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ORIGINAL PAPER

Arthrobacter terrae sp. nov., a psychrophilic actinobacterium with multi copies of *cap*A gene isolated from Antarctic soil

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Abstract A Gram-staining-positive, non-spore-forming, non-flagellated, ellipsoidal, strain Z1-20 ^{T} belonging to the genus *Arthrobacter* was isolated from a soil sample collected from the Zhongshan station, Antarctic. Phylogenetic analysis of the 16S rRNA gene sequences and phylogenetic analysis revealed that strain Z1-20 ^{T} formed a unique single cluster in the genus *Arthrobacter* and shared high 16S rRNA sequence similarities of 97.1% and 96.9% with *A. glacialis* HLT2-12-2 ^{T} and *A. psychrochitiniphilus* GP3^{T}, respectively. Values of Digital DNA-DNA hybridization (dDDH) between strain Z1-20 ^{T} against *A. glacialis* HLT2-12-2 ^{T} and *A. psychrochitiniphilus* GP3^{T} were 20.3% and 13.8%, respectively. Average nucleotide identity (ANI) score between strain Z1-20 ^{T} against *A. glacialis* HLT2-12-2 ^{T} and *A. psychrochitiniphilus* GP3^{T} were 72.5% and 72.1%, respectively. Genes for the synthesis of the osmoprotectant glycine betaine and higher copies of *cap*A gene encoding cold shock protein were found in genome of Z1-20 ^{T} that may help Z1-20 ^{T} in cold-adaptation. Strain Z1-20 ^{T} comprised lysine as the diagnostic diamino acid. Based on the results of phylogenetic, phenotypic and chemotaxonomic features, strain Z1-20 ^{T} represents a novel species of a novel taxon of genus *Arthrobacter*, for which the name *Arthrobacter terrae* gen. nov., sp. nov. is proposed.

Keywords Antarctic · *Arthrobacter* · Polyphasic taxonomy · New species

Introduction

Members of the genus *Arthrobacter* are aerobic, Gram-stain positive, catalase-positive actinobacteria with a high DNA G+C content (Keddie et al. 1986; Stackebrandt et al. 1983), contain MK-9(H_2) or MK-8/MK-9 as the major menaquinones. Two major cell-wall peptidoglycan structural types in *Arthrobacter* species are A3α and A4α (Busse 2016). The genus *Arthrobacter* strains currently comprises 69 species with validly names, frequently isolated from various environments including soils (Gupta et al. 2004; Ganzert et al. 2011), marine environments (Pindi et al. 2010; Cobet et al. 1970), lake water (Dubinina and Zhdanov 1975), marsh (Zhang et al. 2018) and sewage (Kim et al. 2008). It has also been found in the filtration substrate (Ding et al. 2009), the surface of smear-ripened cheeses (Irlinger et al. 2005) and mural paintings (Heyrmanl et al. 2005). Psychrophilic members of the genus *Arthrobacter* including *A. psychrochitiniphilus* (Wang et al. 2009),

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A. alpinus (Zhang et al. 2010), *A. cryoconiti* (Margesin et al. 2012) and *Arthrobacter ruber* (Liu et al. 2018) were obtained from Antarctica and other cold environments. The wide distribution of *Arthrobacter* members is probably due to their nutritional versatility and their resistance to environmental stress factors. Recently, cold-active enzymes such as β-D-galactosidase and α-Amylase have been isolated from *Arthrobacter* species (Kim et al. 2017; Rutkiewicz et al. 2019), which indicated that psychrophilic species of the genus *Arthrobacter* have important potential sources of cold-active enzymes.

During an exploration of Antarctic microbial resources, a Gram-staining-positive, aerobic bacterium, designated strain Z1-20 T was isolated from a soil sample collected in Zhongshan station, Antarctic. In this study, strain Z1-20 ^{T} was characterized taxonomically using a polyphasic approach, and a novel species of the genus *Arthrobacter* is proposed.

Materials and methods

Isolation of microorganism

The strain Z1-20 ^{T} was isolated from a soil sample collected from the Zhongshan station, Antarctic. The soil sample was serially diluted in 1% (w/v) NaCl solution and inoculated onto R2A agar plates (0.5 g yeast extract, 0.5 g peptone, 0.5 g casamino acids, 0.5 g glucose, 0.5 g soluble starch, 0.3 g K_2HPO_4, 0.024 g $MgSO_4$, 0.3 g sodium pyruvate, pH7.0, 15 g agar in 1L) and then incubated at 15 °C for 7–10 days. The isolated strain was routinely cultured on R2A agar plates at 20 °C and maintained at 4 °C. It was also stored as glycerol suspensions (20%, v/v) at − 80 °C.

Phenotypic characterization

Strain Z1-20 ^{T} was grown for 4 days in R2A broth at 20 °C and 180 rpm. An aliquot of culture was stained with crystal violet and Gram's iodine. The morphological characteristics of strain Z1-20 ^{T} were observed using transmission electron microscope (model JEM-1200EX) after 4 days of growth on R2A agar plates. Growth at different temperatures (4, 10, 15, 20, 25, 28 and 37 °C) and different pH (pH 4.0–12.0 at intervals of 1.0 pH unit) were tested on R2A agar plates for 7–10 days. Media with different pH values were prepared using the buffer system described by Xu et al. (2005). The tolerance to different NaCl concentrations (0, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 15 and 20%, w/v) was tested on R2A agar plates as the basal plates by incubating the cultures for 7–10 days at 20 °C. Oxidase production was tested as described by McCarthy and Cross (1984). Catalase activity was detected by the production of bubbles following addition of a drop of 3% (v/v) H_2O_2. Hydrolysis of casein, gelatin, starch and tween 80 and nitrate reduction were determined as described by Cowan and Steel (1965). Carbon source utilization was determined using the API 50CH tests (BioMérieux, Marcy-l'Étoile, France) according to the manufacturer's instructions.

Phylogenetic and genome analyses

PCR amplification of the 16S rRNA gene fragment of the novel strain was performed. The 16S rRNA gene sequence of strain Z1-20 ^{T} was compared against a database of cultured species via the EzBio-Cloud Database (http://www.ezbiocloud.net/) (Yoon et al. 2017a, b) and multiple sequence alignment was programed via CLUSTAL W (MEGA 7.0) (Larkin et al. 2007). Neighbor-joining phylogenetic and maximum-likelihood phylogenetic trees were constructed using MEGA 7.0 (Kumar 2016; Felsenstein 1985; Saitou and Nei 1987), and PHYML phylogenetic tree was generated using the web (http://www.atgc-montpellier.fr/phyml/) after multiple alignment of data by CLUSTAL W (Larkin et al. 2007). Distances (distance options according to the Kimura two-parameter model) and clustering were determined using the neighbor-joining method. Bootstrap analysis was used to evaluate the tree topology of the neighbor-joining data by performing 1000 resamplings (Fitch 1970).

Genomic DNA for the genome sequencing was extracted via the Genomic DNA Rapid Isolation Kit for Bacterial Cell (TIANGEN). The genomic DNA G + C content was determined from whole genome sequence data of the strain Z1-20 ^{T}. Digital DNA-DNA hybridization (dDDH) analysis to establish the precise taxonomic position of strain Z1-20 ^{T} was performed using the GGDC web (http://ggdc.dsmz.de) (Meier-Kolthoff et al. 2013). Average nucleotide identity (ANI) was calculated using the web services available at EzBio-cloud

(https://www.ezbiocloud.net/tools/ani) (Yoon et al. 2017a, b). A maximum-likelihood phylogenetic tree was constructed based on the alignment of 900 single-copy core genes with 26 *Arthrobacter* species, constructed by RAxML-NG (https://github.com/amkozlov/raxml-ng/) with an inferred model by ModelTest (https://github.com/ ddarriba/modeltest/), with 100 bootstrap replicates (Croucher et al. 2015).

Online tool antiSMAH (https://antismash.secondarymetabolites.org/#!/start) was used to predict the gene clusters of secondary metabolites in strains Z1-20 ^{T}, *A. glacialis* HLT2-12-2 ^{T} and *A. psychrochitiniphilus* GP3^{T}. For comparative analyses, Z1-20 ^{T}, *A. glacialis* HLT2-12-2 ^{T} and *A. psychrochitiniphilus* GP3^{T} were selected based on neighbor-joining phylogenetic tree and integrity and similarity of their genomes. GeneMarkS software (Besemer et al. 2001) was used to predict the protein-coding genes of bacterial genome. Comparing the protein sequence of the predicted gene with NR, eggNOG and KEGG databases were performed by diamond blastp. For this analysis, the comparison result with the highest score was selected for annotation and the following cutoff values were applied (e-value < 1e-6 and amino acid sequence identity of at least 40%).

Chemotaxonomic characterization

Biomass for chemotaxonomic analysis was obtained by cultivation in shake flasks (with shaking at about 180 rpm) using R2A liquid medium (1% (w/v) NaCl, pH 7.0) at 20 °C for 4 days. The analysis of peptidoglycan structure was carried out as described by Schumann (Schumann 2011) in DSMZ. Polar lipids were extracted, examined by two-dimensional TLC and identified using published procedures (Minnikin et al. 1984a, b; Minnikin et al. 1984a, b). Menaquinones were isolated using the methods of Minnikin et al. (Minnikin et al. 1984a, b; Minnikin et al. 1984a, b) and separated by HPLC (Kroppenstedt 2004). The cellular fatty acid compositions were determined according to the instructions of the Sherlock Microbial Identification System (MIDI Sherlock version 4.5, MIDI database TSBA40 4.10) (Kroppenstedt 2004; Sasser 1990).

Results and discussion

Morphological and phenotypic characteristic

Bacterial cells of strain Z1-20 ^{T} are ellipsoidal, non-spore-forming, approximately 0.43–0.79 μm wide and 0.71–1.4 μm long (Fig. S1). When tested on R2A agar plates, growth of strain Z1-20 ^{T} was observed at temperatures between 10 and 28 °C, with an optimum growth temperature of 20 °C and within the pH range pH 6.0–9.0, with an optimum of pH 8.0. The strain grew on R2A agar with NaCl concentrations range from 0 to 7% (w/v), with an optimum of 1%. Positive for oxidase, catalase, nitrate reduction, but negative for hydrolysis of casein, gelatin, starch, Tween80. The following substrates in the API 50CH tests were utilized: mannitol, D-mannose, D-glucose, D-fructose, aesculin, iron citrate, potassium gluconate and 2 potassium ketogluconate. Z1-20 ^{T} and the reference strains are shown in Table 1 and Table S1.

Phylogenetic characteristics

The almost-complete 16S rRNA gene sequence (1497 bp) of strain Z1-20 ^{T} was determined and compared against the EzBio-cloud Database (Kim et al. 2012) to retrieve most similar sequences of recognized bacteria. Strain Z1-20 ^{T} showed high sequence similarities to *Arthrobacter* species. The most closed 16S rRNA gene sequence similarity was found to *A. glacialis* HLT2-12-2 ^{T} (97.05%) (Liu et al. 2019), followed by *A. psychrochitiniphilus* GP3^{T} (96.92%) (Wang et al. 2009), *Pseudarthrobacter siccitolerans* 4J27^{T} and *P. phenanthrenivorans* Sphe3^{T}. Neighbor-joining and maximum-likelihood phylogenetic trees showed that the novel strain Z1-20 ^{T} formed a separate branch from the two closely related *Arthrobacter* type strains and *Pseudarthrobacter* clusters (formerly '*Arthrobacter oxydans*' group) (Fig. 1 and Fig. S3). The high consistency of phylogenetic position of strain Z1-20 ^{T} was also supported by the phylogenomic tree (Fig. 2) and other algorithms tested (Fig. S4). Based on the 16S rRNA gene sequence similarity and phylogenetic clustering, the closely related type strains *A. glacialis*, *A. psychrochitiniphilus* and the relative *P. siccitolerans* and *P. phenanthrenivorans*, as well as the type strain *P. polychromogenes* of the genus *Pseudarthrobacter* were chosen as reference

Table 1 Characteristics useful for differentiating strain Z1-20 ^{T} from the most closely related species of the genus *Arthrobacter* and *Pseudarthrobacter*

Characteristic	1	2	3	4	5	6
Colony color	Yellow	Creamy yellow	Yellow	Cream	Yellow	Blue-green
Growth temperature range (°C), optimum	10 – 28, 20	4 – 25, 20 – 25	0 – 25, 20	15 – 35, 30	4 – 37, 30 – 37	10 – 37, 25
Growth pH range, optimum	6 – 9, 8	7 – 8, 7	6 – 8, 7	5 – 9, 7	6.5 – 8.5, 7.0 – 7.5	6 – 11, 9 – 10
NaCl range for growth (%), optimum	0 – 7, 1	0 – 4, 0.5 – 2	0 – 3, 1	0 – 4, 1	NA	NA
Hydrolysis of:	–	–	+	–	NA	NA
Starch	–	–	+	–	NA	NA
Tween 80						
Nitrate reduction	+	+	–	+	+	+
Oxidase production	+	–	–	–	–	NA
Assimilation of						
D-Glucose	+	–	+	+	–	NA
D-Mannose	+	–	–	+	–	NA
D-Maltose	–	+	–	+	–	+
D-Sucrose	–	+	+	+	+	+
D-Trehalose	–	+	–	+	–	–
D-Cellobiose	–	+	–	+	–	NA
D-Gentiobiose	+	+	–	+	–	NA
D-Turanose	–	+	–	+	–	NA
Polar lipid	PG, DPG, PI and GL	PG, DPG, PI, DMG and L	PG, DPG, PI, GL, APL, PL and L*	NA	PG, DPG, PI, MGDG, DMG, TDG and L	PG, DPG, PI, MGDG, DMDG, TMDG and L
Peptidoglycan type	A3α (L-Lys-Thr-Ala_2, A11.27)	A3α (L-Lys-L-Thr-L-Ala_3; A11.28)[a]	A3α (L-Lys-Thr-Ala, A11.25)	A3α (L-Lys-L-Ser-L-Thr-L-Ala; A11.23)	NA	A3α (L-Lys-L-Ser-L-Thr-L-Ala; A11.23)
Major menaquinones	MK-9(H_2)	MK-9(H_2)	MK-9(H_2)	MK-9(H_2)	MK-9(H_2)	MK-9(H_2)
Major fatty acids	anteiso-$C_{15:0}$, anteiso-$C_{17:0}$, iso-$C_{15:0}$	anteiso-$C_{15:0}$, anteiso-$C_{17:0}$, iso-$C_{16:0}$	anteiso-$C_{15:0}$, anteiso-$C_{17:0}$, iso-$C_{16:0}$	anteiso-$C_{15:0}$, $C_{17:0}$, $C_{16:0}$ and iso-$C_{16:0}$	iso-$C_{15:0}$, anteiso-$C_{15:0}$, iso-$C_{16:0}$, $C_{16:0}$ and anteiso-$C_{17:0}$	anteiso-$C_{15:0}$ and anteiso-$C_{17:0}$
G + C content (mol%)*	63.0	61.4	58.5	65.3	67.5	62.9
ANI (%)	–	72.45	72.1	72.9	72.45	72.9
dDDH (%)	-	20.3	13.8	20.1	20.8	20.1

Strains: 1, Z1-20 ^{T}; 2, *A. glacialis* HLT2-12-2 ^{T}; 3, *A. psychrochitiniphilus* GP3^{T}; 4, *P. siccitolerans* 4J27^{T}; 5, *P. phenanthrenivorans* Sphe3^{T}; 6, *P. polychromogenes* WS 1989 ^{T}

PG phosphatidylglycerol; *DPG* diphosphatidylglycerol; *PI* phosphatidylinositol; *GL* unidentified glycolipid; *L* unidentified lipid

Data for reference species were taken from Busse (2016); Busse and Schumann (2019); Kallimanis et al. (2013); Liu et al. (2019); SantaCruz-Calvo et al. (2013); Schippers-Lammertse et al. (1963); Wang et al. (2009) and *the present study. + positive, – negative, NA, no data available

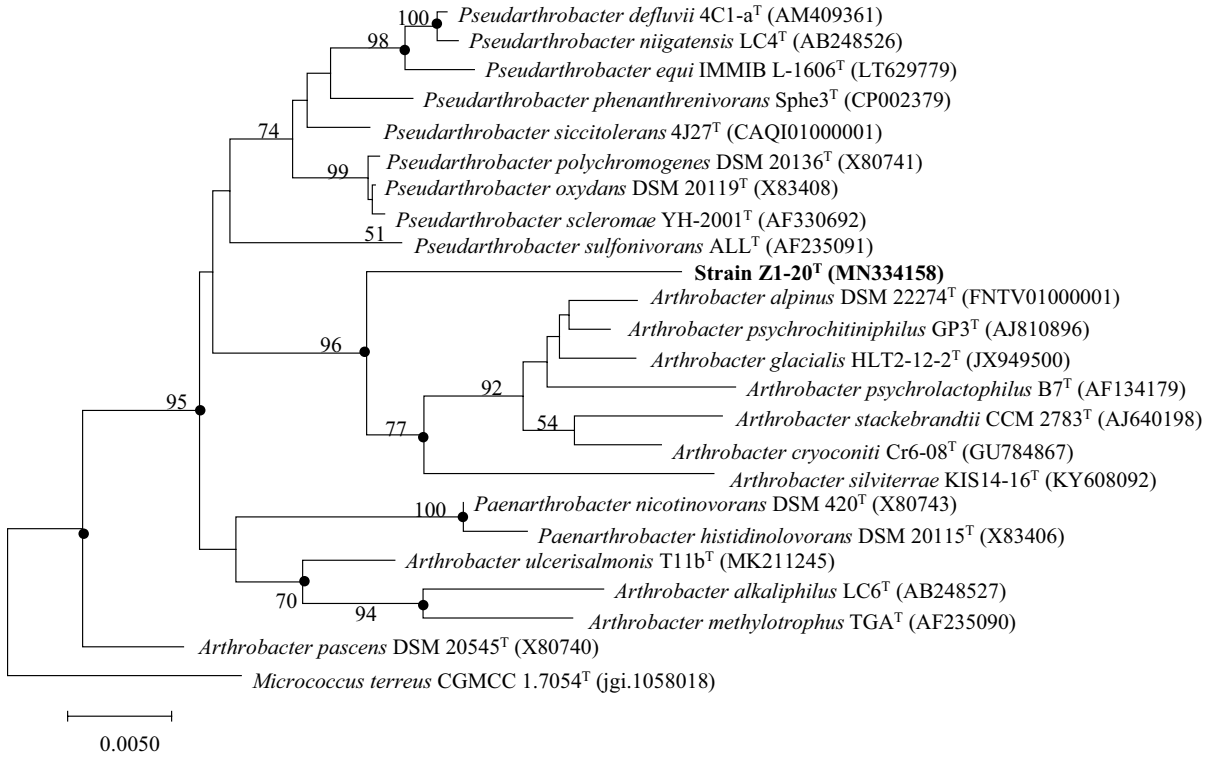

Fig. 1 Neighbor-joining phylogenetic tree based on 16S rRNA gene sequences (1408 bp) showing the phylogenetic position of strain Z1-20 ^{T} within the family Micrococcaceae. Dots (•) indicates the clades that were conserved in the maximum-likelihood phylogenetic tree and PHYML phylogenetic tree. Bootstrap values are shown on nodes in percentages of 1,000 replicates, when greater than 50%. Bar, 5 substitutions per 1000 nt

strains for further comparative study to determine the taxonomic position of the novel strain Z1-20 ^{T}.

Genomic characteristics

The genome size of strain Z1-20 ^{T} was about 4.43 Mb with 4351 genes and 69 tRNA genes and a single 16S rRNA gene. The DNA G+C content of the strain Z1-20 ^{T} was calculated to be 63.0% from genome data. Digital DNA-DNA hybridizations (dDDH) values between strain Z1-20 ^{T} against the reference strains were 13.8–20.8%, which were clearly below the 70% threshold generally accepted for species delineation (Wayne et al. 1987). Average nucleotide identity (ANI) score between strain Z1-20 ^{T} against the reference strains ranged from 72.1 to 72.9%. The ANI values lower than 95% (Kim et al. 2014) found between the new strain and its closest related species could also support strain Z1-20 ^{T} representing a novel species. In addition, maximum-likelihood phylogenomic tree based on the alignment of 900 single-copy core genes showed high consistency of the phylogenetic position of strain Z1-20 ^{T}, which support the designation of strain Z1-20 ^{T} as a novel species (Fig. 2). The above genomic analysis results confirm that the strain Z1-20 ^{T} represents a new taxon.

AntiSMASH analysis of the genome of Z1-20 ^{T} found six type biosynthesis gene clusters: bacteriocin, butyrolactone, terpene, betalactone, T3PKS and NRPS, showing a slight difference with the two reference strains (Table S2). Genes associated with cold adaptation in the genome of strain Z1-20 ^{T} have been revealed (Table 2 and Supplementary file 1) which include cold shock response, osmoprotection protection, oxidative stress risistance and membrane adaptations. Z1-20 ^{T} has an uptake system for organic osmoprotectants, as suggested by the identification of several genes coding for ABC-type glycine betaine/

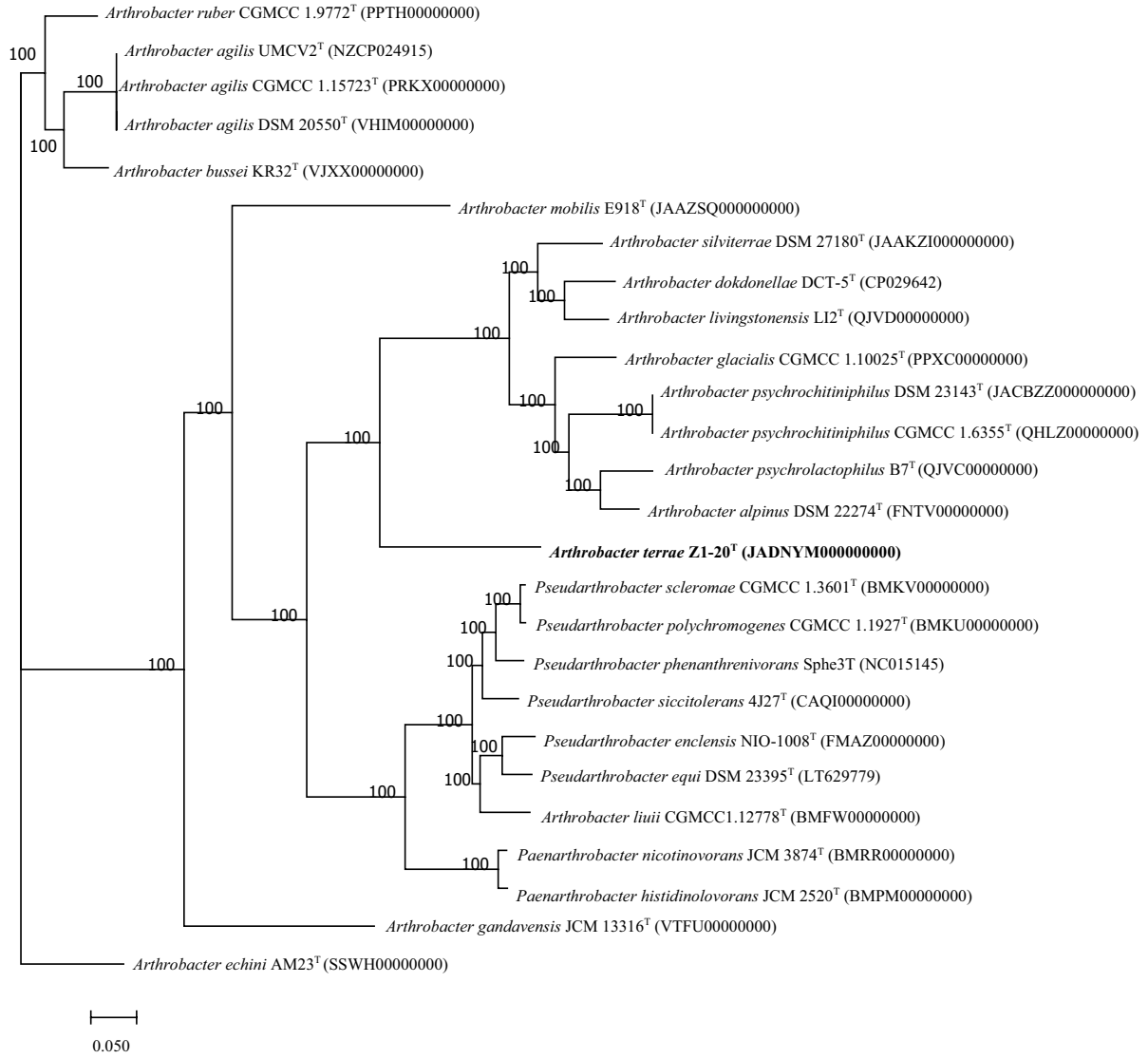

Fig. 2 A maximum-likelihood phylogenetic tree was generated from the alignment of 900 single-copy core genes, with bootstrap support values from 100 replicates. Bold font indicates the position of strain Z1-20 T

proline transporters, as well as a putative betAB pathways for the formation of glycine betaine/proline. It is well known that glycine betaine often acts as a cryoprotectant to protect bacteria from cold environments by preventing cold-induced aggregation of cellular proteins and maintaining membrane fluidity at low temperature (Ko et al. 1994; Chattopadhyay 2002). Besides accumulating osmoprotectants from the environment, strain Z1-20 T is also capable of synthesizing compatible solutes. Two putative pathways are present for the formation of trehalose. Genes predicted to code for trehalose-6-phosphate synthase and trehalose-6-phosphate phosphatase, comprising the OtsAB pathway for trehalose synthesis from UDP-D-glucose and α-D-glucose-6-phosphate, as well as the genes for the alternative TreYZ pathway (Table 2 and Supplementary file 1). Interestingly, there are a higher number of tRNA and copies of gene encoding cold shock protein CapA compared with strain *A. glacialis* HLT2-12-2 T and A. *psychrochitiniphilus* GP3T. CapA can be induced following the cold shock and remain overexpressed several hours

Table 2 Genes linked to environmental stress response in strain Z1-20 ^{T} and the reference strains

Product name	Strains		
	1	2	3
Sigma factors	7	8	9
Oxidative stress resistance	10	13	14
Osmoprotection			
Glycogen metabolism	5	5	9
Trehalose metabolism	5	3	5
Biosynthesis of glycine betaine/proline	2	1	1
Glycine betaine/proline ABC transporter	6	5	5
Cold shock response	11	9	9
Membrane adaptations	2	2	1
Carotenoid biosynthesis	5	5	7

Strains: 1, Z1-20 ^{T}; 2, *A. glacialis* HLT2-12-2 ^{T}; 3, *A. psychrochitiniphilus* GP3^{T}

after the temperature downshift which could be the key factors contributing to the survival ability in cold Antarctic environments (Phadtare et al. 1999). Sufficient number of tRNA in the genome also explains its translational efficiency and survival in the unfavorable conditions in Antarctic.

Chemotaxonomic characterization

The purified amino acids in total hydrolysates (4 N HCl, 100 °C, 16 h) of peptidoglycan were alanine, glutamic, threonine and lysine in a molar ratio of 2.7:1.0:0.4:0.3. The peptidoglycan type was A3α (L-Lys-Thr-Ala2, A11.27) and lysine was the diagnostic diamino acid. The menaquinones of strain Z1-20 ^{T} were MK-9(H_2) (55.5%), MK-8(H_2) (37.7%) and MK-7(H_2) (6.8%), while the polar lipids were phosphatidylglycerol (PG), diphosphatidylglycerol (DPG), phosphatidylinositol (PI) and one unidentified glycolipid (GL) (Fig. S2). There is a distinct difference in the peptidoglycan structures between Z1-20 ^{T} and *Pseudarthrobacter* strains. The peptidoglycan interpeptide chain of Z1-20 ^{T} detected in DSMZ is Lys-Thr-Ala2, corresponding to peptidoglycan structure A11.27, while *Pseudarthrobacter* sp. strains have A3α peptidoglycan type with Lys-Ser-Thr-Ala in the interpeptide corresponding to A11.23 which distinguished distinctly from *Arthrobacter* sp. Strain ZS1-20 ^{T} was composed of the major lipids PG, DPG, PI and one GL, which was also found in the most closed

Table 3 Cellular fatty acid compositions (%) of strain Z1-20 ^{T} and the two most closely related type strains of the genus *Arthrobacter*

Fatty acid	1	2	3
Saturated fatty acid:			
$C_{14:0}$	TR	–	–
$C_{16:0}$	1.7	3.6	TR
Branched:			
iso-$C_{14:0}$	TR	TR	1
iso-$C_{15:0}$	**16.6**	2.6	TR
iso-$C_{16:0}$	**6.6**	**6.6**	TR
Iso-$C_{17:0}$	3.4	–	–
anteiso-$C_{15:0}$	**45.4**	**71.9**	**75.6**
anteiso-$C_{17:0}$	**20.7**	**12.6**	**13.9**

Strains: 1, Z1-20 ^{T}; 2, *A. glacialis* HLT2-12-2 ^{T}; 3, *A. psychrochitiniphilus* GP3^{T}

Data are expressed as percentages of total fatty acids. Major components (> 5.0%) are highlighted in bold. Fatty acids amounting to less than 0.5% in all strains are not shown. TR, trace amount (< 1%); –, not detected

A. glacialis HLT2-12-2 ^{T} and *A. psychrochitiniphilus* GP3^{T}. While the relative *Pseudarthrobacter* strains contained the major compounds DPG, PI, PG and three GL. The almost identical polar lipids profiles and peptidoglycan variations supported that strain Z1-20 ^{T} belongs to the genus *Arthrobacter*. The cellular fatty acids (> 10% of the total fatty acids) were anteiso-$C_{15:0}$ (45.4%), anteiso-$C_{17:0}$ (20.7%) and iso-$C_{15:0}$ (16.6%) (Table 3). The composition profile with anteiso-$C_{15:0}$ as the main fatty acid is typical of species of *Arthrobacter* genus (Lee et al. 2003) that confirmed strain Z1-20 ^{T} belongs to the genus *Arthrobacter*. The above chemotaxonomic characteristics of strain Z1-20 ^{T}, such as peptidoglycan type, major fatty acids, major menaquinone and phospholipids were consistent with its assignment to the genus *Arthrobacter*.

Strain Z1-20 ^{T} differed greatly from the closely related *Arthrobacter* type strains in terms of some of its phylogenetic, biochemical, chemotaxonomic and physiological data (Tables 1, 3 and Table S1). The NaCl tolerance range of Z1-20 ^{T} was slightly higher than *A. glacialis* HLT2-12-2 ^{T} and *A. psychrochitiniphilus* GP3^{T}. The growth under 10 °C was nonvisible. The ability to oxidase production was different from *A. glacialis* HLT2-12-2 ^{T} and *A. psychrochitiniphilus* GP3^{T}. Meanwhile, the content of iso-$C_{15:0}$ of

the fatty acids of strain Z1-20^{T}differed distinctly from the two reference strains, although a relative high proportion of iso-$C_{15:0}$ is common on *Arthrobacter* members such as *A. koreensis* and *A. globiformis* (Lee et al. 2003; Hahne et al. 2019). Furthermore, digital DNA-DNA hybridizations values between strain Z1-20 ^{T} against the type strains of *A. glacialis* HLT2-12-2 ^{T} and *A. psychrochitiniphilus* GP3^T were 20.3% and 13.8%, respectively and average nucleotide identity score between strain Z1-20 ^{T} against *A. glacialis* HLT2-12-2 ^{T} and *A. psychrochitiniphilus* GP3^T were 72.5% and 72.1%, respectively. Based on the phenotypic and genotypic results obtained in this study, it is concluded that strain Z1-20 ^{T} represents a novel species of the genus *Arthrobacter*, for which the name *Arthrobacter terrae* sp. nov. is proposed.

Description of *Arthrobacter terrae* sp. nov

Arthrobacter terrae (ter'rae L. gen. fem. n. terrae, of the earth), Z1-20 ^{T} (=CCTCC AA 2019079 ^{T}=KCTC49361^T), was isolated from a soil sample collected at Zhongshan station, Antarctic. Cells are Gram-staining-positive, non-spore-forming, non-flagellated, ellipsoidal, approximately 0.43–0.79 μm wide and 0.71–1.4 μm long (Fig. S1). Colonies of the novel strain Z1-20 ^{T} are yellow, convex, dry and opaque, with smooth and entire margins and the diameter is 1.0–1.5 mm after incubation on R2A agar for 72 h at 20 °C. Growth occurs at 10–28 °C (optimum 20 °C), at pH 6.0–9.0 (optimum pH 8.0) and in the presence of 0–7% (w/v) NaCl (optimum, 1%). Major polar lipids are phosphatidylglycerol (PG), diphosphatidylglycerol (DPG), phosphatidylinositol (PI) and one unidentified glycolipid (GL). The major fatty acids are anteiso-$C_{15:0}$, anteiso-$C_{17:0}$ and iso-$C_{15:0}$ and the predominant menaquinone is MK-9(H_2). The peptidoglycan type is A3α. The DNA G+C content of the genomic DNA of the type strain is 63.0%.

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Author contributions PJ, XR, WW and GN equally contributed to this work.

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Data availability The genome sequence of *Arthrobacter terrae* Z1-20 ^{T} has been deposited in the GenBank database under the accession number JADNYM000000000. The GenBank accession number of the 16S rRNA gene sequence of strain Z1-20 ^{T} is MN334158.

Declarations

Conflict of interest The authors declare that there are no conflicts of interest.

Ethical approval This article does not contain any studies with human participants and/or animals performed by any of the authors. Moreover, all authors read and approved the final manuscript.

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