Altererythrobacter troitsensis sp. nov., isolated from the sea urchin Strongylocentrotus intermedius

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An aerobic, halotolerant, Gram-negative bacterium was isolated from the sea urchin Strongylocentrotus intermedius and subjected to taxonomic characterization. The strain, designated KMM 6042T, was rod-shaped, motile and yellow-pigmented. Phylogenetic analysis indicated that the strain was most closely related to the type strain of Altererythrobacter dongtanensis, and the level of 16S rRNA gene sequence similarity between the two was 99.0%. However, the DNA–DNA relatedness between the two strains was 34.4 ± 7.6%. Physiological and chemotaxonomic properties clearly distinguished the novel strain from other species of the genus Altererythrobacter. It is thus evident from the phylogenetic and phenotypic analyses that strain KMM 6042T merits recognition as a novel species of the genus Altererythrobacter, for which the name Altererythrobacter troitsensis sp. nov. (type strain, KMM 6042T = KCTC 12303T = JCM 17037T) is proposed.

The genus Altererythrobacter Kwon et al. (2007) accommodates bacteria inhabiting various habitats including marine sediment (Kwon et al., 2007; Matsumoto et al., 2011), seawater (Lai et al., 2009; Seo & Lee, 2010; Park et al., 2011), tidal flats (Fan et al., 2011), the rhizosphere of wild rice (Kumar et al., 2008) and desert sand (Xue et al., 2012). Members of the genus can be characterized by the yellow to orange–red colony colour on agar plates, lack of bacteriochlorophyll a, presence of ubiquinone 10 as the major respiratory quinone, fatty acids rich in C18:1ω7c, DNA G+C content ranging between 54.5 and 67.2 mol% and a mesophilic temperature range for optimal growth. All species can grow in the presence of NaCl, though NaCl is not essential in many cases. Phosphatidylethanolamine (PE), phosphatidylglycerol (PG), diphosphatidylglycerol (DPG), phosphatidylcholine (PC) and sphingolipids are present as the main polar lipid components (Kumar et al., 2008; Park et al., 2011). Some members of the genus exhibit interesting properties including epoxide hydrolase activity (Kwon et al., 2007), production of astaxanthin (Matsumoto et al., 2011) and growth on crude oil (Lai et al., 2009).

During the study of bacterial diversity at a marine bay area, a yellow-pigmented bacterium was isolated from the sea urchin Strongylocentrotus intermedius using conventional isolation techniques and subjected to further taxonomic investigation. The initial study indicated that the isolate was a member of the family Erythrobacteraceae, and based on the results of the taxonomic study conducted using a polyphasic approach, the novel bacterium is proposed as a new species of the genus Altererythrobacter.

Strain KMM 6042T was isolated from the sea urchin Strongylocentrotus intermedius collected from Troitsa Bay in the Gulf of Peter the Great, East Sea. After isolation and purification, the strain was maintained at 28 °C on marine 2216 agar (Difco) and stored at −20 °C in marine broth 2216, supplemented with 20% (w/v) glycerol.
Cell morphology was studied using cells obtained from marine broth cultures. Cells were fixed in 2.5% paraformaldehyde–glutaraldehyde mixture buffered with 0.1 M phosphate (pH 7.2) for 2 h, fixed in 1% osmium tetroxide in the same buffer for 1 h, dehydrated in graded ethanol and substituted by isoamyl acetate. Samples were then dried at the critical point in CO2. Finally, the samples were sputtered with gold in a sputter coater (SC502; Polaron) and observed using a scanning electron microscope (SEM 515; Philips).

Ranges for growth temperature, pH and NaCl concentration and antibiotic susceptibility were determined as described previously (Han et al., 2003). API 20NE, API 20E, API ZYM and API ID 32 GN (bioMérieux) strips were used for biochemical and physiological characterization. For the determination of G+C content, genomic DNA was isolated and the mol% G+C content was determined by the thermal denaturation method as described previously (Marmur & Doty, 1962). The respiratory quinone was analysed according to the method described by Nishijima et al. (1997). The fatty acid composition was determined using the biomass cultivated on marine agar 2216 (Difco) at 25 °C for 24–48 h. Extraction and analysis of cellular fatty acids were performed according to the procedures for the Sherlock Microbial Identification system (MIDI). Polar lipids were analysed using two-dimensional TLC as described previously (Minnikin et al., 1984).

The absorption spectra of aqueous and organic cell extracts were measured between 350 nm and 1100 nm. The aqueous sample was obtained from the culture supernatant prepared from ultrasonicated cells harvested from marine agar plates incubated under dark, aerobic conditions and the organic extract was prepared using an acetone: methanol mixture [7: 2 (v/v)].

DNA extraction, PCR and sequencing of the 16S rRNA gene followed previous procedures (Kim et al., 1998). The sequence data were aligned with those from representative members of selected genera belonging to the family Erythrobacteraceae using PHYDIT version 3.2 (http://plaza.snu.ac.kr/~jchun/phydit/). Phylogenetic trees were reconstructed using the procedures described previously (Nedashkovskaya et al., 2010). DNA–DNA relatedness was estimated using fluorometric methods in combination

Table 1. Comparison of morphological, cultural and physiological properties for strain KMM 6042T and other species of the genus Altererythrobacter

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<td>6.0–10.0</td>
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<td>ND</td>
<td>ND</td>
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<td>7.0</td>
<td>7.5</td>
<td>7.0–8.0</td>
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<td>0–1</td>
<td>0.5–9</td>
<td>0–12</td>
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<td>+</td>
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<td>66.5</td>
<td>63.1</td>
<td>60.3</td>
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*Data from Xue et al. (2012).
†Data from Park et al. (2011).
‡Data from Lai et al. (2009).
with microplates as described previously (Ezaki et al., 1989). The relatedness was measured reciprocally using at least three replicates.

Cells of strain KMM 6042T were Gram-negative, motile and yellow-pigmented. The individual cells were oval or short rod-shaped, and the cell sizes ranged around 0.3–0.5 µm in width and 0.8–1.0 µm in length (Fig. S1, available at IJSEM online). The temperature range for growth was 4–39 °C, and the optimal temperature was 25 °C. Growth occurred between pH 5.8 and 10, and the optimal range was pH 7.2–7.6. Although the strain was isolated from a marine environment, NaCl was not essential for growth. Growth also occurred in the presence of up to 4 % NaCl. Other biochemical and physiological properties of KMM 6042T are listed in the species description in Table 1. The cellular fatty acids were mainly unsaturated, straight chains, comprised primarily of C18:1ω7c (38.7 %), C17:1ω6c (32.9 %) and C16:1ω7c and/or iso-C15:0 2-OH (8.6 %). Minor components included C16:0 (5.4 %), C17:1ω8c (3.4 %), C15:0 2-OH (2.3 %) and C15:0 (2.2 %). The major respiratory quinone was Q-10. The polar lipids consisted of PE, DPG, glycosphingolipids and unknown aminolipids (Fig. S2). Bacteriochlorophyll a was not detected in aqueous or organic extracts of cells (data not shown), but carotenoid pigments were detected at wavelengths between 400 and 600 nm. In the neighbour-joining phylogenetic analysis based on 16S rRNA gene sequences, strain KMM 6042T clearly belonged to the clade encompassed by the genus Altererythrobacter and was mostly related to Altererythrobacter dongtansensis (99.0 % sequence similarity) and Altererythrobacter xinjiangensis (96.8 % sequence similarity) (Fig. 1), which was also supported by high bootstrap values and the same groupings were also found in the maximum-likelihood tree (not shown). The comparison of 16S rRNA gene sequence similarity also showed that the strain was related to Croceicoccus marinus E4A9T (96.2 %). The assignment of strain KMM 6042T to the genus Altererythrobacter was supported by phenotypic and chemotaxonomic properties, including yellow colony colour, lack of bacteriochlorophyll a, Q10 as the major quinone and C18:1ω7c as the major fatty acid.

However, strain KMM 6042T could be readily discriminated from other species of the genus Altererythrobacter using the combination of phenotypic properties (Tables 1, S1). Strain KMM 6042T and A. dongtansensis, the most closely related species, differed in motility, nitrate reduction, hydrolysis of aesculin, starch and Tween 80, and utilization of glucose and malate as well as in a number of enzyme activities. The fatty acid composition also distinguished strain KMM 6042T from other species of the genus Altererythrobacter troitsensis sp. nov.
Table 2. Fatty acid composition of strain KMM 6042T and other species of the genus Altererythrobacter

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<th>Fatty acid (% )</th>
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<td>C14:0</td>
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<td>–</td>
<td>3.2</td>
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<td>3.1</td>
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<td>5.8</td>
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<td>5.0</td>
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*Summed features represent two or three fatty acids that cannot be separated by the Microbial Identification System. Summed feature consisted of C16:1ω7c and/or iso-C15:0 2-OH.

Altererythrobacter (Table 2). Notably, strain KMM 6042T had higher proportion of C17:1ω6c than other species. The DNA–DNA relatedness with the type strain of A. dongtanensis was 34.4±7.6%, which clearly separates the two strains at species level. It is therefore evident from this study that strain KMM 6042T merits recognition as a novel species of the genus Altererythrobacter, for which the name Altererythrobacter troitsensis sp. nov. is proposed.

Description of Altererythrobacter troitsensis sp. nov.

Altererythrobacter troitsensis (troi.tsen’sis. N.L. masc. adj. troitsensis referring to Troitsa Bay, from where the organism was isolated).

Cells are Gram-negative, strictly aerobic, chemooorganotrophic, motile and rod-shaped. Oxidase and catalase-positive. Contains carotenoid pigments but not bacteriochlorophyll a. Forms yellow colonies on marine agar. Cells are rod-shaped, with sizes ranging around 0.3–0.5 μm × 0.8–1.0 μm. Grows optimally in the absence of NaCl, but growth also occurs in the presence of up to 4% NaCl. Grows at temperatures between 4 and 39 °C, and the optimal temperature is 25 °C. Growth occurs between pH 5.8 and 10, and the optimal range is pH 7.2–7.6. Starch and Tweens 20, 40 and 80 are degraded, but not agar, cellulose, chitin, gelatin or DNA. Using the API 20NE strip, only nitrate reduction and aesculin hydrolysis give a positive result. Using the API 20E strip, only acid production from D-mannitol, sucrose and amygdalin give a positive result, and acid production from D-glucose and L-arabinose is weakly positive. Using the API ZYM strip, results for alkaline phosphatase, leucine arylamidase, cystine arylamidase, cystine arylamidase and β-glucosidase activities are positive, and esterase (C4), esterase lipase (C8), acid phosphatase and esterase lipase (C12) give a positive result. And acid production from D-glucose and L-arabinose is weakly positive.
naphthol-AS-BI-phosphohydrolase are weakly positive. Using the API ID 32N strip, positive result for the utilization of maltose, suberate, acetate, lactate, d-glucose, propionate, valerate and 3-hydroxybenzoate. Susceptible to ampicillin, carbencillin and tetracycline, but not to benzylpenicillin, gentamicin, kanamycin, lincomycin, neomycin, oleandomycin and polymyxin B. The main cellular fatty acids are C<sub>18:1</sub>ω7c (38.7 %), C<sub>17:1ω6c</sub> (32.9 %) and a summed feature of C<sub>16:1ω7c</sub> and/or iso-C<sub>15:0</sub> 2-OH (8.6 %). The major isoprenoid quinone is Q-10. The main polar lipids consist of PE, DPG, unknown glycolipids and unknown aminolipids.

The type strain is KMM 6042<sup>T</sup> (=KCTC 12303<sup>T</sup> = JCM 17037<sup>T</sup>), which was isolated from the sea urchin <i>Strongylocentrotus intermedius</i>. The DNA G+C content of the type strain is 65.0 %.

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**References**


