Sphingomonas changbaiensis sp. nov., isolated from forest soil

Jia-Yue Zhang,1 Xing-Yu Liu1,2 and Shuang-Jiang Liu1

1State Key Laboratory of Microbial Resources, Institute of Microbiology, Chinese Academy of Sciences, Beijing, 100101, PR China
2National Engineering Laboratory of Biohydrometallurgy, General Research Institute for Nonferrous Metals, Beijing, 100088, PR China

Bacterial strain V2M44T was isolated from forest soil from the Changbai Mountains, Heilongjiang Province, China. Cells of strain V2M44T were Gram-negative, rod-shaped and 0.3–0.4 μm in diameter and 1.5–2.5 μm long. The cells were strictly aerobic and were motile by means of peritrichous flagella. Growth occurred at 20–33 °C (optimum, 29–31 °C), at pH 5–8 (optimum, pH 6.0–7.0) and in the presence of 0–0.1 % (w/v) NaCl (optimum, 0.05%). Strain V2M44T contained C17:1ω6c (38.9 %) and summed feature 7 (comprising C18:1ω7c, C18:1ω9t and/or C18:1ω12t, 31.5 %) as the major cellular fatty acids and Q-10 as the major respiratory quinone. The major polar lipids were sphingoglycolipid, phosphatidylmonomethylethanolamine, phosphatidylethanolamine, phosphatidylglycerol and diphosphatidylglycerol along with two unidentified phospholipids and four unidentified glycolipids. The major component in the polyamine pattern was sym-homospermidine. The DNA G+C content was 65.8 mol%. Analysis of 16S rRNA gene sequences indicated that strain V2M44T was phylogenetically related to members of the genus Sphingomonas, with sequence similarities ranging from 92.0–95.8 %. Based on these results, it is concluded that strain V2M44T represents a novel species of the genus Sphingomonas, for which the name Sphingomonas changbaiensis sp. nov. is proposed. The type strain is V2M44T (=CGMCC 1.7057T=NBRC 104936T).

The genus Sphingomonas was proposed by Yabuuchi et al. (1990) and has been subsequently emended by Takeuchi et al. (2001), Yabuuchi et al. (2002) and Busse et al. (2003). On the basis of phylogenetic analysis of 16S rRNA gene sequences, polyamine patterns and polar lipid profiles, Takeuchi et al. (2001) proposed that the genus Sphingomonas should be classified into four genera Sphingomonas, Novosphingobium, Sphingobium and Sphingopyxis, however, the phenotypic evidence to support this proposal was weak (Yabuuchi et al., 2002). According to Busse et al. (2003), species of the genus Sphingomonas comprising cluster I as proposed by Takeuchi et al. (2001), with sym-homospermidine as the major polyamine pattern, should be considered as members of Sphingomonas sensu stricto, with Sphingomonas paucimobilis as the type species. Members of this genus are off-white, yellow or orange-pigmented, non-fermentative, Gram-negative, non-motile or motile rods with a single polar flagellum or peritrichous flagella and are characterized by the presence of sym-homospermidine, a unique sphingoglycolipid, Q-10, 2-hydroxymyristic acid and the absence of 3-hydroxy fatty acids. In this study, we report the isolation and identification of a novel isolate, strain V2M44T, from a sample of forest soil.

In an attempt to study the cultured microbial diversity in forest soil from the Changbai Mountains, Heilongjiang Province, China, bacterial strains were isolated by using a serial dilution method (Sait et al., 2002). V2M isolation medium was modified from VL55 medium (Sait et al., 2002) by the addition of (l-glycine, 4 mg SrCl2, 3 mg NaSiO3, 9H2O, 3 mg TiO2, 2 mg Cd(NO3)2·4H2O and 2 mg SnCl2·H2O. Solution 2 contained (l-glyceraldehyde, 20 mg chromotropic acid, 70 mg gallic acid, 30 mg ascorbic acid, 10 mg sodium thioglycolate, 50 mg sodium succinate, 50 mg DL-malic acid, 50 mg saligenin, 50 mg sorbitol, 40 mg salicin, 20 mg barbital, 20 mg aconitic acid, 30 mg creatine and 30 mg sodium deoxycholate.

The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain V2M44T is EU682686.

Figures showing additional phylogenetic trees, scanning and transmission electron micrographs of cells of strain V2M44T and the results of the polar lipid analysis are available as supplementary figures. A supplementary table detailing the cellular fatty acid contents of strain V2M44T is also available with the online version of this paper.
Strain V2M44<sup>T</sup> was isolated from several V2M plates inoculated with the 10<sup>-7</sup> dilution after one week of incubation at 30 °C. Each plate displayed several tiny yellow colonies of strain V2M44<sup>T</sup>

The nearly complete 16S rRNA gene of strain V2M44<sup>T</sup> (1477 bp) was amplified and sequenced according to the method described by Zhang et al. (2003). DNA BLAST searches (Altschul et al., 1990) of 16S rRNA gene similarity using the NCBI database showed that strain V2M44<sup>T</sup> was phylogenetically related to members of the genus Sphingomonas. Alignments of the 16S rRNA gene sequences of members of the genus Sphingomonas were performed with the CLUSTAL_X program (version 1.64b, Thompson et al., 1997) and the alignment positions with insertions or deletions were excluded from calculations. Phylogenetic trees based on 16S rRNA gene sequence analysis were constructed by the neighbour-joining and maximum-parsimony methods with Kimura’s two-parameter calculation model in MEGA version 3.1 (Kumar et al., 2004), and by the maximum-likelihood method in fastDNAml version 1.2.2 (Olsen et al., 1994; Felsenstein, 1981). 16S rRNA gene sequence analysis indicated that strain V2M44<sup>T</sup> was phylogenetically related to members of the genus Sphingomonas, with sequence similarities ranging from 92.0 to 95.8%. In particular, strain V2M44<sup>T</sup> was closely related to Sphingomonas mali NBRC 15500<sup>T</sup> (95.8%), Sphingomonas kaisensis PB56<sup>T</sup> (95.8%), Sphingomonas oligophenolica S213<sup>T</sup> (95.8%), Sphingomonas dokdonensis DS-4<sup>T</sup> (95.6%), Sphingomonas pituitsosa EDIV<sup>T</sup> (95.6%), Sphingomonas prunii NBRC 15499<sup>T</sup> (95.6%), Sphingomonas aerolata NW12<sup>T</sup> (95.4%), Sphingomonas asacharolytica NBRC 15499<sup>T</sup> (95.3%), Sphingomonas azotifigens Y39<sup>T</sup> (95.3%), Sphingomonas trueperi ATCC 12417<sup>T</sup> (95.3%), Sphingomonas desiccabilis C1PD<sup>T</sup> (95.2%), Sphingomonas molluscum KMM 3882<sup>T</sup> (95.2%), Sphingomonas echinoides DSM 1805<sup>T</sup> (95.1%), Sphingomonas astaxanthifaciens TDMA-17<sup>T</sup> (95.1%), Sphingomonas aquatilis JS57<sup>T</sup> (95.0%), and Sphingomonas koreensis JS26<sup>T</sup> (95.0%). The phylogenetic tree (Fig. 1) also indicated that strain V2M44<sup>T</sup> clustered with species of the genus Sphingomonas and the topologies of the maximum-parsimony tree and maximum-likelihood tree were essentially the same (see Supplementary Figs S1 and S2 in IJSEM Online).

The morphological, physiological and biochemical characteristics of strain V2M44<sup>T</sup> were investigated using routine cultivation on diluted tryptic soy broth (D-TSB) medium at 30 °C. The D-TSB medium was 1/5 strength tryptic soy broth at 12, 13, 14, 16, 17.5, 19, 21, 22, 24, 27, 28, 29, 31, 34, 36, 38, 41, 45, 49, 51 and 56 °C. The pH range for growth was tested at pH 4.0, 5.0, 5.5, 6.0, 6.5, 7.0, 7.5, 8.0, 8.5, 9.1 and 9.8 by using D-TSB in which the pH was adjusted by the addition of 5 M NaOH or HCl and verified after autoclaving. Tolerance to NaCl was examined in D-TSB supplemented with 0, 0.05, 0.1, 0.2, 0.3, 0.4, 0.5, 1.0 and 2.0% (w/v) NaCl. Tests for catalase and oxidase activities and for the hydrolysis of casein, starch, Tween 20 and Tween 80 were performed according to Dong & Cai (2001). In addition, strain V2M44<sup>T</sup> was characterized by using API 20NE, API 50CH and API ZYM identification systems (bioMérieux) at 30 °C.

Cells of strain V2M44<sup>T</sup> were Gram-negative, rod-shaped and 0.3–0.4 μm in diameter and 1.5–2.5 μm in length. Cells were strictly aerobic and were motile by means of peritrichous flagella (see Supplementary Fig. S3 in IJSEM Online). Detailed physiological and biochemical characteristics of strain V2M44<sup>T</sup> are presented in the species description and the properties that distinguish the novel strain from closely related species are listed in Table 1.

The cell mass of strain V2M44<sup>T</sup> and S. mali JCM 10193<sup>T</sup> used for chemotaxonomic analyses was produced on D-TSB agar at 30 °C for 3 days. Cellular fatty acids were extracted, methylated and analysed by the Sherlock Microbial Identification System following the manufacturer’s instructions. Isoprenoid quinones were extracted and purified according to the method of Collins (1985) and analysed by HPLC (Wu et al., 1989; Hu et al., 2004). Polymamines were analysed as described previously (Flores & Galston, 1982), with strain S. mali JCM 10193<sup>T</sup> (Takeuchi et al., 1995) as the reference strain in a parallel experiment. Polar lipids were extracted according to the modified method of Kamikura (1993) and separated by TLC on Merck Kieselgel 60-HPTLC by two-dimensional development as described by Ross et al. (1985). Phospholipids were detected with the Zinzadze reagent of Dittmer & Lester (1964). Glycolipids were detected by spraying the plate with 0.5% 1-naphthol in methanol/water (1:1 v/v) and then with sulfuric acid/ethanol (1:1 v/v), followed by heating at 120 °C for 5–10 min (Xin et al., 2001). Whole lipid profiles were detected by spraying with molybdatosphosphoric acid (10 g molybdatosphosphoric acid hydrate in 100 ml ethanol) followed by heating at 120–160 °C (Worliczek et al., 2007).

The predominant isoprenoid quione of strain V2M44<sup>T</sup> was ubiquinone-10 (Q-10). The fatty acid profile of strain V2M44<sup>T</sup> comprised C<sub>17:1</sub><sup>ω6c</sup> (38.9%), summed feature 7 comprising C<sub>18:1</sub><sup>ω7c</sup>, C<sub>18:1</sub><sup>ω9t</sup> and/or C<sub>18:1</sub><sup>ω12t</sup>, 31.5%), C<sub>16:0</sub> (5.3%) and C<sub>17:1</sub><sup>ω8c</sup> (5.2%). The hydroxy fatty acids were C<sub>15:0</sub> 2-OH (4.4%), C<sub>16:0</sub> 2-OH (1.8%) and C<sub>14:0</sub> 2-OH (1.3%). No 3-hydroxy fatty acids were detected in this strain. The fatty acid composition of the
strain V2M44ᵀ is given in more detail in Supplementary Table S1 (available in IJSEM Online). The major polyamine was sym-homospermidine. The major polar lipids were sphingoglycolipid, phosphatidylmonomethylethanolamine, phosphatidylethanolamine, phosphatidylglycerol, diphosphatidylglycerol, two unidentified phospholipids and four unidentified glycolipids (see Supplementary Fig. S4). Phosphatidyldimethylethanolamine and phosphatidylcholine were not detected, distinguishing strain V2M44ᵀ from *S. pituitosa*, *S. pruni*, *S. asaccharolytica* and *S. trueperi* (Denner et al., 2001; Kämpfer et al., 1997). The chemotaxonomic features of strain V2M44ᵀ, including Q-10 as the major isoprenoid quinone, C₁₇ : ₁₀₀₆ₙ and summed feature 7 as the major fatty acids, the absence of 3-hydroxy fatty acids and the presence of sphingoglycolipid are as expected for species closely related to the genus *Sphingomonas* (Busse et al., 2003; Denner et al., 1999, 2001; Kämpfer et al., 1997; Lee et al., 2001; Reddy & Garcia-Pichel, 2007; Romanenko et al., 2007; Takeuchi et al., 1995; Xie & Yokota, 2006; Yoon et al., 2006).

The DNA base composition was determined by thermal denaturation (Marmur & Doty, 1962) and *Escherichia coli* K-12 was used as the reference. The DNA G+C content of strain V2M44ᵀ was 65.8 % (T_m), which is within the range of values (60.7–69.9 %) previously reported for the genus *Sphingomonas*.

Based on the above phenotypic and phylogenetic studies, it is clear that strain V2M44ᵀ is a member of the genus *Sphingomonas*.
**Table 1. Phenotypic characteristics that differentiate strain V2M44T from related members of the genus Sphingomonas**

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
<th>5</th>
<th>6</th>
<th>7</th>
<th>8</th>
<th>9</th>
<th>10</th>
<th>11</th>
<th>12</th>
<th>13</th>
<th>14</th>
<th>15</th>
<th>16</th>
<th>17</th>
</tr>
</thead>
<tbody>
<tr>
<td>Colony colour</td>
<td>Y</td>
<td>LY</td>
<td>OR</td>
<td>PY</td>
<td>Y</td>
<td>DY</td>
<td>LY</td>
<td>O</td>
<td>LY</td>
<td>Y</td>
<td>Y</td>
<td>Y</td>
<td>Y</td>
<td>DY</td>
<td>Y</td>
<td>Y</td>
<td>Y</td>
</tr>
<tr>
<td>Motility</td>
<td>+</td>
<td>–</td>
<td>–</td>
<td>+</td>
<td>–</td>
<td>–</td>
<td>+</td>
<td>+</td>
<td>–</td>
<td>–</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>–</td>
<td>+</td>
<td>+</td>
<td></td>
</tr>
<tr>
<td>Oxidase activity</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Nitrate reduction</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Urease activity</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Gelatin hydrolysis</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Aesculin hydrolysis</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>(+)</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>β-Galactosidase</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Assimilation of:</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>N-Acetyl-D-glucosamine</td>
<td>–</td>
<td>+</td>
<td>+</td>
<td>ND</td>
<td>–</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>ND</td>
<td>+</td>
<td>ND</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Adipate</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>ND</td>
<td>+</td>
<td>–</td>
<td>–</td>
<td>(+)</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>ND</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>L-Arabinose</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>ND</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>(+)</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Caprate</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>ND</td>
<td>+</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>ND</td>
<td>–</td>
<td>ND</td>
<td>–</td>
<td>ND</td>
<td>+</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Citrate</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Gluconate</td>
<td>+</td>
<td>+</td>
<td>(+)</td>
<td>+</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>D-Glucose</td>
<td>(+)</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>(+)</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>(–)</td>
<td>+</td>
<td>+</td>
<td>–</td>
<td>–</td>
<td>+</td>
</tr>
<tr>
<td>Malate</td>
<td>(+)</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Maltose</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>+</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>D-Mannitol</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>ND</td>
<td>+</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>D-Mannose</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>(+)</td>
<td>ND</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Phenylacetate</td>
<td>–</td>
<td>ND</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>DNA G+C content</td>
<td>65.8</td>
<td>65.4–69.9</td>
<td>64.2</td>
<td>66.9</td>
<td>64.5</td>
<td>65.4</td>
<td>65.4</td>
<td>64.8</td>
<td>68.0</td>
<td>65.6</td>
<td>ND</td>
<td>68.3</td>
<td>65.8</td>
<td>63.3</td>
<td>63.0</td>
<td>66.0</td>
<td></td>
</tr>
</tbody>
</table>

*Sphingomonas changbaiensis*. Strain V2M44T exhibited a range of phenotypic characteristics that differentiated it from the currently recognized species of the genus *Sphingomonas* (Table 1), such as urease and β-galactosidase activities, assimilation of various carbon sources and the polar lipid profile. Therefore, it is concluded that strain V2M44T represents a novel species of the genus *Sphingomonas* for which the name of *Sphingomonas changbaiensis* sp. nov. is proposed.

**Description of Sphingomonas changbaiensis** sp. nov.

*Sphingomonas changbaiensis* (chang.bai.en’sis. N.L. fem. adj. *changbaiensis* pertaining to the Changbai mountains, in the north-east of China, from where the type strain was isolated).

Strictly aerobic, Gram-negative, heterotrophic, oxidase- and catalase-positive. Cells are rods of 0.3–0.4 μm in diameter and 1.5–2.5 μm in length and are motile by means of peritrichous flagella. Colonies on D-TSB agar are circular, entire and yellow. No growth is detected on TSB agar, 1/2 strength TSB agar, LB agar, 1/10 strength LB agar, NB agar or 1/2 strength NB agar. Growth occurs on 1/5 and 1/10 strength TSB agar. Growth occurs at 20–33 °C (optimum, 29–31 °C), at pH 5–8 (optimum, pH 6.0–7.0) and in the presence of 0–0.1 % (w/v) NaCl (optimum, 0.05 %). Nitrate is not reduced. Gelatin, aesculin, Tween 20 and Tween 80 are hydrolysed, but casein and starch are not hydrolysed. Urease activity is present, but arginine dihydrolase activity is absent. Indole and H₂S are not produced. Assimilates D-glucose, gluconate, adipate and malate, but not the following compounds: D-mannitol, maltose, L-arabinose, D-mannose, N-acetyl-D-glucosamine, caprate, citrate and phenylacetate. In the API 50 CH test system, acids are produced from glycerol, D-fructose, N-acetylglucosamine, aesculin and ferric citrate. All other API 50 CH test results are negative. In the API ZYM test system, alkaline phosphatase, esterase, lipase (C8), leucine arylamidase, valine arylamidase, cystine arylamidase, α-chymotrypsin, acid phosphatase and naphthol-AS-BI-phosphohydrolase activities are present. Esterase (C4), lipase (C14), trypsin, N-acetyl-β-glucosami-
nidase, α-galactosidase, β-galactosidase, β-glucuronidase, β-glucosidase, α-glucosidase, α-mannosidase and α-fucosidase activities are absent. The predominant cellular fatty acids are C17:0 106c, summed feature 7 (comprising C18:1ω7c, C18:1ω9t and/or C18:1ω12t), C16:0 109c and C15:0 2-ОH. The major isoprenoid quinone is Q-10. The major polyamine is sym-homospermidine. The major polar lipids are sphingoglycolipid, phosphatidylethanolamine and phosphatidylglycerol.

The type strain, V2M44T (=CGMCC 1.7057T=NBRC 104936T), was isolated from forest soil. The DNA G+C content of the type strain is 65.8 mol% (Tm).

Acknowledgements
This work was supported by grants from the National Science Foundation of China (30725001) and the Chinese Academy of Sciences (KSCX2-YW-G-052).

References


