A novel actinomycete, designated strain Sco-B14T, was isolated from volcanic ash collected near Darangshi Oreum (a parasitic or satellite volcano) in Jeju, Republic of Korea. The organism formed well-developed, branched substrate mycelium, on which short chains of non-motile spores were arranged singly or in clusters. Aerial mycelium was not produced. Globose bodies were observed. The reverse colour of colonies was light brown to brown. Diffusible pigments were produced on ISP medium 3 and oatmeal-nitrate agar. Phylogenetic analysis based on 16S rRNA gene sequences showed that strain Sco-B14T formed a lineage within the family Micromonosporaceae and was distinct from established genera. The 16S rRNA gene sequence similarity of strain Sco-B14T to members of related genera of the family was 95.0–95.7 % to type strains of Catellatospora species, 94.7 % to Hamadaea tsunoensis IMSNU 22005T, 94.7 % to Longispora albida K97-0003T and 94.0 % to Catelliglobosispora koreensis LM 042T. 3-Hydroxy-diaminopimelic acid was the diagnostic diamino acid in the cell-wall peptidoglycan. Whole-cell sugars were glucose, rhamnose, ribose, xylose, arabinose, galactose and mannose. The polar lipids included diphosphatidylglycerol, phosphatidylethanolamine and phosphatidylinositol. The menaquinone profile contained MK-10(H4) (49 %), MK-9(H4) (24 %), MK-10(H6) (18 %) and MK-9(H6) (9 %). The predominant fatty acids were iso-C15 : 0 and C17 : 0.

The DNA G+C content was 70.1 mol%. The combination of chemotaxonomic and phylogenetic data clearly separated the isolate from the type strains of all genera in the family Micromonosporaceae. On the basis of the phylogenetic and chemotaxonomic data presented in this paper, strain Sco-B14T is considered to represent a novel species of a new genus in the family Micromonosporaceae, for which the name Allocatelliglobosispora scoriae gen. nov., sp. nov. is proposed. The type strain of Allocatelliglobosispora scoriae is Sco-B14T (=KCTC 19661T =DSM 45362T).

The family Micromonosporaceae Krasil'nikov 1938 emend. Koch et al. 1996, emend. Stackebrandt et al. 1997 is a member of the suborder Micromonosporinae, and contained seven genera according to Stackebrandt et al. (1997) (Micromonospora, Actinoplanes, Dactylosporangium, Catellatospora, Catenuloplanes, Couchioplanes and Pilimelia). Subsequently, the genera Spirilliplanes, Verrucosispora, Virgisporangium, Asanoa, Longispora and Salinispora have been recognized as members of the family Micromonosporaceae on the basis of chemotaxonomic characteristics and phylogenetic relationships (Koch et al., 1996; Stackebrandt et al., 1997). Recently, several new genera have been added to the family: Actinocatenispora (Thawai et al., 2006), Polymorphospora (Tamura et al., 2006), Luedemannella (Ara & Kudo, 2007b), Krasilnikovia (Ara & Kudo, 2007c), Catelliglobosispora (Ara et al., 2008a), Hamadaea (Ara et al., 2008a), Pseudosporangium (Ara et al., 2008b), Planosporangium (Wiese et al., 2008), Rugosimonospora (Monciardini et al., 2009), Plantactinospora (Qin et al., 2009) and Actinuariuspora (Thawai et al., 2010). Catelliglobosispora and Hamadaea were erected by Ara et al. (2008a) by the reclassification of Catellatospora koreensis Lee et al. 2000 and Catellatospora tsunoensis Asano et al. 1989, respectively.

During a study of microbial diversity and bioactive compounds from scoria, a vesicular pyroclastic rock with basaltic composition, strain Sco-B14T was isolated from volcanic ash collected near Darangshi Oreum (a parasitic volcano or satellite cone) in Jeju, Republic of Korea. A volcanic ash sample (1 g) was ground to a powder with a pestle and suspended in 10 ml distilled water. Aliquots of serial dilutions were spread onto starch-casein agar (1 % soluble starch, 0.03 % casein, 0.2 % KNO3, 0.2 % KH2PO4, 0.002 % CaCO3, 0.005 % MgSO4.7H2O, 0.001 % FeSO4.7H2O and 1.8 % agar in distilled water,
pH 7.2) and the plates were incubated at 30 °C for 2 weeks. A single colony was selected and further streaked on ISP medium 2 (Shirling & Gottlieb, 1966). The pure culture was maintained at −20 and −80 °C in 20 % (v/v) glycerol. For cellular fatty acid analyses, *Catelliglobosispora koreensis* LM 042T and *Hamadaea tsunoensis* IMSNU 22005T were grown on ISP medium 2 at 30 °C.

Morphological characteristics of strain Sco-B14T were observed by scanning electron microscopy (model JSM 6700F; JEOL) using a culture grown on ISP medium 3 for 21 days at 30 °C. An agar block with growth was fixed for 1 h with 1 % OsO4 and dehydrated by using a graded series of ethanol or a mixture of ethanol and isoamyl acetate. After critical-point drying with liquid carbon dioxide, the specimen was coated with platinum before observation. For cultural characterization, strain Sco-B14T was grown for 21 days at 30 °C on various agar media as described by Nonomura & Ohara (1969), Prauser & Bergholz (1974) and Shirling & Gottlieb (1966).

Strain Sco-B14T grew well on ISP media 2, 3, 4 and 5 and oatmeal-nitrate agar and showed poor growth on ISP media 6 and 7. The organism formed well-developed, branched substrate mycelium, on which short chains of non-motile spores were arranged singly or in clusters without the formation of aerial mycelium (Fig. 1a). Globose bodies were observed (Fig. 1b). The reverse colour of colonies was light brown to brown. Soluble pigments were brown on ISP medium 3 and oatmeal-nitrate agar.

The ranges of temperature and pH for growth were determined on ISP medium 2 at 4–42 °C and pH 4.1–12.1 (at intervals of 1.0 pH unit). Tolerance of NaCl for growth was tested in the presence of 0–9 % NaCl (at intervals of 1 %). Utilization of carbohydrates as sole carbon sources was tested using ISP medium 9 (Shirling & Gottlieb, 1966) as the basal medium. Carbon sources were filter-sterilized and added to final concentrations of 1 % (for carbohydrates and alcohols) or 0.1 % (for organic acids). Gram staining, oxidase and catalase activities and degradation abilities were determined as described by Lee et al. (2008). Results of these physiological tests are given in the species description.

Genomic DNA was extracted and purified as described previously (Hopwood et al., 1985). PCR-mediated amplification and sequencing of the 16S rRNA gene were performed as described by Lee & Lee (2008). The 16S rRNA gene sequence of strain Sco-B14T was aligned with corresponding sequences obtained from GenBank/EMBL databases using the CLUSTAL_X program (Thompson et al., 1997). Phylogenetic analyses were performed using several programs contained in the PHYLIP suite (Felsenstein, 2008). A phylogenetic tree was constructed by the neighbour-joining method (Saitou & Nei, 1987) from an evolutionary distance matrix calculated with the model of Jukes & Cantor (1969). The tree topology was evaluated by bootstrap analyses based on 1000 resamplings (Felsenstein, 1985).

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For chemotaxonomic characterization, biomass of strain Sco-B14T was obtained from a culture grown in ISP 2 broth for 7 days at 30°C. The isomer of diaminopimelic acid (DAP) in the cell-wall peptidoglycan was determined by the method of Staneck & Roberts (1974). Whole-cell sugars were analysed as described previously (Saddler et al., 1991). Respiratory quinones were extracted according to Collins (1985) and identified by HPLC (Kroppenstedt, 1985). Analysis of polar lipids was performed by TLC as described by Minnikin et al. (1977). The DNA G+C content was determined by HPLC (Mesbah et al., 1989).

Whole-cell hydrolysates contained 3-OH DAP as the diagnostic diamino acid and glucose, rhamnose, ribose, xylose, arabinose, galactose and mannose as whole-cell sugars. The menaquinone profile contained MK-10(H4) (49 %), MK-9(H4) (24 %), MK-10(H6) (18 %) and MK-9(H6) (9 %). The polar lipids included diphosphatidylglycerol, phosphatidylethanolamine and phosphatidylinositol (see Supplementary Fig. S1, available in IJSEM Online). The DNA G+C content of strain Sco-B14T was 70.1 mol%.

Cellular fatty acid methyl esters were prepared by alkaline methanolysis (Minnikin, 1988) and analysed according to the standard protocol of the Microbial Identification System (version 6; MIDI). For this analysis, strain Sco-B14T, Catelliglobopsis koreensis LM 042T and Hamadaea tsunoensis IMSNU 22005T were grown in ISP 2 broth for 7 days at 30°C. The cellular fatty acid profile of strain Sco-B14T included considerable amounts of saturated, iso-, anteiso- and 10-methyl-branched fatty acids. The major fatty acids (>10 % of the total) were iso-C15:0 (21.2 %) and C17:0 (12.3 %). In this study, the fatty acid profiles of Catelliglobopsis koreensis LM 042T and Hamadaea tsunoensis IMSNU 22005T differed slightly from the results of Ara et al. (2008a) with regard to major fatty acids (Supplementary Table S1). The cellular fatty acid profile of strain Sco-B14T was similar to that of Hamadaea tsunoensis IMSNU 22005T but they differed from each other in that strain Sco-B14T did not have iso-C16:0 or anteiso-C17:0 as major components, the major fatty acids found in our study for Catelliglobopsis koreensis LM 042T. The profiles of Catelliglobopsis koreensis LM 042T and Hamadaea tsunoensis IMSNU 22005T also contained C16:1 2-OH, that was not detected in the extract of strain Sco-B14T; this hydroxy fatty acid could therefore be a key fatty acid that differentiates strain Sco-B14T from these type strains.

16S rRNA gene sequence analysis revealed that strain Sco-B14T belongs to the family Micromonosporaceae. Strain Sco-B14T is morphologically similar to members of the genera Catellatospora, Catelliglobopsis and Hamadaea in that it produces short chains of non-motile spores directly from the vegetative mycelium without the formation of aerial mycelium. However, strain Sco-B14T can be readily distinguished from the above genera by using a combination of chemotaxonomic characteristics. Members of the genera Catellatospora, Catelliglobopsis and Hamadaea differ from one another in their menaquinone profiles (Table 1). Strain Sco-B14T shows a complex menaquinone profile including MK-10(H4), MK-9(H4) and MK-10(H6) as major menaquinones, revealing that it can be readily distinguished from the above genera. In addition, members of the genera Catellatospora and Hamadaea contain meso-
Table 1. Characteristics that differentiate strain Sco-B14<sup>T</sup> from other genera of the family *Micromonosporaceae*


<table>
<thead>
<tr>
<th>Taxon</th>
<th>Sporangia</th>
<th>Spore motility</th>
<th>Diamino acid(s)</th>
<th>Whole-cell sugar(s)&lt;sup&gt;*&lt;/sup&gt;</th>
<th>Fatty-acid type</th>
<th>Major menaquinone(s)</th>
<th>Phospholipid type</th>
<th>DNA G+C content (mol%)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sco-B14&lt;sup&gt;T&lt;/sup&gt;</td>
<td>–</td>
<td>–</td>
<td>3-OH DAP</td>
<td>Glc, Rhm, Rib, Xyl, Ara, Gal, Man</td>
<td>3b</td>
<td>10(H&lt;sub&gt;4&lt;/sub&gt;), 9(H&lt;sub&gt;6&lt;/sub&gt;), 10(H&lt;sub&gt;4&lt;/sub&gt;)</td>
<td>PII</td>
<td>70.1</td>
</tr>
<tr>
<td>Actinaurispora</td>
<td>–</td>
<td>–</td>
<td>m-DAP</td>
<td>Glc, Xyl, Man, Gal</td>
<td>3b</td>
<td>9(H&lt;sub&gt;6&lt;/sub&gt;), 10(H&lt;sub&gt;4&lt;/sub&gt;), 9(H&lt;sub&gt;6&lt;/sub&gt;)</td>
<td>PII</td>
<td>72.6</td>
</tr>
<tr>
<td>Actinocatenispora</td>
<td>–</td>
<td>–</td>
<td>m-DAP</td>
<td>Ara, Gal, Xyl</td>
<td>3b</td>
<td>9(H&lt;sub&gt;4&lt;/sub&gt;), 9(H&lt;sub&gt;6&lt;/sub&gt;)</td>
<td>PII</td>
<td>72</td>
</tr>
<tr>
<td>Actinoplanes</td>
<td>+</td>
<td>+</td>
<td>m-DAP</td>
<td>Ara, Xyl</td>
<td>3d</td>
<td>9(H&lt;sub&gt;4&lt;/sub&gt;), 10(H&lt;sub&gt;4&lt;/sub&gt;)</td>
<td>PII</td>
<td>72–73</td>
</tr>
<tr>
<td>Asanoa</td>
<td>–</td>
<td>–</td>
<td>m-DAP</td>
<td>Ara, Gal, Xyl</td>
<td>2d</td>
<td>10(H&lt;sub&gt;6&lt;/sub&gt;), 10(H&lt;sub&gt;4&lt;/sub&gt;)</td>
<td>PII</td>
<td>71–72</td>
</tr>
<tr>
<td>Catellatospora</td>
<td>–</td>
<td>–</td>
<td>m-DAP, 3-OH DAP</td>
<td>Xyl, Man, Gal, Ara, Rhm, Rib, Glc</td>
<td>3b</td>
<td>9(H&lt;sub&gt;4&lt;/sub&gt;)</td>
<td>PII</td>
<td>70–71</td>
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<tr>
<td>Catelliglobosispora</td>
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<td>–</td>
<td>m-DAP</td>
<td>Rhm, Man, Xyl, Gal, Glc</td>
<td>3b</td>
<td>10(H&lt;sub&gt;4&lt;/sub&gt;)</td>
<td>PII</td>
<td>70.4</td>
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<tr>
<td>Catenuoloplanes</td>
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<td>+</td>
<td>l-Lys</td>
<td>Xyl</td>
<td>2c</td>
<td>9(H&lt;sub&gt;6&lt;/sub&gt;), 10(H&lt;sub&gt;4&lt;/sub&gt;)</td>
<td>PIII</td>
<td>71–73</td>
</tr>
<tr>
<td>Couchioplanes</td>
<td>–</td>
<td>+</td>
<td>l-Lys</td>
<td>Ara, Gal, Xyl</td>
<td>2c</td>
<td>9(H&lt;sub&gt;4&lt;/sub&gt;)</td>
<td>PII</td>
<td>70–72</td>
</tr>
<tr>
<td>Dactylosporangium</td>
<td>+</td>
<td>+</td>
<td>m-DAP</td>
<td>Ara, Xyl</td>
<td>3b</td>
<td>9(H&lt;sub&gt;4&lt;/sub&gt;), 9(H&lt;sub&gt;6&lt;/sub&gt;), 9(H&lt;sub&gt;4&lt;/sub&gt;)</td>
<td>PII</td>
<td>71–73</td>
</tr>
<tr>
<td>Hamadaea</td>
<td>–</td>
<td>–</td>
<td>m-DAP, 3-OH DAP</td>
<td>Xyl, Gal, Man, Rib, Ara, Rhm, Glc</td>
<td>3b</td>
<td>9(H&lt;sub&gt;6&lt;/sub&gt;)</td>
<td>PII</td>
<td>70</td>
</tr>
<tr>
<td>Krasilnikovia</td>
<td>–</td>
<td>–</td>
<td>m-DAP</td>
<td>Gal, Man, Xyl, Ara, Rib</td>
<td>2d</td>
<td>9(H&lt;sub&gt;6&lt;/sub&gt;), 9(H&lt;sub&gt;4&lt;/sub&gt;), 9(H&lt;sub&gt;4&lt;/sub&gt;)</td>
<td>PII</td>
<td>71</td>
</tr>
<tr>
<td>Longispora</td>
<td>–</td>
<td>–</td>
<td>m-DAP</td>
<td>Ara, Gal, Xyl</td>
<td>2d</td>
<td>10(H&lt;sub&gt;4&lt;/sub&gt;), 10(H&lt;sub&gt;4&lt;/sub&gt;)</td>
<td>PII</td>
<td>70</td>
</tr>
<tr>
<td>Luedemannella</td>
<td>+</td>
<td>–</td>
<td>m-DAP</td>
<td>Xyl, Gal, Man, Rhm, Rib, Ara</td>
<td>2d</td>
<td>9(H&lt;sub&gt;4&lt;/sub&gt;), 9(H&lt;sub&gt;4&lt;/sub&gt;), 9(H&lt;sub&gt;2&lt;/sub&gt;)</td>
<td>PII</td>
<td>71</td>
</tr>
<tr>
<td>Micromonospora</td>
<td>–</td>
<td>–</td>
<td>m-DAP</td>
<td>Ara, Xyl</td>
<td>3b</td>
<td>10(H&lt;sub&gt;6&lt;/sub&gt;), 10(H&lt;sub&gt;4&lt;/sub&gt;), 9(H&lt;sub&gt;6&lt;/sub&gt;)</td>
<td>PII</td>
<td>71–72</td>
</tr>
<tr>
<td>Pilimelia</td>
<td>+</td>
<td>+</td>
<td>m-DAP</td>
<td>Ara, Xyl</td>
<td>2d</td>
<td>9(H&lt;sub&gt;4&lt;/sub&gt;), 9(H&lt;sub&gt;2&lt;/sub&gt;)</td>
<td>PII</td>
<td>ND</td>
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<tr>
<td>Planosporangium</td>
<td>+</td>
<td>+/−</td>
<td>m-DAP</td>
<td>Ara, Xyl</td>
<td>3b</td>
<td>9(H&lt;sub&gt;4&lt;/sub&gt;), 10(H&lt;sub&gt;4&lt;/sub&gt;)</td>
<td>PII</td>
<td>71.4</td>
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<td>Plantaertiospora</td>
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<td>–</td>
<td>m-DAP</td>
<td>Ara, Gal, Xyl</td>
<td>2d</td>
<td>10(H&lt;sub&gt;4&lt;/sub&gt;), 10(H&lt;sub&gt;4&lt;/sub&gt;), 10(H&lt;sub&gt;4&lt;/sub&gt;)</td>
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<td>–</td>
<td>m-DAP</td>
<td>Xyl</td>
<td>2a</td>
<td>10(H&lt;sub&gt;4&lt;/sub&gt;), 10(H&lt;sub&gt;4&lt;/sub&gt;), 9(H&lt;sub&gt;4&lt;/sub&gt;)</td>
<td>PII</td>
<td>71</td>
</tr>
<tr>
<td>Pseudosporangium</td>
<td>–</td>
<td>–</td>
<td>m-DAP, 3-OH DAP</td>
<td>Ara, Gal, Glc, Man, Rib, Xyl</td>
<td>2d</td>
<td>9(H&lt;sub&gt;4&lt;/sub&gt;)</td>
<td>PII</td>
<td>73.6</td>
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<tr>
<td>Rugosimonospora</td>
<td>+</td>
<td>–</td>
<td>3-OH DAP</td>
<td>Gal, Ara, Xyl</td>
<td>2d</td>
<td>9(H&lt;sub&gt;4&lt;/sub&gt;)</td>
<td>PII</td>
<td>72–73</td>
</tr>
<tr>
<td>Salinispora</td>
<td>–</td>
<td>–</td>
<td>m-DAP</td>
<td>Ara, Gal, Xyl</td>
<td>3a</td>
<td>9(H&lt;sub&gt;4&lt;/sub&gt;)</td>
<td>PII</td>
<td>70</td>
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<tr>
<td>Spirilliplanes</td>
<td>–</td>
<td>–</td>
<td>m-DAP</td>
<td>Ara, Xyl</td>
<td>2d</td>
<td>10(H&lt;sub&gt;4&lt;/sub&gt;)</td>
<td>PII</td>
<td>69</td>
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<tr>
<td>Verrucospora</td>
<td>–</td>
<td>–</td>
<td>m-DAP</td>
<td>Man, Xyl</td>
<td>2b</td>
<td>9(H&lt;sub&gt;4&lt;/sub&gt;)</td>
<td>PII</td>
<td>70</td>
</tr>
<tr>
<td>Virgisporangium</td>
<td>+</td>
<td>–</td>
<td>m-DAP</td>
<td>Ara, Gal, Xyl</td>
<td>2d</td>
<td>10(H&lt;sub&gt;4&lt;/sub&gt;), 10(H&lt;sub&gt;4&lt;/sub&gt;), 10(H&lt;sub&gt;4&lt;/sub&gt;)</td>
<td>PII</td>
<td>71</td>
</tr>
</tbody>
</table>

*Ara, Arabinose; Gal, galactose; Glc, glucose; Man, mannose; Rhm, rhamnose; Rib, ribose; Xyl, xylose.*
DAP and 3-OH DAP as the diagnostic diamino acids in the peptidoglycan and *Catelliglobosispora koreensis* contains meso-DAP, in contrast to strain Sco-B14T, which contains 3-OH DAP as the only diamino acid. 3-OH DAP is also found in the cell-wall peptidoglycan of members of the genera *Pseudosporangium* and *Rugosimonospora*, but they differ from strain Sco-B14T in their menaquinone profiles (Table 1). Differential morphological and chemotaxonomic properties between strain Sco-B14T and genera of the family *Micromonosporaceae* are given in Table 1.

On the basis of the phylogenetic, chemotaxonomic and morphological data presented here, strain Sco-B14T is considered to represent a novel species of a new genus of the family *Micromonosporaceae*, for which the name *Allocatelliglobosispora scoriae* gen. nov., sp. nov. is proposed.

**Description of *Allocatelliglobosispora gen. nov.*

*Allocatelliglobosispora* (Al.lo.ca.tel’li.glo.bo.si’spo’ra. Gr. adj. allo another, the other; N.L. fem. n. Catelliglobosispora a bacterial generic name; N.L. fem. n. Allocatelliglobosispora the other Catelliglobosispora, an organism that is phylogenetically close to *Catelliglobosispora* but chemotaxonomically distinct).

Aerobic, oxidase-negative, catalase-positive and Gram-stain-positive. Substrate mycelium is well-developed, branched and light brown to brown in colour. Short chains of motile spores are borne singly or in clusters from the vegetative mycelium without the formation of aerial mycelium. Globose bodies are observed. 3-OH DAP is the diagnostic diamino acid in the cell-wall peptidoglycan. Whole-cell sugars are glucose, rhamnose, ribose, xylose, arabinose, galactose and mannose. The polar lipids include diphosphatidylglycerol, phosphatidylethanolamine and phosphatidylinositol. The major menaquinone is MK-10(H$_4$). The predominant cellular fatty acids are iso-C$_{15:0}$ and C$_{17:0}$. The DNA G+C content of the type strain of the type species is 70.1 mol%. Phylogenetically, the genus belongs to the family *Micromonosporaceae*. The type species is *Allocatelliglobosispora scoriae*.

**Description of Allocatelliglobosispora scoriae sp. nov.**

*Allocatelliglobosispora* (sco.ri’a. N.L. gen. n. scoriae of scoria, a type of volcanic ash, referring to the site at which the type strain was isolated).

The morphological and chemotaxonomic characteristics are the same as those given in the genus description. Grows well on ISP media 2, 3, 4 and 5 and oatmeal-nitrate agar; poor growth on ISP media 6 and 7. Soluble pigments are brown and are produced only on ISP medium 3 and oatmeal-nitrate agar. Growth occurs at pH 7.1–8.1 and 20–30 °C. Optimal temperature and pH for growth are 30 °C and pH 7.1. No growth in the presence of 1% NaCl. Nitrate is not reduced to nitrite. H$_2$S production is not observed. Aesculin and starch are degraded but CM-cellulose, casein, DNA, hypoxanthine, tyrosine and xanthine are not. Acetate, L-arabinose, citrate, raffinose, Dl-tartrate and D-xylitol are utilized as sole carbon and energy sources. Adonitol, D-arabinose, benzoate, cellobiose, dextran, dulcitol, meso-erythritol, formate, D-fructose, D-galactose, D-glucose, glycerol, myo-inositol, lactose, malate, maltose, D-glucosamine, D-mannosylamine, melibiose, methyl D-glucoside, methyl D-mannoside, L-rhamnose, L-ribose, salicin, D-sorbitol, L-sorbose, sucrose, succrose, trehalose and D-xylose are not utilized.

The type strain, Sco-B14T (=KCTC 19661$^T$ =DSM 45362$^T$), was isolated from volcanic ash collected in Jeju, Republic of Korea.

**Acknowledgements**

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**References**


