**Roseicitreum antarcticum** gen. nov., sp. nov., an aerobic bacteriochlorophyll \(a\)-containing alphaproteobacterium isolated from Antarctic sandy intertidal sediment

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A novel Gram-negative, non-motile bacterium, designated strain ZS2-28\(^T\), was isolated from sandy intertidal sediment samples collected from the coastal regions of the Chinese Antarctic Zhongshan Station on the Larsemann Hills, Princess Elizabeth Land, East Antarctica. Strain ZS2-28\(^T\) was obligately heterotrophic, strictly aerobic, psychrotolerant (growth occurred at 0–33 °C) and moderately halophilic (optimal growth in 7–8 % NaCl). A single major peak at 872–874 nm in the infrared absorption spectrum indicated the presence of bacteriochlorophyll \(a\). Poly-\(\beta\)-hydroxybutyrate accumulation and slime production were also detected. The predominant cellular fatty acid was C\(_{16:0}\) \(3\)-OH, with C\(_{10:0}\) \(3\)-OH, C\(_{16:0}\), C\(_{17:0}\) cyclo, C\(_{19:0}\) \(9\)-cyclo and summed feature 3 (C\(_{18:1}\) \(\omega7\)-c and/or C\(_{18:1}\) \(\omega6\)-c) present in smaller amounts. The respiratory quinone was \(Q\)-10. The main polar lipids were phosphatidyleglycerol, phosphatidylethanolamine, phosphatidylcholine and an unidentified aminolipid. The G + C content of the genomic DNA was 63.3 mol%. Phylogenetic analysis based on 16S rRNA gene sequences indicated that strain ZS2-28\(^T\) formed a distinct evolutionary lineage within the clade containing members of the genera *Roseibaca*, *Roseinatronobacter* and *Rhodobaca* of the class *Alphaproteobacteria*. On the basis of its phylogenetic position, as well as its phenotypic and chemotaxonomic characteristics, strain ZS2-28\(^T\) represents a novel species of a novel genus, for which the name *Roseicitreum antarcticum* gen. nov., sp. nov. is proposed. The type strain is ZS2-28\(^T\) (\(=\)CGMCC 1.8894T =LMG 24863T).

Since aerobic methylotrophs containing bacteriochlorophyll \(a\) were reported by Sato (1978), a variety of aerobic bchl \(a\)-containing bacteria have been identified from different geographical areas and ecological niches (Yurkov, 2006). However, information on aerobic bchl \(a\)-containing bacteria inhabiting the Antarctic intertidal environment is still lacking. Intense seasonal scouring by ice, winter ice encasement, high exposure to UV radiation, high levels of salinity and temperature fluctuations make the Antarctic intertidal zone possibly the world’s most physically disturbed environment (Peck et al., 2006). Here, we describe a novel aerobic bchl \(a\)-containing bacterium, which was isolated from Antarctic sandy intertidal sediment and found to be phylogenetically related to the type strains of *Roseibaca ekhonensis* (Labrenz et al., 2009), *Roseinatronobacter thiooxidans* (Sorokin et al., 2000), *Roseinatronobacter monicus* (Boldareva et al., 2007), *Rhodobaca bogoriensis* (Milford et al., 2000) and *Rhodobaca barguzinensis* (Boldareva et al., 2008), all of which are members of the family *Rhodobacteraceae*.

Strain ZS2-28\(^T\) was isolated from sandy intertidal sediment samples collected from the coastal regions of the Chinese Antarctic Zhongshan Station on the Larsemann Hills, Princess Elizabeth Land, East Antarctica during the 23rd Chinese National Antarctic Research Expedition in March 2007 (Yu et al., 2010). For the isolation of bacteria, 1 g wet sediment from the samples was mixed with 99 ml of sterilized seawater; 10 glass beads (diameter 2–3 mm) were added before shaking at 4 °C for 1 h at 300 r.p.m. and the mixture was further diluted (1 : 10) in sterilized seawater and spread onto natural seawater agar. One isolate was obtained in pure culture after three successive transfers to fresh marine agar 2216 (MA; Difco) and stored at –80 °C in marine broth 2216 (MB; Difco) supplemented with 30 % (v/v) glycerol.

**Abbreviations:** bchl, bacteriochlorophyll; LH, light-harvesting.
Cells of strain ZS2-28T were Gram-negative, non-sporo- 
forming, lemon-shaped and surrounded with slime (see 
Supplementary Fig. S1, available in IJSEM Online). Flagella 
were not found. Cells of strain ZS2-28T grew at 0–33 °C 
(optimum 25–27 °C), at pH 5.0–9.5 (pH optimum 7.0) 
and in 0–15 % (w/v) NaCl (optimum 7–8 %). Strain ZS2-28T 
did not grow photoautotrophically with H₂/CO₂ (80:20, 
v/v) or photoorganotrophically with acetate or glutamate 
under anaerobic conditions. In vivo absorption spectra of 
intact cells grown aerobically in the dark showed only a 
single major peak in the infrared at 872–874 nm (Supplementary Fig. S2), indicating the presence of bchl a. 
However, the lack of significant absorbance near 800 and 
850 nm in the in vivo spectrum indicated that strain ZS2-28T 
synthesized light-harvesting (LH) I photocomplexes (the ‘core’ 
antenna) but lacked an LH II (peripheral) antenna 
system (Zuber & Cogdell, 1995). Although intracytoplasmic 
membranes of the vesicular type were present, only a few 
vesicles were observed per cell and the vesicles seemed 
to be concentrated in the periphery of the cell (Supplementary 
Fig. S3). Strain ZS2-28T was not able to produce bchl 
a anaerobically or grow under anaerobic conditions. Other 
phenotypic characteristics of strain ZS2-28T are given in the 
genus and species descriptions or are shown in Tables 1, 2 
and 3.

Respiratory quinones were extracted and purified according 
to Collins (1985) and were analysed by HPLC (Wu 
et al., 1989). Polar lipid analyses were carried out by the 
identification service of the DSMZ and Dr B. J. Tindall. 
The DNA G+C content (mol%) was determined by HPLC 
according to Mesbah et al. (1989). For fatty acid analyses, 
cell biomass was harvested from cultures grown in MA 
after incubation at 16 °C and/or 27 °C for 7 days. Cellular 
fatty acid analyses were performed according to the 
instructions of the Sherlock Microbial Identification 
System and at Shanghai Public Health Clinical Center, 
Fudan University, P. R. China. Strain ZS2-28T contained 
phosphatidylglycerol, phosphatidylethanolamine, 
phosphatidylcholine and an unidentified aminolipid (Supple-
mentary Fig. S4). The major respiratory quinone detected 
was ubiquinone 10. The DNA G+C content of strain ZS2-
28T was 63.3 mol%. The predominant fatty acid in strain 
ZS2-28T was C₁₈ : 1 (72.56–74.30 %). Fatty acids C₁₈ : 0 
3-H and C₁₉:0ω8c cyclo were also present in strain ZS2-
28T but were absent in the reference strains (Table 3).

For 16S rRNA gene sequencing and phylogenetic analysis, 
DNA was extracted from strain ZS2-28T and purified by 
using a kit (BioDev, Beijing, China). The nearly full-length 
16S rRNA gene was amplified by PCR using universal 
primers 8f (5'-AGAGTTTGATCCTGCGGTTAGAGATTTG-3') 
and 1492r (5’-GTTTAGTCCTGACTACCT-3’) (Weisburg 
et al., 1991). Purified PCR product was ligated to pMD 
18-T (TaKaRa) and cloned according to the manufacturer’s 
instructions. Sequencing reactions were carried out using 
an ABI BigDye 3.1 sequencing kit (Applied BioSystems) 
and an automated DNA sequencer (model ABI3730; 
Applied BioSystems). The nearly complete 16S rRNA gene 
sequence (1429 nt) of strain ZS2-28T was submitted to 
GenBank and EMBL and compared with similar sequences 
using the BLAST program. The identification of phylogenetic 
eighbours and the calculation of pairwise 16S rRNA gene 
sequence similarities were achieved using the EzTaxon 
server (http://www.eztaxon.org/; Chun et al., 2007). 
Sequences were aligned using CLUSTAL_X version 1.8
Table 1. Phenotypic characteristics of strain ZS2-28T and related genera

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>1</th>
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<th>4</th>
<th>5</th>
<th>6</th>
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<td>Cell shape</td>
<td>1</td>
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<td>r</td>
<td>o or r</td>
<td>o or r</td>
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<td>Motility</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>+</td>
<td>+/-</td>
<td>+/-</td>
</tr>
<tr>
<td>Slime production</td>
<td>+</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>+/-</td>
<td>+/-</td>
</tr>
<tr>
<td>Internal photosynthetic membranes</td>
<td></td>
<td>Vesicular</td>
<td>–</td>
<td>–</td>
<td>Vesicular</td>
<td>Vesicular*</td>
</tr>
<tr>
<td>Light-harvesting complex(es)</td>
<td></td>
<td>LH I, LH II</td>
<td>LH I, LH II</td>
<td>LH I</td>
<td>LH I, LH II</td>
<td>LH I, LH II</td>
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<td>+</td>
<td>+</td>
<td>–</td>
<td>–</td>
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<tr>
<td>Anaerobic phototrophism</td>
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<td>–</td>
<td>–</td>
<td>+</td>
<td>+</td>
<td>+</td>
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<tr>
<td>Anaerobic growth</td>
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<td>–</td>
<td>+</td>
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<td>–</td>
<td>–</td>
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<td>Growth below pH 7</td>
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<td>–</td>
<td>–</td>
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<td>+/-</td>
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<tr>
<td>Optimal pH for growth</td>
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<td>8.5–10.0</td>
<td>7.0–9.5</td>
<td>8.0–9.0</td>
<td>6.5–7.5</td>
<td>6.0–8.5</td>
</tr>
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<td>NaCl requirement</td>
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<td>–</td>
<td>+</td>
<td>–</td>
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<td>+/-</td>
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<tr>
<td>NaCl for optimal growth (%)</td>
<td>7.0–8.0</td>
<td>3.0–4.0</td>
<td>2.5</td>
<td>1.0–3.0</td>
<td>0.4–0.6</td>
<td>2.0–5.0</td>
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<tr>
<td>Nitrate reduction</td>
<td>–</td>
<td>+</td>
<td>–</td>
<td>–</td>
<td>+/-</td>
<td>+/-</td>
</tr>
<tr>
<td>DNA G+C content (mol%)</td>
<td>63.3</td>
<td>59.0–61.5</td>
<td>61.0</td>
<td>58.8–59.8</td>
<td>62.9–73.2</td>
<td>58.0–67.7</td>
</tr>
</tbody>
</table>

The internal photosynthetic membranes of Rhodobacter blasticus are lamellar.†Rhodovulum strictum and Rhodovulum steppense are not able to grow below pH 7.‡Rhodobacter vinaykumarii requires NaCl for growth.§Rhodovulum sulfidophilum, Rhodovulum visakhapatnamense and Rhodovulum lacipunicei are able to grow in the absence of NaCl.‖Rhodobacter azotoformans is positive for nitrate reduction; results for Rhodobacter megalophilus and Rhodobacter sphaeroides are not reported.

(Thompson et al., 1997) and edited manually using the BioEdit sequence alignment editor version 5.0.9 (Hall, 1999). The phylogenetic tree was reconstructed using the maximum-likelihood method in the PHYLIP 3.69 software package (Felsenstein, 2009). Relationships among taxa were also determined using the neighbour-joining and maximum-parsimony methods with Kimura 2-state parameter model analyses implemented in the program MEGA version 4 (Tamura et al., 2007).

Pairwise analysis revealed that the novel strain exhibited 16S rRNA gene sequence similarity values of 96.5, 96.2, 95.8, 95.7, 95.6, 95.3, 95.2, 95.2, 95.1 and 94.8% with respect to the type strains of Rhodobacter veldkampii, Roseinatronobacter thiioxidans, Roseinatronobacter monicus, Rhodobaca barguzinensis, Rhodobaca bogoriensis, Paracoccus aminophilus, Haematobacter massilens, Haematobacter missouriensis, Paracoccus homiensis and Roseibaca ekhonensis, respectively. Other species belonging to the class Alphaproteobacteria showed ≤95.0% 16S rRNA gene sequence similarity to strain ZS2-28T. Although there is no precise correlation between 16S rRNA gene sequence similarity and species delineation, it is generally recognized that divergence values of >3% are significant (Stackebrandt & Goebel, 1994). An unrooted tree reconstructed using the maximum-likelihood method showed strain ZS2-28T occupying a phylogenetic position within the family Rhodobacteraceae (Fig. 1). The topology of the phylogenetic trees generated using the maximum-parsimony and neighbour-joining algorithms (Supplementary Figs S5 and S6) was somewhat different from that of the trees constructed using the maximum-likelihood method. Nevertheless, strain ZS2-28T formed a distinct lineage within the clade containing species of the genera Roseibaca, Roseinatronobacter and Rhodobaca in these three phylogenetic trees. The phylogenetic position of strain ZS2-28T was strongly supported by its phenotypic characteristics. Strain ZS2-28T was clearly distinguishable from members of the genera Rhodobaca, Rhodobacter and Rhodovulum by its inability to synthesize bchl a anaerobically or grow under anaerobic conditions (Table 1). Intracytoplasmic membrane systems were present in cells of strain ZS2-28T but were absent in species of the genera Roseinatronobacter and Roseibaca (Table 1). Differences in carbohydrate utilization patterns (Table 2) and fatty acid profiles (Table 3) also differentiated strain ZS2-28T from species of the genera Roseibaca, Roseinatronobacter, Rhodobaca and Rhodobacter. Furthermore, the isolate could be easily distinguished from species of the genera Haematobacter, Paracoccus, Albidovulum, Catellibacterium and Thioclava by its ability to synthesize bchl a (Albuquerque et al., 2002; Tanaka et al., 2004; van Spanning et al., 2005; Sorokin et al., 2005; Helsel et al., 2007; Liu et al., 2008).
Table 2. Chemotaxonomic characteristics of strain ZS2–28<sup>T</sup> and related species

Strains: 1, ZS2–28<sup>T</sup>; 2, *Rhodobusa bogoriensis* DSM 18756<sup>T</sup>; 3, *Roseatintrabacter* thiooxidans DSM 13087<sup>T</sup>; 5, *Rhodobacter capsulatus* DSM 1710<sup>T</sup>; 5, *Roseibaka ekhonensis* DSM 11469<sup>T</sup>. All data were from this study. All strains produced lysine decarboxylase but did not produce agarase, amylase, caseinase, gelatinase or lipase (Tweed 80). Acid was not produced from melibiose, D-mannitol, malic acid, maltose, L-rhamnose, sucrose, casein hydrolysate and yeast extract were utilized. Starch, arbutin, D-adonitol, D-arabinose, L-arabitol, dulcitol, erythritol, D-fucose, L-fucose, benzoate, capric acid, glycerogen, inulin, potassium 2-ketogluconate, potassium 5-ketogluconate, malonate, melezitose, melibiose, methanol, methyl-α-D-glucopyranoside, methyl-α-D-mannopyranoside, methyl-β-D-xylopyranoside, raffinose, L-sorbose, D-tagatose, tartrate, ethanol and xylitol were not utilized. +, Positive; –, negative.

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
<th>5</th>
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<tr>
<td>Enzyme activity</td>
<td></td>
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<tr>
<td>Arginine dihydrolase</td>
<td>+</td>
<td>+</td>
<td>+</td>
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<tr>
<td>Ornithine decarboxylase</td>
<td>+</td>
<td>–</td>
<td>+</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Urease</td>
<td>+</td>
<td>–</td>
<td>+</td>
<td>+</td>
<td>+</td>
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<tr>
<td>β-Galactosidase</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
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<tr>
<td>β-Glucosidase</td>
<td>+</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
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<td>Acid production from:</td>
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<tr>
<td>L-Rhamnose</td>
<td>+</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
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<tr>
<td>L-Arabinose</td>
<td>+</td>
<td>+</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>D-Glucose</td>
<td>–</td>
<td>+</td>
<td>–</td>
<td>–</td>
<td>–</td>
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<tr>
<td>Sucrose</td>
<td>–</td>
<td>–</td>
<td>+</td>
<td>–</td>
<td>+</td>
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<td>Utilization of:</td>
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<tr>
<td>N-Acetylglucosamine, salicin</td>
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<td>–</td>
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<td>+</td>
<td>+</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>L-Arabinose, D-ribose</td>
<td>+</td>
<td>+</td>
<td>–</td>
<td>–</td>
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<tr>
<td>Butyrate</td>
<td>+</td>
<td>–</td>
<td>+</td>
<td>+</td>
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<td>Caproate, aspartate</td>
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<td>+</td>
<td>–</td>
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<td>Fructose, lactate, propionate</td>
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<td>+</td>
<td>+</td>
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<td>+</td>
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<td>Gentiose, gluconate, amygdalin</td>
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<td>–</td>
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<td>Lactose, D-lyxose, D-arabitol, inositol, aesculin, phenylacetic acid</td>
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<td>D-Mannose, D-mannitol, trehalose</td>
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<td>D-Sorbitol</td>
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<td>+</td>
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<tr>
<td>L-Xylose</td>
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</table>

Based on the phenotypic and phylogenetic evidence presented here, strain ZS2–28<sup>T</sup> represents a novel species of a novel genus, for which the name *Roseicitreum antarcticum* gen. nov., sp. nov. is proposed. Characteristics that differentiate *Roseicitreum* gen. nov. from other bchl <i>a</i>-containing species of genera in the same cluster are given in Table 1.

Table 3. Fatty acid composition of strain ZS2–28<sup>T</sup> and related species

Values are percentages of total fatty acids. —, Not detected.

<table>
<thead>
<tr>
<th>Fatty acid*</th>
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<th>4</th>
<th>5</th>
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<tbody>
<tr>
<td>C&lt;sub&gt;10:0&lt;/sub&gt; 3-OH</td>
<td>1.39/1.08</td>
<td>–</td>
<td>–</td>
<td>–</td>
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<tr>
<td>C&lt;sub&gt;14:0&lt;/sub&gt;</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>0.34</td>
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<tr>
<td>C&lt;sub&gt;16:0&lt;/sub&gt;</td>
<td>4.01/6.72</td>
<td>2.18</td>
<td>4.26</td>
<td>3.88</td>
<td>1.82</td>
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<tr>
<td>C&lt;sub&gt;17:0&lt;/sub&gt; cyclo</td>
<td>1.71/1.36</td>
<td>–</td>
<td>0.10</td>
<td>0.45</td>
<td>–</td>
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<tr>
<td>C&lt;sub&gt;17:1&lt;/sub&gt;ω8c</td>
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<td>0.26</td>
<td>0.40</td>
<td>0.20</td>
<td>1.08</td>
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<td>C&lt;sub&gt;18:0&lt;/sub&gt;</td>
<td>–</td>
<td>0.22</td>
<td>0.33</td>
<td>2.20</td>
<td>–</td>
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<tr>
<td>C&lt;sub&gt;18:1ω7c&lt;/sub&gt;</td>
<td>74.30/72.56</td>
<td>86.10</td>
<td>82.55</td>
<td>84.72</td>
<td>82.32</td>
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<td>11 methyl C&lt;sub&gt;18:1ω7c&lt;/sub&gt;</td>
<td>3.67/8.19</td>
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<td>4.83</td>
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<tr>
<td>C&lt;sub&gt;19:0ω8c&lt;/sub&gt; cyclo</td>
<td>1.96/4.53</td>
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<tr>
<td>Summed features‡</td>
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<td>7.35/2.59</td>
<td>2.71</td>
<td>2.12</td>
<td>5.55</td>
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<tr>
<td>7</td>
<td>2.39/–</td>
<td>4.22</td>
<td>5.51</td>
<td>–</td>
<td>4.51</td>
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</table>

*All data were obtained after growth on MA for 7 days. 1, 2, 3 and 4 were incubated at 27 °C; strains 1 and 5 at 16 °C.

†Cells were grown at 27 °C/16 °C.

‡Summed features are groups of two or three fatty acids that cannot be separated by GLC with the MIDI system. Summed feature 3 comprises C<sub>16:1ω7c</sub> and/or iso-C<sub>15:0</sub> 2-OH. Summed feature 7 comprises an unknown fatty acid of equivalent chain length 18.846 and/or C<sub>19:1ω6c</sub>.

Description of *Roseicitreum* gen. nov.

*Roseicitreum* (Ro.se.i.ci’re.um. L. adj. roseus rose-coloured; L. neut. n. citreum citron, lemon; N.L. neut. n. *Roseicitreum* pink lemon).

Gram-negative, obligately heterotrophic, strictly aerobic, non-motile and moderately halophilic. Cells contain bchl <i>a</i> and poly-β-hydroxybutyrate. Intracytoplasmic membrane systems are present. Slime production-positive. Does not grow photoautotrophically with H<sub>2</sub>/CO<sub>2</sub> (80 : 20, v/v) or photo-organotrophically with acetate or glutamate anaerobically. Positive for cytochrome oxidase and catalase. The predominant cellular fatty acid is C<sub>18:1ω7c</sub>. The respiratory quinone is Q-10. The polar lipids phosphatidylethanolamine and phosphatidylglycerol are present. The type species of the genus is *Roseicitreum antarcticum*.

Description of *Roseicitreum antarcticum* sp. nov.

*Roseicitreum antarcticum* (an.tar.ci’cu.m. L. neut. adj. antarcticum southern, belonging to Antarctica).

Cells are lemon-shaped, 0.5–0.8 × 1–2 μm. Colonies on MA are pink-coloured, convex, circular, smooth and 1–2 mm in diameter after 3 days of incubation at 27 °C. With prolonged aerobic cultivation in the light, colony colour changes to red. Bchl <i>a</i> is produced with a single major peak at 872–874 nm in the infrared absorption
Thalassobacter oligotrophus CECT 6294T (AJ631302)
Thalassobius mediterraneus CECT 5383T (AJ878874)
Thioclava pacifica TL 2 (AY567191)
Rhodovulum sulfidophilum DSM 1374T (D16423)
Roseiceirem antarcticum ZS-28T (FJ196006)
Roseinatronobacter thiooxidans ALG 1T (AF249749)
Roseibacca exhalensins EL-50 (AJ805746)
Roseinatronobacter monicus ROS 39 (DQ659236)
Rhodobacca bogoriensis LB1T (AF248636)
Rhodobacca banguiensis VKM B-2406 (EF584833)
Rhodobacter velikhampi ATCC 33703T (D16421)
Albidovulum inspectum BPF FR-10T (AF465833)
Paracoccus denticrinitis ATCC 17741T (Y16927)
Cateelibacterium nectriaphilum AST4T (AB101543)
Rhodobacter capsulatus ATCC 11161T (D16428)
Haemobacter misrquorum CCUG 52607T (DG342315)
Mannirhabdus alcalophilus HTCC 2654T (DQ615443)
Donghicolana ebuneans SW-4T (DQ687965)
Loktanella salicilasha LMG 21507T (AJ440997)
Wenmonis marina HY34T (DQ042063)
Oceanicola granulosa HTCC 2516T (AY248966)
Roseovarius tolerans Eko Lake-172T (Y11551)
Salinisatisbacter flavus ISL40T (FJ252707)
Ruegeria lacucaeauteri PT-115T (ACN01000031)
Antarctobacter heliotermes EL-219T (Y11552)
Pelagicola litorea CL-ES2T (EF192392)

Fig. 1. Phylogenetic tree reconstructed using the maximum-likelihood method showing the position of strain ZS2-28T and the type strains of related species based on 16S rRNA gene sequence analysis. Bootstrap values ≥50% (based on 100 resampled datasets) are given at branch points. GenBank accession numbers of 16S rRNA gene sequences are given in the parentheses. Bar, 1% sequence divergence.

Spectrum. Growth occurs at 0–33 °C (optimum 25–27 °C), at pH 5–9.5 (optimum pH 7.0) and in 0–15 % (w/v) NaCl (optimum 7–8 %). Indole production and Voges–Proskauer reaction are negative. Negative for reduction of nitrate and production of hydrogen sulfide. Positive for arginine dihydrolase, lysine decarboxylase, ornithine decarboxylase, urease, β-galactosidase and β-glucosidase activities. Negative for gelatinase, agarase, caseinase, amylase and lipase (Tweed 80) activities. The following substrates are utilized as sole carbon and energy sources: L-arabinose, cellobiose, D-galactose, gentiobiose, D-glucose, maltose, D-mannose, L-rhamnose, D-ribose, sucrose, trehalose, turanose, D-xylose, D-mannitol, adipic acid, glucuronate, malic acid, glycogen, amygdalin, pyruvate, casein hydrolysate and yeast extract. The following substrates are not utilized as sole carbon sources: starch, D-arabinose, D- and L-fucose, fructose, lactose, D-lyxose, melezitose, melibiose, raffinose, L-sorbose, D-tagatose, L-xyllose, methyl-α-D-glucopyranoside, methyl-α-D-mannopyranoside, methyl-β-D-xylpyranoside, D-adonitol, D- and L-arabitol, dulcitol, erythritol, inositol, D-sorbitol, xylitol, N-acetylglucosamine, arbutin, aesculin, inulin, salicin, glycogen, potassium 2-ketogluconate, potassium 5-ketogluconate, capric acid, trisodium citrate, phenylacetic acid, lactate, propionate, butyrate, benzoate, caproate, malonate, methanol, succinate, tartrate, ethanol, propanol, aspartate and glycolate. Acid is produced from L-rhamnose and L-arabinose but not from D-glucose, melibiose, sucrose, D-mannitol, inositol, D-sorbitol and amygdalin. Susceptible to (μg per disk, unless otherwise stated) erythromycin (15), chloromycetin (30), ciprofloxacin (5) and norflaxacin (10); resistant to ampicillin (30), amoxicillin (1), penicillin (75), piperacillin (100), polymyxin B (100 U), tetracycline (30) and vancomycin (30). The predominant cellular fatty acid is C18:1ω7c, with C10:0 3-OH, C16:0, C17:0 cyclo, C19:0 8c8c cyclo and summed feature 3 (C16:1ω7c and/or iso-C15:0 2-OH) present in smaller amounts.

The type strain, ZS2-28T (=CGMCC 1.8894T =LMG 24863T), was isolated from sandy intertidal sediment samples collected from coastal regions of the Chinese Antarctic Zhongshan Station on the Larsemann Hills, Princess Elizabeth Land, East Antarctica. The DNA G+C content of the type strain is 63.3 mol% (determined by HPLC).

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References


