Georgenia ruanii sp. nov., a novel actinobacterium isolated from forest soil in Yunnan (China), and emended description of the genus Georgenia

Wen-Jun Li, Ping Xu, Peter Schumann, Yu-Qin Zhang, Rüdiger Pukall, Li-Hua Xu, Erko Stackebrandt and Cheng-Lin Jiang

Correspondence
Wen-Jun Li
wjli@ynu.edu.cn

1Laboratory for Conservation and Utilization of Bio-Resources, Yunnan Institute of Microbiology and Yunnan University, Kunming, Yunnan, 650091, People’s Republic of China
2DSMZ – Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH, Inhoffenstrasse 7b, D-38124 Braunschweig, Germany
3Institute of Medicinal Biotechnology, Chinese Academy of Medical Sciences and Peking Union Medical College, Beijing 100050, People’s Republic of China

A Gram-positive, motile, short-rod-shaped strain, designated YIM 004T, was isolated from a forest-soil sample collected from Lijiang, Yunnan Province, China, and was investigated using a polyphasic taxonomic approach. The isolate contained chemotaxonomic markers that corresponded to those of its phylogenetic neighbour, Georgenia muralis, i.e. it possessed peptidoglycan type A4a with lysine as the diagnostic cell-wall diamino acid, the predominant menaquinone was MK-8(H4) and the major fatty acid was ai-C15 : 0. The G+C content of the genomic DNA was 72.9 mol%. Strain YIM 004T exhibited a 16S rRNA gene sequence similarity of 97.3 % and a DNA–DNA relatedness value of 18 % with respect to G. muralis DSM 14418T. On the basis of the phenotypic and genotypic differences between the isolate and G. muralis, strain YIM 004T represents a novel species of the genus Georgenia, for which the name Georgenia ruanii sp. nov. is proposed. The type strain is YIM 004T (= CCTCC AB 204065T = DSM 17458T = KCTC 19029T). In addition, an emended description of the genus Georgenia is presented.

The genus Georgenia was proposed by Altenburger et al. (2002) with a single species, Georgenia muralis, the type strain of which was isolated from a medieval wall painting in the church of St Georgen in Styria, Austria. The cells were Gram-positive, oxidase- and catalase-positive, non-sporulating and non-motile and exhibited a rod–coccus cycle.

In the course of a screening programme for new antibiotics, some mesophilic bacteria that contained both type I and type II polyketide biosynthesis pathway genes were screened and identified by means of polyphasic taxonomy (Xu et al., 2003, 2005a, b). The present investigation was designed to clarify the taxonomic position of another novel strain containing these genes. Strain YIM 004T was isolated from a forest-soil sample collected from Lijiang, Yunnan Province, China, after 2 weeks incubation at 28 °C on ISP 2 agar (Shirling & Gottlieb, 1966). Comparative 16S rRNA gene sequence analysis revealed the isolate to be a member of the suborder Micrococccinae. On the basis of phenotypic and genotypic evidence, the novel isolate represents a novel species of the genus Georgenia.

All physiological and biochemical tests were performed at 28 °C. The colony morphology was determined after 3 days incubation at 28 °C on ISP 2 and TSA [trypticase soy broth (BBL), 3 %, w/v; Bacto agar (Difco), 1.5 %, w/v] medium. Colour determination was achieved using colour chips from the ISCC–NBS colour charts (standard sample no. 2106) (Kelly, 1964). Gram staining was carried out using the standard Gram reaction and was examined by light microscopy (BH-2 microscope; Olympus). Cell motility was investigated on Luria–Bertani swarming agar (0.3 %, w/v). Cellular morphology was studied by using a JEM-1010 electron microscope (JEOL) with cells from exponentially growing cultures. Oxidase activity was determined using a 1 % solution of tetramethyl-p-phenylenediamine (Kovács, 1956). Catalase activity was determined by assessing the production of bubbles after the addition of 3 % H2O2. The temperature range and optimum for growth were

These authors contributed equally to this work.

The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain YIM 004T is DQ203185.

A transmission electron micrograph of cells of strain YIM 004T is available as a supplementary figure with the online version of this paper.
tested at 4–55 °C on ISP 2 medium. The pH range and optimum for growth, tolerance of sodium chloride and phenol and susceptibility to antibiotics were examined as described by Xu et al. (2005a). Carbon utilization and acid production were tested using Micro-biochemical tubes (Hangzhou Tianhe Micro-organism Reagent). Some other physiological properties were tested by using the API ID 32E test kit (bionMérieux).

The cells of strain YIM 004^T were short rod-shaped (0.5–0.8 x 1.4–2.0 μm) and motile (amphitrichous, i.e. the cell has a single flagellum at each end, as shown in Supplementary Fig. S1 available in IJSEM Online). The cells were Gram-positive and chemo-organotrophic, with a respiratory-type metabolism. Endospores and poly-β-hydroxyalkanoate were not formed. The strain could not grow in the presence of sodium chloride at concentrations above 5%. The temperature range for growth was 10–37 °C and the pH range for growth was 6.5–10.0. Optimal growth occurred at 28–30 °C and at pH 7.0. The results of the other physiological and biochemical analyses are summarized in the species description.

Analysis of sugars from whole-cell hydrolysates was performed using procedures described by Stanek & Roberts (1974). Purified peptidoglycan preparations were obtained after disruption of the cells by shaking with glass beads and subsequent trypsin digestion according to the method of Schleifer (1985). The amino acids and peptides in the cell-wall hydrolysates were analysed by two-dimensional ascending TLC on cellulose plates using the solvent systems of Schleifer & Kandler (1972). The N-terminal amino acid of the interpeptide bridge was determined by dinitrophenylation as described by Schleifer (1985). The molar ratios of the amino acids were determined by GC and GC-MS of the N-heptafluorobutyryl amino acid isobutyl esters (MacKenzie, 1987). Analysis of the enantiomers of the peptidoglycan amino acids was performed by GC of the N-pentafluoropropionyl amino acid isopropyl esters (Frank et al., 1980) on an L-Chirasil-Val column (Macherey-Nagel) as described by Groth et al. (1999).

Polar lipids were extracted from cultures grown in TSB, examined by two-dimensional TLC and identified using published procedures (Minnikin et al., 1979; Collins & Jones, 1980). Menaquinones were isolated using the method of Collins et al. (1977) and were analysed by HPLC (Groth et al., 1997). Analysis of the whole-cell fatty acid pattern was performed using previously described methods involving the MIDI system (Microbial ID) (Kroppenstedt, 1985; Meier et al., 1993). The G+C content of the DNA was determined by reversed-phase HPLC of nucleosides according to Mesbah et al. (1989).

The molar ratio of the amino acids in the peptidoglycan hydrolysate (4 M HCl, 16 h at 100 °C) was approximately 3.1 : 2.4 : 1.0 for alanine/glutamic acid/lysine. Glutamic acid and smaller amounts of alanine were detected as N-terminal amino acids because of the incomplete cross-linkage of the interpeptide bridge. Enantiomeric analysis of the peptidoglycan amino acids revealed almost equimolar amounts of L- and D-glutamic acid and an L-alanine/D-alanine ratio of approximately 2 : 1. The peptides D-Ala = L-Lys = L-Ala and L-Lys = L-Ala were detected in the partial hydrolysate (4 M HCl, 45 min at 100 °C) of the peptidoglycan of strain YIM 004^T. From these data, it was concluded that strain YIM 004^T possesses peptidoglycan of type A4z, with lysine as the diagnostic cell-wall diamino acid and an interpeptide bridge comprising L-Lys = L-Ala = L-Glu. The cell-wall sugars consisted of galactose and rhamnose. The polar lipids were phosphatidylglycerol, phosphorylcholine, diphosphatidylglycerol and an unknown phospholipid. The menaquinone pattern was composed of MK-8(H_4), MK-7(H_4), MK-9(H_4) (90:2:1). The major fatty acids were ai-C_{15:0} and i-C_{15:0}; the detailed cellular fatty acid profile is reported in the species description. The G+C content of genomic DNA from strain YIM 004^T was 72.9 mol%.

Genomic DNA for PCR amplification was prepared from cells lysed by microwaves: a small amount of biomass was transferred from solid medium to a new Eppendorf tube. After the cells had been washed with 1 ml PBS (pH 8.0) and 1 ml washing buffer [50 mM Tris/ HCl, pH 7.7; 25 mM EDTA; 0.1 % SDS; 0.1 % polyvinylpyrrolidone (PVP)], 50 μl lysis buffer (50 mM Tris/HCl, pH 8.0; 25 mM EDTA; 3 % SDS; 1.2 % PVP) was added to resuspend the cells, which were then heated at 700 W in a microwave oven for 45 s. Next, 400 μl warm extraction buffer [10 mM Tris/HCl, pH 8.0, 1 mM EDTA, 0.5 M sodium acetate, 1.2 % PVP (pre-warmed at 65 °C)] was added immediately and mixed with the cell suspension. An equal volume of phenol/chloroform was used for extraction. The DNA was precipitated with 2-propanol. The DNA was washed with 70 % ethanol and dissolved using 20 μl TE solution.

PCR amplification and 16S rRNA gene sequencing were carried out as described previously (Cui et al., 2001). After a preliminary BLAST analysis (Altschul et al., 1997), the sequence of strain YIM 004^T was aligned with those of related members of the class Actinobacteria, which had been retrieved from the GenBank database using the BLAST2 algorithm (Tatusova & Madden, 1999). Sequence similarities were determined by using CLUSTAL X (Thompson et al., 1997). A phylogenetic tree was constructed, using the neighbour-joining method of Saitou & Nei (1987), from k_{nu e} values (Kimura, 1980, 1983) with MEGA, version 2.1 (Kumar et al., 2001). The topology of the phylogenetic tree was evaluated by using the bootstrap resampling method of Felsenstein (1985), with 1000 replicates.

The almost-complete 16S rRNA gene sequence (1516 nt) was determined for strain YIM 004^T. Phylogenetic analysis of strain YIM 004^T revealed that the isolate was most closely related to G. muralis DSM 14418^T, the 16S rRNA gene sequence similarity value being 97.3 %, and the two strains formed a distinct clade within the suborder Micrococccinae (Fig. 1).
strain YIM 004T contains an interpeptide bridge composed of L-Lys and using a UV-Vis spectrophotometer (model UV1601; Shimadzu). Genomic DNAs from strains YIM 004T and DSM 14418T were prepared according to the method of Marmur (1961); purified genomic DNAs were cut to generate DNA fragments between 400 and 800 bp in size. Sheared genomic DNA (about 100 μg) from each sample was added to 2 × SSC (1 × SSC is 0.15 M sodium chloride plus 0.015 M sodium citrate) and then denatured by raising the temperature to 100 °C and cooled to the melting temperature in the spectrophotometer. The samples were kept at the melting temperature for 3 min and the absorbance at 260 nm was recorded at 30 s intervals for a total of 30 min. The initial reassociation kinetics were determined by using linear regression analysis. The percentage DNA homology for these two micro-organisms was calculated using the equation described by De Ley et al. (1970). All statistical analyses were performed using the EXCEL software (Microsoft). The DNA–DNA relatedness value obtained was 18 % (mean from two experiments), significantly lower than the 70 % value considered to be the threshold for the delineation of genomic species (Wayne et al., 1987).

The results of the 16S rRNA gene sequence analysis clearly demonstrated that strain YIM 004T is closely related to Georgenia muralis DSM 14418T. Both organisms contain MK-8(H4) as the predominant menaquinone and have the same peptidoglycan type (A4α) with lysine as the diagnostic cell-wall diamino acid. These properties support the inclusion of strain YIM 004T within the genus Georgenia. However, strain YIM 004T contains an interpeptide bridge composed of L-Lys→L-Ala→L-Glu, while the peptidoglycan of G. muralis has peptidoglycan subunits that are cross-linked via a single L-glutamic acid residue. In addition, strain YIM 004T differs from G. muralis DSM 14418T by the presence of phosphatidylinositol, by possessing larger amounts of iso-C15:0 and by some other phenotypic characteristics, as shown in Table 1.

The DNA–DNA relatedness data provide conclusive evidence that the novel isolate (YIM 004T) and G. muralis DSM 14418T are members of different genomic species (Wayne et al., 1987). Strain YIM 004T therefore represents a novel species of the genus Georgenia, for which the name Georgenia ruanii sp. nov. is proposed. As a consequence of newly reported characteristics not included in the original description of strain DSM 14418T, the description of the genus Georgenia Altenburger et al. 2002 needs to be emended.

Emended description of Georgenia Altenburger et al. 2002

The description is based on that given by Altenburger et al. (2002). Cells are coccoid or rod-shaped that may exhibit a rod–coccus life cycle. Gram-positive, non-sporulating and motile or non-motile. Aerobic, but growth under anaerobic conditions can also occur. Oxidase- and catalase-positive. The peptidoglycan type is A4α (based on lysine as diagnostic diamino acid). The major menaquinone is MK-8(H4). The polar lipids are diphasphatidylglycerol and phosphatidylglycerol; phosphatidylglycerol and mannoside or phosphatidylinositol can occur. There is a predominance of iso- and anteiso-branched fatty acids, with ai-C15:0 as a major component. The G+C content of the genomic DNA is 70–73 mol%. Phylogenetically, the genus is a member of the suborder Micrococccineae, order Actinomycetales. The type species is Georgenia muralis.

Description of Georgenia ruanii sp. nov.

Georgenia ruanii [ru.a’ni.i. N.L. gen. n. ruanii of Ruan, named in honour of Ji-Sheng Ruan (born in 1926), a Chinese microbiologist who devotes himself to the study of actinomycete taxonomy].

Displays the following properties in addition to those described above for the genus. Colonies are 1.1–1.2 mm in diameter, circular, entire, slightly convex, opaque and pale...
The following characteristics apply to both strains: A4a-type peptidoglycan with lysine as the diagnostic cell-wall diamino acid; MK-8(H4) as the predominant menaquinone; the assimilation of fructose, glucose, arabinose, galactose, sucrose, maltose, cellobiose, melibiose and salicin; the hydrolysis of starch and asesculin; the presence of lysine decarboxylase, β-glucosidase, N-acetylglucosaminidase and x-glucosidase activities; and the absence of H2S and indole production, urease, arginine dihydrolase, α-galactosidase and β-glucuronidase. +, Positive; −, negative; w, weakly positive.

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>YIM 004T</th>
<th>G. muralis DSM 14418T</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cell morphology</td>
<td>Short rods</td>
<td>Rod–coccus cycle</td>
</tr>
<tr>
<td>Motility</td>
<td>+</td>
<td>−</td>
</tr>
<tr>
<td>pH tolerance</td>
<td>6.5–10.0</td>
<td>6.0–9.0</td>
</tr>
<tr>
<td>Maximum NaCl concentration for growth (%, w/v)</td>
<td>5</td>
<td>7</td>
</tr>
<tr>
<td>Maximum temperature for growth (°C)</td>
<td>37</td>
<td>45</td>
</tr>
<tr>
<td>Utilization of D-mannose</td>
<td>+</td>
<td>w</td>
</tr>
<tr>
<td>Nitrate reduction</td>
<td>−</td>
<td>+</td>
</tr>
<tr>
<td>β-Galactosidase</td>
<td>+</td>
<td>−</td>
</tr>
<tr>
<td>N-Acetyl-β-glucosaminidase</td>
<td>+</td>
<td>−</td>
</tr>
<tr>
<td>Cystine arylamidase</td>
<td>−</td>
<td>+</td>
</tr>
<tr>
<td>Hydrolysis of Tween 80</td>
<td>DPG, PG, PI, 1 PL</td>
<td>DPG, PG, PIM, 2 PLs, GL</td>
</tr>
<tr>
<td>Polar lipids*</td>
<td>L-Lys→L-Ala→L-Glu</td>
<td>L-Lys→L-Ala→L-Glu</td>
</tr>
<tr>
<td>Peptidoglycan interpeptide bridge</td>
<td>i-C15:0 (78.3 %);</td>
<td>i-C15:0 (66.6 %);</td>
</tr>
<tr>
<td>Major fatty acids (&gt; 5 %)</td>
<td>i-C15:0 (14.9 %)</td>
<td>i-C14:0 (6.0 %)</td>
</tr>
<tr>
<td>DNA G+C content (mol%)</td>
<td>72.9</td>
<td>70.0</td>
</tr>
</tbody>
</table>

*DPG, Diphosphatidylglycerol; GL, unknown glycolipid; PG, phosphatidylglycerol; PI, phosphatidilinositol; PIM, phosphatidilinositol mannoside; PL, unknown phospholipid.

Table 1. Characteristics used to differentiate between strain YIM 004T and its closest phylogenetic neighbour, G. muralis DSM 14418T.

The type strain, YIM 004T (= CCTCC AB 204065T = DSM 17458T = KCTC 19029T), was isolated from soil in Lijiang, Yunnan Province, China.
Acknowledgements

This research was supported by the National Basic Research Program of China (project no. 2004CB719601), the National Natural Science Foundation of China (project no. 30600001) and the Yunnan Provincial Natural Science Foundation (project no. 2004C0002Q). W.-J. Li was also supported by the Program for New Century Excellent Talent in University (NCET).

References


