***Sphingomonas aquatilis* sp. nov., *Sphingomonas koreensis* sp. nov. and *Sphingomonas taejonensis* sp. nov., yellow-pigmented bacteria isolated from natural mineral water**

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The taxonomic status of four strains from several mineral water sources in Taejon, Korea, was examined. The DNA base compositions of these strains ranged from 62 to 66 mol%. All of the strains contained sphingolipids and ubiquinone 10 as the main respiratory quinone. The cellular fatty acids of these strains included octadecenoic acid, hexadecanoic acid and 2-hydroxymyristic acid, without 3-hydroxy fatty acids. On the basis of morphological, physiological and chemotaxonomic characteristics, together with 16S rDNA sequence comparison and DNA–DNA reassociation data, three new species of the genus *Sphingomonas* are proposed for the strains isolated from natural mineral water: *Sphingomonas aquatilis* sp. nov. for strain JSS7^T (= KCTC 2881^T = KCCM 41067^T), *Sphingomonas koreensis* sp. nov. for strains JSS26^T (= KCTC 2882^T = KCCM 41069^T) and JSS28 (= KCTC 2883 = KCCM 41066) and *Sphingomonas taejonensis* sp. nov. for strain JSS54^T (= KCTC 2884^T = KCCM 41068^T).

Keywords: *Sphingomonas*, mineral water, taxonomy

INTRODUCTION

As industry develops, environmental pollution becomes an increasing problem. Recently, water pollution has become more serious and concern has also increased about the quality of natural mineral water. In most natural mineral waters, bacterial cells are assumed to exist under starvation conditions and growth will be limited primarily by low concentrations of suitable carbon and energy sources. Therefore, it has been presumed that the conditions in most mineral water used for drinking make it difficult for bacteria to grow (Manaia *et al.*, 1990; Quevedo-Sarmiento *et al.*, 1986; Taylor *et al.*, 1983). However, yellow-pigmented bacterial colonies were frequently encountered on nutrient agar isolation plates when we investigated the

microbial ecosystems present in natural mineral water samples. The isolation and characterization of some bacteria from natural mineral waters has been reported (Manaia *et al.*, 1990; Quevedo-Sarmiento *et al.*, 1986; Taylor *et al.*, 1983), but there has been little study regarding yellow-pigmented bacteria. Therefore, we isolated and identified yellow-pigmented bacteria from natural mineral water from several places in the city of Taejon, Korea. The isolates were yellow-pigmented, Gram-negative, aerobic and motile rods with single polar flagella and contained ubiquinone 10 (Q-10) and 2-hydroxy fatty acids without 3-hydroxy fatty acids. On the basis of these characteristics, we judged that the isolates belonged to the genus *Sphingomonas*.

The genus *Sphingomonas* was first proposed by Yabuuchi *et al.* (1990) and later emended by Takeuchi *et al.* (1993). Members of the genus *Sphingomonas* are yellow-pigmented, Gram-negative, aerobic, non-spore-forming, non-fermentative, motile or non-motile rods and are characterized chemotaxonomically by the presence of Q-10, 2-hydroxy fatty acids and

Abbreviation: Q-10, ubiquinone 10.

The GenBank accession numbers for the 16S rDNA sequences of strains JSS7^T, JSS26^T, JSS28 and JSS54^T are respectively AF131295, AF131296, AF031240 and AF131297.

sphingolipid and the absence of 3-hydroxy fatty acids (Balkwill *et al.*, 1997; Kawahara *et al.*, 1994; Nohynek *et al.*, 1995; Takeuchi *et al.*, 1993, 1995; Wilkes *et al.*, 1996; Yabuuchi *et al.*, 1979, 1990).

In this study, we report the morphological, biochemical and phylogenetic characteristics of yellow-pigmented bacteria isolated from natural mineral water. We also propose that four of the isolates be assigned to three new species of *Sphingomonas*, *Sphingomonas aquatilis* sp. nov., *Sphingomonas koreensis* sp. nov. and *Sphingomonas taejonensis* sp. nov.

METHODS

Micro-organisms and cultures. The bacterial strains used in this study were isolated from natural mineral water in Taejon, Korea. Samples (250 ml) were collected in sterile bottles and filtered through a 0.45 µm Millipore filter. Filters were placed face-up on nutrient agar (Difco) plates and incubated at 30 °C for 7 d. Yellow-pigmented colonies were observed and isolated. The type strains of *Sphingomonas paucimobilis*, KCTC 2885^T (= IFO 13935^T = ATCC 29837^T), and *Sphingomonas yanoikuyae*, KCTC 2818^T (= IFO 15102^T = ATCC 51230^T), were obtained from the Korean Collection for Type Cultures, Taejon, Korea, as reference strains. The strains used are listed in Table 1. All strains were cultured routinely on nutrient agar and on trypticase soy agar for fatty acid analysis. The cultures were incubated at 30 °C for 2 d.

Determination of phenotypic characteristics. Cell morphology was examined by light microscopy. Motility was determined with an optical microscope using the hanging drop technique (Skerman, 1967). The flagellum type was determined by transmission electron microscopy using cells from the exponential growth phase. Cells were negatively stained with 1% (w/v) phosphotungstic acid and, after air-drying, the grids were examined by using a model CM-20 transmission electron microscope (Philips). The API 20NE and API ID32GN systems (bioMérieux) were used for physiological and biochemical characteristics. API ID32GN galleries were used to determine the carbohydrate assimilation pattern of the organisms. All API tests were performed in accordance with the manufacturer's directions. Fermentative acid production and oxidative acid production from carbohydrates were tested by growth in OF basal medium (Difco) supplemented with 0.5–1% carbohydrate [soft-agar

stabs with (fermentative) and without (oxidative) sterile mineral oil overlay]. The OF medium tubes were incubated at 30 °C for 10 d.

Cellular fatty acid analysis. Bacterial cultures were harvested from trypticase soy agar for total cellular fatty acid analysis. Fatty acids were extracted by following the Microbial Identification System instructions, as described previously (Lee *et al.*, 1996; Yang *et al.*, 1993).

Sphingolipid analysis. The long-chain bases of the cellular sphingolipids were analysed as described by Yano *et al.* (1982).

DNA base composition. DNA was extracted and purified by a modification of the method of Marmur (1961). The G + C content of DNA was determined by the reverse-phase HPLC method described by Tamaoka & Komagata (1984).

DNA–DNA hybridization. DNA–DNA hybridization was carried out by fluorometric hybridization in microdilution wells using biotinylated DNA (Ezaki *et al.*, 1989).

Identification of isoprenoid quinone. Isoprenoid quinones were extracted with chloroform/methanol (2:1, v/v) and purified by TLC on Merck Kieselgel 60 F₂₅₄ plates (20 × 20 cm, 0.5 mm thick) using a mixture of petroleum ether and diethyl ether (9:1, v/v) as the solvent and then analysed by HPLC as described by Shin *et al.* (1996).

16S rDNA sequence analysis. 16S rDNA sequencing from the four strains was described by Yoon *et al.* (1998). Two primers described by Stackebrandt & Liesack (1993), 9F (5'-GAGTTTGATCCTGGCTCAG-3'; positions 9–27 according to *Escherichia coli* 16S rRNA numbering) and 1542R (5'-AGAAAGGAGGTGATCCAGCC-3'; positions 1542–1525), were used for amplification of the 16S rRNA gene. The 5' ends of the two primers were phosphorylated using T4 polynucleotide kinase (New England Biolabs) according to the instructions of the Strandase ssDNA preparation kit (Novagen). The 16S rRNA gene was amplified as described by Yoon *et al.* (1997) in separate reactions containing phosphorylated 9F plus non-phosphorylated 1542R and phosphorylated 1542R plus non-phosphorylated 9F primers. PCR products were precipitated with 1 µl 1% (w/v) glycogen, 9 µl 3 M sodium acetate (pH 5.2) and 70 µl 2-propanol and resuspended in 10 µl distilled water. Strands containing phosphorylated primer from PCR products were selectively digested using λ exonuclease according to the Strandase ssDNA preparation kit instructions. The ssDNA templates produced were used directly for the sequencing

Table 1. *Sphingomonas* strains included in this study

Culture collections are abbreviated as: KCTC, Korean Collection for Type Cultures, Taejon, Korea; IFO, Institute for Fermentation, Osaka, Japan; KCCM, Korean Culture Center of Microorganisms, Seoul, Korea. All taxa listed are positive for sphingolipid and have Q-10 as the major isoprenoid quinone.

Strain	Other designation	Source	DNA G + C content (mol %)
JSS7 (= KCTC 2881 ^T)	KCCM 41067 ^T	Natural mineral water, Korea	63
JSS26 (= KCTC 2882 ^T)	KCCM 41069 ^T	Natural mineral water, Korea	66
JSS28 (= KCTC 2883)	KCCM 41066	Natural mineral water, Korea	66
JSS54 (= KCTC 2884 ^T)	KCCM 41068 ^T	Natural mineral water, Korea	63
<i>Sphingomonas paucimobilis</i> KCTC 2885 ^T	IFO 13935 ^T	–	64
<i>Sphingomonas yanoikuyae</i> KCTC 2818 ^T	IFO 15102 ^T	–	62

reaction. Sequencing was performed as described by Kim *et al.* (1995) using [³⁵S]dATP α S and a DNA sequencing kit (USB) according to the manufacturer's instructions.

Phylogenetic analysis. The 16S rDNA sequences of strains JSS7^T, JSS26^T, JSS28 and JSS54^T were aligned with 16S rRNA and rDNA sequences of representatives of the genus *Sphingomonas* and related taxa by using the CLUSTAL W software (Thompson *et al.*, 1994). Gaps at the 5' and 3' ends of the alignment were omitted from further analysis. Evolutionary distance matrices were calculated by using the algorithm of Jukes & Cantor (1969) with the DNADIST program within the PHYLIP package (Felsenstein, 1993). A phylogenetic tree was constructed by using the neighbour-joining method (Saitou & Nei, 1987) as implemented within the NEIGHBOR program of the same package. The stability of relationships was assessed by bootstrap analysis of 1000 data sets with the programs SEQBOOT, DNADIST, NEIGHBOR and CONSENSE of the PHYLIP package.

RESULTS AND DISCUSSION

Morphological and physiological characteristics

All of the strains were Gram-negative, motile rods with single polar flagella (Fig. 1). All of the isolates gave positive results for aesculin hydrolysis, β -galactosidase, oxidase, catalase and assimilation of glucose and negative results for nitrate reduction, indole production, glucose acidification, arginine hy-

drolisis, urease, gelatin hydrolysis and assimilation of 2-ketogluconate, 5-ketogluconate, adipate, D-ribose, D-sorbitol, glycogen and phenylacetate. Table 2 shows differential characteristics for 20 *Sphingomonas* species; isolates JSS7^T, JSS26^T, JSS28 and JSS54^T can be differentiated from other *Sphingomonas* species on the basis of the results of several tests included in Table 2.

Chemotaxonomic characteristics

All of the isolates contained Q-10 and sphingolipid and the DNA base composition (G+C content) ranged from 63 to 66 mol%. The major whole-cell fatty acids in the test strains were octadecenoic acid (18:1), hexadecanoic acid (16:0) and 2-hydroxy-myristic acid (14:0 2-OH), which was the predominant hydroxy fatty acid (Table 3). Three of the isolates, JSS26^T, JSS28 and JSS54^T, contained 2-hydroxy-pentadecanoic acid (15:0 2-OH) and 2-hydroxy-hexadecanoic acid (16:0 2-OH) in addition to 2-hydroxymyristic acid. None of the strains contained 3-hydroxy fatty acids.

DNA–DNA reassociation analysis

As shown in Table 4, DNA–DNA reassociation values between the four isolates and all of the other strains tested were less than 26%. Isolates JSS26^T and JSS28 exhibited high levels of homology (90–102%) with each other, but lower levels of homology with JSS7^T (16–18%) and JSS54^T (11–15%). The DNA–DNA reassociation values between JSS7^T and the other three isolates and between JSS54^T and the other three isolates were less than 18%.

Phylogenetic analysis

Nearly complete 16S rDNA sequences (positions 28–1524, *E. coli* numbering) were determined for JSS7^T, JSS26^T, JSS28 and JSS54^T. The primary structures of the 16S rDNA sequences of these strains were compared with each other and with those of closely related reference strains. A phylogenetic tree based on K_{nuc} values, shown in Fig. 2, indicates that these strains belong to the genus *Sphingomonas*.

The levels of 16S rDNA sequence similarity confirmed that isolates JSS7^T, JSS26^T, JSS28 and JSS54^T all belong to the genus *Sphingomonas*. Three of the isolates (JSS7^T, JSS26^T and JSS28) were most closely related to *Sphingomonas asaccharolytica*, *Sphingomonas pruni* and *Sphingomonas mali*, and formed a distinct cluster with these strains (Fig. 2). Two of these strains (JSS26^T and JSS28) had identical 16S rDNA gene sequences, implying that they may be members of the same species. The levels of sequence similarity between these strains and *S. asaccharolytica*, *S. pruni* and *S. mali* were somewhat lower (97.8–98.1%). Isolate JSS7^T was phylogenetically most closely related to strains JSS26^T and JSS28, but was always separated

Fig. 1. Transmission electron micrograph of strain JSS54^T. Bar, 1 μ m.

Table 2. Morphological and physiological characteristics of *Sphingomonas* species

Taxa are identified as: 1, *S. chlorophenolica*; 2, *S. yanoikuyae*; 3, *S. suberifaciens*; 4, *S. macrogoltabidus*; 5, *S. adhaesiva*; 6, *S. terrae*; 7, *S. capsulata*; 8, *S. subarctica*; 9, *S. rosa*; 10, *S. natatoria*; 11, *S. mali*; 12, *S. pruni*; 13, *S. asaccharolytica*; 14, *S. parapaucimobilis*; 15, *S. sanguinis*; 16, *S. paucimobilis*; 17, *S. trueperi*; 18, *S. aquatilis* JSS7^T; 19, *S. koreensis* JSS26^T; 20, *S. taejonensis* JSS54^T. Strain JSS28 gave identical results to JSS26^T. All taxa are positive for motility and aesculin hydrolysis and negative for Gram staining. Cells are rod-shaped. Characteristics are scored as: +, positive; –, negative; w, weak; NT, not tested. Data in columns 1, 3–15 and 17 were taken from Kämpfer *et al.* (1997), Takeuchi *et al.* (1993, 1995) and Yabuuchi *et al.* (1990, 1999).

Characteristic	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
Colony colour*	Y	Y	W	Y	Y	Y	Y	Y	Y	O	Y	Y	Y	Y	Y	Y	Y	Y	Y	PY
Reduction of nitrate	NT	–	–	–	–	–	–	NT	W	–	–	–	–	+	–	–	NT	–	–	–
Hydrolysis of gelatin	NT	–	–	–	–	–	–	NT	–	–	–	–	–	–	–	–	+	–	–	–
Assimilation of:																				
Adipate	–	–	–	–	–	W	–	–	–	+	W	–	–	–	–	–	–	–	–	–
Caprate	–	+	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	+	–	+
Citrate	–	+	–	–	–	–	–	+	–	–	–	–	–	+	–	–	–	–	–	–
D-Melibiose	–	+	NT	–	+	–	–	NT	+	NT	+	+	+	+	+	+	+	–	+	–
D-Sucrose	–	+	NT	–	+	–	+	NT	+	NT	+	+	W	+	+	+	+	+	+	–
Gluconate	–	+	NT	–	–	–	+	–	+	–	+	+	–	+	–	–	–	–	–	–
L-Arabinose	–	+	–	+	–	–	+	+	+	+	+	+	+	+	+	+	+	+	–	–
Malate	–	+	–	–	+	+	+	+	+	–	–	–	–	+	+	+	+	–	+	+
Maltose	–	+	–	+	–	–	+	+	+	+	+	+	+	+	+	+	+	+	–	–
Mannose	–	–	–	–	+	–	+	–	+	–	+	+	+	+	+	+	+	–	–	–
N-Acetylglucosamine	–	+	–	–	+	–	+	+	W	–	+	+	+	+	+	+	+	+	+	–
Rhamnose	–	+	NT	–	–	–	+	+	+	NT	+	+	+	W	–	–	–	+	+	–
Salicin	–	+	NT	–	+	–	–	NT	+	NT	+	+	W	+	+	+	+	W	+	–
Oxidative acid production (OF medium) from:																				
Glycerol	NT	+	NT	–	+	–	+	NT	–	NT	–	–	–	–	+	–	–	–	–	–
Rhamnose	–	+	NT	–	+	–	+	NT	+	NT	+	–	–	+	+	–	–	+	W	–

*o, Orange; PY, pale yellow; Y, yellow; w, white.

Table 3. Cellular fatty acid profiles of isolates and reference strains

Summed features represent groups of two or three fatty acids that could not be separated by GLC with the MIDI system: summed feature 4 contained one or more of 15:0 iso 2-OH and/or 16:1 ω 7*t*; summed feature 7 contained one or more of 18:1 ω 7*c*, 18:1 ω 9*t* and/or 18:1 ω 12*t*. ND, Not detected.

Fatty acid	<i>S. paucimobilis</i> KCTC 2885 ^T	<i>S. yanoikuyae</i> KCTC 2818 ^T	JSS7 ^T	JSS26 ^T	JSS28	JSS54 ^T
Saturated fatty acids:						
14:0	1.52		0.52	0.70	1.85	0.95
15:0	0.52		ND	ND	0.23	0.26
16:0	9.26		15.40	20.58	12.98	8.82
17:0	0.29		ND	ND	ND	ND
18:0	0.72		ND	1.04	0.55	0.40
Unsaturated fatty acids:						
16:1 ω 5 <i>c</i>	0.71		2.90	0.81	1.28	1.56
17:1 ω 8 <i>c</i>	0.50		ND	ND	0.35	ND
17:1 ω 7 <i>c</i>	ND		0.83	ND	ND	ND
17:1 ω 6 <i>c</i>	1.76		1.59	ND	1.47	1.57
18:1 ω 5 <i>c</i>	3.42		3.12	1.51	1.76	1.81
Hydroxy fatty acids:						
14:0 2-OH	6.36		7.44	10.86	9.42	10.08
15:0 2-OH	0.16		ND	ND	0.29	0.34
16:0 2-OH	ND		0.84	ND	0.79	0.82
Summed feature 4	2.67		15.75	4.61	2.06	2.06
Summed feature 7	72.11		51.60	59.89	66.97	71.33

from those strains on a distinct branch of the tree (Fig. 2). The level of sequence similarity between it and JSS26^T and JSS28 was 97.0%. Isolate JSS54^T was

most closely related to *Sphingomonas macrogoltabidus*. However, a comparison of levels of sequence similarity between it and JSS54^T (97.7%) revealed that isolate

Table 4. DNA–DNA reassociation values for various *Sphingomonas* strains

Strain	Reassociation (%) with labelled DNA from:			
	JSS7 ^T	JSS26 ^T	JSS28	JSS54 ^T
JSS7 ^T	100	18	16	11
JSS26 ^T	16	100	90	15
JSS28	14	102	100	16
JSS54 ^T	18	15	11	100
<i>S. adhaesiva</i> KCTC 2812 ^T	11	17	16	11
<i>S. aromaticivorans</i> IFO 16084 ^T	10	11	9	16
<i>S. asaccharolytica</i> KCTC 2825 ^T	18	5	14	16
<i>S. capsulata</i> IFO 12533 ^T	9	16	20	7
<i>S. macrogoltabidus</i> KCTC 2813 ^T	7	6	16	19
<i>S. mali</i> KCTC 2826 ^T	14	7	18	14
<i>S. parapaucimobilis</i> KCTC 2815 ^T	14	12	22	9
<i>S. paucimobilis</i> KCTC 2885 ^T	18	12	27	13
<i>S. pruni</i> KCTC 2824 ^T	16	9	14	10
<i>S. rosa</i> KCTC 2821 ^T	10	11	11	9
<i>S. sanguinis</i> IFO 13937 ^T	18	10	16	5
<i>S. stygia</i> IFO 16085 ^T	16	6	9	18
<i>S. subarctica</i> IFO 16058 ^T	8	9	11	17
<i>S. subterranea</i> IFO 16086 ^T	13	10	16	12
<i>S. terrae</i> KCTC 2814 ^T	13	7	11	26
<i>S. yanoikuyae</i> KCTC 2818 ^T	21	14	8	13
<i>S. natatoria</i> IFO 15649 ^T	12	10	11	13
<i>S. suberifaciens</i> KCTC 2841 ^T	20	10	9	8
<i>Brevundimonas subvibrioides</i> IFO 16000 ^T	24	8	12	7

JSS54^T represents a distinct species of the genus *Sphingomonas*.

As mentioned above, the chemotaxonomic and physiological characteristics and phylogenetic data showed that all of the isolated strains that we studied are members of the genus *Sphingomonas*.

Conclusions

Members of the genus *Sphingomonas* contain sphingoglycolipid with the long-chain base dihydrosphingosin and do not contain lipopolysaccharide. They contain Q-10 and 2-hydroxymyristate and do not contain 3-hydroxy fatty acids. The DNA G+C content of *Sphingomonas* species is 62–67 mol%. The strains isolated from natural mineral water that we studied here have these characteristics.

Isolate JSS54^T has pale yellow colonies and gave negative results in assimilation of carbon sources with the exception of caprate and malate by the API 20NE and API ID32GN tests. These results show the isolate JSS54^T can be differentiated from other *Sphingomonas* species. Strains JSS7^T, JSS26^T and JSS28 also have different physiological characteristics, as shown in Table 2.

A comparison of the 16S rDNA sequences of isolates JSS7^T, JSS26^T and JSS54^T with sequences reported

previously (Takeuchi *et al.*, 1995; Nohynek *et al.*, 1996) resulted in relatively high levels of similarity (97.0–98.1%), but DNA–DNA reassociation values between these isolates and all of the other type strains tested were less than 27%. These values demonstrate that the four isolates are not related to any of the previously described taxa at the species level.

On the basis of morphological, physiological and chemotaxonomic characteristics, together with DNA–DNA hybridization and 16S rDNA sequence comparison data, we propose that the isolates from natural mineral water from Korea should be assigned to three new species of the genus *Sphingomonas*: *Sphingomonas aquatilis* (for strain JSS7^T = KCTC 2881^T), *Sphingomonas koreensis* (for strains JSS26^T = KCTC 2882^T and JSS28 = KCTC 2883) and *Sphingomonas taejonensis* (for strain JSS54^T = KCTC 2884^T).

Description of *Sphingomonas aquatilis* sp. nov.

Sphingomonas aquatilis (a.qua.til'is. L. f. adj. *aquatilis* aquatic, growing in water).

Cells are Gram-negative rods, motile with single polar flagella. Colonies are circular, entire, low-convex, smooth, opaque and yellow. Indole, urease and arginine dihydrolase are not produced. Catalase, oxidase and β -galactosidase are positive. Gelatin is not liquified and glucose is not fermented. Reduction of nitrate and

Fig. 2. Phylogenetic tree indicating the position of strains JSS7^T, JSS26^T, JSS28^T and JSS54^T within the radiation of members of the genus *Sphingomonas* and related taxa. Sequence accession numbers are given for each strain. Bootstrap values are indicated. Bar, 0.01 accumulated change per nucleotide.

hydrolysis of aesculin are negative. Caprate, D-sucrose, glucose, L-arabinose, maltose, N-acetylglucosamine, rhamnose and salicin are assimilated; 2-ketogluconate, 5-ketogluconate, adipate, citrate, D-melibiose, D-ribose, D-sorbitol, gluconate, glycogen, malate, mannose and phenylacetate are not assimilated. Acid is produced oxidatively from glucose and rhamnose but not from glycerol. The G + C content of the DNA is 63 mol%. The major isoprenoid quinone is ubiquinone Q-10. The major non-polar fatty acids are 18:1 ω 7c and 16:0 and the major 2-hydroxy fatty acid is 14:0 2-OH. Sphingolipid is present.

The type strain is JSS7^T (= KCTC 2881^T, KCCM 41067^T), which was isolated from natural mineral water of Taejon City, Korea.

Description of *Sphingomonas koreensis* sp. nov.

Sphingomonas koreensis (ko.re.en'sis. N.L. f. adj. *koreensis* of Korea, from where the new organisms were isolated).

Cells are Gram-negative, motile rods with single polar flagella. Colonies are circular, entire, low-convex, smooth, opaque and yellow. Indole, urease and arginine dihydrolase are not produced. Catalase, oxidase and β -galactosidase are positive. Gelatin is not liquified and glucose is not fermented. Reduction of nitrate and hydrolysis of aesculin are negative. D-Melibiose, D-sucrose, glucose, malate, maltose, N-acetylglucosamine, rhamnose and salicin are assimilated; 2-ketogluconate, 5-ketogluconate, adipate, caprate, citrate, D-ribose, D-sorbitol, gluconate, glycogen, L-arabinose, mannose and phenylacetate are not assimilated. Acid is weakly produced oxidatively from glucose and rhamnose, but not from glycerol. The G + C content of the DNA is 66 mol%. The major isoprenoid quinone is ubiquinone Q-10. The major non-polar fatty acids are 18:1 ω 7c and 16:0; the major 2-hydroxy fatty acids are 14:0 2-OH, 15:0 2-OH and 16:0 2-OH. Sphingolipid is present.

Strains were isolated from natural mineral water from Taejon City, Korea. The type strain is JSS26^T (=

KCTC 2882^T = KCCM 41069^T) and JSS28 (= KCTC 2883 = KCCM 41066) is a reference strain.

Description of *Sphingomonas taejonensis* sp. nov.

Sphingomonas taejonensis (tae.jon.en'sis. N.L. f. adj. *taejonensis* of Taejon, Korea, the geographical origin of the new species).

Cells are Gram-negative, motile rods with single polar flagella. Colonies are circular, entire, low-convex, smooth, opaque and pale yellow. Indole, urease and arginine dihydrolase are not produced. Catalase, oxidase and β -galactosidase are positive. Gelatin is not liquified and glucose is not fermented. Reduction of nitrate and hydrolysis of aesculin are negative. Caprate, glucose and malate are assimilated; 2-keto-gluconate, 5-ketogluconate, adipate, citrate, D-melibiose, D-ribose, D-sorbitol, D-sucrose, gluconate, glycogen, L-arabinose, maltose, mannose, N-acetylglucosamine, phenylacetate, rhamnose and salicin are not assimilated. Acid is weakly produced oxidatively from glucose, but not from rhamnose and glycerol. The G + C content of the DNA is 63 mol %. The major isoprenoid quinone is ubiquinone Q-10. The major non-polar fatty acids are 18:1 ω 7c, 16:0, 16:1 ω 7t and 17:1 ω 6c; the major 2-hydroxy fatty acids are 14:0 2-OH, 15:0 2-OH and 16:0 2-OH. Sphingolipid is present.

The type strain, JSS54^T (= KCTC 2884^T = KCCM 41068^T), was isolated from natural mineral water from Taejon City, Korea.

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