Risungbinella pyongyangensis gen. nov., sp. nov., a mesophilic member of the family Thermoactinomycetaceae isolated from an agricultural soil sample

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A mesophilic strain, designed MC 210T, was isolated from an agricultural soil sample from Pyongyang, Democratic People’s Republic of Korea, and its taxonomic position was investigated by using a polyphasic approach. The novel strain grew well on PYI medium, and no diffusible pigments were produced. The optimum temperature for growth was 37 °C. The aerial mycelium was well developed, but not fragmented. The strain was Gram-reaction-positive and non-motile and formed endospores on the aerial mycelium. Phylogenetic analysis based on the 16S rRNA gene sequence indicated that strain MC 210T belongs to the family Thermoactinomycetaceae. Strain MC 210T showed 16S rRNA gene sequence similarities of 92.90 and 92.54 % to the type strains of Geothermomicrobium terrae and Shimazuella kribbensis, respectively. The cell wall of strain MC 210T contained meso-diaminopimelic acid, glutamic acid and alanine as the diagnostic amino acids, and whole-cell hydrolysates contained glucose, arabinose and galactose. Strain MC 210T contained anteiso-C15 : 0, iso-C14 : 0, C14 : 0, anteiso-C15 : 0, C16 : 0 and iso-C13 : 0 as the major cellular fatty acids. The main polar lipids were phosphatidylethanolamine, phosphatidylmethylethanolamine, phosphatidylglycerol, diphosphatidylglycerol, two unknown aminophospholipids, an unknown aminolipid, three unknown phospholipids and five unknown polar lipids. The predominant menaquinone was MK-7. The G+C content of the genomic DNA was 42.1 mol%. On the basis of our phylogenetic, physiological and chemotaxonomic data, strain MC 210T is considered to represent a novel genus and species, for which we propose the name Risungbinella pyongyangensis gen. nov., sp. nov., in the family Thermoactinomycetaceae. The type strain of Risungbinella pyongyangensis is MC 210T (CCTCC AA 2013021T = NRRL B-59118T).

Tsilinsky (1899) proposed a new genus Thermoactinomyces with the capacity to grow at high temperatures (50–55°C), which was the first described member of the family Thermoactinomycetaceae (Matsuo et al., 2006). At the time of writing, on the basis of 16S rRNA gene sequence analysis, as well as chemotaxonomic and physiological characterization, the family Thermoactinomycetaceae accommodates 14 genera: Thermoactinomyces (Tsilinsky, 1899), Laceyella, Thermoflavimicrobium, Seinonella (Yoon et al., 2005), Planifilum (Hatayama et al., 2005), Mechercharmeyces (Matsuo et al., 2006), Shimazuella (Park et al., 2007), Desmospora (Yassin et al., 2009), Kroppensteinia (von Jan et al., 2011), Marininema (Li et al., 2012), Melghirimyces (Addou et al., 2012), Lihuaxueella (Yu et al., 2012), Hazenella (Buss et al., 2013), Polycladomyces (Tsubouchi et al., 2013) and Geothermomicrobium (Zhou et al., 2014). All known members of the family Thermoactinomycetaceae are Gram-positive, aerobic and thermophilic, with the exception of three mesophilic species, Seinonella...
Strain MC 210T was isolated from a soil sample collected from an agricultural field in Mangyongdae District (39° 00.18’ N, 125° 38.45’ E), Pyongyang City, Democratic People’s Republic of Korea. Samples taken from the top soil layer were collected and transferred into sterile polypropylene bags. The samples were kept frozen on ice during transport to the laboratory and stored at 4°C until use. Isolation was carried out using the standard dilution plating method on R2A agar (BD) at 37°C. The novel strain was cultured routinely on R2A agar and stored by lyophilization.

For 16S rRNA gene sequencing and phylogenetic analysis, genomic DNA was extracted from a fresh culture of strain MC 210T following the methods of Sambrook et al. (1989). Primers 27f (5′-AGTTTGATCCTGGCTCAG-3′) and 1540r (5′-AAGAGGAGGTATCCAGC-3′) were used for amplification of the 16S rRNA gene (Lane, 1991). PCR and 16S rRNA gene sequencing were carried out as described by Lin et al. (2004). Sequence similarity was investigated using NCBI BLAST and pairwise alignment was calculated using the EzTaxon database (Chun et al., 2007). Phylogenetic analysis was performed by using the software package MEGA version 5.0 (Tamura et al., 2011) after multiple alignment of the data via CLUSTAL_X (Thompson et al., 1997).

Evolutionary distances were calculated using the distance options according to Kimura’s two-parameter model (Kimura, 1980). Clustering using the neighbour-joining (Saitou & Nei, 1987), maximum-parsimony (Fitch, 1971) and maximum-likelihood (Felsenstein, 1981) methods was determined by using bootstrap values based on 1000 replicates (Felsenstein, 1985). Close-neighbour-interchange (search level = 2, random additions = 100) was applied in the maximum-parsimony analysis. Type strains of all species in the family Thermoactinomycetaceae were included in the phylogenetic trees. The root position was estimated by using the sequence of Mycobacterium tuberculosis H37Rv (Kubica et al., 1972) as an outgroup.

The almost-complete 16S rRNA gene sequence of strain MC 210T (1413 bp) was determined in this study. 16S rRNA gene sequence comparisons indicated that strain MC 210T was most closely related to members of the genera Geothermocribium, Lihuaxuella, Laceyella, Shimazuella, Hazenella and Thermoactinomyces, especially Geothermocribium terrae YIM 777562T (92.90 %), Lihuaxuella thermophila YIM 77831T (92.85 %), Laceyella putida KCTC 3666T (92.76 %), Laceyella sacchari KCTC 9790T (92.76 %), Laceyella sediminis RHA1T (92.71 %), Shimazuella kribbensis KCTC 9933T (92.54 %), Hazenella coriacea 23436T (92.19 %) and Thermoactinomyces daquis H-18T (92.12 %). Lower sequence similarities (<92 %) were found with representative members of the other genera shown in Fig. 1. Phylogenetic analysis of the 16S rRNA gene sequence of strain MC 210T revealed that the strain belonged to a separate line within the family Thermoactinomycetaceae that is distinct from all other genera within the family, and formed a relatively well-supported clade (supported by a bootstrap value of 76 %) with S. kribbensis KCTC 9933T in the neighbour-joining tree (Fig. 1). However, the relatively high sequence divergence (>7.1 %) showed that the isolate was distantly related to described taxa. The topologies of the trees generated with the maximum-parsimony and maximum-likelihood algorithms were similar (Figs S1 and S2, available in the online Supplementary Material). Therefore, we selected G. terrae YIM 77562T, with the highest gene sequence similarity (92.9 %), and S. kribbensis KCTC 9933T, forming the most robust clade, as the reference strains for phenotypic characterization and fatty acid analysis.

Cultural characteristics of strain MC 210T were tested on ISP 2, ISP 3, ISP 4 and ISP 5 agar (all prepared as described by Shirling & Gottlieb, 1966), nutrient agar, potato-glucose agar and Czapek’s agar prepared as described by Dong & Cai (2001), tryptic soya agar (TSA), Bennett’s agar (Atlas, 1993), PYI agar (5.0 g proteose peptone, 1.0 g yeast extract, 2.0 g CaCl2, 2.0 g MgCl2, 100 ml distilled water, pH 7.0) and marine agar (MA) at 37°C for 2–5 days. The morphological characteristics of 3-day-old cultures of strain MC 210T grown on PYI agar were observed by light microscopy (BX51; Olympus) and scanning electron microscopy (Zeiss Sigma). The Gram reaction was tested by a modified method of Gerhardt et al. (1994). Growth at 4, 10, 18, 22, 28, 37, 42 and 50°C was tested on PYI agar by incubating cells for 7 days. Through continuous observation, the temperature range and optimum temperature for growth were determined. NaCl tolerance was examined with 0, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12 and 15 % (w/v) NaCl, also on PYI agar as basal medium, at 37°C. The pH range for growth was tested at pH 4, 5, 6, 7, 8 and 9 (using the buffer system described by Xu et al. 2005) at 37°C for 7 days by culturing the strain in PYI broth. Growth under anaerobic conditions (approx. 4–10 % CO2) was determined after incubation in a BBIL GasPak anaerobic jar (Becton Dickinson) on PYI agar supplemented with 0.1 % KNO3. Carbon-source utilization was investigated by the methods described by Shirling & Gottlieb (1966) and Locci (1989). Nitrogen-source utilization was determined according to Williams et al. (1989). Catalase activity was detected by the production of bubbles after the addition of a drop of 3 % (v/v) H2O2. Oxidase activity was determined by the oxidation of tetramethyl p-phenylenediamine (Kovacs, 1956). Tests for hydrolysis of cellulose, gelatin, starch and Tweens 20, 40, 60 and 80, milk coagulation and peptonization, utilization of urea and nitrate reduction were performed as described by Gonzalez et al. (1978). Hydrolysis of casein, hypoxanthine, tyrosine and xanthine was tested using the substrate concentrations described by Cowan & Steel (1965).
To measure the G+C content of the chromosomal DNA, genomic DNA from the novel strain was extracted and purified as described by Moore & Dowhan (1995) and degraded enzymically into nucleosides and the G+C content was then determined as described by Mesbah et al. (1989) using reversed-phase HPLC (UltiMate 3000; Dionex). Cell biomass for the analysis of respiratory quinones was obtained from cultivation in a shaking flask containing PYI broth at 37°C. Respiratory quinones were extracted from lyophilized cells as described by Collins et al. (1977) and were identified by HPLC as described by Xie & Yokota (2003). The isomer type of diaminopimelic acid (DAP) in the peptidoglycan was determined by using the method described by Staneck & Roberts (1974). For cellular fatty acid (CFA) analysis, strain MC 210T and the reference strains were grown in PYI broth at 37°C, and cells grown to late-exponential phase were used in this study. The methods used for harvesting, saponification, methylation and extraction of CFAs were as described in the protocol of the Sherlock Microbial Identification System (MIDI) version 6.0. Separation and identification of fatty acid methyl esters was performed using a Hewlett Packard 6890N gas chromatograph, with MIDI Sherlock database TSBA 6 (Sasser, 1990). For polar lipid analysis, strain MC 210T and the reference strains were grown in PYI broth at 37°C. Polar lipids were extracted and analysed by two-dimensional TLC (silica gel plates, layer thickness 0.2 mm; Merck) according to Tindall (1990). The composition of the amino acids and sugars in the cell-wall peptidoglycan was analysed according to the procedures developed by Hasegawa et al. (1983) and Tang et al. (2009) using cellulose TLC plates.

Fig. 1. Neighbour-joining phylogenetic tree based on 16S rRNA gene sequences (1413 bp) showing the relationship of strain MC 210T to representative members of the family Thermactinomycetaceae. Bootstrap values (expressed as percentages of 1000 replications) above 50% are shown at branch points. The sequence of Mycobacterium tuberculosis H37RvT was used as an outgroup. Bar, 0.02 substitutions per nucleotide position.
Strain MC 210T could grow on R2A agar, MA, PYI agar and TSA, while no growth occurred on ISP 2, ISP 3, ISP 4, ISP 5, Czapek’s agar, Bennett’s agar or potato-glucose agar. Morphological observation of a 3-day-old culture of MC 210T revealed that this new isolate shared the morphological characteristics already described for the family Thermoactinomycesaceae, with white aerial mycelium and pale-yellow substrate mycelium which was well developed. Substrate mycelium was branched, but not fragmented. Spores (1.0–1.2 μm in diameter; Fig. 2a), with the structure and properties of bacterial endospores, formed singly on the aerial mycelium (Fig. 2b) and were non-motile. No diffusible pigments were produced on the media tested.

The temperature range for growth of strain MC 210T was 22–42 °C, with the optimum temperature being 37 °C. The pH range for growth was 6.0–8.0, with optimum growth at pH 7.0. NaCl was not required for growth, but was tolerated up to 8% (w/v), with optimum growth at 0–2% (w/v) NaCl. Activities of oxidase and catalase were positive, and activity of urease was negative. Detailed physiological and biochemical characteristics of the novel isolate are given in Table 1 and in the species description.

The chemotaxonomic properties of strain MC 210T are compared with those of members of other genera of the family Thermoactinomycesaceae in Table 1. The cell-wall peptidoglycan of the strain MC 210T contained meso-DAP as the DAP isomer, which is consistent with other members of the family, except members of the genera Marininema and Melghirimyces, which contain l,l-DAP. In addition, glutamic acid and alanine were found in the cell-wall peptidoglycan, which differentiated the novel strain and the related S. kribbensis KCTC 9933T from members of other genera within the family Thermoactinomycesaceae.

The cell-wall sugars of MC 210T consisted of glucose, arabinose and galactose. The predominant menaquinone in S. kribbensis KCTC 9933T was MK-9, whereas MK-7 was the major respiratory quinone found in strain MC 210T, which was similar to most members of the family Thermoactinomycesaceae (including G. terrae YIM 77562T). On the other hand, the main polar lipid pattern of strain MC 210T (Fig. S3) contained phosphatidylethanolamine, phosphatidyldimethylethanolamine, phosphatidylglycerol, diphosphatidylglycerol, two unknown aminophospholipids, an unknown aminolipid, three unknown phospholipids and five unknown polar lipids, which is a particular feature that distinguishes the strain from G. terrae YIM 77562T, which did not contain an unknown aminolipid, and S. kribbensis KCTC 9933T, from which the three unknown phospholipids were absent (Table 1). The CFA profile of strain MC 210T showed clear differences from those of the reference strains (Table 2). As shown in Table 2, the predominant CFAs of strain MC 210T (>5%) were anteiso-C13 : 0, iso-C14 : 0, C14 : 0, anteiso-C15 : 0, C16 : 0 and iso-C13 : 0. The strain also contained iso-C15 : 0, C18 : 0, C12 : 0 and C13 : 0 as minor fatty acids. Strain MC 210T and the two reference strains were particularly different with respect to their CFA profiles, as strain MC 210T contained significantly larger proportions of the major fatty acids C14 : 0, iso-C13 : 0 and anteiso-C13 : 0 and a smaller proportion of iso-C15 : 0, which indicated that the novel isolate has a CFA profile that is clearly distinct from those of the closely related strains G. terrae YIM 77562T and S. kribbensis KCTC 9933T. The DNA G+C content of strain MC 210T was 42.1 mol%.

Phenotypic and molecular studies indicate that strain MC 210T can be distinguished clearly from members of other genera of the family Thermoactinomycesaceae. Examination of the growth temperature, NaCl tolerance, melanin
Table 1. Characteristics that differentiate strain MC 210\textsuperscript{T} from related members of the family *Thermoactinomycetaceae*

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>1</th>
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<th>7</th>
<th>8</th>
<th>9</th>
<th>10</th>
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</thead>
<tbody>
<tr>
<td>Colour of aerial mycelium</td>
<td>White</td>
<td>White\textsuperscript{a}</td>
<td>ND\textsuperscript{b}</td>
<td>ND\textsuperscript{c}</td>
<td>White</td>
<td>White</td>
<td>White</td>
<td>White</td>
<td>ND</td>
<td>Yellow–white</td>
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<tr>
<td>Melanin production</td>
<td>+</td>
<td>−</td>
<td>+</td>
<td>ND</td>
<td>White</td>
<td>White</td>
<td>White</td>
<td>White</td>
<td>+</td>
<td>−</td>
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<tr>
<td>Growth on 25 mg novobiocin ml\textsuperscript{−1}</td>
<td>+</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>−</td>
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<tr>
<td>Temperature for growth (°C)</td>
<td>22–42</td>
<td>20–37\textsuperscript{a}</td>
<td>30–60\textsuperscript{b}</td>
<td>28–65\textsuperscript{c}</td>
<td>30–65</td>
<td>35–65</td>
<td>28–65</td>
<td>28–70</td>
<td>22–45</td>
<td>45–60</td>
</tr>
<tr>
<td>Tolerance of 8 % (w/v) NaCl</td>
<td>+</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
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<td>Degradation of:</td>
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<tr>
<td>Starch</td>
<td>+</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>−</td>
<td>−</td>
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<tr>
<td>Casein</td>
<td>+</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
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<tr>
<td>Hypoxanthine</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>+</td>
<td>−</td>
<td>−</td>
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<tr>
<td>Gelatin liquefaction</td>
<td>+</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
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<td>+</td>
</tr>
<tr>
<td>Polar lipids\textsuperscript{†}</td>
<td>PE, PME, PG, DPG, 2APL, AL, 3PL, SL</td>
<td>PE, PME, PG, DPG, 4AL, 2L</td>
<td>PE, PME PG, DPG, APL, PL, 3L</td>
<td>PE, PME, PG, DPG, APL, 3PL</td>
<td>DPG, PE, DPG, APL, PI, PL</td>
<td>DPG, PE, DPG, PME, PI, PL</td>
<td>DPG, PE, DPG, PME, PI, PL</td>
<td>DPG, PE, DPG, PME, PI, PL</td>
<td>DPG, PE, DPG, PME, PI, PL</td>
<td>DPG, PE, DPG, PME, PI, PL</td>
</tr>
<tr>
<td>Cell-wall peptidoglycan</td>
<td>meso-DAP, Glu, Ala</td>
<td>meso-DAP, Glu, Ala</td>
<td>meso-DAP</td>
<td>meso-DAP\textsuperscript{†}</td>
<td>meso-DAP</td>
<td>meso-DAP</td>
<td>meso-DAP</td>
<td>meso-DAP</td>
<td>meso-DAP</td>
<td>meso-DAP</td>
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<tr>
<td>Cell-wall sugars\textsuperscript{‡}</td>
<td>Glc, Ara, Gal</td>
<td>No characteristic sugars\textsuperscript{d}</td>
<td>Glc, Gal, Man, Rib, Rha\textsuperscript{b}</td>
<td>Glc, Gal, Man, Rib, Rha\textsuperscript{b}</td>
<td>Xyl, Ara, Glc</td>
<td>Xyl, Ara, Glc</td>
<td>Rib, Glc</td>
<td>Rib, Xyl, Glc</td>
<td>NA</td>
<td>NA</td>
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<tr>
<td>Predominant menaquinone (&gt;10 % peak-area ratio)</td>
<td>MK-7</td>
<td>MK-9</td>
<td>MK-7</td>
<td>MK-7</td>
<td>MK-7</td>
<td>MK-8</td>
<td>MK-9</td>
<td>MK-8</td>
<td>MK-7</td>
<td>MK-8</td>
</tr>
<tr>
<td>Other menaquinones</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
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<td>−</td>
</tr>
<tr>
<td>DNA G + C content (mol%)</td>
<td>42.1</td>
<td>39.4\textsuperscript{a}</td>
<td>45.6\textsuperscript{b}</td>
<td>55.6\textsuperscript{c}</td>
<td>49.0</td>
<td>48.0</td>
<td>47.9</td>
<td>48.6</td>
<td>37.8</td>
<td>47.0</td>
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</table>

\*Data taken from: a, Park et al. (2007); b, Zhou et al. (2014); c, Yu et al. (2012).

\†DPG, Diphosphatidylglycerol; PE, phosphatidylethanolamine; PG, phosphatidylycerol; PI, phosphatidylinositol; PIM, phosphatidylinositol mannosides; PME, phosphatidylmethylethanolamine; AL, unknown aminolipid; APL, unknown aminophospholipid; PL, unknown phospholipid; L, unknown polar lipid;

\‡Ara, Arabinose; Gal, galactose; Glc, glucose; Man, mannose; Rha, rhamnose; Rib, ribose; Xyl, xylose.
production, DNA G+C content, menaquinone composition, polar lipid pattern and CFA profile revealed that strain MC 210T did not belong to any previously reported genus of the family Thermoactinomycetaceae. On the basis of the results presented in this study, strain MC 210T represents a novel genus and species in the family Thermoactinomycetaceae, for which the name Risungbinella pyongyangensis gen. nov., sp. nov. is proposed.

**Description of Risungbinella gen. nov.**

Risungbinella (Ri.sung.bin.el’la. N.L. fem. dim. n. Risungbinella named after Professor SungBin Ri, a microbiologist from Kim Il Sung University, Democratic People’s Republic of Korea).

Aerial mycelium is white and substrate mycelium is white to pale yellow and is not fragmented. Endospores are formed singly on flexuous branches of the aerial mycelium. Soluble pigments are not produced. The cell-wall peptidoglycan contains meso-DAP, glutamic acid and alanine, and the cell-wall hydrolysate contains glucose, arabinose and galactose. The major polar lipids are phosphatidylethanolamine, phosphatidylmethylethanolamine, phosphatidylglycerol, diphosphatidylglycerol, two unknown aminophospholipids, an unknown aminolipid, three unknown phospholipids and five unknown polar lipids. The only menaquinone detected is MK-7. Major fatty acids (>5%) are anteiso-C13:0, iso-C14:0, C14:0, anteiso-C15:0, C16:0 and iso-C13:0. The DNA G+C content of the type strain of the type species is 42.1 mol%. The type species is Risungbinella pyongyangensis.

### Table 2. CFA contents of strain MC 210T and the type strains of phylogenetically related species

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<th>Fatty acid</th>
<th>1</th>
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<td>Straight-chain</td>
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<tr>
<td>C12:0</td>
<td>2.47</td>
<td>-</td>
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<tr>
<td>C13:0</td>
<td>2.40</td>
<td>-</td>
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<tr>
<td>C14:0</td>
<td>13.87</td>
<td>4.36</td>
<td>2.56</td>
<td>1.73</td>
<td>2.6</td>
<td>2.8</td>
<td>2.24</td>
<td>1.16</td>
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<tr>
<td>C15:0</td>
<td>11.82</td>
<td>19.49</td>
<td>2.73</td>
<td>6.84</td>
<td>7.2</td>
<td>3.8</td>
<td>2.62</td>
<td>1.61</td>
<td>-</td>
<td>3.22</td>
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<tr>
<td>C17:0</td>
<td>1.62</td>
<td>-</td>
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<tr>
<td>C18:0</td>
<td>3.50</td>
<td>10.08</td>
<td>1.09</td>
<td>2.86</td>
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*Summed features are groups of two or three fatty acids that could not be separated by GLC with the MIDI System. Summed feature 2 contains C14:0 3-OH and/or iso-C16:1; summed feature 3 contains C16:1ω7c and/or C16:1ω6c; summed feature 5 contains anteiso-C18:0 and/or C18:2ω6,9c; summed feature 8 contained C18:1ω7c and/or C18:1ω6c.
Description of *Risungbinella pyongyangensis* sp. nov.

*Risungbinella pyongyangensis* (pyong.yang.en’sis. N.L. fem. adj. *pyongyangensis* pertaining to Pyongyang City, from where the type strain was isolated).

Displays the following properties in addition to those described for the genus. Cells are Gram-reaction-positive, aerobic and mesophilic. Grows well on PYI agar and slightly on R2A agar, MA and TSA. After 3 days of incubation at 37°C on PYI agar, colonies are white, dried and wrinkled. Growth occurs at 22–42°C, pH 6.0–8.0 and 0–8% (w/v) NaCl. The optimal temperature, pH and NaCl concentration for growth are 37°C, pH 7.0 and 0–2% (w/v) NaCl. Positive for oxidase, catalase, gelatin liquefaction, reduction of nitrate and hydrolysis of casein, starch, L-tyrosine and Tweens 20, 40, 60 and 80. Negative for urease, milk coagulation, milk peptonization and hydrolysis of cellulose, hypoxanthine and xanthine. Growth occurs in the presence of 25 mg novobiocin ml⁻¹. Mannose, xylose, inositol, maltose, rhamnose, galactose, glucose, cellobiose and mannitol can be utilized as sole carbon sources, but lactose, raffinose, ribose, fructose and arabinose are not utilized. L-Asparagine, L-ornithine, L-phenylalanine, L-cysteine, L-tryptophan, L-threonine, L-tyrosine and L-methionine are utilized as sole nitrogen sources, but not L-histidine, L-arginine, L-lysine, L-glutamic, L-serine, L-proline, L-alanine, L-valine or L-cystine.

The type strain, MC 210^T (=CCTCC AA 2013021^T =NRRL B-59118^T), was isolated from an agricultural soil sample collected from Pyongyang City, Democratic People’s Republic of Korea.

Acknowledgements

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References


