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Aureimonas leprariae sp. nov., Isolated from a *Lepraria* sp. Lichen

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Abstract

A Gram-negative, motile, aerobic and coccoid rod-shaped bacterium, designated strain YIM132180^T, was isolated from a *Lepraria* sp. lichen collected from Pu'er, Yunnan Province, China. The strain grew at 15–35 °C (optimum, 25–28 °C), at 0–2% (w/v) NaCl (optimum, 0–1%) and at pH 6.0–9.0 (optimum, pH 7.0). The 16S rRNA gene sequence showed that strain YIM132180^T had highest similarity (96.4%) with *Aureimonas endophytica* 2T4P-2-4^T, followed by *Aureimonas ureilytica* NBRC 106430^T (95.7%) and *Aureimonas rubiginis* CC-CFT034^T (95.6%). Phylogenetic analysis showed that the strain grouped with species of the genus *Aureimonas*. The genomic sequence was 4,779,519 bp and contained 4584 coding sequences (CDSs), 54 RNA genes, 3 complete rRNA genes and 47 tRNA genes. The major fatty acids (>10%) of strain YIM132180^T were $C_{18:1}$ ω7c, $C_{16:0}$ and $C_{19:0}$ cyclo ω8c. The predominant menaquinone was ubiquinone 10 (Q-10). The polar lipid profile comprised diphosphatidylglycerol, phosphatidylcholine, phosphatidylmethylethanolamine, phosphatidylethanolamine, phosphatidylglycerol, unidentified phospholipid, amino lipid, lipid and most importantly sulfoquinovosyldiacylglycerol (SQDG). Based on the draft genome sequence, the G+C content of strain YIM132180^T was 68.4 mol%. The results of the polyphasic taxonomic study, including phenotypic, chemotaxonomic, and phylogenetic analyses, showed that strain YIM132180^T represents a novel species of the genus *Aureimonas*, for which the name *Aureimonas leprariae* sp. nov. is proposed. The type strain is YIM 132180^T (=KCTC 72462^T = CGMCC 1.17389^T).

Introduction

The family *Aurantimonadaceae* currently contains six genera: *Aurantimonas* [1], *Fulvimarina* [2], *Martelella* [3], *Aureimonas* [4], *Jiella* [5] and *Mangrovicella* [6]. *Aurantimonas altamirensis*, *Aurantimonas ureilytica* and *Aurantimonas frigidaquae* of the genus *Aurantimonas* were reclassified as *Aureimonas altamirensis*, *Aureimonas ureilytica* and *Aureimonas frigidaquae* [4] based on the presence or absence of the glycolipid sulfoquinovosyldiacylglycerol (SQDG) and 16S rRNA gene sequence analyses. At the time of writing, the genus *Aureimonas* includes 13 species with validly published names: *Aureimonas ureilytica*, *Aureimonas frigidaquae* and *Aureimonas altamirensis* (type species) isolated from air, a water-cooling system and the walls of Altamira Cave, respectively; *Aureimonas phyllosphaerae*, *Aureimonas jatrophae* [7], *Aureimonas ferruginea* and *Aureimonas rubiginis* from leaf tissues of *Jatropha curcas* L.[8]; *Aureimonas glaciistagni* from a melt pond on Arctic sea ice [9]; *Aureimonas galii* and *Aureimonas pseudogalii* from the phyllosphere of *Galium album* [10]; *Aureimonas glaciei* from an ice core [11]; *Aureimonas endophytica* from

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Aegiceras corniculatum [12]; *Aureimonas populi* from poplar tree bark [13]. Lichens are structured associations of a fungus with a cyanobacteria and/or green algae in a symbiotic relationship, which provide specific habitats for diverse bacterial communities, including actinomycetes [14]. During a study of the diversity of microorganism present in lichen samples, a novel bacterium YIM 132180^T was isolated.

Materials and Methods

Isolation and Maintenance of the Organisms

During an exploration of the cultivable bacterial diversity of lichens in Pu'er (23°07′N, 101°03′E), Yunnan Province, China, we isolated a novel strain, designated strain YIM132180^T from the lichen of genus *Lepraria*. The lichen sample was air-dried at 28 °C for a week, and each sample was homogenized with 20 ml of sterile water using a glass homogenizer [14]. Serial dilutions of the samples (200 µl) were plated onto humic acid-vitamin (HV) agar (humic acid 1.0 g, Na_2HPO_4 0.5 g, KCl 1.7 g, $MgSO_4{\cdot}7H_2O$ 0.05 g, $FeSO_4{\cdot}7H_2O$ 0.01 g, $CaCl_2$ 1 g, agar 18 g, B-vitamins 3.7 mg, pH 7.2) [15]. After incubation at 28 °C for 2–4 week, colonies were picked up and inoculated onto International Streptomyces Project Medium 2 (ISP 2; Difco) [16] to obtain the pure isolates. Strain YIM 132180^T was isolated with the preceding method and was preserved in 20% (v/v) glycerol suspensions at − 80 °C. In order to verify the evolutionary position of the novel strains, we obtained the reference strain, *A. endophytica* 2T4P-2-4^T from China General Microbiological Culture Collection Centre (CGMCC).

Phenotypic Characteristics

Cell morphology and flagella were observed using transmission electron microscopy (JEM-2100; JEOL) after 3 days of incubation on ISP 2 at 28 °C. Cell motility determination was examined by observing the development of turbidity throughout a tube using ISP 2 semisolid medium containing 0.4% agar [17]. Gram staining was performed according to the steps of the standard Gram reaction [18]. Catalase activity was observed via the reaction of fresh cells with 3% (v/v) H_2O_2 and oxidase activity was tested using oxidase reagent (bioMérieux) [19]. Anaerobic growth was determined after 2 weeks of incubation at 28 °C using the GasPak EZ Anerobe Pouch system (BD). The growth temperature of strain YIM132180^T on ISP 2 agar was determined at 4, 8, 10, 15, 20, 25, 28, 30, 35, 37, 40 and 45 °C. Salt tolerance was measured on ISP 2 supplemented with various concentrations of NaCl (0% and 1–10% at intervals of 1%). The pH range (pH 4.0–13.0, at intervals of 1 pH unit) for growth was tested in ISP 2 broth at 28 °C using the buffer system described by Xu et al. [20]. Hydrolysis of casein; gelatin; Tween 20, 40, 80; starch and cellulose; H_2S production; nitrite reduction and anaerobic characteristics were investigated as described by Tindall et al. [21]. Carbon and nitrogen sources utilization were tested by Biolog GEN III microplate. In addition, other physiological and biochemical tests of strain YIM 132180^T and the reference strain 2T4P-2-4^T were determined by using API ZYM, API 20NE and API 50CH kits (bioMérieux) according to the manufacturer's instructions.

16S rRNA Gene Sequencing and Phylogenetic Analysis

Extraction of genomic DNA and PCR amplification of the 16S rRNA gene were performed as described by Li et al. [22]. The purified PCR products were cloned using the pEASY-T1 Cloning Kit to obtain the almost-complete 16S rRNA gene sequence according to the manufacturer's instructions. For the identification, the almost-complete 16S rRNA gene sequence of strain was submitted to EzBioCloud (www.ezbiocloud.net) [23] and NCBI for BLAST search. Multiple alignments with corresponding sequences of the closely related strains were aligned using CLUSTAL X 1.83 [24]. Phylogenetic trees were generated based on three algorithms: neighbour-joining [25], maximum-likelihood [26] and maximum-parsimony [27], using MEGA 7.0 program [28]. The evolutionary distance matrices of the trees were calculated using Kimura's two-parameter model. The topologies of the phylogenetic trees were evaluated by bootstrap analyses after 1000 replications.

Genomic Analysis

The genome sequence of YIM 132180^T was tested by BGI (Wuhan, People's Republic of China) using an Illumina Hiseq 4000 sequencer. The processed reads data were assembled by using SOAPdenovo version 2.04 [29] short sequence group assembly software, and the optimal assembly result was obtained after several adjustments. The short oligonucleotide of assembled results was further polished using SOAP aligner 2.21 [30].

Chemotaxonomic Characterisation

For the chemotaxonomic analyses of quinones, fatty acids and polar lipids, the strain YIM 132180^T and the reference strain 2T4P-2-4^T were cultured on ISP 2 agar at 28 °C for 4 days. The composition of cellular fatty acids was extracted and analysed according to the standard protocol of the Microbial Identification System (MIDI) [31, 32]. Menaquinones were extracted from freeze-dried cells according to the methods of Collins et al. and analysed using HPLC [33,

34]. The polar lipids were investigated using two-dimensional TLC, as described by Minnikin et al. [35].

Results and Discussion

Phenotypic Characteristics

Strain YIM 132180^T was Gram-negative, non-spore-forming, motile with flagella, aerobic and coccoid rod-shaped (1.1–1.2 × 1.3–1.8 μm; Fig. S1). Colonies with diameters of 0.5–1.5 mm were tiny, smooth, convex and yellow after 3 days of incubation on ISP agar. Growth occurs on ISP 2, ISP 4, ISP 5, R2A and NA agar, but not on TSA and Czapek's agar. The strain YIM132180^T grew at 15–35 °C (optimum, 25–28 °C), at pH 6.0–8.0 (optimum, pH 7.0) and in the presence of 0–2% (w/v) NaCl (optimum, 0–1%). Catalase and oxidase tests were positive. Hydrolysis of starch, gelatin, Tween 40 and nitrate reduction were positive, but hydrolysis of casein, cellulose, Tweens 20, 80 and H_2S production were negative. In API ZYM tests, acid phosphatase, alkaline phosphatase, esterase (C_4), esterase lipase (C_8), leucine arylamidase, valine arylamidase, cystine arylamidase, trypsin, chymotrypsin, naphthol-AS-BI-phosphohydrolase, β-galactosidase, *N*-acetyl-β-glucosaminidase activities are positive, but lipase (C_{14}), α-galactosidase, β-glucuronidase, α-glucosidase, β-glucosidase, α-mannosidase and α-fucosidase activities are negative. In the Biolog GEN III system tests, the species can assimilate of dextrin, D-maltose, D-cellobiose, gentiobiose, sucrose, D-turanose, D-raffinose, D-melibiose, β-methyl-D-glucoside, *N*-acetyl-D-glucosamine, *N*-acetyl-β-D-mannosamine, *N*-acetyl-β-D-galactosamine, 1% NaCl, α-D-glucose, D-mannose, D-fructose, D-galactose, 3-methyl-glucose, D-fucose, L-fucose, L-rhamnose, inosine, 1% sodium lactate, D-sorbitol, D-mannitol, D-arabitol, myo-inosine, glycerol, D-glucose-6-phosphate, D-fructose-6-phosphate, D-aspartic acid, rifamycin SV, minocycline, L-alanine, L-aspartic acid, L-glutamic acid, L-histidine, L-pyroglutamic acid, L-serine, lincomycin, pectin, D-galactonic acid lactone, D-glucuronic acid, mucic acid, quinic acid, D-saccharic acid, tetrazolium violet, tetrazolium blue, D-lactic acid methyl ester, L-lactic acid, α-keto-glutaric acid, D-malic acid, L-malic acid, bromo-succinic-acid, nalidixic acid, potassium tellurite, Tween 40, β-hydroxy-D, L-butyric acid, propionic acid and acetic acid. In the API 50CH strips, acid is produced from D-arabinose, L-arabinose, methyl β-D-xylopyranoside, aesculin, salicin, cellobiose, maltose, starch, D-lyxose, D-fucose, L-fucose, L-arabitol, but not from glycol, erythritol, D-adonitol, D-galactose, D-glucose, D-fructose, D-mannose, L-sorbose, L-rhamnose, dulcitol, inositol, mannitol, sorbitol, methyl α-D-mannopyranoside, methyl α-D-glucopyranoside, *N*-acetylglucosamine, amygdalin, arbutin, lactose, melezitose, D-sucrose, trehalose, inulin, melezitose, raffinose, glycogen, xylitol, D-gentiobiose, turanose, D-tagatose, L-arabitol, gluconate, 2-ketogluconate and 5-ketogluconate. Details of physiological and biochemical analyses of strain YIM 132180^T are presented in Table 1 and in the species description.

16S rRNA Gene Sequencing and Phylogenetic Analysis

The almost-complete 16S rRNA gene sequence of strain YIM 132180^T (1475 bp; GenBank accession number MN495985) was obtained. Comparative analysis of 16S rRNA gene sequences using the EzBioCloud server indicated that strain YIM 132180^T shows high level of similarity with *A. endophytica* 2T4P-2-4^T (96.4%), *Aureimonas ureilytica* NBRC 106430^T (95.7%) and *A. rubiginis* CC-CFT034^T (95.6%). The neighbour-joining phylogenetic tree (Fig. 1) based on the almost-complete 16S rRNA gene sequence (1475 bp) showed that strain YIM 132180^T was closely related to *A. endophytica* 2T4P-2-4^T and *A. rubiginis* CC-CFT034^T. The maximum-likelihood (Fig. S2) and maximum-parsimony algorithms (Fig. S3) also verified the relation.

Genomic Analysis

The draft genome sequence of strain YIM 132180^T (4,779,519 bp) contains 40 contigs with N50 contig length of 213,101 bp (GenBank accession number VZDO00000000). Based on the draft genome, the G+C content of strain YIM32180^T was determined to be 68.4 mol%. The genome of strain YIM 132180^T contains 4638 genes, 4584 coding sequences (CDSs), 54 RNA genes, 3 complete rRNA genes and 47 tRNA genes based on the genomic analysis.

Chemotaxonomic Characterisation

The major cellular fatty acids (>10%) contained $C_{18:1}$ ω7c (49.5%), C-$_{16:0}$ (23.1%) and $C_{19:0}$ cyclo ω8c (12.8%) and the cellular fatty acid contents of strain YIM132180^T and the related species of genus *Aureimonas* are shown in Table 2. The predominant quinone of YIM 132180^T was ubiquinone 10 (Q-10) which is consistent with other species of the genus *Aureimonas*. The polar lipid profile comprised diphosphatidylglycerol (DPG), phosphatidylmethylethanolamine (PME), phosphatidylethanolamine (PE), phosphatidylglycerol (PG), phosphatidylcholine (PC), unidentified phospholipid (PL), amino lipid (AL), lipid (L) and sulfoquinovosyldiacylglycerol (SQDG) (Fig. S4) which was the special chemotaxonomic feature of genus *Aureimonas*. The characteristics of polar lipid profile, in which strain YIM 132180^T contained a unidentified

Table 1 Differential characteristics between strain YIM 132180^T and closely related species within the genus *Aureimonas*

Characteristic	1	2	3[a]
Isolation source	Lichen	Bark	Rust
Colony colour	Yellow	Light yellow	Pale yellow
Morphology	Coccoid rod	Coccoid rod	Short rod
Cell size (μm)	1.1–1.2 × 1.3–1.8	1.7–1.9 × 1.9–2.5[b]	1.3 × 2.3
Flagellation	>1, Polar	>1, Polar[b]	NA
Colony morphology	Circular, convex, smooth	Circular, convex, rough	Circular, entire, smooth
Growth at (°C)	15–35	15–37	20–30
pH range for growth	6–8	6–9	5–8
Tolerance of NaCl (%, w/v)	0–2	0–3	0–1
Nitrate reduction	+	−	−[b]
Hydrolysis of			
Starch	+	−	NA
Gelatin	+	−	NA
Tween 20	−	+	+[b]
Tween 40	+	−	+[b]
PNPG	+	−	+
Fermentation of			
D-glucose	+	−	+
Assimilation of			
D-glucose	−	+	+
L-arabinose	−	+	+
N-acetyl-D-glucosamine	+	+	−
D-maltose	+	+	−
Malic acid	+	−	−
Enzyme activity			
Esterase lipase (C_8)	+	−	+
Valine arylamidase	+	+	−
Cystine arylamidase	+	+	−
Trypsin	+	+	−
Chymotrypsin	+	−	−
β-Galactosidase	+	−	−
Alkaline phosphatase	+	+	−
α-Glucosidase	−	−	+
N-acetyl-β-glucosaminidase	+	+	−
Quinone	Q-10	Q-10	Q-10
DNA G + C content (mol%)	68.4	69.8[b]	67.7

Strains: 1, YIM 132180^T; 2, *Aureimonas endophytica*, 2T4P-2-4^T; 3, *Aureimonas rubiginis*, CC-CFT034^T. All strains were positive for catalase, oxidase, urease, but negative for hydrolysis of cellulose and Tween 80. In API 20NE kits, all strains were positive for assimilation of D-mannose and D-mannitol. In the API ZYM kits, all strains were positive for esterase (C_4), leucine arylamidase, naphthol-AS-BI-phosphohydrolase. All data were obtained from this study unless indicated otherwise. +, Positive; −, negative

NA no data available

[a]Data from Lin et al. [8]

[b]Data from Li et al. [12]

PL, while it is absent in *A. endophytica* 2T4P-2-4^T. The G+C content of strain YIM132180^T was 68.4 mol%, which was lower than strain *A. endophytica* 2T4P-2-4^T (69.8 mol%), but higher than strain *A. rubigini*s CC-CFT034^T (67.7 mol%) based on the draft genome data.

Taxonomic Conclusion

In conclusion, from the results of tests of the phylogenetic, chemotaxonomic, some morphologic and physiological features of YIM 132180^T, and the low levels of 16S rRNA gene sequence similarity (<97%) with its close relatives, it

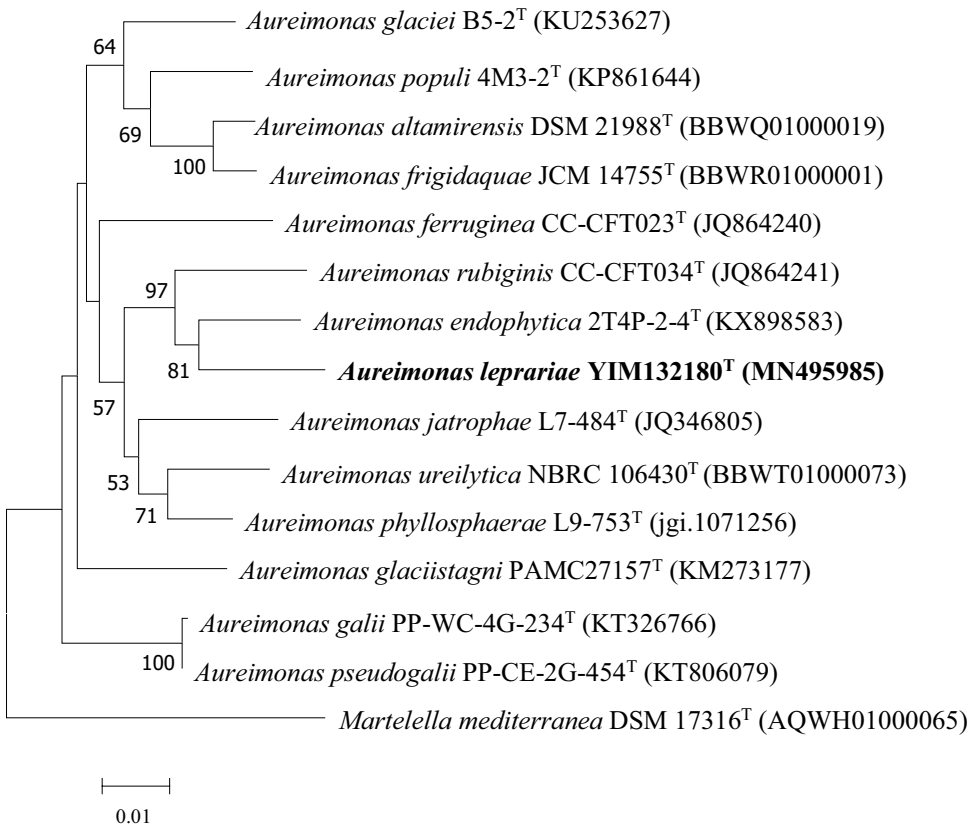

Fig. 1 Neighbour-joining phylogenetic tree based on 16S rRNA gene sequences showing the phylogenetic location of strain YIM 132180^T with related taxa. Numbers at nodes indicate the level of bootstrap support (>50%) based on 1000 replications. *Martelella mediterranea* DSM 17316^T (AQWH01000065) was used as an outgroup. Bar 0.01 substitutions per nucleotide position

Table 2 Cellular fatty acid compositions of strain YIM 132180^T and related strain *Aureimonas endophytica* 2T4P-2-4^T

Fatty acid	1	2
$C_{14:0}$	3.0	TR
$C_{14:0}$ 2-OH	1.2	–
$C_{16:0}$	**23.1**	**14.7**
$C_{17:0}$	1.1	TR
$C_{18:0}$	2.4	1.7
$C_{18:1}$ 2-OH	2.9	3.3
$C_{18:0}$ 3-OH	TR	TR
$C_{18:1}$ ω7c	**49.5**	**65.7**
$C_{19:0}$ cyclo ω8c	**12.8**	4.5
Summed feature 3[a]	2.6	6.5

All data were obtained from this study. Strains: 1, YIM 132180^T; 2, *Aureimonas endophytica*, 2T4P-2-4^T. Values are percentages of total fatty acids. The major fatty acids (greater than 10%) are shown bold

TR, trace (less than 1%); –, not detected

[a]Summed feature 3 contains $C_{16:1}$ ω7c and/or $C_{16:1}$ ω6c

is obvious that strain YIM 132180^T represents a novel species of genus *Aureimonas*, for which the name *A. leprariae* sp. nov. is proposed.

Description of *Aureimonas leprariae* sp. nov.

Aureimonas leprariae (le.pra'ri.ae. N.L. gen. n. *leprariae* referring to the isolation of the organism from the lichen genus *Lepraria*).

Cells (approximately 1.1–1.2 × 1.3–1.8 μm in size) are Gram-negative, non-spore-forming, motile with flagella, aerobic and coccoid rod-shaped. Colonies with diameters of 0.5–1.5 mm were tiny, smooth, convex and yellow after 3 days of incubation on ISP 2 agar at 28 °C. Good growth occurs on ISP 2, ISP 5 and R2A agar, whereas poor growth occurs on ISP 4 and NA agar, and no growth occurs on TSA and Czapek's agar. The growth temperature is between 15 and 35 °C (optimum, 25–28 °C), pH range is from 6.0 to 8.0 (optimum, pH 7.0) and the species can tolerate less than 2% (w/v) NaCl stress (optimum, 0–1%). Catalase and oxidase tests were positive. Hydrolysis of starch, gelatin, Tween 40 and nitrate reduction were positive, but hydrolysis of casein, cellulose, Tweens 20, 80 and H_2S production were negative. The major cellular fatty acids contain $C_{18:1}$ ω7c, $C_{16:0}$ and $C_{19:0}$ cyclo ω8c. The polar lipid profile comprised DPG, PME, PE, PG, PC, SQDG, unidentified PL, AL and L. The G+C content of the genomic DNA is 68.4 mol%.

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Author Contributions KZ: performed the experiments and wrote the manuscript; L-QJ and G-DL: analysed the data; S-BS and Q-YL: performed the study; D-FA and LL: analysed the data; X-YW: collected the lichen samples; L-SW: identified the lichen samples; YJ: guided the experiments and revised the manuscript; C-LJ: designed the study.

Compliance with Ethical Standards

Conflict of interest The authors declare that they have no conflict of interest.

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