**Sphingomonas lutea** sp. nov., isolated from freshwater of an artificial reservoir

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An aerobic, Gram-stain-negative, gliding and yellow-pigmented bacterium, designated strain JS5\(^{\text{T}}\), was isolated from freshwater of Juam reservoir, Republic of Korea. Cells were catalase-positive and oxidase-negative. The neighbour-joining phylogenetic tree based on 16S rRNA gene sequences showed that strain JS5\(^{\text{T}}\) forms an independent lineage within the genus *Sphingomonas*. Strain JS5\(^{\text{T}}\) was related distantly to *Sphingomonas parvus* GP20-2 (98.2% 16S rRNA gene sequence similarity), *Sphingomonas sediminicola* Dae 20\(^{\text{T}}\) (96.8%) and *Sphingomonas daechungensis* CH15-11\(^{\text{T}}\) (96.7%). The major fatty acids of strain JS5\(^{\text{T}}\) were C\(_{16:0}\), summed feature 3 comprising C\(_{16:1}\)ω7c and/or C\(_{16:1}\)ω6c and summed feature 8 comprising C\(_{18:1}\)ω7c and/or C\(_{18:1}\)ω6c. The predominant isoprenoid quinone of the isolate was ubiquinone-10. The DNA G+C content of strain JS5\(^{\text{T}}\) was 65 mol%. Phenotypic characteristics distinguished strain JS5\(^{\text{T}}\) from related species of the genus *Sphingomonas*. On the basis of the evidence presented in this study, a novel species, *Sphingomonas lutea* sp. nov., is proposed to accommodate strain JS5\(^{\text{T}}\) (=KCTC 23642\(^{\text{T}}\) = JCM 18309\(^{\text{T}}\)).

The genus *Sphingomonas* belonging to the family *Sphingomonadaceae* of the class *Alphaproteobacteria* was erected by Yabuuchi *et al.* (1990) with *Sphingomonas paucimobilis* as the type species. The genus description has been subsequently emended by Takeuchi *et al.* (1993, 2001), Yabuuchi *et al.* (1999, 2002), Busse *et al.* (2003) and Chen *et al.* (2012). Members of this genus are Gram-stain-negative, strictly aerobic, chemoheterotrophic and non-sporulating rods with ubiquinone-10 (Q-10) as the major respiratory quinone, sym-homospermidine as the major polyamine and sphingoglycolipids as the characteristic polar lipids. The G+C content of their DNA varies between 62 and 68 mol% and the major fatty acids are C\(_{18:1}\)ω7c and/or C\(_{18:1}\)ω6c (Chen *et al.*, 2012). Based on 16S rRNA gene sequences, polyamine patterns and polar lipid profiles, the genus *Sphingomonas* has been divided into four genera, *Sphingomonas*, *Novosphingobium*, *Sphingobium* and *Sphingopyxis* (Takeuchi *et al.*, 2001). At the time of writing, the genus *Sphingomonas* consists of 91 species with validly published names. Species of the genus *Sphingomonas* have been isolated from various environmental habitats such as soil, water, air, desert sand, freshwater sediment, plants, marine bivalve, glacier and heavy metal mine (Takeuchi *et al.*, 1995; Lee *et al.*, 2001; Yang *et al.*, 2006; Romanenko *et al.*, 2007; An *et al.*, 2011, 2013; Huang *et al.*, 2012; Kim *et al.*, 2014; Ahn *et al.*, 2015; Zhu *et al.*, 2015; Liu *et al.*, 2015; Feng *et al.*, 2016). The present study reports on the taxonomic characterization of a *Sphingomonas*-like bacterial strain, JS5\(^{\text{T}}\), which was isolated from freshwater of an artificial lake. Strain JS5\(^{\text{T}}\) was isolated from freshwater of Juam artificial reservoir (35° 00′ N 127° 14′ E) located in Jeonnam Province, Republic of Korea, in December 2010. The reservoir was constructed in 1992 to supply mainly drinking water, and its area and capacity was 1010 km\(^2\) and 4.6×10\(^8\) tons, respectively. At the time of water sampling, water temperature, pH and dissolved oxygen concentration were 9.9 °C, 6.9 and 8.6 mg l\(^{-1}\), respectively. Isolation of bacteria was achieved with the standard dilution plating technique using Reasoner’s 2A (R2A; Becton Dickinson) agar at 25 °C for 7 days. The isolate was routinely cultured on R2A agar and preserved at −80 °C as a suspension in distilled water containing 20% (v/v) glycerol. Reference strains *Sphingomonas parvus* KACC 12865, *Sphingomonas daechungensis* KCTC 23718\(^{\text{T}}\) and *Sphingomonas sediminicola* KCTC 12629\(^{\text{T}}\) were purchased from the respective culture collections. The name ‘*S. parvus*’ has been effectively published (Ahn *et al.*, 2015), but not validated. Nonetheless, we used ‘*S. parvus*’ KACC 12865 as a reference for the phenotypic and genotypic experiments because the strain ‘*S. parvus*’ GP20-2 was found to be the closest relative of strain JS5\(^{\text{T}}\).
Bacterial DNA preparation, PCR amplification and sequencing of the 16S rRNA gene were carried out as described previously (Chun & Goodfellow, 1995). Identification of phylogenetic neighbours and calculation of pairwise 16S rRNA gene sequence similarities were achieved using the EzTaxon-e server (http://www.ezbiocloud.net; Kim et al., 2012) and the BLAST search program at the NCBI website (http://blast.ncbi.nlm.nih.gov/Blast.cgi). The novel sequence and related sequences were aligned by using CLUSTAL W (Thompson et al., 1994), and the alignment was refined using BioEdit version 7.2.0 (Hall, 1999). Phylogenetic analysis was performed by using the software package MEGA version 6.06 (Tamura et al., 2013). Phylogenetic trees were inferred using the neighbour-joining (Saitou & Nei, 1987), maximum-likelihood (Felsenstein, 1993) and maximum-parsimony (Fitch, 1971) algorithms. The distance matrix of the neighbour-joining method was generated according to the model of Jukes & Cantor (1969). The robustness of the topology in the neighbour-joining phylogenetic tree was evaluated by bootstrap analyses (Felsenstein, 1985) based on 1000 resamplings. For DNA G+C content calculations, the DNA sample was prepared in triplicate and values were determined by the thermal denaturation method of Marmur & Doty (1962).

The 16S rRNA gene sequence of strain JS5 was a continuous stretch of 1428 nt. The closest relatives of strain JS5 were ‘S. parvus’ GP20-2 (98.2 % 16S rRNA gene sequence similarity), S. sediminicola Daee 20T (96.8 %) and S. daechungensis CH15-11T (96.7 %). Levels of 16S rRNA gene sequence similarity between strain JS5 and other members of the genus Sphingomonas were less than 96 %. The neighbour-joining tree (Fig. 1) showed that strain JS5 formed a distinct branch with the clade comprising ‘S. parvus’ with 99 % bootstrap support. The trees based on other methods showed essentially similar topology (Fig. S1, available in the online Supplementary Material).

DNA–DNA hybridization was performed by the membrane filter technique using the DIG High Prime DNA Labelling and Detection Starter kit II (Roche Molecular Biochemicals) according to the method described in detail by Lee et al. (2003), with the modification that the hybridization temperature was 64 °C. Strain JS5 and ‘S. parvus’ KACC 12865 shared a low level of DNA–DNA relatedness (45 %). This value is below the threshold (70 %) for determining bacterial species (Wayne et al., 1987), and strongly suggested that the new isolate belongs to a separate genomic species in the genus Sphingomonas.

Growth on various standard bacteriological media was tested by using nutrient agar (NA; Becton Dickinson), R2A agar, plate-count agar (PCA; Becton Dickinson), marine agar (MA; Becton Dickinson) and tryptic soy agar (TSA; Becton Dickinson) according to the manufacturer’s instructions. Cells grown on R2A agar at 30 °C for 2–3 days were used for the physiological and biochemical tests. The Gram reaction test of cells grown on R2A agar at 30 °C for 2–14 days was performed by using the bioMérieux Gram stain kit according to the manufacturer’s instructions and the Ryu non-staining KOH method (Powers, 1995). Cell morphology was observed by phase-contrast (ICC50; Leika) and scanning electron (JSM-7100F; Jeol) microscopy using cells grown at 30 °C for 4 days on R2A agar and for 3 days in R2A broth, respectively. Motility was examined by observing cells grown in wet mounts using phase-contrast microscopy (ICC50; Leika). Flagellation was determined with transmission electron microscopy (CM-20; Philips) using cells cultured for 48 h in R2A broth. Growth at various NaCl concentrations (0–3 %, w/v, using increments of 0.5 %) was investigated on R2A agar prepared according to the formula of R2A agar medium except that no NaCl was used. The growth experiment at pH 4–11 (increments of 1 pH units) was performed using R2A broth medium containing 100 mM acetate buffer, 100 mM NaH2PO4/Na2HPO4 buffer and 100 mM NaHCO3/Na2CO3 buffer, at pH 4–5, 6–8 and 9–11, respectively. The optimal temperature and temperature range for growth was tested on R2A agar at 4, 10, 15, 20, 25, 30, 37, 40 and 45 °C. Anaerobic growth was tested on R2A agar in a jar containing the AnaeroPack-Anaero (Mitsubishi Gas Chemical), which works as an oxygen absorber and CO2 generator, for up to 10 days. Catalase and oxidase activities were tested in 3 % (v/v) hydrogen peroxide and oxidase reagent (bioMérieux), respectively. Acid production from sugars was tested as described by Yamaguchi & Yokoe (2000). Simons’ citrate test was carried out in Simmons’ citrate agar (Sigma). Indole production was determined with Kovacs’ indole reagent on SIM agar (Becton Dickinson). H2S production was determined on Kligler iron agar (Becton Dickinson) according to Smibert & Krieg (1994). Degradation of the following macromolecules was tested using R2A agar as the basal medium and incubation at 30 °C for 10 days (all w/v; all Sigma): CM-cellulose (1 %), casein (2 % skimmed milk), chitin (0.5 % colloidal chitin), hypoxanthine (0.5 %), starch (1 %), Tween 20 (1 %), Tween 80 (1 %) and xanthine (0.5 %). Degradation was revealed by the formation of clear zones around the colonies either directly (Tindall et al., 2007) or after flooding with adequate staining solutions (Smibert & Krieg, 1994). Decomposition of xylan (1 %, w/v) was tested using R2A agar as the basal medium (Barrow & Feltham, 1993). DNase activity was determined with DNase test agar (Becton Dickinson). The presence of flexirubin-type pigments was tested using the KOH test as described by Bernardet et al. (2002). Cell extracts for carotenoid pigment analysis were prepared with methanol (Klassen & Foght, 2008) and the absorption spectrum (200–800 nm) was recorded using a UV/VIS spectrophotometer (Ultrispec 2100 pro; Biochrom). Some physiological characteristics and enzyme activities were determined using API 20NE and API ZYM kits (bioMérieux) and GN2 MicroPlates (Biolog) prepared according to the instructions of the manufacturers. Antibiotic resistance was determined with the disc diffusion method (Bauer et al., 1966) using commercial antibiotic-impregnated discs (Becton Dickinson).
After 5 days of incubation at 30 °C on R2A agar, the results were interpreted according to the guidelines set out by the CLSI (2009). Cells were Gram-stain-negative, motile by gliding and rod shaped, approximately 0.2 µm in diameter and 0.5–0.9 µm in length (Fig. S2). Colonies were circular, convex, smooth, 0.5–1.0 mm in diameter and yellow on R2A agar after 10 days. Strain JS5T was sensitive to the following antibiotics (µg per disc, unless otherwise indicated): amikacin (30), chloramphenicol (30), erythromycin (15), gentamicin (10), kanamycin (30) and vancomycin (30), but resistant to ampicillin (10), nalidixic acid (30), penicillin (10 IU), streptomycin (10) and tetracycline (30). The detailed results of morphological, physiological and biochemical analyses are given in Table 1 and the species description.

For cellular fatty acid analysis, strain JS5T and the reference strains were grown on R2A agar and harvested at late exponential growth phase, i.e. after 3 days at 30 °C. Extraction of fatty acid methyl esters and separation by GC were performed by using the Instant FAME method of the Microbial Identification System (MIDI) version 6.1 and the TSBA6 database. For analyses of polar lipids, polyamine patterns

**Fig. 1.** Neighbour-joining phylogenetic tree based on 1322 nt in unambiguously aligned 16S rRNA gene sequences, showing the relationships between strain JS5T and members of the genus Sphingomonas. Numbers at nodes are levels of bootstrap support (>70%) based on neighbour-joining analyses of 1000 resampled data sets. The sequence of *Escherichia coli* KCTC 2441T (EU014689) was used as an outgroup. Closed circles indicate that the corresponding nodes were also recovered in trees generated with the maximum-parsimony and maximum-likelihood algorithms. Bar, 0.02 nucleotide substitutions per position.
Table 1. Phenotypic characteristics that differentiate strain JS5\textsuperscript{T} from other Sphingomonas species

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
</tr>
</thead>
<tbody>
<tr>
<td>Isolation source</td>
<td>Freshwater</td>
<td>Ginseng-field soil</td>
<td>Freshwater sediment</td>
<td>Eutrophic reservoir sediment</td>
</tr>
<tr>
<td>Colony colour</td>
<td>Yellow</td>
<td>Pale orange</td>
<td>Yellow</td>
<td>Pale yellow</td>
</tr>
<tr>
<td>Optimum growth temperature ((^\circ)C)</td>
<td>25–30</td>
<td>35</td>
<td>30</td>
<td>28–30</td>
</tr>
<tr>
<td>Motility</td>
<td>Gliding</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Growth at/with:</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>10(^\circ)C</td>
<td>+</td>
<td>+</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>0.5 % (w/v) NaCl</td>
<td>+</td>
<td>–</td>
<td>+</td>
<td>W*</td>
</tr>
<tr>
<td>Oxidase</td>
<td>–</td>
<td>+</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Reducation of nitrate</td>
<td>–</td>
<td>–</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Enzyme activity (API ZYM):</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>(\alpha)-Chymotrypsin</td>
<td>–</td>
<td>w</td>
<td>w</td>
<td>–</td>
</tr>
<tr>
<td>Cystine arylamidase</td>
<td>–</td>
<td>+</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>(\beta)-Galactosidase</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>+</td>
</tr>
<tr>
<td>(\alpha)-Glucosidase</td>
<td>–</td>
<td>+</td>
<td>w</td>
<td>w</td>
</tr>
<tr>
<td>(\beta)-Glucosidase</td>
<td>–</td>
<td>w</td>
<td>w</td>
<td>+</td>
</tr>
<tr>
<td>Trypsin</td>
<td>–</td>
<td>+</td>
<td>–*</td>
<td>–</td>
</tr>
<tr>
<td>Hydrolysis of:</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Tween 20</td>
<td>+</td>
<td>–</td>
<td>–</td>
<td>W</td>
</tr>
<tr>
<td>Assimilation of (Biolog):</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>D-Galactose</td>
<td>–</td>
<td>+</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Gentibiose</td>
<td>–</td>
<td>w</td>
<td>–</td>
<td>+</td>
</tr>
<tr>
<td>D-Gluconic acid</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>+</td>
</tr>
<tr>
<td>(\alpha)-D-Glucose</td>
<td>–</td>
<td>+</td>
<td>W</td>
<td>+</td>
</tr>
<tr>
<td>Glycly L-aspartic acid</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>+</td>
</tr>
<tr>
<td>Glycly L-glutamic acid</td>
<td>+</td>
<td>+</td>
<td>–</td>
<td>+</td>
</tr>
<tr>
<td>L-Glutamic acid</td>
<td>W</td>
<td>W</td>
<td>w</td>
<td>+</td>
</tr>
<tr>
<td>L-Histidine</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>+</td>
</tr>
<tr>
<td>(\beta)-Hydroxybutyric acid</td>
<td>+</td>
<td>+</td>
<td>–</td>
<td>+</td>
</tr>
<tr>
<td>Melibiose</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>+</td>
</tr>
<tr>
<td>Succinic acid</td>
<td>–</td>
<td>w</td>
<td>–</td>
<td>+</td>
</tr>
<tr>
<td>Trehalose</td>
<td>–</td>
<td>+</td>
<td>W</td>
<td>w</td>
</tr>
<tr>
<td>Turanose</td>
<td>–</td>
<td>+</td>
<td>–</td>
<td>+</td>
</tr>
<tr>
<td>Tween 40</td>
<td>–</td>
<td>–</td>
<td>+</td>
<td>–</td>
</tr>
<tr>
<td>Acid production from:</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Glucose</td>
<td>–</td>
<td>–</td>
<td>+</td>
<td>–</td>
</tr>
<tr>
<td>Xylose</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>+</td>
</tr>
<tr>
<td>DNA G+C content (mol%)\dagger</td>
<td>64.9</td>
<td>67.2\textsuperscript{a}</td>
<td>67.9\textsuperscript{b}</td>
<td>65.6\textsuperscript{c}</td>
</tr>
</tbody>
</table>

\*Results differ from those reported by An \textit{et al.} (2013) and Huy \textit{et al.} (2014).

and isoprenoid quinones, cells grown in R2A broth for 3 days at 30\(^\circ\)C were harvested and freeze-dried. Polar lipids were extracted, separated by two-dimensional TLC and identified by spraying the plates with appropriate detection reagents (Minnikin \textit{et al.}, 1984; Komagata & Suzuki, 1987). Polyamines were extracted and analysed according to

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Schenkel et al. (1995). Isoprenoid quinones were extracted and purified according to Minnikin et al. (1984) and analysed by HPLC as described by Collins (1994) using an isocratic solvent system [methanol/2-butanol (2 : 1, v/v)].

The fatty acid profile of strain JS5<sup>T</sup> is detailed in Table 2. The predominant fatty acids (>10.0% of the total) were summed feature 8 (C<sub>18:1ω7c</sub> and/or C<sub>18:1ω6c</sub>) (34.8%), summed feature 3 (C<sub>16:0</sub>ω7c and/or C<sub>16:0</sub>ω6c) (16.3%) and C<sub>16:0</sub> (16.4%). C<sub>14:0</sub> 2-OH was not detected in the novel isolate, but C<sub>18:1ω</sub> 2-OH was present (3.4%). Furthermore, the relatively low level or absence of C<sub>14:0</sub> 2-OH in strain JS5<sup>T</sup> and the reference strains found in our study have been described in several Sphingomonas species (An et al., 2013; Asker et al., 2007a; Chung et al., 2011; Kim et al., 2007; Srivinasan et al., 2011; Yi et al., 2010). The major respiratory quinone detected was Q-10. The major polar lipids were diphosphatidylglycerol, phosphatidylcholine, phosphatidylethanolamine, phosphatidylglycerol, sphingoglycolipid and two unidentified glycolipids; two unidentified lipids were also detected (Fig. S3). The polyamine pattern showed the presence of sym-homospermidine as the major polyamine.

A number of phenotypic characteristics and the fatty acid profile clearly distinguished strain JS5<sup>T</sup> from closely related Sphingomonas species. Strain JS5<sup>T</sup> was motile by gliding while the related strains were non-motile. Strain JS5<sup>T</sup> contained a greater proportion of summed feature 3, but lower proportion of summed feature 8 than the related strains. Therefore, strain JS5<sup>T</sup> should be classified as representing a novel species within the genus Sphingomonas, for which the name Sphingomonas lutea sp. nov. is proposed.

**Table 2. Cellular fatty acid composition (%) of strain JS5<sup>T</sup> and related Sphingomonas species**

<table>
<thead>
<tr>
<th>Fatty acid</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
</tr>
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<tbody>
<tr>
<td>Straight-chain saturated</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>C&lt;sub&gt;14:0&lt;/sub&gt;</td>
<td>2.1</td>
<td>1.3</td>
<td>1.3</td>
<td>TR</td>
</tr>
<tr>
<td>C&lt;sub&gt;15:0&lt;/sub&gt;</td>
<td>TR</td>
<td>2.3</td>
<td>TR</td>
<td></td>
</tr>
<tr>
<td>C&lt;sub&gt;16:0&lt;/sub&gt;</td>
<td>16.4</td>
<td>20.1</td>
<td>19.9</td>
<td>16.4</td>
</tr>
<tr>
<td>C&lt;sub&gt;17:0&lt;/sub&gt;</td>
<td>–</td>
<td>4.8</td>
<td>–</td>
<td>TR</td>
</tr>
<tr>
<td>C&lt;sub&gt;18:0&lt;/sub&gt;</td>
<td>7.7</td>
<td>5.8</td>
<td>2.4</td>
<td>1.7</td>
</tr>
<tr>
<td>C&lt;sub&gt;14:0&lt;/sub&gt; 2-OH</td>
<td>–</td>
<td>–</td>
<td>1.0</td>
<td>–</td>
</tr>
<tr>
<td>C&lt;sub&gt;18:1ω&lt;/sub&gt; 2-OH</td>
<td>3.4</td>
<td>1.4</td>
<td>9.8</td>
<td>2.5</td>
</tr>
<tr>
<td>Monounsaturated</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>C&lt;sub&gt;16:1ω5c&lt;/sub&gt;</td>
<td>3.9</td>
<td>TR</td>
<td>TR</td>
<td>2.2</td>
</tr>
<tr>
<td>C&lt;sub&gt;17:1ω6c&lt;/sub&gt;</td>
<td>5.2</td>
<td>11.7</td>
<td>1.3</td>
<td>4.1</td>
</tr>
<tr>
<td>C&lt;sub&gt;17:1ω6c&lt;/sub&gt;</td>
<td>TR</td>
<td>1.9</td>
<td>–</td>
<td>TR</td>
</tr>
<tr>
<td>C&lt;sub&gt;18:1ω9c&lt;/sub&gt;</td>
<td>3.0</td>
<td>2.1</td>
<td>TR</td>
<td></td>
</tr>
<tr>
<td>11-methyl C&lt;sub&gt;18:1ω7c&lt;/sub&gt;</td>
<td>3.1</td>
<td>4.8</td>
<td>3.8</td>
<td>1.3</td>
</tr>
<tr>
<td>Summed features*</td>
<td></td>
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</tr>
<tr>
<td>3</td>
<td></td>
<td>16.3</td>
<td>1.4</td>
<td>5.9</td>
</tr>
<tr>
<td>4</td>
<td></td>
<td>TR</td>
<td>–</td>
<td>1.7</td>
</tr>
<tr>
<td>8</td>
<td></td>
<td>34.8</td>
<td>40.1</td>
<td>49.7</td>
</tr>
</tbody>
</table>

*Summed features are groups of two or three fatty acids that cannot be separated by GC with the MIDI system. Summed feature 3 contained C<sub>16:1ω7c</sub> and/or C<sub>16:1ω6c</sub>; summed feature 4 contained iso-C<sub>17:1ω</sub> and/or anteiso-C<sub>17:1ω</sub>; summed feature 8 contained C<sub>18:1ω7c</sub> and/or C<sub>18:1ω6c</sub>.

Description of Sphingomonas lutea sp. nov.

*Sphingomonas lutea* (lu’t.e.a. L. fem. adj. lutea yellow-coloured).

Cells are Gram-stain-negative, aerobic, non-spore-forming, motile by gliding and rod shaped, approximately 0.2 µm in diameter and 0.5–0.9 µm in length. Colonies are circular, convex, smooth, 0.5–1.0 mm in diameter and yellow on R2A agar after 5 days of growth. Growth occurs on R2A and NA but not on MA, PCA or TSA. Growth occurs at 10–37°C (optimum, 25–30°C), at pH 6–8 (optimum, pH 7) and with 0–0.5% (w/v) NaCl. Catalase-positive and oxidase-negative. Flexirubin-type pigments are absent. Methanol extracts show the spectrum typical of carotenoid pigments with maximum absorption at 451 nm and shoulders at 426 and 477 nm. Nitrate is not reduced to nitrite. Indole and H<sub>2</sub>S are not produced. Aesculin and Tween 20 are hydrolysed, but arginine, casein, chitin, CM-cellulose, DNA, gelatin, hypoxanthine, starch, Tween 80, urea, xanthine and xylan are not. Negative for assimilation of adipic acid, arabinose, capric acid, glucose, malic acid, maltose, mannitol, mannose, phenylacetic acid, potassium gluconate, trisodium citrate and N-acetyl-glucosamine.

Negative for acid production from fructose, galactose, glucose, lactose, maltose, mannitol, mannose, rhamnose, sucrose, trehalose and xylene. In the API ZYM gallery, alkaline phosphatase, esterase (C4), esterase lipase (C8) and leucine arylamidase activities are present; acid phosphatase, naphthol-AS-BI-phosphohydrolase and valine arylamidase are weakly positive; but α-chymotrypsin, cystine arylamidase, α-fucosidase, α-galactosidase, β-galactosidase, N-acetyl-β-glucosaminidase, α-glucosidase, β-glucosidase, β-glucuronidase, lipase (C14), α-mannosidase and trypsin activities are absent. In the GN2 Microplate system, the following substrates are assimilated: glycyl l-glutamic acid, β-hydroxybutyric acid and l-proline; the following substrates are weakly assimilated: 2-aminoethanol, 2,3-butanediol, glucose 1-phosphate, glucose 6-phosphate, l-glutamic acid, DL-α-glycerol phosphate, putrescine, thymidine and uridine; other substrates are not assimilated. The predominant fatty acids (>10.0% of the total) are C<sub>16:0</sub> summed feature 3 (C<sub>16:1ω7c</sub> and/or C<sub>16:1ω6c</sub>) and summed feature 8 (C<sub>18:1ω7c</sub> and/or C<sub>18:1ω6c</sub>). The major respiratory quinone is Q-10. The major polar lipids are diphosphatidylglycerol, phosphatidylcholine, phosphatidylethanolamine,
phosphatidylglycerol, sphingoglycolipid and two unidentified glycolipids; two unidentified lipids are also detected. The major polyamine is sym-homospermidine.

The type strain is JS5T (=KCTC 23642T=JCM 18309T), isolated from freshwater of Juam reservoir, Republic of Korea. The DNA G+C content of the type strain is 64.9 mol%.

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**References**


