A Gram-positive, coccoid, non-spore-forming bacterium, designated strain 3-6<sup>T</sup>, was isolated from farmland soil and subjected to a polyphasic taxonomic analysis. Comparative analysis of the 16S rRNA gene sequence revealed that the strain represented a novel member of the suborder Micrococcinae. Its nearest phylogenetic neighbour was the type strain of *Georgenia muralis* (94.2% 16S rRNA gene sequence similarity). Chemotaxonomic characteristics of strain 3-6<sup>T</sup> were as follows: the major menaquinone was MK-8(H<sub>4</sub>); the polar lipids consisted mainly of diphosphatidylglycerol, phosphatidylglycerol and one unknown glycolipid; the predominant fatty acids were anteiso-C<sub>15 : 0</sub>, anteiso-C<sub>17 : 0</sub> and iso-C<sub>16 : 0</sub>; mycolic acids were absent. A new murein type, L-Lys–Gly–L-Glu–L-Glu (A<sub>4</sub>–), was found in the peptidoglycan of the cell wall. The DNA G+C content was 69.8 mol%. On the basis of morphological, chemotaxonomic and phylogenetic characteristics, it is suggested that strain 3-6<sup>T</sup> represents a novel species of a new genus within the suborder Micrococcinae, for which the name *Ruania albidiflava* gen. nov., sp. nov. is proposed. The type strain of *Ruania albidiflava* is 3-6<sup>T</sup> (=CGMCC 4.3142<sup>T</sup> = DSM 18029<sup>T</sup> = JCM 13910<sup>T</sup> = PCM 2644<sup>T</sup>).

According to the estimation performed by Hammond (1995), the number of bacteria that have been successfully isolated and identified comprises only a small portion of the total that exist in nature. In the past decade, the Micrococcinae (Stackebrandt et al., 1997) has been one of the most studied suborders in the class Actinobacteria; numerous novel taxa in this suborder have been cultured and described (Martin et al., 1997; Groth et al., 1999a, b, 2001, 2002; von Wintzingerode et al., 2001; Altenburger et al., 2002; Takahashi et al., 2006). In the current study, we describe a bacterium isolated from farmland soil collected in Shandong Province, China, and propose a novel species of a new genus in the suborder Micrococcinae.

Farmland soil samples were collected from a cotton field in Shandong Province. A 1 g soil sample was suspended in 10 ml sterile distilled water and mixed thoroughly by shaking overnight at room temperature. The suspension was serially diluted and spread onto yeast extract–starch agar (JCM medium no. 42) plates, followed by incubation for 1 week under humid conditions at 28 °C. The organism thus isolated, designated strain 3-6<sup>T</sup>, was picked and transferred to fresh nutrient agar for purification. The pure culture was tested for growth in various media and was maintained on nutrient agar slants at 4 °C.

For observation of colony and cell morphology, strain 3-6<sup>T</sup> was grown on nutrient agar, R agar (Groth et al., 1999b) and trypticase soy agar (TSA; BBL) for up to 5 days at 28 °C. Light and scanning electron micrographs were taken according to methods described previously (Huang et al., 2004). The presence of flagella was examined via transmission electron microscopy of 48- and 72-h plate cultures. The temperature range for growth was determined by incubating inoculated slant agar cultures (R medium, pH 7.0) at 4, 10, 15, 20, 28, 37 and 45 °C. Growth was also assessed on R agar plates at initial pH values of 3.5–13.5. The lower pH values of the test medium were obtained according to the method described by Cui et al. (2005) and pH values above 10.5 by using a buffer system of disodium hydrogen phosphate (0.15 M)/sodium hydroxide (6 M). API 50CH and API ZYM kits (bioMérieux) were used to test acid production from carbohydrates and enzyme activities, respectively. In
Cell mass of strain 3-6\textsuperscript{T} was collected from 4-day cultures and subjected to analysis. Genomic DNA extraction and PCR amplification of the 16S rRNA gene from strain 3-6\textsuperscript{T} were performed by using an established method (Chun & Goodfellow 1995). The PCR product was purified and cloned into the vector pMD 18-T (Takara) by using the method and reagents provided by the manufacturer. The almost-complete nucleotide sequence of the 16S rRNA gene was obtained according to the process described by Groth et al. (2006), except that M13 sequencing primers were used. Preliminary phylogenetic analysis was performed with the BLAST search program available at NCBI. Sequences were loaded into the software package MEGA, version 3.1 (Kumar et al., 2004), and this was followed by a series of programmed phylogenetic calculations. Neighbour-joining (Saitou & Nei, 1987) and maximum-parsimony (Fitch, 1971) trees were constructed separately as described by Gu et al. (2006).

Cell mass of strain 3-6\textsuperscript{T} was collected from 4-day cultures in liquid R medium. Isoprenoid quinones were purified according to the methods of Collins (1985) and analysed by HPLC (Wu et al., 1989) by using an HP-1050 (Hewlett Packard) chromatograph equipped with a Zorbax ODS C18 (250 × 4.6 mm, inner diameter 5 μm) column. The mobile phase was acetonitrile/2-propanol (2:1) at a flow rate of 1 ml min\textsuperscript{-1}, and menaquinones were detected by absorption at 270 nm. Polar lipids were extracted and identified by two-dimensional TLC (Lechevalier et al., 1977; Minnikin et al., 1984). The fatty acid profile was determined according to the GC techniques described by Sasser (1990) and Kämpfer & Kroppenstedt (1996). The acid methanolysis procedure was used to detect mycolic acids (Minnikin et al., 1975). To determine the peptidoglycan structure, purified cell wall was prepared according to the method of Lechevalier & Lechevalier (1970). Amino acids and peptides in the cell-wall hydrolysates were examined by TLC as described by Schleifer (1985). Whole-cell sugars consisted mainly of galactose and glucose. The major menaquinone was the partially saturated menaquinone MK-8(H\textsubscript{4}). Phosphatidylglycerol, di-phosphatidylglycerol and one unknown glycolipid were found as major polar lipids. Cellular fatty acid analysis revealed predominant amounts of the branched fatty acids anteiso-C\textsubscript{15:0} (37.3 %), anteiso-C\textsubscript{17:0} (14.7 %) and iso-C\textsubscript{16:0} (14.3 %) and smaller amounts of C\textsubscript{18:1}ω9c (9.5 %), iso-C\textsubscript{15:0} (7.9 %), C\textsubscript{16:0} (5.9 %), iso-C\textsubscript{17:0} (2.6 %) and C\textsubscript{14:0} (1.9 %). The complete fatty acid profile is given in Supplementary Table S2 in IJSEM Online. Mycolic acids were not present. The G+C content of the genomic DNA of strain 3-6\textsuperscript{T} was 69.8 mol%.

The nearest phylogenetic neighbours of strain 3-6\textsuperscript{T}, as determined by analysis of the almost-complete 16S rRNA gene sequences, were found to be members of the suborder Micrococcineae. Highest sequence similarity was obtained with Georgiina muralis 1A-C\textsuperscript{T} (94.2 %). The position of strain 3-6\textsuperscript{T} relative to its phylogenetic neighbours is shown in the neighbour-joining tree (Fig. 1) and was confirmed in the maximum-parsimony tree (see Supplementary Fig. S2 in IJSEM Online). The pattern of its 16S rRNA gene sequence signature nucleotides is shown in Table 1, which was calculated according to the method of Lechevalier & Lechevalier (1980). The G+C content of the genomic DNA of strain 3-6\textsuperscript{T} was determined by the thermal denaturation method (Marmur & Doty, 1962) with Escherichia coli K-12 as a control.
indicated that strain 3-6T does not belong to any recognized family within the suborder Micrococcineae, having the fewest signature nucleotide differences with Georgenia (seven of 33 positions) and the Bogoriellaceae (eight of 33 positions) (Stackebrandt et al., 1997; Stackebrandt & Schumann, 2000).

Characteristics that differentiate strain 3-6T from other representatives of the nearest neighbours detected by 16S rRNA gene sequence analysis are given in Table 2. It is evident from the genotypic and phenotypic data presented that strain 3-6T represents a novel species of a new genus within the suborder Micrococcineae, for which the name Ruania albidiflava gen. nov., sp. nov. is proposed.

**Description of Ruania gen. nov.**

Ruania (Ru.an’i.a. N.L. fem. n. Ruania named after Ji-Sheng Ruan, a Chinese microbiologist who has made great contributions to the development of actinomycete taxonomy in China).

**Table 1. Patterns of 16S rRNA gene signature nucleotides that define strain 3-6T, the genera Beutenbergia, Georgenia and Salana and the family Bogoriellaceae**

Positions are numbered according to the *E. coli* numbering scheme. The following signature nucleotides were identical in all taxa analysed: 41:401 (G–C), 45:396 (U–G), 142:221 (C–G), 248:276 (C–G), 258:268 (G–C), 1244:1293 (C–G) and 1310:1327 (G–C).

<table>
<thead>
<tr>
<th>Position</th>
<th>Strain 3-6T</th>
<th>Georgenia</th>
<th>Bogoriellaceae</th>
<th>Beutenbergia</th>
<th>Salana</th>
</tr>
</thead>
<tbody>
<tr>
<td>589:650</td>
<td>U–A</td>
<td>U–A</td>
<td>C–G</td>
<td>U–A</td>
<td>U–A</td>
</tr>
<tr>
<td>610</td>
<td>A</td>
<td>A</td>
<td>A</td>
<td>A</td>
<td>A</td>
</tr>
<tr>
<td>612:628</td>
<td>U–A</td>
<td>G–C</td>
<td>C–G</td>
<td>G–C</td>
<td>C–G</td>
</tr>
<tr>
<td>616:624</td>
<td>G–C</td>
<td>G–C</td>
<td>G–C</td>
<td>G–C</td>
<td>G–C</td>
</tr>
<tr>
<td>615:625</td>
<td>A–U</td>
<td>A–U</td>
<td>G–C*</td>
<td>A–U</td>
<td>A–U</td>
</tr>
<tr>
<td>863</td>
<td>U</td>
<td>U</td>
<td>U</td>
<td>A*</td>
<td>U</td>
</tr>
<tr>
<td>1134:1140</td>
<td>C–G</td>
<td>C–G</td>
<td>C–G</td>
<td>C–G</td>
<td>C–G</td>
</tr>
<tr>
<td>1254:1283</td>
<td>G–U</td>
<td>G–C</td>
<td>G–C</td>
<td>G–C</td>
<td>G–C</td>
</tr>
<tr>
<td>1414:1486</td>
<td>U–G</td>
<td>C–G</td>
<td>C–G</td>
<td>U–A</td>
<td>U–A</td>
</tr>
</tbody>
</table>

*Errors in the signatures indicated in Altenburger et al. (2002) have been corrected here.
Table 2. Differential characteristics of strain 3-6T and related taxa

Data for reference taxa were taken from Altenburger et al. (2002) (Georgenia), Groth et al. (1997) (Bogoriella), Groth et al. (1999b) (Beutenbergia) and von Wintzingerode et al. (2001) (Salana). All taxa have the same major menaquinone, MK-8(H4). DNA G+C contents given are for the type strain of the type species.

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>Strain 3-6T</th>
<th>Georgenia</th>
<th>Bogoriella</th>
<th>Beutenbergia</th>
<th>Salana</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cell morphology</td>
<td>Coccoid</td>
<td>Rod–coccus</td>
<td>Irregular rod, coccoid</td>
<td>Rod–coccus</td>
<td>Rod, coccoid, club-like</td>
</tr>
<tr>
<td>DNA G+C content (mol%)</td>
<td>70</td>
<td>70</td>
<td>70</td>
<td>75</td>
<td></td>
</tr>
<tr>
<td>Polar lipids*</td>
<td>PG, DPG, IGL</td>
<td>PG, DPG, PIM, 2PL, GL</td>
<td>PI, PG, DPG, 1PL</td>
<td>PI, DPG, 3PL</td>
<td>PG, DPG, PLs</td>
</tr>
<tr>
<td>Major fatty acid(s)</td>
<td>anteiso-C15 : 0, anteiso-C17 : 0, iso-C16 : 0</td>
<td>anteiso-C15 : 0, iso-C14 : 0, iso-C15 : 1</td>
<td>anteiso-C15 : 0, anteiso-C15 : 0</td>
<td>iso-C16 : 0, C14 : 0, C16 : 0</td>
<td></td>
</tr>
</tbody>
</table>

*DPG, Diphosphatidylglycerol; nGL, n unknown glycolipid(s); PG, phosphatidylglycerol; PI, phosphatidylinositol; PIM, phosphatidylinositol mannoside; nPL, n unknown phospholipid(s).

Gram-positive, aerobic, mesophilic, moderately halotolerant, non-acid-fast, non-motile, non-spore-forming cocci. The rod–coccus life cycle is not detected. The peptidoglycan type is A4z with an L-Lys–Gly–L-Glu–L-Glu interpeptide bridge. The predominant menaquinone is MK-8(H4). The main fatty acid is anteiso-C15 : 0 (12-methyl tetradecanoic acid). The major polar lipids are phosphatidylglycerol, phosphatidylglycerol and one unknown glycolipid. Mycolic acids are absent. The 16S rRNA gene sequence signature nucleotides are listed in Table 1. The genus belongs phylogenetically to the suborder Micrococccineae, order Actinomycetales. The type species is Ruania albidiflava.

Description of Ruania albidiflava sp. nov.

Ruania albidiflava (al.bi.di.flava. L. adj. albidus white; L. fem. adj. flava yellow; N.L. fem. adj. albidiflava whittest yellow).

Cells are 0.5–0.8 μm in diameter. Colonies are convex and moist, with a pale yellow colour. Growth occurs at 20–37 °C with an optimum at 28 °C, and at a wide initial pH range of 5.5–12.5 with an optimum at pH 6.5–10.5. Can tolerate up to 10% (w/v) NaCl. Catalase-positive, oxidase-negative. The methyl red test is positive, but indole and Voges–Proskauer reactions are negative. Nitrate is reduced to nitrite. H2S is not produced. Potato starch is decomposed, but adenine, casein, ascuscin, gelatin, hippurate, hypoxantine, tyrosine, urea and xanthine are not. Acids are produced from arbutin, salicin, D-ribose, methyl β-D-xylopyranoside, D-fructose, ascin, D-maltose, D-arabinose, L-arabinose, D-xyllose, L-rhamnose, L-lyxose and L-fucose, but not from glycerol, erythritol, L-xylene, D-adonitol, D-galactose, D-glucose, D-mannose, L-sorbose, dulcitol, inositol, D-mannitol, D-sorbitol, methyl α-D-ribofuranoside, methyl α-D-glucopyranoside, N-acetylglucosamine, amygdalin, D-cellobiose, D-lactose, D-melibiose, sucrose, D-trehalose, inulin, D-melezitose, D-raffinose, starch, glycojen, xylitol, gentiobiose, D-turanose, D-tagatose, D-fucose, D-l-arabitol, potassium 2-ketogluconate or potassium 5-ketogluconate. Utilizes the following substrates as sole carbon sources: acetate, D-lactate, D-melezitose, L-alanine, L-cysteine, L-leucine, L-methionine, L-proline, methyl α-D-glucoside, oxalate, D-fructose, D-glucose, D-glutamic acid, D-malate, D-ribose, D-sorbitol, D-trehalose, glycerol, D-arginine, L-fucose and sucrose. The following substrates are not utilized: citrate, D-cellobiose, D-galactose, D-inulin, D-lactulose, D-mannitol, D-mannose, D-raffinose, D-rhamnose, D-sorbose, D-xyllose, dulcitol, erythritol, glycojen, inositol, L-arabinose, L-leucinamide, L-ornithine, L-phenylalanine, L-tyrosine, L-valine, malate, malonate, nicotinamide, salcin and succinate. In the API ZYM assay, tests are positive for cystine arylamidase, α-fucosidase, alkaline phosphatase, esterase lipase (C8), leucine arylamidase, valine arylamidase, acid phosphatase, naphthol-AS-BI-phosphohydrolase, α-galactosidase, β-galactosidase, α-glucosidase, β-glucosidase, N-acetyl-α-glucosaminidase and α-mannosidase, but negative for esterase (C4), lipase (C14), trypsin, chymotrypsin and β-glucuronidase. Cells are susceptible to ampicillin (10 μg), chloramphenicol (30 μg), ciprofloxacin (5 μg), erythromycin (15 μg), gentamicin (10 μg), kanamycin (30 μg), neomycin (30 μg), polymyxin B (300 IU), rifampicin (15 μg) and streptomycin (10 μg). Not susceptible to nitrofurantoin (300 μg) or oxacillin (1 μg). Whole-cell sugars are galactose and glucose. The G+C content of the genomic DNA is 69.8 mol%. Other chemotaxonomic characteristics are as described for the genus.

The type strain, 3-6T ( = CGMCC 4.3142T = DSM 18029T = JCM 13910T = PCM 2644T), was isolated from farmland soil collected in Shandong Province, China.
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References


