**Mongoliicoccus roseus** gen. nov., sp. nov., an alkaliphilic bacterium isolated from a haloalkaline lake

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Two pink, non-motile, aerobic, alkaliphilic, halotolerant, Gram-negative cocci, designated MIM28T and MIM29, were isolated from the surface water of a haloalkaline lake on the Mongolia Plateau. The isolates grew optimally at 30–33 °C, at pH 8–9 and with 3–4 % (w/v) NaCl. The isolates were chemoheterotrophic and could assimilate carbohydrates, organic acids and amino acids. The major respiratory quinone was menaquinone MK-7. The major polar lipids were phosphatidylcholine and phosphatidylethanolamine. The predominant cellular fatty acids were iso-C15 : 0 (13.8–17.5 %), anteiso-C15 : 0 (10.5–11.2 %), iso-C16 : 0 (4.3–4.6 %), iso-C17 : 0 (3.8–5.3 %), anteiso-C17 : 0 (3.7–7.1 %), C16 : 0 (4.6–6.6 %), iso-C17 : 0 3-OH (4.6–5.8 %), summed feature 3 (C16 : 1ω7c and/or C16 : 1ω6c; 4.0–6.4 %) and summed feature 9 (iso-C17 : 1ω9c and/or C16 : 0 10-methyl; 10.4–12.5 %). Phylogenetic analysis based on 16S rRNA gene sequences showed that the isolates were most closely related to *Litoribacter ruber* YIM CH208T (93.6 % 16S rRNA gene sequence similarity), the genus *Echinicola* (90.4–92 %) and other members of the family *Cyclobacteriaceae* (87.8–90 %). The DNA G+C contents of strains MIM28T and MIM29 were 62.8 and 62.2 mol%. On the basis of morphology, physiology, fatty acid composition, phylogeny and 16S rRNA gene sequence analysis, the isolates are assigned to a novel species of a new genus, for which we propose the name *Mongoliicoccus roseus* gen. nov., sp. nov.; the type strain of the type species is MIM28T (=ACCC 05511T =KCTC 19808T).

In marine and freshwater environments, bacteria of the phylum *Bacteroidetes* play an important role as major degraders of organic compounds such as chitin, cellulose and agar (Cottrell & Kirchman, 2000; Höfle, 1992; Nedashkovskaya et al., 2003). Because of these particular abilities, they can occur with a high abundance in aquatic environments. The phylum *Bacteroidetes* comprises four classes, *Bacteroidia*, *Flavobacteriia*, *Sphingobacteriia* and *Cytophagia*, according to Bergey’s Manual of Systematic Bacteriology (Ludwig et al., 2010). Although members of the family *Cyclobacteriaceae*, class *Cytophagia*, have been found in a wide variety of habitats (Anil Kumar et al., 2010b), many novel genera and species of this family have been isolated from haloalkaline environments, for example *Indibacter alkaliphilus* (Anil Kumar et al., 2010a), *Nitritalea halalkaliphila* (Anil Kumar et al., 2010b), *Litoribacter ruber* (Tian et al., 2010) and *Echinicola jeungdonensis* (Kim et al., 2011), and *Fontibacter flavus* was isolated from a hot spring (Kämpfer et al., 2010).

Saline and alkaline lakes are highly productive and a valuable source of novel micro-organisms (Jones et al., 1998). Soda lakes also show evidence of active decomposition processes (Grant et al., 1990). Most isolates from these environments produce important biochemical enzymes at alkaline pH (Joshi et al., 2008). An analysis of bacterial diversity in Baer soda lake on the Mongolia Plateau revealed that nearly 37 % of clones represented new taxa (Ma et al., 2004). The Mongolia Plateau has thousands of saline and alkaline lakes. However, few bacterial strains...
have been isolated and investigated. To date, the described members of the family *Cyclobacteriaceae* are rods or horseshoe-shaped. This study describes two coccoid isolates of the family *Cyclobacteriaceae*.

Two strains, designated MIM28T and MIM29, were isolated from Lake Horsememo, a soda lake located in Hunsandake Desert, China on the Mongolia Plateau (42° 58' N 115° 23' E; pH 9.0; 4%, w/v, salinity) in August 2009. The isolates were obtained using standard dilution-plating methods on marine agar 2216 (MA; Difco) with medium adjusted to pH 9. The isolates were maintained on MA with incubation at 30 °C for 48 h and preserved at −80 °C in marine broth 2216 (MB; Difco) supplemented with 20% glycerol. For reference, *L. ruber* YIM CH208T (Tian et al., 2010) was used for comparative testing under the same conditions.

Cell size and morphology was observed by electron microscopy. Gram-staining was tested by the standard procedure according to Gerhardt *et al.* (1994) using cells grown for 48 h at 30 °C on MA. Motility was examined by the hanging-drop method (Bowman, 2000). Anaerobic growth in MB was tested using an anaerobic environment system (Bactron III-2), according to the manufacturer's instructions. Conditions for growth were tested in trypticase soy broth (Guangdong Huankai Microbial Sci. & Tech.) at pH 4–11 (at intervals of 0.5 pH units), with 0–10% (w/v) NaCl (at intervals of 0.5% NaCl) and at 0–45 °C (at intervals of 1 °C). For pH tests, appropriate biological buffers (pH 4–6, acetate buffer; pH 7–11, Tris/HCl buffer) were used to adjust the pH of the medium prior to sterilization. Growth was determined by measuring optical density at 540 nm. Acid production, carbon utilization and enzymic activities were determined using the API 50 CH, API 20 NE and API ZYM systems (bioMérieux), according to the manufacturer's instructions. Additional carbon utilization tests were done using the GN2 MicroPlate system (Biolog). Antibiotic sensitivity was determined by the disc-diffusion method (Bauer *et al.*, 1966). H2S production was detected in modified MB medium supplemented with 0.01% (w/v) L-cysteine.

Cell biomass for quantitative fatty acid analysis was obtained by scraping cells incubated on trypticase soy agar (Guangdong Huankai Microbial Sci. & Tech.) at 30 °C after 48 h for strains MIM28T and MIM29 and after 6 days for *L. ruber* YIM CH208T, which grew very slowly. Fatty acid esters were prepared and analysed according to the protocol of Sasser (1990) using the Sherlock Microbial Identification System version 6.1 (MIDI) and the standard MIS library TSBA version 6.0. Menaquinones were extracted according to the method of Collins *et al.* (1977) and analysed by HPLC (Groth *et al.*, 1997). Polar lipids were separated by two-dimensional TLC with standard markers as controls (Komagata & Suzuki, 1987) and further identified by spraying with appropriate detection reagents (Collins & Jones, 1980).

Genomic DNA was extracted from cultures as described by Wisotzkey *et al.* (1990). The G+C content of the genomic DNA was determined from melting point (Tm) curves (Sly *et al.*, 1986) using genomic DNA from *Escherichia coli* K-12 as the reference. Amplification and sequencing of the 16S rRNA gene was carried out according to the method of Du *et al.* (2006). To identify the nearest taxa, a BLAST search of public databases was first carried out and closely related sequences were retrieved for further phylogenetic analysis (Altschul *et al.*, 1990). The sequence alignment was created using CLUSTAL X version 2.0 with the default penalties and modified manually. Sequence similarity was calculated using the subprogram DNADIST within PHYLIP version 3.6 (Felsenstein, 1989). Maximum-likelihood phylogenetic analysis was performed using PHYLIP (Felsenstein, 1989). Neighbour-joining analysis was performed using MEGA4 (Kumar *et al.*, 2008) based on Kimura's two-parameter rule (Kimura, 1980). The topology of trees was evaluated by bootstrap analysis based on 1000 resamplings.

To determine whether strains MIM28T and MIM29 belonged to the same species, DNA–DNA hybridization was done as described by Huß *et al.* (1983). 16S rRNA gene sequence similarities between the isolates and members of family *Cyclobacteriaceae* were <93% and thus below the cut-off value of 97% proposed by Tindall *et al.* (2010) for the separation of species; therefore, further DNA–DNA hybridization was not done.

The isolates were Gram-negative, aerobic, non-motile cocci (0.7–1.2 μm in diameter) (Fig. S1, available in IJSEM Online). The coccus shape distinguished the isolates from the rod-shaped members of the family *Cyclobacteriaceae* (Anil Kumar *et al.*, 2010b), including members of the genera *Litoribacter* (Tian *et al.*, 2010) and *Echinicola* (Kim *et al.*, 2011; Nedashkovskaya *et al.*, 2006, 2007). Colonies on MA at 30 °C were circular, smooth, shiny, pink, opaque and convex with entire margins. Strains MIM28T and MIM29 grew at 4–42 °C (optima of 33 and 30 °C, respectively) and with 0–10% NaCl (optima of 3 and 4%, respectively) (Table 1). The isolates were sensitive to 24 antibiotics and resistant to five, as detailed in the species description. The isolates could be differentiated from members of the genus *Litoribacter* by temperature range for growth (4–42 versus 20–37 °C) and from members of the genus *Echinicola* by NaCl concentration range for growth (0–10 versus 0–15% NaCl). Strains MIM28T and MIM29 grew at pH 6–10 (optima of pH 9 and 8, respectively). Anaerobic growth could not be observed. The major respiratory quinone was a menaquinone with seven isoprene units (MK-7). The major polar lipids comprised phosphatidylcholine and phosphatidylethanolamine, which differentiated the isolates from *L. ruber* YIM CH208T (Fig. S2). The DNA G+C content of strains MIM28T and MIM29 was 62.8 and 62.2 mol%, respectively, which is considerably higher than the range observed for members of the family *Cyclobacteriaceae* (33.7–49 mol%) but similar to that observed for *Salinibacter ruber* (66.3–66.7%) (Antón *et al.*, 2002). DNA–DNA relatedness between the isolates was 80.1%, which is higher than the 70% threshold recommended by Wayne *et al.* (1987) for assigning strains to the same species.
Table 1. Characteristics that differentiate strain MIM28<sup>T</sup> from members of the family Cyclobacteriaceae

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
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<th>6</th>
<th>7</th>
<th>8</th>
<th>9</th>
<th>10</th>
<th>11</th>
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<td>C</td>
<td>R</td>
<td>R</td>
<td>R</td>
<td>R</td>
<td>R</td>
<td>CB</td>
<td>RH</td>
<td>R</td>
<td>CBB</td>
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<td>Cell dimensions (μm)</td>
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<tr>
<td>Length</td>
<td>0.7–1.2</td>
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<td>0.8–2.3</td>
<td>0.9–5.0</td>
<td>2.0–3.0</td>
<td>2.0–3.0</td>
<td>1.1–4.8</td>
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<td>3–8</td>
<td>1.0–3.0</td>
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<tr>
<td>Width</td>
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<td>0.4–0.8</td>
<td>0.3–0.5</td>
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<td>0.3</td>
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<td>Colony colour&lt;sup&gt;b&lt;/sup&gt;</td>
<td>P</td>
<td>R</td>
<td>PR/Y/YO</td>
<td>Y/O/R R/O</td>
<td>R/P</td>
<td>R/P</td>
<td>R/P</td>
<td>R/P</td>
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<td>P</td>
<td>P</td>
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<tr>
<td>DNA G+C content (mol%)</td>
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<td>45.1</td>
<td>44–46.9</td>
<td>35.3–41</td>
<td>49</td>
<td>42.7±1</td>
<td>38.4</td>
<td>35–43</td>
<td>33.7–45.2</td>
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<td>NaCl for growth (%)</td>
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<td>0–9</td>
<td>0–15</td>
<td>0–6</td>
<td>1–22</td>
<td>0–8</td>
<td>0–6</td>
<td>0–5.9</td>
<td>0–15</td>
<td>0–5.5</td>
<td>5–20</td>
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<td>2</td>
<td>0–3.4</td>
<td>2–5</td>
<td>0–6</td>
<td>1–2</td>
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<td>1–5</td>
<td>1</td>
<td>10–15</td>
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<td>Growth temperature (°C)</td>
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<td>20–37</td>
<td>6–44</td>
<td>4–40</td>
<td>25–40</td>
<td>15–40</td>
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<td>2 to 37</td>
<td>4–42</td>
<td>0–40</td>
<td>25–45</td>
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<td>33</td>
<td>28</td>
<td>20–32</td>
<td>37/25</td>
<td>37</td>
<td>30–37</td>
<td>30–35</td>
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<td>6–9</td>
<td>6–10</td>
<td>7.5–12</td>
<td>7.5–12</td>
<td>7–9</td>
<td>5.5–10.5</td>
<td>6–9</td>
<td>6.5–12</td>
<td>6.0–9.0</td>
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<tr>
<td>Optimum</td>
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<td>8.5</td>
<td>7</td>
<td>8.0/7.0</td>
<td>10</td>
<td>10</td>
<td>7</td>
<td>7.5</td>
<td>7.5–8</td>
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<td>7.5–8.0</td>
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<tr>
<td>D-Xylose</td>
<td>W</td>
<td>+</td>
<td>V</td>
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<td>V</td>
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<td>ND</td>
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<td>Galactose</td>
<td>+</td>
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<td>–</td>
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<td>+</td>
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<tr>
<td>D-Fructose</td>
<td>+</td>
<td>–</td>
<td>V</td>
<td>V</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>V</td>
<td>+</td>
<td>W</td>
<td>ND</td>
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<tr>
<td>Arbutin</td>
<td>+</td>
<td>–</td>
<td>ND</td>
<td>V</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
<td>+</td>
<td>–</td>
<td>W</td>
<td>ND</td>
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<tr>
<td>API 20 NE</td>
<td>Urea</td>
<td>+</td>
<td>–</td>
<td>V</td>
<td>V</td>
<td>V</td>
<td>V</td>
<td>V</td>
<td>ND</td>
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<tr>
<td>Protease (gelatin)</td>
<td>+</td>
<td>–</td>
<td>–</td>
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<td>ND</td>
<td>+</td>
<td>ND</td>
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<tr>
<td>API ZYM</td>
<td>Esterase (C4)</td>
<td>W</td>
<td>+</td>
<td>V</td>
<td>V</td>
<td>V</td>
<td>V</td>
<td>ND</td>
<td>ND</td>
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<td>W</td>
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<tr>
<td>Lipase (C14)</td>
<td>–</td>
<td>+</td>
<td>–</td>
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<td>V</td>
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<td>β-Galactosidase</td>
<td>+</td>
<td>–</td>
<td>+</td>
<td>+</td>
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<tr>
<td>α-Mannosidase</td>
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<td>V</td>
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<td>Utilization of:</td>
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<td>Tween 40</td>
<td>–</td>
<td>+</td>
<td>–</td>
<td>V</td>
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<td>V</td>
<td>V</td>
<td>ND</td>
<td>–</td>
<td>+</td>
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<tr>
<td>Tween 80</td>
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<td>–</td>
<td>V</td>
<td>V</td>
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<td>–</td>
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<td>–</td>
<td>V</td>
<td>–</td>
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<tr>
<td>myo-Inositol</td>
<td>+</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
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<td>–</td>
<td>–</td>
<td>–</td>
<td>V</td>
<td>–</td>
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<tr>
<td>Maltose</td>
<td>+</td>
<td>+</td>
<td>V</td>
<td>V</td>
<td>–</td>
<td>+</td>
<td>W</td>
<td>V</td>
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<tr>
<td>Mannitol</td>
<td>W</td>
<td>+</td>
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<td>–</td>
<td>V</td>
<td>+</td>
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</tbody>
</table>

<sup>a</sup>C, Coccus; CB, coccobacillus (short filaments with rounded ends or rods); CR, slightly curved rod; R, rod; RH, ring-like or horseshoe-shaped.

<sup>b</sup>LP, Light pink; O, orange; P, pink; R, red; YO, yellow-orange.

Table S1 shows the results of the API and Biolog GN2 tests. Strain MIM28<sup>T</sup> used 58 substrates and strain MIM29 used 63 substrates, with 54 substrates used by both isolates (considering a weakly positive response as positive). The isolates produced acid from 21 substrates in total, 19 by strain MIM28<sup>T</sup> and 20 by strain MIM29, with 18 substrates common to both. With API 20 NE, 10 positive reactions were observed with both isolates. With API ZYM tests, strain MIM28<sup>T</sup> was positive for 16 enzymes and strains MIM29 was positive for 15 enzymes. Overall, with carbon source utilization, substrate for acid production and enzyme activity, the isolates could be differentiated from members of the Cyclobacteriaceae such as YIM CH208<sup>T</sup> and members of the genus Echinicola (Table 1).
There were differences in fatty acid composition between the isolates and *L. ruber* YIM CH208T and members of the genus *Echinicola*, particularly in chain length and some of the major fatty acids (Table 2). The fatty acid compositions of the two isolates were similar and were dominated by iso-C₁₅ : ₀, anteiso-C₁₅ : ₀, iso-C₁₆ : ₀ and iso-C₁₇ : ₀ 3-ОH (>5%), but some small differences existed (Table S2). In strain MIM28ᵀ the proportion of the major fatty acid iso-C₁₅ : ₀ was lower (13.8%) than in *L. ruber* YIM CH208T (32.8%) and members of the genus *Echinicola* (17.3–31.4%) and the proportion of iso-C₁₆ : ₀ was much higher (13.0%) than in *L. ruber* YIM CH208T (1.7%) and the genus *Echinicola* (<1.3%).

Almost-complete 16S rRNA gene sequences were obtained from strain MIM28ᵀ (1403 bp) and strain MIM29 (1485 bp). Sequence similarity between the isolates was high (99.8% 16S rRNA gene sequence similarity). The search of public databases found that the isolates’ 16S rRNA gene sequences were most similar to those of *Rhodonellum psychrophilum* 4-5-25 (GU112990; 96.0%), *L. ruber* YIM CH208ᵀ (94.0%) and *Echinicola jeungdonensis* HMD3054ᵀ (92.0%). The lowest 16S rRNA gene sequence similarity between the isolates and other members of the *Cyclobacteriaceae* was observed with *Fontibacter flavus* CC-GZM-130ᵀ (87.8% similarity). Phylogenetic analysis based on maximum-likelihood and neighbour-joining showed that the two

### Table 2. Cellular fatty acid compositions of strain MIM28ᵀ and members of the family *Cyclobacteriaceae*

<table>
<thead>
<tr>
<th>Fatty acid (%)</th>
<th>1</th>
<th>2*</th>
<th>3</th>
<th>4</th>
<th>5</th>
<th>6</th>
<th>7</th>
<th>8</th>
<th>9†</th>
<th>10</th>
<th>11</th>
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<tbody>
<tr>
<td>C₁₄ : ₀</td>
<td>0.2</td>
<td>0.3 (tr)</td>
<td>ND</td>
<td>1.0</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
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<td>4.1</td>
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<tr>
<td>C₁₅ : ₀</td>
<td>ND</td>
<td>ND</td>
<td>0.8–23.5</td>
<td>0.5–3.8</td>
<td>56.8</td>
<td>ND</td>
<td>ND</td>
<td>ND</td>
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</tr>
<tr>
<td>iso-C₁₅ : ₁ G</td>
<td>ND</td>
<td>1.6 (3.0)</td>
<td>ND</td>
<td>1.9–10.1</td>
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<td>ND</td>
<td>tr</td>
<td>9.4</td>
<td>1.9</td>
<td>ND</td>
<td>3.2</td>
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<tr>
<td>iso-C₁₆ : ₀</td>
<td>13.8</td>
<td>32.8 (ND)</td>
<td>17.3–31.4</td>
<td>18.9–31.2</td>
<td>ND</td>
<td>47.9</td>
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</table>

*Values in parentheses were taken from Tian et al. (2010).
†Values in parentheses were taken from Raj & Maloy (1990), Nedashkovskaya et al. (2005) and Ying et al. (2006).
‡Summed features represent two or three fatty acids that cannot be separated by the Microbial Identification System. Summed feature 3 consisted of C₁₆ : ₁ 107c and/or C₁₆ : ₁ 106c. Summed feature 4 consisted of anteiso-C₁₇ : ₁ B and/or iso-C₁₇ : ₁ I. Summed feature 9 consisted of iso-C₁₇ : ₁ 109c and/or C₁₆ : ₀ 10-methyl.
§Summed feature contains C₁₆ : ₁ 107c and/or iso-C₁₅ : ₀ 2-ОH; 34.5%.

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isolates formed a robust lineage with bootstrap support of 100 % (Fig. 1) within a cluster also comprising L. ruber YIM CH208T and the genus Echinicola (bootstrap support values of 88 and 85 % in maximum-likelihood and neighbour-joining trees, respectively). On the basis of phenotypic, chemotaxonomic and phylogenetic analysis, strains MIM28T and MIM29 represent a novel species in a new genus, for which the name Mongoliicoccus roseus gen. nov., sp. nov. is proposed.

**Description of Mongoliicoccus gen. nov.**

Mongoliicoccus [Mon.go.li.ic.occ.’us. N.L. n. Mongolia Mongolia; N.L. masc. n. coccus (from Gr. masc. n. kokkos grain) coccus; N.L. masc. n. Mongoliicoccus a coccus from Mongolia, referring to the isolation of the type strain from the Mongolia Plateau].

Cells are Gram-negative cocci. Positive for catalase and oxidase. Aerobic and chemoheterotrophic. The predominant fatty acids are iso-C₁₅ : ₀, anteiso-C₁₅ : ₀, iso-C₁₆ : ₀, C₁₆ : ₀, iso-C₁₇ : ₀ 3-0H, summed feature 3 (C₁₆ : ₁₅₀7c and/or C₁₆ : ₁₀₆c) and summed feature 9 (iso-C₁₇ : ₁₆₀9c and/or C₁₆ : ₀ 10-methyl). The major respiratory quinone is MK-7. The major polar lipids are phosphatidylcholine and phosphatidylethanolamine. Halotolerant and alkaliphilic, but NaCl is not needed for growth. The genus Mongoliicoccus belongs to the family Cyclobacteriaceae, order Sphingobacteriales, class Sphingobacteriia, phylum Bacteroidetes. The type species is Mongoliicoccus roseus.

**Description of Mongoliicoccus roseus sp. nov.**

Mongoliicoccus roseus (ro.se.us. L. masc. adj. roseus rose-coloured).

The species description is based on properties of two strains. The main characteristics are those given for the genus. In addition, cells are 0.7–1.2 μm in diameter. Colonies on MA after >3 days at 30 °C are pink, circular, smooth and convex. Grows at 4–42 °C (optimum 30–33 °C), at pH 6–10 (optimum 8–9) and with 0–10 % (w/v) NaCl (optimum growth at 5 % NaCl).
3–4 %). Degrades starch and ascorbic acid. Does not hydrolyse TWEENs 20, 40 or 80. Nitrate is reduced to nitrite. H2S is not produced from L-cysteine. Acid is produced from D-xylene, galactose, D-glucose, D-fructose, D-mannose, amylodextrin, arbutin, aesculin, salicin, cellobiose, maltose, lactose, succrose, inulin, raffinose, starch, β-gentiobiose, turanose and 2-ketogluconate. Grows in Z-glucosidase, D-glucose, D-fructose, D-mannose, adonitol, L-arabinose, cellobiose, i-erythritol, D-galactose, gentiobiose, α-D-glucose, myo-inositol, L-αctulose, lactulose, maltose, D-mannitol, D-mannose, D-melibiose, D-psicose, raffinose, D-rhamnose, D-sorbitol, sucrose, trehalose, turanose, pyruvic acid methyl ester, acetic acid, citric acid, D-galacturonic acid, D-glucuronic acid, D-glucosaminic acid, D-glucuronic acid, α-ketoglutaric acid, DL-lactic acid, quinic acid, D-alanine, L-alanylglycine, L-asparagine, L-aspartic acid, L-glutamic acid, L-histidine, L-leucine, L-ornithine, L-propyrolactamic acid, D-serine, L-serine, DL-carnitine, inosine, uridine, thymidine, 2,3-butanediol, DL-α-ketoglutaric acid, DL-lactic acid, quinic acid, α-ketovaleric acid, malonic acid, D-saccharic acid, α-D-glucose, D-glucosaminidase and α-myosomalidase. Sensitive to vancomycin (30 μg/disc unless otherwise indicated) vancomycin (30), norfloxacin (10), amikacin (30), kanamycin (30), cefalexin (30), piperacillin (100), minocycline (30), vibramycin (30), cefoperazone (75), polymyxin B (300 U), ofloxacin (5), midecamycin (10 U), clindamycin (2), chloromycetin (30), furazolidone (30), tetracycline (30), ampicillin (10), ciprofloxacin (5), penicillin (30), erythromycin (15), novobiocin (5), te-tracycline (30), ampicillin (10), ciprofloxacin (5), penicillin (10 U), clindamycin (2), chloromycetin (30), furazolidone (300), polymyxin B (300 U), oxofloxacin (5), midecamycin (30), minocycline (30), vibramycin (30), cefoperazone (75), rocephin (30), cefuroxime (30), cephadrine (30), cefazolin (30), cefalexin (30), Piperacillin (100) and carbenicillin (100), but resistant to amikacin (30), kanamycin (30), gentamicin (10), fortum (30) and oxacillin (1).

The type strain is MIM28T (=ACC C 05511T =KCTC 19808T), isolated from an alkaline saline lake on the Mongolia Plateau. The DNA G+C content of the type strain is 62.8 mol% (Tm). Strain MIM29 (=ACC C 05592 =KCTC 23452) is also a strain of this species.

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References


