	ND	+
Starch	-	-	-	ND	+	-	+	+	+	+	+	-	+
Aesculin	+	+	-	+	-	-	+	+	+	+	+	+	+
Tween 80	+	+	+	+	-	ND	+	V	+	-	V	+	-
Gelatin	-	-	-	-	-	-	-	-	-	-	-	+	-
Urea	-	-	-	+	+	-	+	+	+	+	+	+	-
Assimilation of:													
D-Mannitol	-	-	-	-	+	-	+	-	-	-	-	+	-
D-Melibiose	+	+	-	+	+	+	+	+	+	+	+	-	ND
D-Raffinose	-	-	-	ND	+	+	+	+	+	+	+	+	+
D-Ribose	-	-	-	ND	+	-	-	-	-	-	-	+	-
D-Xylose	-	-	-	ND	+	+	+	+	+	+	-	+	-
Glycerol	-	-	-	-	+	-	V	-	-	+	+	+	-
Inositol	-	-	-	ND	-	-	-	-	-	-	-	+	-
Inulin	+	+	-	ND	+	-	V	V	-	+	+	+	+
L-Arabinose	-	+	-	-	+	-	+	+	-	+	+	+	+
L-Rhamnose	-	-	-	-	+	-	-	+	v	+	+	+	-
L-Sorbose	-	-	-	ND	+	-	-	-	-	-	-	ND	ND
Acid production from:													
D-Glucose	+	-	+	ND	-	+	+	+	+	+	+	+	+
D-Mannitol	-	-	-	ND	-	-	+	-	-	-	-	-	-
D-Sucrose	+	+	+	+	-	-	+	+	+	+	+	-	ND
D-Trehalose	+	+	+	+	+	-	-	-	-	-	-	ND	ND
L-Arabinose	+	+	-	+	-	-	-	+	+	+	+	-	+
L-Rhamnose	+	-	-	-	+	-	-	V	-	+	-	-	-
DNA G+C content (mol%)	41.0	45.0	38.9	36.9	38.5	38.7	39.0	39.9-40.5	39.3-40.0	44.0-44.2	37.3	39.3	36.3

[a] Data from this study utilize the same conditions as described in this paper.

pH growth range was between pH 6.0 and pH 9.0, and the NaCl growth range was between 0 and 5% (w/v). The optimum temperature, pH, and NaCl concentration were 31°C, pH 7.0, and 0.5~1.0% NaCl (w/v), respectively. The phenotypic and chemotaxonomic characteristics that differentiated Strain IBFC2009^T from previously described *Sphingobacterium* species are listed in Table 1.

16S rRNA gene sequence and phylogenetic analysis

Almost complete 16S rRNA gene sequence of Strain IBFC2009^T was obtained, and the GenBank accession no. for the 16S rRNA gene sequence of Strain IBFC2009^T was GQ339910 (1,453 bp). Preliminary sequence comparisons with 16S rRNA gene sequences deposited in the GenBank database indicated that Strain IBFC2009^T belonged to the genus *Sphingobacterium*. The strain showed the highest sequence similarities with the type strains of *S. composti* T5-12^T and 4M24^T (94.6% and 94.4%, respectively). According to the phylogenetic tree (Fig. 3), Strain IBFC2009^T formed a compact cluster with *S. composti* T5-12^T, *S. composti* 4M24^T, *S. daejeonense* TR6-04^T, and *S. mizutaii* ATCC 33299^T.

Cellular fatty acids and G+C content

The major fatty acids were summed feature 3 (iso-$C_{15:0}$ 2-OH and/or $C_{16:1}$ ω7*c*, 34.4%), iso-$C_{15:0}$ (22.4%), $C_{16:0}$ 3-OH (15.2%), and iso-$C_{17:0}$ 3-OH (12.8%), including typical features for members of the genus *Sphingobacterium* (Steyn *et al*., 1998; Takeuchi and Yokota, 1992). In contrast to other *Sphingobacterium* species, Strain IBFC2009^T contained a unique $C_{14:0}$ 2-OH (3.2%) content, had a larger of $C_{16:0}$ 3-OH (15.2%) and iso-$C_{15:0}$ 3-OH (5.8%) content, but had a smaller of $C_{16:0}$ (1.8%) content. The cellular fatty acid profiles of Strain IBFC2009^T and *Sphingobacterium* species are presented in Table 2. The DNA G+C content for the genus *Sphingobacterium* ranged from 36.0 mol% (Ten *et al.*, 2006)

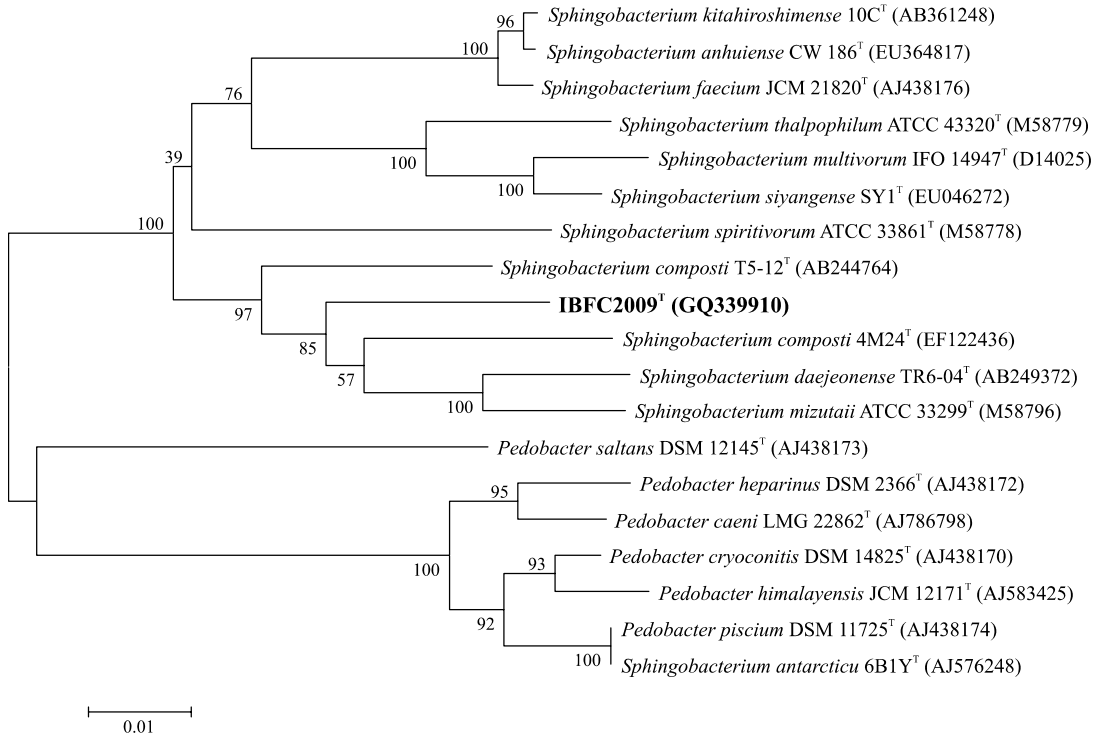

Fig. 3. Phylogenetic tree generated using the neighbor-joining method based on the 16S rRNA gene sequence of Strain IBFC2009^T. Numbers at nodes represent bootstrap percentages based on 1,000 samplings. Bar, 0.01 changes per nucleotide position. The maximum-parsimony tree showed essentially the same topology (data not shown).

Table 2. Cellular fatty acid of Strain IBFC2009^T and *Sphingobacterium* species

Strains: 1, IBFC2009^T; 2, *S. composti* 4M24^T; 3, *S. composti* T5-12^T; 4, *S. kitahiroshimense* 10C^T (Matsuyama *et al*., 2008); 5, *S. siyangense* SY1^T (Liu *et al.*, 2008); 6, *S. daejeonense* TR6-04^T (Kim *et al.*, 2006); 7, *S. spiritivorum* NBRC 14948^T; 8, *S. multivorum* NBRC 14947^T; 9, *S. mizutaii* ATCC 33299^T; 10, *S. thalpophilum* NBRC 14963^T; 11, *S. faecium* NBRC 15299^T [data in Columns 7∼11 are from Takeuchi and Yokota (1992) and Steyn *et al.* (1998)]; 12, *S. antarcticum* MTCC 675^T (Shivaji *et al.*, 1992); 13, *S. anhuiense* CW 186^T (Wei *et al.*, 2008). +, Fatty acid is detected but its content was not reported; -, <1% or not detected; Summed features are groups of two or three fatty acids that could not be separated by GLC using the MIDI system. Summed feature 3 contained $C_{16:1}$ *ω7c*/iso-$C_{15:0}$ 2-OH.

Fatty acid	1[a]	2[a]	3[a]	4	5	6	7	8	9	10	11	12	13
$C_{14:0}$	2.0	-	1.3	-	3.9	-	-	2.7	-	3.2	-	+	1.3
$C_{14:0}$ 2-OH	3.2	-	-	-	-	-	-	-	-	-	-	-	-
iso-$C_{15:0}$	22.4	27.9	26.1	28.9	32.9	45.6	30.1	22.2	30.0	17.7	24.6	29.0	32.2
anteiso-$C_{15:0}$	-	-	-	-	2.7	2.6	-	-	-	-	-	-	1.2
iso-$C_{15:0}$ 3-OH	5.8	3.3	2.4	-	3.0	1.5	2.2	3.2	3.0	4.3	3.7	-	2.7
iso-$C_{15:1}$ G	-	-	-	-	-	-	-	-	-	-	-	-	1.1
$C_{16:0}$	1.8	-	4.9	-	10.9	3.4	3.5	7.8	-	6.0	4.5	+	3.6
$C_{16:0}$ 2-OH	-	-	-	-	-	-	-	-	-	3.2	-	-	-
$C_{16:0}$ 3-OH	15.2	2.3	1.2	-	6.4	-	2.7	5.3	-	6.3	2.1	-	2.0
$C_{16:0}$ 10-methyl	-	-	-	-	-	-	-	-	-	-	1.4	-	-
$C_{16:1}$ ω5c	-	-	1.4	-	-	-	-	-	-	-	1.5	-	-
iso-$C_{17:0}$ 3-OH	12.8	20.1	11.3	12.8	5.9	16.6	12.5	7.1	22.1	10.0	10.0	-	9.8
$C_{17:1}$	-	-	-	-	-	-	-	-	-	-	-	+	-
$C_{18:0}$	-	-	2.2	-	-	-	-	-	-	-	-	-	1.7
iso-$C_{17:1}$ ω9c	-	1.6	7.4	-	1.1	2.9	1.7	-	3.7	-	-	-	-
iso-$C_{15:1}$ F	-	-	3.1	-	-	-	-	-	-	-	-	-	-
$C_{18:1}$ ω5c	-	-	1.9	-	-	-	-	-	-	-	-	-	
Summed feature 3[a]	34.4	37.6	25.8	40.3	24.1	23.8	42.7	49.0	35.1	47.8	48.1	56.0	33.7
Unknown (ECL 13.566)	-	-	-	-	-	-	-	-	1.3	1.3	1.4	-	-

[a] Data from this study utilize the same conditions as described in this paper. Strains were grown on NA at 31°C for 48 h.

to 44.2 mol% (Takeuchi and Yokota, 1992). The DNA G+C content of Strain IBFC2009^T (41.0 mol%) was within this range.

Discussion

The genus *Sphingobacterium* was proposed to be negative for Gram staining and gelatinase and indole production, and positive for catalase and oxidase (Dong and Cai, 2001). Aside from the above-mentioned common characteristics, Strain IBFC2009^T had several other unique vital characteristics when compared with other *Sphingobacterium* species: aesculin was hydrolyzed, but DNA was not hydrolyzed; D-melibiose and inulin were assimilated, but L-arabinose was not assimilated; and acids were produced from D-glucose, L-arabinose, and L-rhamnose.

The genus *Sphingobacterium* had iso-$C_{15:0}$ 2-OH, $C_{16:1}$ $\omega7c$, iso-$C_{15:0}$ and iso-$C_{17:0}$ 3-OH as the main fatty acids (Takeuchi and Yokota, 1992; Steyn *et al*., 1998). Fatty acid results were, to some extent, dependent on the medium used, culturing time, and temperature (Yongmanitchai and Ward, 1991). The reported data of fatty acids on the genus *Sphingobacterium* were obtained using different methods or media (e.g., R2A, NB, TSA, TYB, and TSA, among others). In this study, the fatty acids of two closest relative species (two *S. composti* species) were studied on the same conditions with Strain IBFC2009^T (grown on NA at 31°C for 48 h). Strain IBFC2009^T contained a unique $C_{14:0}$ 2-OH (3.2%) content, had a greater $C_{16:0}$ 3-OH (15.2%) and iso-$C_{15:0}$ 3-OH (5.8%) content, but had a lesser $C_{16:0}$ (1.8%) content. The cellular fatty acid profiles suggested that it should be classified in the genus *Sphingobacterium* as a novel species.

The hybridization method applied could be disregarded if the highest 16S rDNA sequence similarity was less than 97.0% (Stackebrandt and Goebel, 1994; Keswani and Whitman, 2001). Strain IBFC2009^T showed the highest sequence similarities with the type strains of *S. composti* T5-12^T and 4M24^T (94.6% and 94.4%, respectively). In addition, according to the phylogenetic tree (Fig. 1), Strain IBFC2009^T formed a compact cluster with *S. composti* T5-12^T, *S. composti* 4M24^T, *S. daejeonense* TR6-04^T, and *S. mizutaii* ATCC 33299^T; therefore, the results demonstrated that Strain IBFC2009^T was not related to any other species of the genus *Sphingobacterium* at the species level.

On the basis of phenotypic and phylogenetic studies, it is demonstrable that Strain IBFC2009^T should represent a novel species of the genus *Sphingobacterium*, for which the name *Sphingobacterium bambusae* sp. nov. is proposed.

Description of *Sphingobacterium bambusae* sp. nov.

Sphingobacterium bambusae (bam.bu'sa.e. L. gen. n. Bambusa, of/from bamboo).

Cells are Gram-negative, non-motile, non-spore-forming rods, 0.5~0.8 μm wide, and 1.2~2.5 μm long for aerobic growth at 31°C. Colonies grown on NB are smooth, convex, round, glossy, yellow, and 1.0~2.0 mm in diameter after 2 d of incubation at 31°C on NA. The temperature, pH, and NaCl concentration ranges for growth are 11°C~39°C, pH 6.0~9.0, and 0~5% NaCl (w/v), respectively. Strain IBFC 2009^T tests are positive for catalase and oxidase, but negative for arginine decarboxylase, H_2S production, indole, lysine decarboxylase, methyl red, nitrate reduction, ornithine decarboxylase, phenylalanine ammonia lyase, tryptophan ammonia lyase, and the Voges-Proskauer reaction. Glucose is not fermented. Aesculin and Tween 80 are hydrolyzed, but CM-cellulose, DNA, gelatin, mannan, pectine, starch, urea, and xylan are not. The strain assimilates D-glucose, D-maltose, D-melibiose, D-sucrose, and inulin; however, it does not assimilate arginine monohydrochloride, ascorbic acid, benzaldehyde, citric acid, cysteine, D-fructose, D-fucose, D-galactose, D-galacturonic acid, D-mannitol, D-mannose, D-raffinose, D-ribose, D-sorbitol, D-xylose, glycerol, glycin, glycogen, inositol, kreatine, lactic acid, lactoflavin, lactose, L-arabinose, L-arginine, L-cystine, L-cystine mono hydrochloride, L-lactamine, L-lysine, L-phenyl alanine, L-proline, L-rhamnose, L-sorbose, L-threonine, malic acid, maltose, oxalic acid, propionic acid, pyro, sodium malonate, sodium oxalate, starch, tannin, tryptophan, and valeric acid. Acids are produced from D-fructose, D-galactose, D-glucose, D-lactose, D-maltose, D-mannose, D-raffinose, D-sucrose, D-trehalose, D-xylose, ethanol, glycerol, inulin, L-arabinose, and L-rhamnose, but not from D-mannitol, D-ribose, D-sorbitol, glycogen, inositol, L-sorbose, and starch. The major fatty acids are summed feature 3 (iso-$C_{15:0}$ 2-OH and/or $C_{16:1}$ $\omega7c$), iso-$C_{15:0}$, $C_{16:0}$ 3-OH, and iso-$C_{17:0}$ 3-OH. The G+C content of the genomic DNA is 41.0 mol%.

The type strain, IBFC2009^T (=CCTCC AB 209162^T =KCTC 22814^T), was isolated from the soil of a bamboo plantation, which was collected from Hangzhou, China.

Acknowledgements

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References

Cappuccino, J.D. and N. Sherman. 2002. Microbiology: A Laboratory Manual, 6th ed. Benjamin Cummings, San Francisco, USA.

Dong, X.Z. and M.Y. Cai. 2001. Identification Manual for Routine Bacteriology. Scientific Press, Beijing, China.

Felsenstein, J. 1985. Confidence limits on phylogenies: An approach using the bootstrap. *Evolution* 39, 783-791.

Fitch, W.M. 1972. Toward defining the course of evolution: Minimum change for a specific tree topology. *Syst. Zool.* 20, 406-416.

Gerhardt, P., R.G.E. Murray, W.A. Wood, and N.R. Krieg. 1994. Methods for General and Molecular Bacteriology. American Society for Microbiology, Washington, D.C., USA.

Holmes, B., R.J. Owen, and D.G. Hollis. 1982. *Flavobacterium spiritivorum*, a new species isolated from human clinical specimens. *Int. J. Syst. Bacteriol.* 32, 157-165.

Keswani, J. and W.B. Whitman. 2001. Relationship of 16S rRNA sequence similarity to DNA hybridization in prokaryotes. *Int. J. Syst. Evol. Microbiol.* 51, 667-678.

Kim, K.H., L.N. Ten, Q.M. Liu, W.T. Im, and S.T. Lee. 2006. *Sphingobacterium daejeonense* sp. nov., isolated from a compost sample. *Int. J. Syst. Evol. Microbiol.* 56, 2031-2036.

Kumar, S., K. Tamura, and M. Nei. 2004. MEGA3: Integrated software for molecular evolutionary genetics analysis and sequence alignment briefings. *Bioinformatics* 5, 150-163.

Liu, R., H. Liu, C.X. Zhang, S.Y. Yang, X.H. Liu, K.Y. Zhang, and R. Lai. 2008. *Sphingobacterium siyangense* sp. nov., isolated from farm soil. *Int. J. Syst. Evol. Microbiol.* 58, 1458-1462.

Marmur, J. and P. Doty. 1962. Determination of the base composition of deoxyribonucleic acid from its thermal denaturation temperature. *J. Mol. Biol.* 5, 109-118.

Matsuyama, H., H. Katoh, T. Ohkushi, A. Satoh, K. Kawahara, and I. Yumoto. 2008. *Sphingobacterium kitahiroshimense* sp. nov., isolated from soil. *Int. J. Syst. Evol. Microbiol.* 58, 1576-1579.

Saitou, N. and M. Nei. 1987. The neighbor-joining method: A new method for reconstructing phylogenetic trees. *Mol. Biol. Evol.* 4, 406-425.

Sasser, M. 1990. Identification of bacteria by gas chromatography of cellular fatty acids. MIDI Technical Note 101. MIDI. Newark, DE, USA.

Shivaji, S., M.K. Ray, N.S. Rao, L. Saisree, M.V. Jagannadham, G.S. Kumar, G.S.N. Reddy. and P.M. Bhargava. 1992. *Sphingobacterium antarcticus* sp. nov., a psychrotrophic bacterium from the soils of Schirmacher Oasis, Antarctica. *Int. J. Syst. Bacteriol.* 42, 102-106.

Stackebrandt, E. and B.M. Goebel. 1994. Taxonomic note: A place for DNA-DNA reassociation and 16S rRNA sequence analysis in the present species definition in bacteriology. *Int. J. Syst. Bacteriol.* 44, 846-849.

Steyn, P.L., P. Segers, M. Vancanneyt, P. Sandra, K. Kersters, and J.J. Joubert. 1998. Classification of *heparinolytic* bacteria into a new genus, *Pedobacter*, comprising four species: *Pedobacter heparinus* comb. nov., *Pedobacter piscium* comb. nov., *Pedobacter africanus* sp. nov., and *Pedobacter saltans* sp. nov. Proposal of the family Sphingobacteriaceae fam. nov. *Int. J. Syst. Bacteriol.* 48, 165-177.

Takeuchi, M. and A. Yokota. 1992. Proposals of *Sphingobacterium faecium* sp. nov., *Sphingobacterium piscium* sp. nov., *Sphingobacterium heparinum* comb. nov., *Sphingobacterium thalpophilum* comb. nov., and two genospecies of the genus *Sphingobacterium*, and synonymy of *Flavobacterium yabuuchiae* and *Sphingobacterium spiritivorum*. *J. Gen. Appl. Microbiol.* 38, 465-482.

Ten, L.N., Q.M. Liu, W.T. Im, Z. Aslam, and S.T. Lee. 2006. *Sphingobacterium composti* sp. nov., a novel DNase-producing bacterium isolated from compost. *J. Microbiol. Biotechnol.* 16, 1728-1733.

Thompson, J.D., T.J. Gibson, F. Plewniak, F. Jeanmougin, and D. Higgins. 1997. The Clustal-X windows interface: Flexible strategies for multiple sequence alignment aided by quality analysis tools. *Nucleic Acids Res.* 24, 4876-4882.

Wei, W., Y. Zhou, X. Wang, X. Huang, and R. Lai. 2008. *Sphingobacterium anhuiense* sp. nov., isolated from forest soil. *Int. J. Syst. Evol. Microbiol.* 58, 2098-2101.

Yabuuchi, E., T. Kaneko, I. Yano, C.W. Moss, and N. Miyoshi. 1983. *Sphingobacterium gen. nov*., *Sphingobacterium spiritivorum* comb. nov., *Sphingobacterium multivorum* comb. nov., *Sphingobacterium mizutae* sp. nov., and *Flavobacterium indologenes* sp. nov.: Glucose-nonfermenting Gram-negative rods in CDC groups IIk-2 and IIb. *Int. J. Syst. Bacteriol.* 33, 580-598.

Yongmanitchai, W. and O.P. Ward. 1991. Growth of and omega-3 fatty acid production by *Phaeodactylum tricornutum* under different culture conditions. *Appl. Environ. Microbiol.* 57, 419-425.

Yoo, S.H., H.Y. Weon, H.B. Jang, B.Y. Kim, S.W. Kwon, S.J. Go, and E. Stackebrandt. 2007. *Sphingobacterium composti* sp. nov., isolated from cotton-waste composts. *Int. J. Syst. Evol. Microbiol.* 57, 1590-1593.