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- β -hydroxybutyrate accumulation and slime production were also detected. The predominant cellular fatty acid was C_{18:1 ω 7c}, with C_{10:0} 3-OH, C_{16:0}, C_{17:0} cyclo, C_{19:0 ω 8c} cyclo and summed feature 3 (C_{16:1 ω 7c} and/or iso-C_{15:0} 2-OH) present in smaller amounts. The respiratory quinone was Q-10. The main polar lipids were phosphatidylglycerol, 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 1.8894^T =LMG 24863^T).

Since aerobic methylotrophs containing bacteriochlorophyll (bchl) *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 *Rhodobacteriaceae*.

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.

The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain ZS2-28^T is FJ196006.

Six supplementary figures are available with the online version of this paper.

Rhodobaca bogoriensis DSM 18756^T, *Rhodobacter capsulatus* DSM 1710^T, *Roseibaca ekhonensis* DSM 11469^T and *Roseinatronobacter thiooxidans* DSM 13087^T were obtained from DSMZ and used as reference strains.

Cell morphology was examined by using phase-contrast microscopy (CX; Olympus) and transmission electron microscopy (JEM-1200EX; JEOL). The internal membrane systems were viewed from ultrathin sections using a transmission electron microscope. Colony morphology was observed on MA after incubation at 27 °C for 72 h. *In vivo* absorption spectra were measured in 60 % (w/v) sucrose solution using a Beckman DU800 spectrophotometer (Biebl & Drews, 1969). Polyhydroxybutyrate granules were identified by Nile Blue A staining (Ostle & Holt, 1982) using fluorescence microscopy (CX; Olympus). Growth at different temperatures was determined in MB for 5–30 days. Growth at 0–20 % (w/v) NaCl (increments of 1 %) was tested in a medium containing (l⁻¹) 5 g MgCl₂, 2 g MgSO₄, 0.5 g CaCl₂, 1 g KCl, 5 g peptone and NaCl at the appropriate test concentration, adjusted to pH 7.5 with KOH (Smibert & Krieg, 1994). Growth at pH 4–11 was determined in MB by using the following buffer system: pH 4–5, 0.1 M citric acid/0.1 M sodium citrate; pH 6–8, 0.1 M KH₂PO₄/0.1 M NaOH; pH 9–10, 0.1 M NaHCO₃/0.1 M Na₂CO₃; pH 11, 0.05 M Na₂HPO₄/0.1 M NaOH. Growth under anaerobic conditions was determined by incubation in an anaerobic chamber (AnaeroJar; Oxoid). Tests for photolithoautotrophic or photoorganotrophic growth were performed according to the methods of Labrenz *et al.* (1999). Hydrolysis of casein, starch, Tween 80 and gelatin was determined as described by Smibert & Krieg (1994) on MA. Activities of constitutive enzymes and other physiological properties were determined by using API 20 E, API 20 NE and VITEK 2 GN strips (bioMérieux) according to the manufacturer's instructions, except that the inoculum was prepared by suspending cells in 3 % sea salts solution (Sigma). Utilization of carbon sources was determined in a basal medium containing (l⁻¹) 0.54 g NH₄Cl, 30 g NaCl, 3 g MgCl₂·6H₂O, 2 g K₂SO₄, 0.2 g K₂HPO₄, 0.01 g CaCl₂, 0.006 g FeCl₃·6H₂O, 0.005 g Na₂MoO₄·7H₂O, 0.004 g CuCl₂·2H₂O and 6 g Tris. Utilization of substrates in the API 50 CH system and the following carbon sources (0.1 %, w/v) was tested: lactate, malate, propionate, pyruvate, butyrate, benzoate, caproate, malonate, methanol, succinate, tartrate, ethanol, propanol, casein hydrolysate, yeast extract, aspartate and glycolate. Additionally, antimicrobial susceptibility testing was performed by using the agar diffusion method using antibiotic-impregnated discs (Oxoid) as described by Buczolits *et al.* (2002).

Cells of strain ZS2-28^T were Gram-negative, non-spore-forming, lemon-shaped and surrounded with slime (see Supplementary Fig. S1, available in IJSEM Online). Flagella were not found. Cells of strain ZS2-28^T grew at 0–33 °C (optimum 25–27 °C), at pH 5.0–9.5 (optimum pH 7.0) and in 0–15 % (w/v) NaCl (optimum 7–8 %). Strain ZS2-28^T 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 ZS2-28^T 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 ZS2-28^T was not able to produce bchl *a* anaerobically or grow under anaerobic conditions. Other phenotypic characteristics of strain ZS2-28^T 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 ZS2-28^T contained phosphatidylglycerol, phosphatidylethanolamine, phosphatidylcholine and an unidentified aminolipid (Supplementary Fig. S4). The major respiratory quinone detected was ubiquinone 10. The DNA G + C content of strain ZS2-28^T was 63.3 mol%. The predominant fatty acid in strain ZS2-28^T was C_{18:1ω7c} (72.56–74.30 %). Fatty acids C_{10:0} 3-OH and C_{19:0ω8c} cyclo were also present in strain ZS2-28^T but were absent in the reference strains (Table 3).

For 16S rRNA gene sequencing and phylogenetic analysis, DNA was extracted from strain ZS2-28^T 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'-AGAGTTTGATCCTGGCTCAG-3') and 1492r (5'-GGTACCTTGTTACGACTT-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 ZS2-28^T was submitted to GenBank and EMBL and compared with similar sequences using the BLAST program. The identification of phylogenetic neighbours 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 ZS2-28^T and related genera

Taxa: 1, strain ZS2-28^T; 2, *Roseinatronobacter* (two species); 3, *Roseibaca* (one species); 4, *Rhodobaca* (two species); 5, *Rhodobacter* (12 species); 6, *Rhodovulum* (12 species). Data for *Roseinatronobacter*, *Roseibaca*, *Rhodobaca*, *Rhodobacter* and *Rhodovulum* are from Eckersley & Dow, 1980; Imhoff, 1991; Milford *et al.*, 2000; Sorokin *et al.*, 2000; Boldareva *et al.*, 2007; Boldareva *et al.*, 2008; Labrenz *et al.*, 2009; Chakravarthy *et al.*, 2009 (also cited in Girija *et al.*, 2010; Venkata Ramana *et al.*, 2009 and Kompantseva *et al.*, 2010). l, Lemon-shaped; o, ovoid; r, rod-shaped; NR, not reported; +, positive; −, negative; −/+ or +/−, variable reaction between species (where the first sign indicates the result of the type species). The quinone system of strain ZS2-28^T was Q-10, identical to that of the other genera.

Characteristic	1	2	3	4	5	6
Cell shape	l	o or l	r	o or r	o or r	o to r
Motility	−	−	−	+	+ / −	+ / −
Slime production	+	−	−	− / +	+ / −	NR
Internal photosynthetic membranes	Vesicular	−	−	Vesicular	Vesicular*	Vesicular
Light-harvesting complex(es)	LH I	LH I, LH II	LH I, LH II	LH I	LH I, LH II	LH I, LH II
Aerobic phototrophism	+	+	+	−	−	−
Anaerobic phototrophism	−	−	−	+	+	+
Anaerobic growth	−	−	−	+	+	+
Photoautotrophic growth	−	−	−	−	+ / −	+ / −
Growth below pH 7	+	−	+	−	+	+ / −†
Optimal pH for growth	7.0–8.0	8.5–10.0	7.0–9.5	8.0–9.0	6.5–7.5	6.0–8.5
NaCl requirement	−	−	+	− / +	− / +‡	− / +§
NaCl for optimal growth (%)	7.0–8.0	3.0–4.0	2.5	1.0–3.0	0–4.0	2.0–5.0
Nitrate reduction	−	+	−	+	− / +	NR
DNA G + C content (mol%)	63.3	59.0–61.5	61.0	58.8–59.8	62.9–73.2	58.0–67.7

*The internal photosynthetic membranes of *Rhodobacter blasticus* are lamellar.

†*Rhodovulum strictum* and *Rhodovulum steppenseis* are not able to grow below pH 7.

‡*Rhodobacter vinaykumarii* requires NaCl for growth.

§*Rhodovulum sulfidophilum*, *Rhodovulum visakhapatnamense* and *Rhodovulum lacipunice* 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, 95.1 and 94.8 % with respect to the type strains of *Rhodobacter veldkampii*, *Roseinatronobacter thiooxidans*, *Roseinatronobacter monicus*, *Rhodobaca barguzinensis*, *Rhodobaca bogoriensis*, *Paracoccus aminophilus*, *Haematobacter massiliensis*, *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 ZS2-28^T. 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 ZS2-28^T 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 ZS2-28^T 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 ZS2-28^T was strongly supported by its phenotypic characteristics. Strain ZS2-28^T 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 ZS2-28^T 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 ZS2-28^T 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^T and related species

Strains: 1, ZS2-28^T; 2, *Rhodobaca bogoriensis* DSM 18756^T; 3, *Roseinatronobacter thiooxidans* DSM 13087^T; 5, *Rhodobacter capsulatus* DSM 1710^T; 5, *Roseibaca ekhonensis* DSM 11469^T. All data were from this study. All strains produced lysine decarboxylase but did not produce agarase, amylase, caseinase, gelatinase or lipase (Tween 80). Acid was not produced from melibiose, D-mannitol, inositol, D-sorbitol or amygdalin. Pyruvate, cellobiose, D-glucose, 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, glycogen, 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.

Characteristic	1	2	3	4	5
Enzyme activity					
Arginine dihydrolase	+	–	+	+	+
Ornithine decarboxylase	+	–	–	+	+
Urease	+	–	+	+	–
β -Galactosidase	+	–	+	+	+
β -Glucosidase	+	–	–	–	–
Acid production from:					
L-Rhamnose	+	–	–	–	+
L-Arabinose	+	+	–	–	–
D-Glucose	–	–	+	–	–
Sucrose	–	–	–	+	+
Utilization of:					
N-Acetylglucosamine, salicin	–	+	–	–	+
Adipic acid	+	–	+	–	–
L-Arabinose, D-ribose	+	+	–	–	–
Butyrate	–	+	–	+	–
Caproate, aspartate	–	–	+	+	–
Fructose, lactate, propionate	–	+	+	+	+
D-Galactose, turanose	+	–	+	+	+
Gentiobiose, gluconate, amygdalin	+	–	–	–	–
Glycerin	+	–	–	–	+
Glycolate	–	–	+	–	–
Lactose, D-lyxose, D-arabitol, inositol, aesculin, phenylacetic acid	–	–	–	–	+
D-Mannose, D-mannitol, trehalose	+	+	–	–	+
D-Sorbitol	–	–	+	+	+
Succinate	–	+	+	+	–
Trisodium citrate	–	–	+	+	+
Propanol	–	–	–	+	–
D-Xylose	+	+	+	–	–
L-Xylose	–	+	+	–	–

Based on the phenotypic and phylogenetic evidence presented here, strain ZS2-28^T 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 *a*-containing species of genera in the same cluster are given in Table 1.

Table 3. Fatty acid composition of strain ZS2-28^T and related species

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

Fatty acid*	1†	2	3	4	5
C _{10:0} 3-OH	1.39/1.08	–	–	–	–
C _{14:0}	–/0.43	–	–	0.34	–
C _{16:0}	4.01/6.72	2.18	4.26	3.88	1.82
C _{17:0} cyclo	1.71/1.36	–	0.10	0.45	–
C _{17:1ω8c}	–	0.26	0.40	0.20	1.08
C _{18:0}	–	0.22	0.33	2.20	–
C _{18:1ω7c}	74.30/72.56	86.10	82.55	84.72	82.32
11 methyl C _{18:1ω7c}	3.67/8.19	4.16	4.83	2.66	–
C _{19:0ω8c} cyclo	1.96/4.53	–	–	–	–
Summed features‡					
3	7.35/2.59	2.71	2.12	5.55	6.71
7	2.39/–	4.22	5.51	–	4.51

*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_{16:1 ω 7c} and/or iso-C_{15:0} 2-OH. Summed feature 7 comprises an unknown fatty acid of equivalent chain length 18.846 and/or C_{19:1 ω 6c}.

Description of *Roseicitreum* gen. nov.

Roseicitreum (Ro.se.i.ci'tre.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 *a* and poly- β -hydroxybutyrate. Intracytoplasmic membrane systems are present. Slime production-positive. Does not grow photoautotrophically with H₂/CO₂ (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_{18:1 ω 7c}. The respiratory quinone is Q-10. The polar lipids phosphatidylglycerol, phosphatidylethanolamine and phosphatidylcholine are present. The type species of the genus is *Roseicitreum antarcticum*.

Description of *Roseicitreum antarcticum* sp. nov.

Roseicitreum antarcticum (an.tarc'ti.cum. L. neut. adj. *antarcticum* southern, belonging to Antarctica).

Cells are lemon-shaped, 0.5–0.8 × 1.0–2.0 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 *a* is produced with a single major peak at 872–874 nm in the infrared absorption

Fig. 1. Phylogenetic tree reconstructed using the maximum-likelihood method showing the position of strain ZS2-28^T and the type strains of related species based on 16S rRNA gene sequence analysis. Bootstrap values $\geq 50\%$ (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 (Tween 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, gluconate, malic acid, glycerol, 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-xylose, melibiose, raffinose, L-sorbose, D-tagatose, L-xylose, methyl- α -D-glucopyranoside, methyl- α -D-mannopyranoside, methyl- β -D-xylopyranoside, 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 (μ g per disk, unless otherwise stated) erythromycin (15), chloramphenicol (30), ciprofloxacin (5) and norfloxacin (10); resistant to amikacin (30), ampicillin (10), benzylpenicillin (10 U), carbenicillin (100), cefazolin sodium (40), cefoperazone (30), ceftazidime (30), ceftriaxone sodium (5), cefuroxime (30), cotrimoxazole (75), doxycycline (30), furazolidone (300), gentamicin (10), kanamycin (30), minocycline (30), neomycin (30),

oxacillin (1), penicillin (75), piperacillin (100), polymyxin B (100 U), tetracycline (30) and vancomycin (30). The predominant cellular fatty acid is C_{18:1} ω 7c, with C_{10:0} 3-OH, C_{16:0}, C_{17:0} cyclo, C_{19:0} ω 8c cyclo and summed feature 3 (C_{16:1} ω 7c and/or iso-C_{15:0} 2-OH) present in smaller amounts.

The type strain, ZS2-28^T (=CGMCC 1.8894^T =LMG 24863^T), 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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