Antonie van Leeuwenhoek (2017) 110:1077–1086
DOI 10.1007/s10482-017-0882-y

ORIGINAL PAPER

Altererythrobacter lauratis sp. nov. and *Altererythrobacter palmitatis* sp. nov., isolated from a Tibetan hot spring

Chang-Guo Yuan · Xing Chen · Zhao Jiang · Wei Chen · Lan Liu · Wen-Dong Xian · Mipeshwaree Devi Asem · Xiao-Yang Zhi · Wen-Jun Li

Received: 22 December 2016 / Accepted: 25 April 2017 / Published online: 3 May 2017

Abstract Two Gram-negative, moderately thermophilic, yellow-pigmented, rod-shaped and motile bacterial strains, designated YIM 75003^T and YIM 75004^T, were isolated from sediment samples collected from the Tagejia hot spring in Tibet, western China. The taxonomic affiliation of the two strains was investigated by a polyphasic approach. Pairwise comparison of the 16S rRNA gene sequences showed that strains YIM 75003^T and YIM 75004^T are closely related to *Altererythrobacter buctense* M0322^T (97.2 and 97.1% respectively), while sharing 99.9% sequence similarity against each other. Optimum growth of the two strains was observed at 37–45 °C, pH 8.0 and in the presence of 1–6% NaCl (w/v). Their predominant respiratory quinone was found to be ubiquinone 10. The major fatty acids in both the strains were identified as summed feature 8 ($C_{18:1}$ $\omega 6c$ and/or $C_{18:1}$ $\omega 7c$) and summed feature 4 ($C_{17:1}$ anteiso B and/or iso I). Their major polar lipid profiles were found to be diphosphatidylglycerol, phosphatidylcholine, phosphatidylethanolamine, phosphatidylglycerol and sphingoglycolipid. The DNA G+C contents of strains YIM 75003^T and YIM 75004^T were determined to be 61.3 and 60.1 mol%, respectively. The DNA-DNA hybridization values between strains YIM 75003^T and YIM 75004^T, and between the two strains and their closely related phylogenetic neighbour *A. buctense* M0322^T (=CGMCC 1.12871^T) were less than 70%. Based on the morphological and physiological properties, phylogenetic analyses, chemotaxonomic characteristics and DNA–DNA relatedness values, the two strains can be distinguished from each other and from their phylogenetically closely related strain. Strains YIM 75003^T and YIM 75004^T are, therefore, considered to represent two novel species of the genus *Altererythrobacter*, for which the names *Altererythrobacter lauratis* sp. nov. (type strain YIM 75003^T = KCTC 52606^T = CCTCC AB2016268^T) and *Altererythrobacter palmitatis* sp. nov. (type strain YIM 75004^T = KCTC 52607^T = CCTCC AB2016270^T) are proposed.

Chang-Guo Yuan, Xing Chen and Zhao Jiang have contributed equally to this work.

Electronic supplementary material The online version of this article (doi:10.1007/s10482-017-0882-y) contains supplementary material, which is available to authorized users.

C.-G. Yuan · Z. Jiang · X.-Y. Zhi (✉) · W.-J. Li (✉)
Yunnan Institute of Microbiology, Yunnan University, Kunming 650091, People's Republic of China
e-mail: xyzhi@ynu.edu.cn

W.-J. Li
e-mail: liwenjun3@mail.sysu.edu.cn

X. Chen · W. Chen
China Tobacco Yunnan Industrial Co. Ltd., Kunming 650231, People's Republic of China

L. Liu · W.-D. Xian · M. D. Asem · W.-J. Li
State Key Laboratory of Biocontrol and Guangdong Provincial Key Laboratory of Plant Resources, School of Life Sciences, Sun Yat-Sen University, Guangzhou 510275, People's Republic of China

Keywords *Altererythrobacter lauratis* sp. nov. · *Altererythrobacter palmitatis* sp. nov. · Polyphasic taxonomy · Tagejia hot spring

Introduction

Hot springs are one of the extreme ecosystems with limited life forms due to their harsh conditions. Despite the extreme environments, Tibet's hot springs have been reported to possess diverse microbial communities, including several novel taxa (Huang et al. 2011). Microorganisms from such extreme habitats may be an important source for novel enzymes and metabolites applicable to biotechnological industries (Song et al. 2009). The genus *Altererythrobacter*, belonging to the family Erythrobacteraceae, was first described by Kwon et al. (2007), and emended subsequently by Xue et al. (2012, 2016). At the time of writing, the genus contains 25 species with validly published names, the majority of which were isolated from deep-sea sediment (e.g. Wu et al. 2014; Zhang et al. 2016a) or sea water (e.g. Park et al. 2011). Phylogenetically, the genus is polyphyletic in nature with members of this genus being grouped along with the genera *Erythrobacter* and *Porphyrobacter* within the family Erythrobacteraceae. The characteristic features of this genus include Gram-staining negative, absence of bacteriochlorophyll *a* (Bchl *a*) and Q-10 as dominant respiratory quinone. Only four species have been reported to possess flagella (Seo and Lee 2012; Nedashkovskaya et al. 2013; Wu et al. 2014; Zhao et al. 2017). During an investigation of microbial diversity of hot springs, two yellow-pigmented, moderately thermophilic strains were isolated from samples collected from the Tagejia geothermal fields of the Tibetan Plateau. This paper reports the taxonomic characterization of the two strains YIM 75003^T and YIM 75004^T as novel species of the genus *Altererythrobacter*.

Materials and methods

Strains and culture conditions

Strains YIM 75003^T and YIM 75004^T were isolated from samples collected from the Tagejia geothermal field (29°24′51.11″N, 86°43′58.02″E) by serial dilution plating on Cellulose-Casamino (CC) agar (Microcrystalline cellulose, 1.0 g; Casamino acid, 1.0 g; KNO_3, 0.2 g; Na_2HPO_3, 0.5 g; $MgSO_4$, 0.05 g; $FeSO_4$, 0.01 g; Agar, 12.0 g; Distilled water, 1 L; pH 7.2 ± 0.2). The isolation plates were kept incubated at 45 °C for 15 days. Single colonies were repeatedly streaked on Reasoner's 2A agar (R2A agar; Reasoner and Geldreich 1985) for purification, and pure cultures were routinely cultivated on the same medium. Both strains were stored as glycerol suspensions (20%, v/v) at −80 °C. The type strain *Altererythrobacter buctense* M0322^T (=CGMCC 1.12871^T) was obtained from the China General Microbiological Culture Collection Center (CGMCC) and was cultivated on R2A agar at 30 °C for comparative taxonomic work.

Morphological, physiological and biochemical characterization

For morphological studies, strains YIM 75003^T and YIM 75004^T were cultured at 45 °C on R2A agar adjusted to pH 7.2. Morphology was examined by light microscopy (model BH2; Olympus) and transmission electron microscopy (JEM-2100; JEOL). Gram staining was carried out by using the standard Gram staining procedure and confirmed by KOH lysis test (Buck 1982). Growth at different temperatures (4, 10, 15, 20, 28, 37, 45, 50, 55, 60, 65 and 70 °C) and NaCl tolerance (0–12.0% w/v, at intervals of 1.0 unit) was determined using R2A broth. The pH range (4.0–11.0, at intervals of 1.0 pH unit) for growth was tested in R2A broth using the buffer system described by Xu et al. (2005). Growth on several media such as nutrient agar (NA), trypticase soy agar (TSA) (Waksman 1967), Luria–Bertani (LB) agar (Atlas 1997), R2A agar, MR agar (Zhang et al. 2016b) and other media at 45 °C were also evaluated. Oxidase activity was tested via the oxidation of tetramethyl-*p*-phenylenediamine (Kovacs 1956). Catalase activity was detected by assessing the production of bubbles on addition of a drop of 3% (v/v) H_2O_2. H_2S production, milk peptonization and coagulation, urease activity and hydrolysis of cellulose, gelatin, starch and Tweens (20, 40 and 80) were performed as described by Gonzalez et al. (1978). Sole carbon source utilization was determined using the methods described by Shirling and Gottlieb (1966) and Locci

(1989), while sole nitrogen source utilization was examined according to Williams et al. (1989). Cellular pigments were extracted as described by Rainey et al. (2003) using culture grown on R2A broth under darkness, and absorbance of the pigments were measured with a U-4100 spectrophotometer (HITACHI, Japan). Other biochemical tests were carried out using the API 20NE, API ZYM and API 50CHB/E test strips (bioMérieux) according to the manufacturer's instructions. Antibiotic susceptibility tests were performed by the agar-diffusion method on R2A agar (30 °C, 4 days) after plating with bacterial suspensions equivalent to 0.5 McFarland standards.

Chemotaxonomy

The polar lipids were prepared as described by Minnikin et al. (1979) and identified by two-dimensional TLC (Collins and Jones 1980). Menaquinones were extracted (Collins et al. 1977) and analysed using HPLC (Kroppenstedt 1982). Cellular fatty acids analysis was performed by using the Microbial Identification System (Sherlock Version 6.1; MIDI database: TSBA6; Sasser 2001). Biomass for fatty acid analysis was obtained from cells grown on R2A agar at 30 °C for 4 days. The G+C contents of the genomic DNAs were determined by using reversed-phase HPLC (Mesbah et al. 1989), with *Escherichia coli* DH5α as the reference strain.

Molecular analysis and DNA–DNA hybridization

Extraction of genomic DNAs and PCR amplification of the 16S rRNA genes were performed as described by Li et al. (2007). The amplicons were purified, cloned into Trans1-T1 chemically competent cells using *pEASY*-T1 vector and sequenced by Sangon Biotech (Shanghai). The sequences were compared with available 16S rRNA gene sequences of validly published species from the EzBioCloud server (Yoon et al. 2016). Multiple alignments with sequences of the most closely related taxa were carried out by using CLUSTAL_X program (Thompson et al. 1997). Phylogenetic analyses were performed by using three tree-making algorithms: neighbour–joining (Saitou and Nei 1987), maximum-likelihood (Felsenstein 1981) and maximum-parsimony (Fitch 1971). The dendrograms were generated by using the MEGA version 6.0 software package (Tamura et al. 2013). Kimura's two parameter model (Kimura 1980) was used to calculate evolutionary distance matrices of the neighbour–joining tree. Bootstrap analysis was performed with 1000 replications (Felsenstein 1985). *Caulobacter vibrioides* CB51^T (AJ009957) was used as outgroup. DNA–DNA relatedness was studied between strains YIM 75003^T and YIM 75004^T, and with the phylogenetically closely related strain *A. buctense* M0322^T (=CGMCC 1.12871^T) using the fluorometric micro-well method (Ezaki et al. 1989; Christensen et al. 2000) at 45 °C as the optimal hybridization temperature. One of the two DNA molecules for hybridization was labeled while the other was immobilized, and vice versa. Six replications were done for each sample and the two extreme values (highest and lowest) for each sample were excluded. The relatedness values are expressed by calculating the means of the remaining four values.

Results and discussion

Phenotypic characteristics

Cells of strains YIM 75003^T and YIM 75004^T were observed to be Gram-negative, aerobic, rod-shaped and motile. Transmission electron microscopy showed that strain YIM 75003^T measured 0.3–0.7 μm in width and 1.2–3.8 μm in length, while strain YIM 75004^T measured about 0.3–0.7 μm in width and 0.8–1.6 μm in length (Fig. S1). Both the strains possessed a polar flagellum (Fig. S1). Colonies of the two strains on R2A agar after 3 days of incubation at 45 °C were yellow-pigmented. While colonies of strain YIM 75003^T were smooth and measured approximately 1.5–2 mm in diameter, those of strain YIM 75004^T were found to be rough and approximately 0.6–0.8 mm in diameter. Both strains were found to grow well on R2A and MR agar, but not on LB agar, TSA or NA. Growth was observed at a temperature range of 10–55 °C (optimum, 37–45 °C) and in the presence of up to 11% NaCl (w/v) (optimum, 1–6%). The two strains showed optimum growth at pH 8.0 but differed in their pH range for growth. Strain YIM 75003^T exhibited growth at pH 5.0–11.0 while strain YIM 75004^T at pH 5.0–9.0. The two strains were observed to be positive for catalase, oxidase and cellulase activities, but negative for H_2S production and urease activity. The two strains utilised acetate

sodium, citrate sodium, fucose, glycerol, inositol, malate sodium, maltose, mannitol, mannose, succinate sodium, sucrose, alanine, arginine, cysteine, glycine, isoleucine, ornithine, phenylalanine, proline, serine, tyrosine, threonine and valine as sole carbon or nitrogen sources, but not arabinose, fructose, galactose, glucose, glycine, rhamnose or xylose. While strain YIM 75003^T utilised pyruvate sodium and saccharose, strain YIM 75004^T could utilise ribose, sorbose and xylitol. Other biochemical activities as determined by the API 20NE, API ZYM and API 50CHB/E test strips (bioMérieux) are presented in Supplementary Table S1. The pigment extracts of the two strains showed absorption maxima at 453 and 480 nm, and did not exhibit any characteristic absorbance at 805 and 830–890 nm indicating the absence of Bchl *a*. The two strains were found to be sensitive to amikacin (30 μg), cefuroxime sodium (30 μg), chloramphenicol (30 μg), erythromycin (15 μg), gentamicin (10 μg), penicillin (10 IU), piperacillin (100 μg) polymyxin B (300 IU), sulfamethoxazole (300 μg), tetracycline (30 μg) and vancomycin (30 μg), but resistant to ethylhydrocupreine (5 μg). Furthermore, strain YIM 75004^T was sensitive to ciprofloxacin (5 μg) and oxacillin (1 μg), but not strain YIM 75003^T. Detailed physiological characteristics of the two strains are given in the species description, and the differential characteristics between strains YIM 75003^T, YIM 75004^T and the closely related type strains of the genus *Altererythrobacter* are listed in Table 1.

Chemotaxonomy

The major respiratory quinone identified in strains YIM 75003^T and YIM 75004^T was observed to be ubiquinone-10 (Q-10), however small percentages of Q-8 and Q-9 were also detected. The major fatty acids (>10%) of strains YIM 75003^T were summed feature 8 ($C_{18:1}$ $\omega6c$ and/or $C_{18:1}$ $\omega7c$), summed feature 4 ($C_{17:1}$ anteiso B and/or iso I) and $C_{16:0}$, while for strain YIM 75004^T were summed feature 8 ($C_{18:1}$ $\omega6c$ and/or $C_{18:1}$ $\omega7c$), summed feature 4 ($C_{17:1}$ anteiso B and/or iso I), $C_{17:1}$ $\omega6c$ and $C_{16:0}$ (Table 2). The major polar lipid profiles of strains YIM 75003^T and YIM 75004^T consisted of diphosphatidylglycerol, phosphatidylcholine, phosphatidylethanolamine, phosphatidylglycerol and sphingoglycolipid (Fig. S2). While two unidentified glycolipids and four unidentified lipids were also detected in the former as minor polar lipids, two unidentified glycolipids and two unidentified lipids were found in the latter (Fig. S2). The G+C contents of strains YIM 75003^T and YIM 75004^T were determined to be 61.3 and 60.1 mol%, respectively.

Phylogenetic analysis and DNA–DNA relatedness value

Sequence comparison of the almost complete 16S rRNA gene sequences of strains YIM 75003^T (GenBank Accession Number KX808673) and YIM 75004^T (KX808674) using the NCBI-BlastN analyses showed that the two strains are closely related to members of the genus *Altererythrobacter* and showed high sequence similarities with *A. buctense* M0322^T (97.2 and 97.1%, respectively). The two strains however showed 99.9% sequence similarity among themselves. Phylogenetic trees based on 16S rRNA gene sequences were generated using the 1343 unambiguously aligned positions that remained after trimming in the MEGA 6 software. In the neighbour–joining phylogenetic tree (Fig. 1), the two strains formed a close clade with *A. buctense* M0322^T, *A. salegens* XY-R17^T and *A. atlanticus* 26DY36^T. The stability of the neighbour–joining tree was supported by the dendrograms generated with maximum likelihood and maximum parsimony methods (Figs. S3 and S4). Since the sequence similarities among the two strains and with *A. buctense* M0322^T were above 97%, DNA–DNA hybridization experiments were performed between strains YIM 75003^T, YIM 75004^T and *A. buctense* M0322^T (= CGMCC 1.12871^T) to determine their genomic DNA relatedness. The DNA–DNA relatedness values of strains YIM 75003^T and YIM 75004^T with *A. buctense* M0322^T (=CGMCC 1.12871^T) was determined to be 53.0 ± 2.2 and 41.5 ± 1.1%, respectively, while the two strains had a relatedness value of 44.8 ± 1.4% between themselves (Table S2). These values are less than cut-off point (70%) for the delineation of genomic species (Wayne et al. 1987).

Based on the phylogenetic analysis (Fig. 1) and comparison of the phenotypic and chemotaxonomic markers such as presence of Q-10 as respiratory quinone (Fig. S2), strains YIM 75003^T and YIM 75004^T should be affiliated to the genus *Altererythrobacter*. The major polar lipid profiles of the two strains were found to be similar to that of *A. salegens* XY-R17^T (Liang et al. 2016), but can be differentiated

Table 1 Different characteristics of strains YIM 75003^T, YIM 75004^T with phylogenetically related species of the genus *Altererythrobacter*

Characteristic	1	2	3	4[b]	5[c]
Source of isolation	Hot spring sediment	Hot spring sediment	Mudstone core[a]	Mangrove sediment	Marine sediment
Cell shape	Short rod	Short rod	Short rod[a]	Short rod	Ovoid-rod
Motility	+	+	–	–	–
Oxidase	+	+	+	–	+
Growth range (optimum)					
Temperature (°C)	10–55 (37–45)	10–55 (37–45)	15–40 (30)[a]	10–35 (30)	20–40 (35)
pH	5–11 (8)	5–9 (8)	5–10 (6–7)[a]	6.5–8 (7–7.5)	6–8.5 (6.5)
NaCl (%)	0–11 (1–6)	0–11 (1–6)	0–4 (0)[a]	2–10 (3–8)	0–6 (2)
Hydrolysis of					
Aesculin	+	+	+[a]	+	–
Tween 20	+	–	+[a]	+	–
Tween 40	–	+	ND[a]	+	+
Tween 80	–	–	–[a]	–	+
Nitrate reduction	–	+	–	+	–
Urease activity	–	–	–/(+[a])	–	–
Utilization of					
Galactose	–	–	+	–	–
Glycerol	+	+	–	ND	–
Pyruvate	+	–	+	ND	–
Ribose	–	+	–	ND	ND
Sorbose	–	+	+	ND	ND
Xylitol	–	+	+	ND	–
Aspartic acid	–	–	+	ND	–
Histidine	–	+	+	ND	–
Lysine	–	+	+	ND	ND
Enzyme activity (API ZYM)					
Cystine arylamidase	–	+	+	+	+
β-Glucuronidase	–	–	+	+	–
Leucine arylamidase	+	–	–	+	+
Assimilation of (API 20NE)					
N-Acetylglucosamine	–	–	+	–	+
Capric acid	–	+	–	–	–
Acid production from					
D-fructose	+	–	–	+	–
Mannitol	–	–	+	ND	+
D-xylose	+	+	–	ND	ND
Sensitive to					
Ciprofloxacin	–	+	+	+	ND
Ethylhydrocupreine	–	–	+	ND	ND
Piperacillin	+	+	–	ND	ND
DNA G+C content (mol%)	61.3	60.1	64.6[a]	64.7	54.5

Strains: *1* YIM 75003^T; *2* YIM 75004^T; *3 A. buctense* M0322^T (= CGMCC 1.12871^T); *4 A. salegens* XY-R17^T; *5 A. epoxidivorans* JCS350^T. Unless stated otherwise, data are taken from this study

+ positive, − negative, *ND* Not determine or data not available in relevant literature

[a] Data from Zhang et al. (2016b)

[b] Data from Liang et al. (2016)

[c] Data from Kwon et al. (2007)

Table 2 Cellular fatty acid composition of strains YIM 75003^T, YIM 75004^T and their closely related strains

Fatty acids (%)	1	2	3		4	5	
	This study	This study	This study	Zhang et al. (2016b)	Liang et al. (2016)	Kumar et al. (2008)	Kwon et al. (2007)
Saturated fatty acids							
$C_{12:0}$	*Tr*	–	–	–	–	–	–
$C_{14:0}$	*Tr*	*Tr*	*Tr*	*Tr*	–	–	–
$C_{16:0}$	16.8	10.2	13.0	2.7	3.1	4.5	3.1
$C_{17:0}$	3.9	3.6	1.6	–	*Tr*	–	–
$C_{18:0}$	*Tr*	*Tr*	*Tr*	1.6	1.0	–	–
$C_{17:0}$ cyclo	–	–	–	–	–	–	6.9
Branched fatty acids							
Iso-$C_{14:0}$	–	–	*Tr*	–	–	–	–
$C_{15:1}$ *ω6c*	–	–	*Tr*	*Tr*	–	–	–
$C_{16:1}$ *ω5c*	–	*Tr*	*Tr*	0.7	4.9	1.4	2.2
$C_{17:1}$ *ω8c*	1.3	1.8	2.3	2.6	0.9	0.8	–
$C_{17:1}$ *ω6c*	7.4	10.7	5.2	6.6	9.5	12.1	–
$C_{18:1}$ *ω7c*	–	–	–	–	–	43.7	46.9
$C_{18:1}$ *ω5c*	–	–	*Tr*	0.8	1.5	0.8	–
$C_{18:1}$*ω7c* 11-methyl	4.4	3.2	9.2	22.0	10.2	7.8	–
Hydroxy fatty acids							
$C_{14:0}$ 2-OH	*Tr*	*Tr*	*Tr*	1.2	2.2	7.9	–
$C_{15:0}$ 2-OH	1.5	1.8	0.7	1.0	0.8	1.2	–
$C_{16:0}$ 2-OH	1.2	1.3	1.7	2.8	–	0.7	–
Summed feature 3*	7.1	8.4	26.1	29.4	10.2	16.1	32.9
Summed feature 4*	25.0	26.6	17.5	–	–	–	–
Summed feature 8*	30.2	30.8	20.9	27.7	49.2	–	–

Taxa: *1* YIM 75003^T; *2* YIM 75004^T; *3 A. buctense* M0322^T (=CGMCC 1.12871^T); *4 A. salegens* XY-R17^T; *5 A. epoxidivorans* JCS350^{T-}

Biomass for data from this study was collected from cultures grown on R2A agar at 30 °C. Values are percentage of total fatty acids. *Tr* trace, mean values less than 0.5%

* Summed features represent two or three fatty acids that cannot be separated by GLC with MIDI system. Summed Feature 3: $C_{16:1}$ *ω6c* and/or $C_{16:1}$ *ω7c*; Summed Feature 4: $C_{17:1}$ anteiso B and/or iso I; Summed Feature 8: $C_{18:1}$ *ω6c* and/or $C_{18:1}$ *ω7c*

from the closely related type strain *A. buctense* M0322^T by the presence of diphosphatidylglycerol and sphingoglycolipid (Zhang et al. 2016b). Other characteristics that differentiate the two strains from related type strains of the genus *Altererythrobacter* included differences in growth conditions (temperature and pH ranges for growth), utilization of carbon and nitrogen sources, as well as the proportions of some fatty acids (Tables 1, 2). Notably the two strains can also be differentiated from each other in the hydrolysis of Tweens 20 and 40, nitrate reduction, utilization of pyruvate, ribose, saccharose, sorbose, xylitol, histidine and lysine, activities of cystine arylamidase and leucine arylamidase, and acid production from D-fructose. In addition, the DNA–DNA relatedness value between them is moderately low, indicating that the two strains YIM 75003^T and YIM 75004^T merit classification as two novel species within the genus *Altererythrobacter*, for which the names *Altererythrobacter lauratis* sp. nov. and *Altererythrobacter palmitatis* sp. nov. are proposed, respectively.

Description of *Altererythrobacter lauratis* sp. nov.

Altererythrobacter lauratis [lau.ra'tis. N.L. n. *lauras*, *atis*, laurate (chemical); N.L. gen. n. *lauratis* of laurate, because it oxidises laurate].

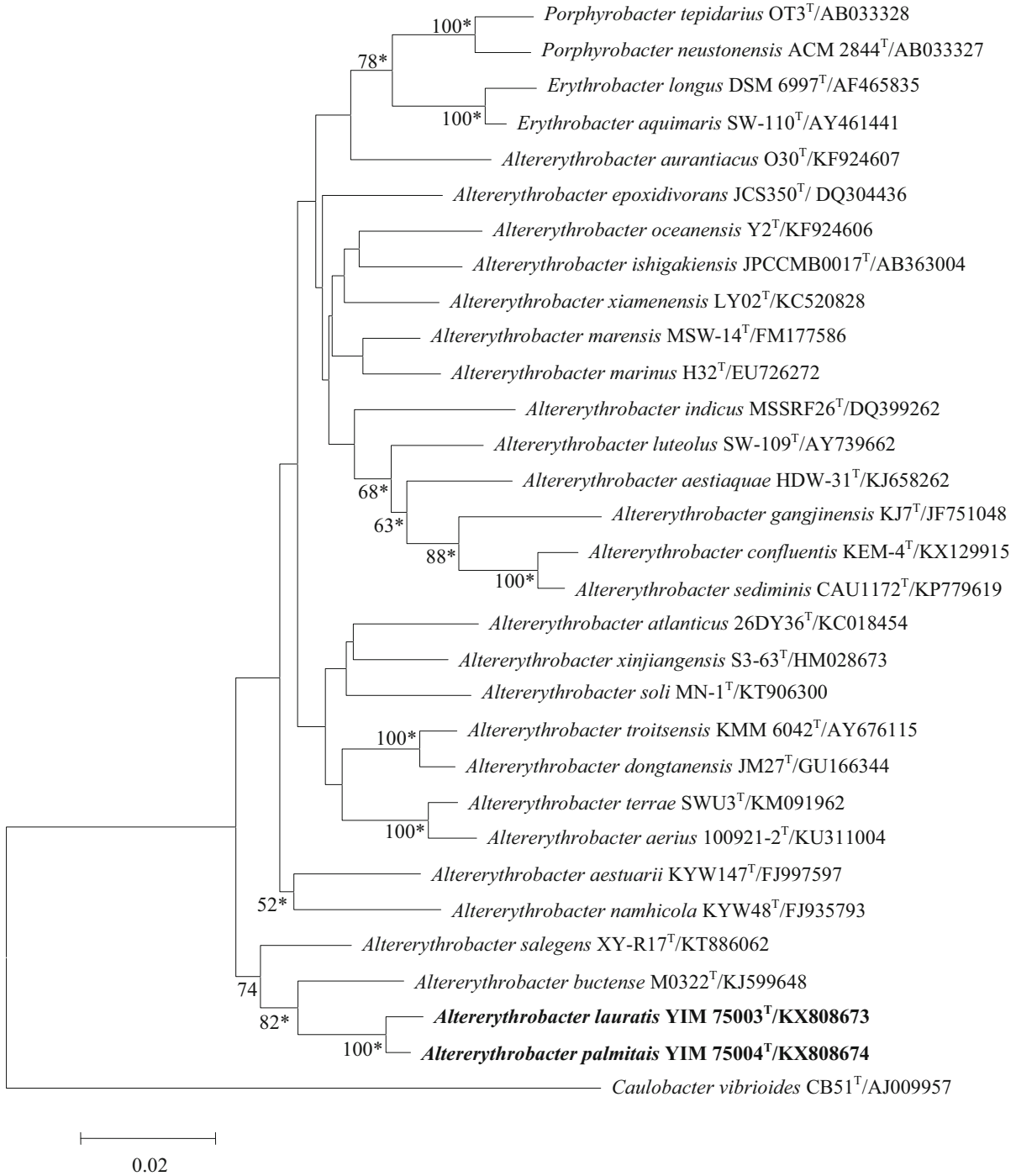

Fig. 1 Neighbor–joining phylogenetic tree based on 16S rRNA gene sequences, showing the position of strains YIM 75003^T and YIM 75004^T among related species of the family Erythrobacteraceae. The sequence of *Caulobacter vibrioides* CB51^T/AJ009957 was used as outgroup. *Asterisks* indicate branches of the tree that were also found in dendrograms generated with the maximum-likelihood and maximum-parsimony algorithms. *Numbers* on branch nodes are bootstrap values (1000 resamplings, only values over 50% are given). *Bar* represents 0.02 substitutions per nucleotide position

Cells are Gram-negative, aerobic, motile and short rods (approximately 0.3–0.7 × 1.2–3.8 μm). Colonies on R2A agar are smooth, convex, circular and yellow-pigmented. Growth occurs on R2A and MR agar but not on LB agar, NA or TSA. Growth occurs at 10–55 °C (optimum, 37–45 °C), pH 5.0–11.0 (optimum, pH 8.0) and 0–11% NaCl (w/v) (optimum, 1–6%). Does not contain Bchl *a* as a photosynthetic pigment. Positive for catalase and oxidase activities. Hydrolyses cellulose and Tween 20, but not chitin, starch or Tweens 40 and 80. H_2S is not produced. The respiratory quinone is Q-10. The polar lipids are diphosphatidylglycerol, phosphatidylcholine, phosphatidylethanolamine, phosphatidylglycerol, sphingoglycolipid, two unidentified glycolipids and four unidentified lipids. The major fatty acids (>10%) are summed feature 8 ($C_{18:1}$ $\omega6c$ and/or $C_{18:1}$ $\omega7c$), summed feature 4 ($C_{17:1}$ anteiso B and/or iso I) and $C_{16:0}$.

The type strain, YIM 75003^T (=KCTC 52606^T = CCTCC AB2016268^T), was isolated from the hot spring of Tagejia geothermal field in Tibet, western China. The DNA G+C content of the type strain is 61.3%. The GenBank accession number for the 16S rRNA gene sequence of strain YIM 75003^T is KX808673. The taxon number of the strain in the Digital Protologue database is TA00084.

Description of *Altererythrobacter palmitatis* sp. nov.

Altererythrobacter palmitatis [pal.mi.ta'tis. N.L. n. *palmitas*, *atis* palmitate (chemical); N.L. gen. n. *palmitatis* of palmitate, because it oxidises palmitate].

Cells are Gram-negative, aerobic, motile and short rods (approximately 0.3–0.7 × 0.8–1.6 μm). Colonies on R2A agar are dry, convex, circular and yellow-pigmented. Grows well on R2A and MR agar but not on LB agar, NA or TSA. Growth occurs at 10–55 °C (optimum, 37–45 °C), pH 5.0–9.0 (optimum, pH 8.0) and 0–11% NaCl (w/v) (optimum, 1–6%). Does not contain Bchl *a* as a photosynthetic pigment. Positive for catalase and oxidase activities. Hydrolyses cellulose and Tween 40, but not chitin, starch or Tweens 20 and 80. H_2S is not produced. The respiratory quinone is Q-10. The polar lipids are diphosphatidylglycerol, phosphatidylcholine, phosphatidylethanolamine, phosphatidylglycerol, sphingoglycolipid, two unidentified glycolipids and two unidentified lipids. The major fatty acids (>10%) are summed feature 8 ($C_{18:1}$ $\omega6c$ and/or $C_{18:1}$ $\omega7c$), summed feature 4 ($C_{17:1}$ anteiso B and/or iso I), $C_{17:1}$ $\omega6c$ and $C_{16:0}$.

The type strain, YIM 75004^T (=KCTC 52607^T = CCTCC AB2016270^T), was isolated from the hot spring of Tagejia geothermal field in Tibet, western China. The DNA G+C content of the type strain is 60.1%. The GenBank Accession Number for the 16S rRNA gene sequence of strain YIM 75004^T is KX808674. The taxon number of the strain in the Digital Protologue database is TA00085.

Acknowledgements We are grateful to Prof. Yu-Guang Zhou (CGMCC, China) for providing the reference type strain and Prof. Aharon Oren, the Hebrew University of Jerusalem, for suggesting the Latin names of the new strains. This work was supported by the Key Project of International Cooperation of Ministry of Science & Technology (MOST) (No. 2013DFA31980), Science and technology infrastructure work project (No. 2015FY110100) and project of China Tobacco Yunnan Industrial Co. Ltd. (No. 2015CP01). W.-J. Li was also supported by Guangdong Province Higher Vocational Colleges & Schools Pearl River Scholar Funded Scheme (2014).

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