**Xiangella phaseoli** gen. nov., sp. nov., a member of the family *Micromonosporaceae*

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A novel endophytic actinomycete, designated strain NEAU-J5\(^T\) was isolated from roots of snap bean (*Phaseolus vulgaris* L.). Comparative analysis of the 16S rRNA gene sequence indicated that NEAU-J5\(^T\) is phylogenetically related to members of the family *Micromonosporaceae*. The whole-cell sugars were galactose, mannose and glucose. The predominant menaquinones were MK-9(H4) and MK-9(H6). The major fatty acids were C\(_{16:0}\), C\(_{18:0}\), C\(_{17:1}\), iso-C\(_{15:0}\) and C\(_{17:0}\). The phospholipids were phosphatidylglycerol, phosphatidylethanolamine, phosphatidylcholine, phosphatidylinositol and phosphatidylinositol mannoside. The DNA G+C content was 72.2 mol%. On the basis of the morphological and chemotaxonomic characteristics, phylogenetic analysis and characteristic patterns of 16S rRNA gene signature nucleotides, strain NEAU-J5\(^T\) represents a novel species of a new genus within the family *Micromonosporaceae*, for which the name *Xiangella phaseoli* gen. nov., sp. nov. is proposed. The type strain of *Xiangella phaseoli* is strain NEAU-J5\(^T\) (=CGMCC 4.7038\(^T\)=DSM 45730\(^T\)).

The family *Micromonosporaceae* was first described by Krasil’nikov (1938), and its description has been subsequently emended by Goodfellow et al. (1990), Koch et al. (1996), Stackebrandt et al. (1997) and Zhi et al. (2009) on the basis of chemotaxonomic data and 16S rRNA gene sequence analysis. At present, the family *Micromonosporaceae* comprises 28 genera. During an investigation exploring potential sources of novel species and novel natural products, a strain designated NEAU-J5\(^T\) was isolated from snap bean root which was collected from Harbin, Heilongjiang province, north China. In this study, the taxonomic status of this strain is reported based on phylogenetic, chemotaxonomic and phenotypic evidence.

Strain NEAU-J5\(^T\) was isolated from snap bean root collected from Harbin, Heilongjiang province, north China (45° 45′ N 126° 41′ E). In the open, the plant was tagged and stored in a clean plastic bag until used (approximately 24 h). The root sample was air-dried for 24 h at room temperature and then washed with an ultrasonic step (160 W, 15 min) to remove the surface soils and adherent epiphytes completely. After drying, the sample was cut into pieces of 5–10 mm in length and then subjected to a seven-step surface sterilization procedure: a 60 s wash in sterile tap water containing cycloheximide (100 mg l\(^{-1}\)) and nalidixic acid (20 mg l\(^{-1}\)), followed by a wash in sterile water, a 5 min wash in 5% NaOCl, a 10 min wash in 2.5% Na\(_2\)S\(_2\)O\(_3\), a 5 min wash in 75% ethanol, a wash in sterile water and a final rinse in 10% NaHCO\(_3\) for 10 min. The rinsed root sample was transferred temporarily onto sterile filter paper to eliminate excess moisture and then placed on a plate of humic acid–vitamin agar (HV) (Hayakawa & Nonomura, 1987) supplemented with cycloheximide (50 mg l\(^{-1}\)). After 21 days of aerobic incubation at 28 °C, colonies were transferred and purified on oatmeal agar (ISP medium 3) and incubated at 28 °C for 2–3 weeks.

Morphological properties were observed by light microscopy (ECLIPSE E200, Nikon) and scanning electron microscopy (S-3400N, Hitachi) using cultures grown on ISP3 agar for 21 days. Cultural characteristics were determined by growth on tap-water agar (Gordon et al., 1974), glucose–yeast–malt (GYM) agar (Lerch & Ettinger, 1972), M8 agar (Castiglione et al., 2008), sucrose–nitrate agar (Waksman medium 1), yeast extract–starch agar

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**Abbreviation:** DAP, diaminopimelic acid.

The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain NEAU-J5\(^T\) is JQ073732.

Three supplementary figures and two supplementary tables are available with the online version of this paper.
(JCM medium 61), Modified Bennett’s (MB) agar (Jones, 1949), Czapek’s agar (Raper & Fennell, 1965) and International Streptomyces Project (ISP) media 2–7 (Shirling & Gottlieb, 1966) at 28 °C for 14–21 days. The Colour Harmony Manual (Jacobson et al., 1958) was used to determine the names and designations of colony colours. The temperature range for growth was determined on ISP3 agar after incubation for 14–21 days. The pH range and NaCl tolerance for growth were determined in tryptic soy broth (TSB) in Erlenmeyer flasks for 14 days at 28 °C. Decomposition of cellulose, hydrolysis of starch, reduction of nitrate, liquefaction of gelatin and production of H2S were examined as described previously (Gordon et al., 1974). Utilization of carbohydrates as sole carbon sources was tested using ISP medium 9 as basal medium according to the method of Shirling & Gottlieb (1966). The utilization of amino acids as nitrogen sources was tested as described by Williams et al. (1983).

Fig. 1. Neighbour-joining tree showing the phylogenetic position of strain NEAU-J5T and type species of recognized genera of the family Micromonosporaceae based on 16S rRNA gene sequences. Streptomyces ambofaciens ATCC 23877T was used as an outgroup. Asterisks indicate branches that were also found using maximum-likelihood (Felsenstein, 1981) methods. Numbers at branch points indicate bootstrap percentages (based on 1000 replicates); only values >30 % are indicated. Bar, 0.01 substitutions per nucleotide position.
The freeze-dried cells used for chemotaxonomic analysis were obtained from cultures grown in TSB on a rotary shaker for 14 days at 28 °C. The isomers of diaminopimelic acid (DAP) in peptidoglycan were analysed by HPLC using an Agilent TC-C18 Column (250 × 4.6 mm internal diameter 5 μm) with a mobile phase consisting of acetonitrile: 0.05 mol l⁻¹ phosphate buffer pH 7.2 15:85 at a flow rate of 0.5 ml min⁻¹. The peak detection used an Agilent G1321A fluorescence detector with a 365 nm excitation and 455 nm longpass emission filters (McKerrow et al., 2000). The N-acyl group of muramic acid in peptidoglycan was determined by the method of Uchida et al. (1999). The whole-organism sugars were analysed according to the procedures developed by Lechevalier & Lechevalier (1980). Phospholipids in cells were extracted and identified by using the method of Minnikin et al. (1984). Menquinones were extracted from freeze-dried biomass and purified according to the protocol of Collins (1985). Extracts were analysed by the HPLC–UV method using Agilent Extend-C18 Column (150 × 4.6 mm, internal diameter 5 μm), typically at 270 nm. The mobile phase was acetonitrile:propyl alcohol (60:40, v/v) and the flow rate was set to 1.0 ml min⁻¹ and the run time was 60 min. The injection volume was 20 μl, and the chromatographic column was controlled at 40 °C (Wu et al., 1989).

Mycolic acids were checked by the acid methanolysis method as described previously (Minnikin et al., 1980). Cellular fatty acids were analysed by GC-MS using the method of Xiang et al. (2011).

Genomic DNA of strain NEAU-J5T was extracted as described previously by Lee et al. (2003) and PCR amplification of 16S rRNA gene was carried out according to the procedures described by Loqman et al. (2009). The PCR product was purified and cloned into the vector pMD19-T (Takara) and sequenced by an Applied Biosystems DNA sequencer (model 3730XL) and software provide by the manufacturer. Almost full-length 16S rRNA gene sequence was obtained and aligned with multiple sequences obtained from the GenBank/EMBL/DDBJ databases using CLUSTAL_X 1.83 software (Thompson et al., 1997). The alignment was manually verified and adjusted prior to the construction of phylogenetic trees. Phylogenetic trees were generated with the neighbour-joining (Saitou & Nei, 1987) and maximum-likelihood (Felsenstein, 1981) algorithms using MEGA 5.05 (Tamura et al., 2011). The stability of the clades in the trees was appraised using a bootstrap value with 1000 repeats (Felsenstein, 1985). A distance matrix was generated using Kimura’s two-parameter model (Kimura, 1980). All positions containing gaps and missing data were eliminated from the dataset (complete deletion option). Streptomyces ambofaciens ATCC 23877T was used as an outgroup. The DNA G+C content of the genomic DNA was determined by the thermal denaturation method as described by Mandel & Marmur (1968), and Escherichia coli JM109 was used as the reference strain. Nucleotides and nucleotide pairs in the 16S rRNA gene of strain NEAU-J5T and closely related members of the family Micromonosporaceae were determined after manual verification of the CLUSTAL_X sequence alignment.

The almost-complete 16S rRNA gene sequence (1512 bp) of strain NEAU-J5T showed a close relationship with members of family Micromonosporaceae. 16S rRNA gene sequence comparisons revealed that strain NEAU-J5T was most closely related to Micromonospora olivasterospora MK-70T (98.38 %), Jishengella endophytica 202201T (98.35 %), Micromonospora rhizosphaerae 211018T (98.11 %), Micromonospora yanggranensis FXJ6.011T (98.04 %), Micromonospora pattaloongensis TJ2-2T (97.95 %), Micromonospora auratingina TT1-11T (97.91 %), Micromonospora endolithica AA-459T (97.77 %) and Verrucosispora gilhommensis DSM 44337T (97.75 %). A neighbour-joining phylogenetic tree (Fig. 1) indicated that the new isolate belonged to the family Micromonosporaceae and was closely affiliated with the members of the genera Verrucosispora, Jishengella and Micromonospora, an association that was supported by maximum-likelihood (see Fig. S1, available in IJSEM Online).

The inclusion of strain NEAU-J5T in the family Micromonosporaceae was also supported by the presence of an almost complete set of family-specific signature nucleotides (Zhi et al., 2009) in its 16S rRNA gene sequence. However, when the signature nucleotide positions of strain NEAU-J5T were compared with those of its closest relatives, there were several nucleotide pair differences from the genera Jishengella, Micromonospora and Verrucosispora (see Table S1).

Fig. 2. Scanning electron micrograph of substrate mycelium of strain NEAU-J5T grown on ISP3 agar for 21 days at 28 °C. Bar, 1 μm.
Table 1. Characteristics of the genus *Xiangella* gen. nov. (strain NEAU-J5<sup>T</sup>) and genera in the family *Micromonosporaceae*

Data for reference genera were taken from Ørskov (1923), Couch (1950), Kane (1966), Thiemann et al. (1967), Asano & Kawamoto (1986), Yokota et al. (1993), Rheims et al. (1998), Kudo et al. (1999), Tamura et al. (1994, 1997, 2001, 2006), Lee & Hah (2002), Matsumoto et al. (2003), Maldonado et al. (2005), Thawai et al. (2006, 2010), Ara & Kudo (2006, 2007a, b), Ara et al. (2008a, b), Wiese et al. (2008), Monciardini et al. (2009), Qin et al. (2009), Inahashi et al. (2010), Lee & Lee (2011), Xie et al. (2011), Li et al. (2011) and Jia et al. (2013). +, Present; –, absent; m-DAP, *meso*-diaminopimelic acid; Ara, arabinose; Gal, galactose; Glc, glucose; Man, mannose; Rha, rhamnose; Rib, ribose; Xyl, xylose. Fatty acid types are classified according to Kroppenstedt (1985) and phospholipid types according to Lechevalier et al. (1981).

<table>
<thead>
<tr>
<th>Genus</th>
<th>Sporangium</th>
<th>Spore motility</th>
<th>Diamino acid (s)</th>
<th>Diagnostic sugars</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><strong>Xiangella</strong></td>
<td>–</td>
<td>–</td>
<td><em>m</em>-DAP</td>
<td>Man, Glc, Gal</td>
<td>3a</td>
<td>9(*H&lt;sub&gt;4&lt;/sub&gt;,8,2&lt;sub&gt;10&lt;/sub&gt;), 8(*H&lt;sub&gt;8&lt;/sub&gt;)</td>
<td>III</td>
<td>72.2</td>
</tr>
<tr>
<td><strong>Jishengella</strong></td>
<td>–</td>
<td>–</td>
<td><em>m</em>-DAP</td>
<td>Xyl, Man, Ara, Rib, Glc</td>
<td>3a</td>
<td>9(*H&lt;sub&gt;6&lt;/sub&gt;,8), 10(*H&lt;sub&gt;4&lt;/sub&gt;)</td>
<td>II</td>
<td>72</td>
</tr>
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<td><strong>Verrucosispora</strong></td>
<td>–</td>
<td>–</td>
<td><em>m</em>-DAP</td>
<td>Man, Xyl</td>
<td>2d</td>
<td>*9(<em>H&lt;sub&gt;4&lt;/sub&gt;)</em></td>
<td>II</td>
<td>70</td>
</tr>
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<td><strong>Micromonospora</strong></td>
<td>–</td>
<td>–</td>
<td><em>m</em>-DAP</td>
<td>Ara, Xyl</td>
<td>3b</td>
<td>10(*H&lt;sub&gt;4,6&lt;/sub&gt;), 9(*H&lt;sub&gt;4,6&lt;/sub&gt;)</td>
<td>II</td>
<td>71–72</td>
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<td><strong>Actinocatenispora</strong></td>
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<td>–</td>
<td><em>m</em>-DAP</td>
<td>Ara, Gal, Xyl</td>
<td>3b</td>
<td>9(*H&lt;sub&gt;4,6&lt;/sub&gt;)</td>
<td>II</td>
<td>72</td>
</tr>
<tr>
<td><strong>Actinoplanes</strong></td>
<td>+</td>
<td>+</td>
<td><em>m</em>-DAP</td>
<td>Ara, Xyl</td>
<td>2d</td>
<td>*9(*H&lt;sub&gt;4&lt;/sub&gt;), 10(<em>H&lt;sub&gt;4&lt;/sub&gt;)</em></td>
<td>II</td>
<td>72–73</td>
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<tr>
<td><strong>Allocatteliglobosispora</strong></td>
<td>–</td>
<td>–</td>
<td>3-OH-DAP</td>
<td>Glc, Rha, Rib, Xyl, Ara, Gal, Man</td>
<td>3b</td>
<td>10(*H&lt;sub&gt;4&lt;/sub&gt;), 9(*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><em>m</em>-DAP</td>
<td>Ara, Gal, Xyl</td>
<td>2d</td>
<td>10(*H&lt;sub&gt;6,8&lt;/sub&gt;)</td>
<td>II</td>
<td>71–72</td>
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<tr>
<td><strong>Catellatospora</strong></td>
<td>–</td>
<td>–</td>
<td><em>m</em>-DAP</td>
<td>Ara, Gal, Xyl, or only Xyl</td>
<td>3b</td>
<td>9(*H&lt;sub&gt;6,8&lt;/sub&gt;), 10(*H&lt;sub&gt;4&lt;/sub&gt;)</td>
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<td>70–71</td>
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<td>–</td>
<td><em>m</em>- and 3-OH-DAP</td>
<td>Rha, Man, Xyl, Gal, Glc</td>
<td>3b</td>
<td>10(*H&lt;sub&gt;4&lt;/sub&gt;)</td>
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<td><strong>Catenuloplanes</strong></td>
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<td>L-Lys</td>
<td>Xyl</td>
<td>2c</td>
<td>9(*H&lt;sub&gt;6&lt;/sub&gt;)</td>
<td>III</td>
<td>71–73</td>
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<tr>
<td><strong>Couchioplanes</strong></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>
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<td>70–72</td>
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<tr>
<td><strong>Dactylosporangium</strong></td>
<td>+</td>
<td>+</td>
<td><em>m</em>-DAP</td>
<td>Ara, Xyl</td>
<td>3b</td>
<td>9(*H&lt;sub&gt;4,6,8&lt;/sub&gt;)</td>
<td>II</td>
<td>71–73</td>
</tr>
<tr>
<td><strong>Hamadaea</strong></td>
<td>–</td>
<td>–</td>
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<td>Xyl, Gal, Man, Rib, Ara, Rha</td>
<td>3b</td>
<td>9(*H&lt;sub&gt;4&lt;/sub&gt;)</td>
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<td><strong>Krasilnikovia</strong></td>
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<td>–</td>
<td><em>m</em>-DAP</td>
<td>Gal, Ara, Xyl</td>
<td>2d</td>
<td>9(*H&lt;sub&gt;6,4,8&lt;/sub&gt;)</td>
<td>II</td>
<td>71</td>
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<td><strong>Longispora</strong></td>
<td>–</td>
<td>–</td>
<td><em>m</em>-DAP</td>
<td>Ara, Gal, Xyl</td>
<td>2d</td>
<td>10(*H&lt;sub&gt;6,8&lt;/sub&gt;)</td>
<td>II</td>
<td>70</td>
</tr>
<tr>
<td><strong>Luedemannella</strong></td>
<td>+</td>
<td>–</td>
<td><em>m</em>-DAP</td>
<td>Gal, Man, Rha, Rib, Xyl, Ara</td>
<td>2d</td>
<td>9(*H&lt;sub&gt;6,4,2,8&lt;/sub&gt;)</td>
<td>II</td>
<td>71</td>
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<tr>
<td><strong>Phytolabianus</strong></td>
<td>–</td>
<td>–</td>
<td><em>m</em>-DAP, l-Lys</td>
<td>Gal, Glc, Man, Rib, Xyl</td>
<td>2d</td>
<td>9(*H&lt;sub&gt;6,10&lt;/sub&gt;), 10(*H&lt;sub&gt;4&lt;/sub&gt;)</td>
<td>II</td>
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<tr>
<td><strong>Phytomonospora</strong></td>
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<td>–</td>
<td><em>m</em>-DAP</td>
<td>Gal, Glc, Rib, Man</td>
<td>2d</td>
<td>8(*H&lt;sub&gt;2&lt;/sub&gt;), 9(*H&lt;sub&gt;2&lt;/sub&gt;), 10(*H&lt;sub&gt;2,4,6&lt;/sub&gt;)</td>
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<td>70</td>
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<tr>
<td><strong>Pilimelia</strong></td>
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<td>+</td>
<td><em>m</em>-DAP</td>
<td>Ara, Xyl</td>
<td>2d</td>
<td>9(*H&lt;sub&gt;6,10&lt;/sub&gt;)</td>
<td>II</td>
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<td>–</td>
<td><em>m</em>-DAP</td>
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<td>10(*H&lt;sub&gt;6,8,4&lt;/sub&gt;)</td>
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<td><strong>Plantactinospora</strong></td>
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<td>3b</td>
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<td>–</td>
<td><em>m</em>-DAP</td>
<td>Xyl</td>
<td>2a</td>
<td>9(*H&lt;sub&gt;6,4,8&lt;/sub&gt;)</td>
<td>II</td>
<td>71</td>
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<td><strong>Pseudosporangium</strong></td>
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<td><em>m</em>- and 3-OH-DAP</td>
<td>Ara, Gal, Glc, Man, Xyl</td>
<td>2d</td>
<td>9(*H&lt;sub&gt;4&lt;/sub&gt;)</td>
<td>II</td>
<td>73.6</td>
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<td><strong>Rugosimonospora</strong></td>
<td>–</td>
<td>–</td>
<td>3-OH-DAP</td>
<td>Ara, Gal, Xyl</td>
<td>2c</td>
<td>9(*H&lt;sub&gt;6,8&lt;/sub&gt;)</td>
<td>II</td>
<td>72–73</td>
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<td><strong>Salinispora</strong></td>
<td>–</td>
<td>–</td>
<td><em>m</em>-DAP</td>
<td>Ara, Gal, Xyl</td>
<td>3a</td>
<td>9(*H&lt;sub&gt;4&lt;/sub&gt;)</td>
<td>II</td>
<td>70–73</td>
</tr>
<tr>
<td><strong>Spirilliplanes</strong></td>
<td>+</td>
<td>–</td>
<td><em>m</em>-DAP</td>
<td>Ara, Xyl</td>
<td>2d</td>
<td>10(*H&lt;sub&gt;4&lt;/sub&gt;)</td>
<td>II</td>
<td>69</td>
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<td><strong>Virgisporangium</strong></td>
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<td>+</td>
<td><em>m</em>-DAP</td>
<td>Ara, Gal, Man, Rha, Xyl</td>
<td>2d</td>
<td>10(*H&lt;sub&gt;6,8&lt;/sub&gt;)</td>
<td>II</td>
<td>71</td>
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<tr>
<td><strong>‘Wangella’</strong></td>
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<td>–</td>
<td><em>m</em>-DAP</td>
<td>Rib, Glc, Gal</td>
<td>1a</td>
<td>9(*H&lt;sub&gt;4&lt;/sub&gt;,6)</td>
<td>III</td>
<td>62.5</td>
</tr>
</tbody>
</table>

*Distinct values are for type strains of type species of the genus.*
Morphological observation of a 21 day-old culture of strain NEAU-J5T grown on ISP3 agar revealed that it formed extensively branched substrate mycelia without fragmentation. Aerial hyphae and sporangia were not present. Non-motile spores (0.60 × 0.69 μm) were borne singly on the substrate mycelium. The spore surface was unevenly warty (Fig. 2). Strain NEAU-J5T grew well on M8, tap-water, Czapek’s, yeast extract–starch, ISP2, ISP3 and ISP4 agar, moderately on MB and ISP6 agar and poorly on GYM, sucrose–nitrate and ISP7 agar, but no growth was observed on ISP5 medium. No soluble pigments were produced on any of the media tested. Colonies were orange, turning to black with age on most tested media. Growth of strain NEAU-J5T occurred in the pH range 5–11 and 0–3% NaCl (w/v), with optimum growth at pH 7.0 and 1% NaCl (w/v). The temperature range for growth was 18–37 °C, with the optimum temperature being 28 °C. Detailed physiological and biochemical properties are given in the species description.

Strain NEAU-J5T contained meso-diaminopimelic acid as a diamino acid. Whole-cell hydrolysates comprised galactose, mannose and glucose. The acyl type of the cell wall polysaccharides was glycolyl. Mycolic acids were not detected. The predominant menaquinones were MK-9(H₄) (59.03%) and MK-9(H₆) (30.63%), with MK-9(H₇) (3.31%), MK-9(H₈) (2.93%), MK-8(H₇) (2.73%), MK-9(H₁₀) (1.09%), MK-9 (0.28%) as minor components. The phospholipid profile consisted of phosphatidylmethylthanolamine, phosphatidyethanolamine, phosphatidylcholine, phosphatidylinositol and phosphatidylinositol mannoside (Fig. S2). The major cellular fatty acids were C₁₆:0 (41.99%), C₁₈:0 (21.07%), C₁₇:1₀7c (10.82%), iso-C₁₅:0 (5.85%), C₁₇:0 (4.91%), C₁₈:1₀9c (3.32%), C₁₄:0 (2.87%), 10-methyl C₁₇:0 (2.67%), anteiso-C₁₇:0 (1.84%), iso-C₁₄:0 (1.80%) and C₁₅:0 (1.55%) (see Table S2 and Fig. S3). Strain NEAU-J5T can be readily distinguished from the most closely related genera in the family Micromonosporaceae by the phospholipid type. Members of the genera Jishengella, Micromonaspora and Verrucosispora correspond to phospholipid type PIII, in contrast to strain NEAU-J5T, which belongs to phospholipid type PII (Lechevalier et al., 1981). The fatty acid pattern also differentiates strain NEAU-J5T from the genera Micromonaspora and Verrucosispora, as the two genera have a 3b or 2d type, in contrast to the novel isolate, which is of type 3a (Kroppenstedt, 1985). Furthermore, the major menaquinones and the whole-cell sugars of strain NEAU-J5T differ from those of the most closely related phylogenetic neighbours of the family Micromonosporaceae (Table 1).

In conclusion, using a combination of morphological and chemotaxonomic data, phylogenetic analysis and the signature nucleotide pattern of the 16S rRNA gene, strain NEAU-J5T is readily distinguishable from known actinomycetes belonging to the family Micromonosporaceae and thus this isolate can be considered as representative of a new genus. Therefore, we propose that strain NEAU-J5T represents a novel species of a new genus within the family Micromonosporaceae, for which the name Xiangella phaseoli gen. nov., sp. nov. is proposed.

**Description of Xiangella gen. nov.**

_Xiangella_ (Xi.ang.el’la. N.L. fem. dim. n. Xiangella named after Hua Xiang, a Chinese microbiologist).

Aerobic, Gram-positive and non-acid-fast actinomycetes. Cells form extensively branched substrate mycelia, which carry singly unevenly warty-surfaced spores (0.60 × 0.69 μm). Spores are non-motile. Cell walls contain meso-diaminopimelic acid, and mannose, galactose and glucose are the whole-cell sugars. The acyl type of the cell wall polysaccharides is glycolyl. Mycolic acids are absent. The major menaquinones are MK-9(H₄), MK-9(H₆). Phosphatidylmethylthanolamine, phosphatidyethanolamine, phosphatidylcholine, phosphatidylinositol and phosphatidylinositol mannoside are present, corresponding to phospholipid type PIII. The major cellular fatty acids are C₁₆:0, C₁₈:0, C₁₇:1₀7c, iso-C₁₅:0, C₁₁:0, corresponding to fatty acid type 3a. The type species of the genus is _Xiangella phaseoli._

**Description of Xiangella phaseoli sp. nov.**

_Xiangella phaseoli_ (pha.se’o.li. N.L. masc. n. Phaseolus botanical genus name; N.L. gen. n. phaseoli of Phaseolus, referring to the isolation of the first strains from _Phaseolus vulgaris_).

Chemotaxonomic and general characteristics are the same as given above for the genus. Grows well on M8, tap-water, Czapek’s, yeast extract–starch, ISP2, ISP3 and ISP4 agar; moderately on MB and ISP6 agar; poorly on GYM, sucrose–nitrate and ISP7 agar; no growth is observed on ISP5 agar. No diffusible pigment is detected on any of the tested media. Colonies are orange to black with age on most tested media. Positive for liquefaction of gelatin and negative for hydrolysis of starch, decomposition of cellulose, reduction of nitrate and production of H₂S. Arabinose, galactose, glucose, inositol, maltose, mannose, mannotol, raffinose, rhamnose, sorbitol and sucrose are utilized as sole carbon sources, but fructose, lactose, ribose and xylose are not. Arginine, asparagine, creatine, glutamine and threonine are utilized as sole nitrogen sources, but alanine, aspartic acid, glutamic acid, glycine and tyrosine are not. Tolerates up to 3% NaCl and grows at temperatures between 18 and 37 °C, with an optimum temperature of 28 °C. Growth occurs at initial pH values between 5 and 11, the optimum being pH 7.0.

The type strain is NEAU-J5T (=CGMCC 4.7038T=DSM 45730T), which was isolated from snap bean root collected...
from Harbin, Heilongjiang Province, north China. The DNA G+C content of the type strain is 72.2 mol%.

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