Description of Sandaracinobacter Hominis Sp. Nov., Isolated From Human Skin

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Abstract

Strain SZY PN-1^T, representing a novel Gram-negative, aerobic, non-motile, rod-shaped and yellow-pigmented bacterium, was isolated from a skin sample of a healthy Chinese people. Growth of SZY PN-1^T optimally occurred at pH 7.0, at 30 ºC and tolerate up to 1.0 % (w/v) NaCl. According to the absorption spectrum, carotenoid was present in the cells. Comparative analysis of the 16S rRNA gene revealed that strain SZY PN-1^T shared high similarities with *Sandaracinobacter sibiricus* RB16-17^T (97.1 %) and *Sandaracinobacter neustonicus* JCM 30734^T (96.6 %), respectively. Phylogenetic analysis of 16S rRNA gene sequences together with protein-concatamer tree showed that SZY PN-1^T formed a separate branch within the genus *Sandaracinobacter*. The DNA G+C content of the strain SZY PN-1^T was 65.0 % (genome). The polar lipid profile included phosphatidylethanolamine, phosphatidylglycerol, two sphingoglycolipids, diphosphatidylglycerol, five unidentified glycolipids and seven unidentified lipids. The predominant fatty acids (> 10.0 %) were identified as $C_{18:1}$ *ω7c* and/or $C_{18:1}$ *ω6c*, $C_{17:1}$ *ω6c*, $C_{16:1}$ *ω7c* and/or $C_{16:1}$ *ω6c*. The major respiratory quinone was ubiquinone Q-10. Based on the phenotypic and genotypic features, we proposed *Sandaracinobacter hominis* sp. nov. with type strain SZY PN-1^T (= KCTC 82150^T = NBRC 114675^T).

Introduction

The genus *Sandaracinobacter*, which belongs to the family *Sphingosinicellaceae* within the order *Sphingomonadales*, comprises two species with validly published names: *Sandaracinobacter sibiricus* RB16-17^T (Yurkov et al. 1997) and *Sandaracinobacter neustonicus* JCM 30734^T (Lee et al. 2020). Members of this genus are Gram-negative, long rods, aerobic bacteria, forming yellow to yellow-orange colonies for carotenoid pigments. Up to date, the members of the ecology of genus *Sandaracinobacter* and related *Sphingosinicellaceae* spp. were reported from environmental samples including varied lakes (Yurkov and Gorlenko. 1990; Gich et al. 2006; Cai et al. 2018; Phurbu et al. 2020), seawater (Lee et al. 2020), soil (Jia et al. 2015), and so on. In this study, we described a member of genus *Sandaracinobacter*, designated SZY PN-1^T, which was isolated from a skin sample of a healthy human.

Materials And Methods

Isolation and cultivation

Cutaneous samples of the antecubital fossa for culture were obtained from healthy people during an investigation for the diversity of skin microbiota in 2019, in the Guangdong Provincial Hospital of Traditional Chinese Medicine, Guangzhou, PR China. Culture swabs (Miraclean, China) were used to collect samples from the antecubital fossa from each volunteer. And then the swabs were placed into a tube containing 2 mL of sterile saline solution, respectively. The fresh sample was immediately brought into the laboratory and inoculated onto BCYE*α* agar, R2A agar and their modified medium at 28-32 °C under aerobic conditions. Single colonies were obtained by streaking onto fresh medium several times.

Among those single colonies, a circular and yellow opaque colony (strain designed as SZY PN-1^T) was obtained. Subsequently, cell lysate was used as template DNA for universal bacterial 16S rRNA gene PCR followed by direct Sanger sequencing to obtain partial nucleotide sequences, which resulted in a lower similarity comparing with other species. The strain was subjected to taxonomic analysis based on phenotypic, physiological and phylogenetic studies and maintained as cells suspension in glycerol (30 %, w/v) at -80 °C.

16S rRNA analysis and phylogeny

For phylogenetic characterization, The DNA extraction, primers used, as well as PCR amplification of the 16S rRNA were described previously (Li et al. 2007). The amplicon was purified by using a PCR purification kit (Sangon Biotech, China). Then, the purified PCR product was cloned into *Escherichia coli* DH5α chemically competent cells using PMD-19T vector and sequenced by a Sanger platform as described by Giovannoni (Giovannoni et al. 1991). The cloned 16S rRNA gene sequence of SZY PN-1^T was compared with other sequences on the EzBioCloud server (http://www.ezbiocloud. net) (Yoon et al. 2017) and the sequences of related species used for the analysis were retrieved. The SZY PN-1^T strain sequence was aligned to those of related type strains using clustal_w. Gaps at the 5’ and 3’ ends of the alignment were manually removed. Phylogenetic tree reconstructions were performed based on the neighbor-joining (NJ) (Saitou et al. 1987), maximum-likelihood (ML) (Felsenstein et al. 1981) and maximum-parsimony (MP) (Fitch et al. 1971) algorithms by using the mega version 7.0 (Kumar et al. 2016). The evolutionary distance and topology of the phylogenetic trees were evaluated by Kimura's two-parameter model (Kimura 1980) and bootstrap analysis based on 1000 replicates (Felsenstein 1985). *Rhodospirillum rubrum* ATCC 11170^T was used as an outgroup.

Genome sequences analysis

Whole-genome sequencing was performed for strain SZY PN-1^T using 100bp paired-end sequencing method with the Illumina Hiseq 2000 platform. The raw data was filtered, and high quality paired-end reads were assembled using the soap *de novo* version 2.04 (Yarza et al. 2014). The completeness and contamination of the assembled genome sequence were evaluated by using CheckM (Abbas et al. 2014). For phylogenomic tree reconstruction, marker genes were extracted from 18 genomes available for the family *Sphingosinicellaceae* using amphora2 (Parks et al. 2015). Sequences of amino acid were aligned separately by using muscle (Wu and Scott 2012) and were checked to remove the poorly aligned regions via Gblocks (Castresana et al. 2010). Then, cleaned alignments were concatenated using perl script (https://github.com/ nylander/catfasta2phyml). The protein-concatamer tree was generated using the RAxML method by applying the default parameter (Edgar 2004) and visualized using the online Tree of Life program version 4.2 (https://itol. embl. de/) (Stamatakis 2014).

The genomic relatedness of strains SZY PN-1^T to the Whole Genome Shotgun sequences of all species type strains in the *Sandaracinobacter* available in public databases was determined by several methods: average nucleotide identity (ANI) and average amino acid identity (AAI). The ANI with the blastn algorithm

(ANIb) and using the MUMmer ultrarapid aligning tool (ANIm) were calculated by the online Ribocon GmbH- version 3.0.20 software (http://jspecies. ribohost.com/jspeciesws/) (Richter et al. 2015). The AAI values were calculated using the CompareM software of the online server (https://github.com/dparks1134/CompareM).

Phenotypic and biochemical characteristics

To determine the optimal growth conditions, strain SZY PN-1^T was cultured on R2A agar, BCYEα agar, Columbia blood agar, Haemophilus chocolate 2 agar, chocolate agar with PolyViteX (PVX agar), MacConkey agar and Mueller-Hinton agar (MH), CHAB agar (cysteine heart agar supplemented with 9% heated sheep red blood cells), tryptic soy agar (TSA), and lysogeny broth medium (LB). The temperature for growth was evaluated by culturing strain SZY PN-1^T on R2A medium at different temperatures (4, 10, 15, 20, 25, 28, 30, 32, 37 and 45 ℃) for 5 days. For determining the growth of pH conditions (pH 5–11, prepared using the buffer system described by Xu et al. (2005) and NaCl tolerance at various concentrations (0, 0.2, 0.4, 0.6, 0.8, 1.0., 2.0, 3.0, 4.0, 5.0, 6.0 %, w/v), strain SZY PN-1^T was kept incubated at 30 ℃, and checked after 5 days. Growth was also tested under anaerobic conditions by using the anaerobic bag (BioMérieux, France) and 5 % CO_2 condition for 5 days at 30 °C. Gram staining was performed using the Gram staining kit (BaSo, China), according to the manufacturer's instructions. Cell size, morphology and flagella insertion were observed under the transmission electron microscopy (JEM-1400, JEOL) with cultures grown in R2A medium for 2 days. Cell motility was assessed by the hanging-drop method as described by Smibert and Krieg (1994). Spores formation was observed as previously described (Logan et al. 2009) after incubating the strains on R2A agar.

Activities of oxidase, catalase and urease, Voges–Proskauer (VP), gelatin liquefaction, H_2S production and nitrate reduction, hydrolysis of starch, casein, aesculin and Tweens 20, 40, 60 and 80 were investigated according to the conventional procedures as previously described (Aslanzadeh 2006; Hansen and Sørheim 1991; Smibert and Krieg 1994). The Bacteriochlorophyll α (BChl α) and carotenoid pigment analysis were performed using the middle-late logarithmic phase as described by Saga et al. (2005). Then the cells were washed with NaCl-saturated and the pigments were extracted with acetone/methanol (7:2, v/v). The absorption spectrum of the cell extractive at 200–900 nm was analysed by using Gen5™ (Biotek). Other biochemical activities of strain SZY PN-1^T were performed using API 20NE, API ZYM, and API 50CH kits (bioMérieux) according to the manufacturer's instructions. All tests were performed in duplicate, and *Polymorphobacter* fuscus CGMCC 1.12714^T was used as control.

Chemotaxonomy

The fatty acid profile, polar lipids and respiratory quinones of strain SZY PN-1^T were analysed in this study. The cellular fatty acid profiles were determined for SZY PN-1^T and reference strains grown on R2A plates incubated at 30 °C for 72 h. Fatty acids were harvested, saponified, methylated and extracted according to standard protocols as described for the Sherlock Microbial Identification System (Sasser 1990). The analysis of cellular fatty acid was performed using a gas chromatograph (7890B, Agilent)

with the MIDI Microbial Identification System using the TSBA6 method and the Microbial Identification Sherlock software package version 6.1 (MIDI 2008). Polar lipids of strain SZY PN-1^T were extracted, separated by two-dimensional thin-layer chromatography on silica gel G 60 plates (Merck; Germany) and further analysed according to the method described by Minnikin *et al*. (Minnikin et al. 1979) and Collins and Jones (Collins and Jones 1980). Respiratory quinones were extracted, purified and analysed by using high-performance liquid chromatography (HPLC) (Kroppenstedt et al. 1982) following the process of Collins *et al.* (1977).

Results And Discussion

16S rRNA phylogeny

The cloned sequence of the 16S rRNA gene of SZY PN-1^T has been deposited in NCBI GenBank under accession number MW135304. Comparison of the 16S rRNA gene sequences of SZY PN-1^T (1409 bp) with those of other species showed that the closest sequence was that of *S. sibiricus* strain RB16-17 (97.1 % sequence similarity), followed by *S. neustonicus* JCM 30734^T (96.6 % sequence similarity) and other type strains with less than 94.2 % sequence similarity within the family *Sphingosinicellaceae*, which is lower than the threshold (98.65 %) for bacterial species demarcation (Kim et al 2014). The maximum-likelihood tree based on 16S rRNA gene sequences demonstrated that strain SZY PN-1^T formed a monophyletic clade that was part of a branch with the genus *Sandaracinobacter* comprised of *S. sibiricus* RB16-17 and *S. neustonicus* JCM 30734^T (Fig. 1). A similar result was obtained when using the neighbor-joining and maximum-parsimony algorithms (Fig. S1-2, available in the online version of this article), which also revealed that strain SZY PN-1^T representing a novel species within the genus *Sandaracinobacter.*

Genome features

The Whole Genome Shotgun project of strain SZY PN-1^T has been deposited at DDBJ/ENA/GenBank under the accession JADCUC000000000, with the genomic size of 3.53 Mbp and the DNA G+C content of 65.0 %. The protein-concatamer tree based on 29 marker genes (*frr*, *infC*, *nusA*, *pgk*, *pyrG*, *rplA*, *rplB*, *rplC*, *rplD*, *rplE*, *rplF*, *rplK*, *rplL*, *rplM*, *rplN*, *rplP*, *rplS*, *rplT*, *rpmA*, *rpsB*, *rpsC*, *rpsE*, *rpsI*, *rpsJ*, *rpsK*, *rpsM*, *rpsS*, *smpB*, *tsf*) indicated that the novel strain SZY PN-1^T clustered within the genus *Sandaracinobacter*, forming a clade with the strain *S. neustonicus* JCM 30734^T (Fig. 2). The threshold limits (95.0–96.0 % ANI and 95 % AAI) for delineation of bacterial species were considered as recommended (Chun et al. 2018; Thompson et al. 2013). The estimated results confirmed that strain SZY PN-1^T represented a novel genomic species within the genus *Sandaracinobacter*, with ANI values ≤ 85.0 % and AAI values ≤ 76.0 % with the genome of *S. neustonicus* JCM 30734^T, which was the closest relative comparing by 16S rRNA and whole-genome sequence. The detailed characteristics of the genomes of the strain SZY PN-1^T, and other type strains within the genus *Sandaracinobacter* are listed in Table S1.

Phenotypic characteristics

Strain SZY PN-1^T showed good growth on R2A and BCYE*α* agar; weak growth on Columbia blood agar, MH agar, TSA and LB agar; but not on *Haemophilus* chocolate 2 agar, chocolate agar with PolyViteX (PVX agar, Bio-caring, China), CHAB agar and MacConkey agar (Bio-caring, China). After incubation for 72 h at 30 ℃ on R2A agar media, the colonies were 1–2 mm in diameter, circular, convex, a little hard and yellow coloured. Strains were able to grow at temperatures ranging between 10 and 37 ℃ (optimum, 30 ℃), pH 6.0–8.0 (optimum, pH 7.0) and in the presence of up to 1.0 % (w/v) NaCl with optimum growth at non-additional NaCl on R2A. Cell of strain SZY PN-1^T was observed to be Gram-negative, aerobic, non-spore-forming and non-motile. The strain was enhanced by the presence of 5% CO_2. Transmission electron microscopy image showed that the strain was a rod, 0.71–0.97 μm long and 0.53–0.63 μm wide without flagella, as shown in Fig. 3. The absorption spectrum of pigments extracted from the cells showed two peaks at 452 and 478 nm (Fig S3), indicating the presence of carotenoids. No peaks were detected above 600 nm, which showed that the strain SZY PN-1^T was absent in BChl α.

The strain was positive for catalase activity but negative for oxidase activity and hydrolysed starch, casein, aesculin, gelatin, Tween 40, Tween 60 but not Tweens 20 and 80. Activities of urease, Voges–Proskauer test, H_2S production and nitrate reduction were negative. The detailed phenotypic and physiological characteristics of strain SZY PN-1^T are summarized and compared with *P. fuscus* CGMCC 1.12714^T and closely related *Sandaracinobacter* species in Table 1.

Chemotaxonomy

Summed feature 8 ($C_{18:1}$ *ω7c* and/or $C_{18:1}$ *ω6c*; 41.8 %), $C_{17:1}$ *ω6c* (12.5 %) and summed feature 3 ($C_{16:1}$ *ω7c* and/or $C_{16:1}$ *ω6c*; 10.9 %) were the predominant cellular fatty acids (>10.0 %) in SZY PN-1^T, which are in agreement with the composition of fatty acids in *S. neustonicus*. Detailed fatty acid compositions are shown in Table 2. Polar lipids of strain SZY PN-1^T contained phosphatidylethanolamine (PE), phosphatidylglycerol (PG) and sphingoglycolipids (SGLs) as major polar lipids (Fig. S4). Diphosphatidylglycerol (DPG), unidentified glycolipids (GLs) and unidentified lipids (Ls) were also present as minor polar lipids. The respiratory quinones comprised ubiquinones Q-10 (92.2 %) and Q-11 (7.8 %), whereas ubiquinone Q-11 was absent in *S. sibiricus* RB16-17 and *S. neustonicus* JCM 30734^T within the genus *Sandaracinobacter.* Moreover, strain SZY PN-1^T lacked ubiquinone Q-9, which was found to present in the strain of *S. sibiricus* RB16-17.

Taxonomic conclusion

Based on the low 16S rRNA gene sequence and other phenotypic characteristics, strain SZY PN-1^T could be distinguished from the related species within the genus *Sandaracinobacter*. The physiological and chemotaxonomic characteristics, including cellular fatty acid and polar lipid profiles, also indicated that strain SZY PN-1^T was similar to the species within the genus *Sandaracinobacter*. These results revealed

that strain SZY PN-1^T should be classified as representing a novel species of the genus *Sandaracinobacter*, for which we propose the name *Sandaracinobacter hominis* sp. nov.

Description of *Sandaracinobacter hominis* sp. nov.

Sandaracinobacter hominis (ho'mi.nis. L. n. *homo*, *-inis*, a human, man, person; L. gen. masc. n. *hominis*, of man, signifying the isolation of strains from human skin).

Cells are Gram-negative, aerobic and rod-shaped, being 0.71–0.97 μm long and 0.53–0.63 μm wide without flagella. Growth occurs from 10 to 37 ºC (optimal at 30 ºC). Cells absorb at 430-490 nm, because of the presence of carotenoids. In the API ZYM strip, it is positive for alkaline phosphatase, esterase (C4), leucine arylamidase, trypsin, acidic phosphatase, naphthol-AS-BI-phosphohydrolase and *α*-glucosidase, and weakly positive for esterase lipase (C8) and α-chymotrypsin. Negative results are obtained for lipase (C14), valine arylamidase, cystine arylamidase, *α*-galactosidase, *β*-galactosidase, *β*-glucuronidase, *β*-glucosidase, *N*-acetyl-*β*-glucosaminidase, *α*-mannosidase and *α*-fucosidase. In the API 20NE strip, positive reactions are observed for hydrolysis of aesculin, *β*-galactosidase, assimilation of glucose and maltose, but reactions are negative for acid production from glucose, arginine dihydrolase, Assimilation of arabinose, mannose, mannitol, *N*-acetyl-d-glucosamine, gluconate, caprate, adipate, malate, citrate and phenylacetate. In the API 50CHB/E strip, positive reactions for esculin ferric citrate, negative reactions for glycerol, erythritol, d-arabinose, l-arabinose, d-ribose, d-xylose, L-xylose, d-adonitol, methyl *β*-d-xylopyranoside, d-galactose, d-glucose, d-fructose, d-mannose, L-sorbose, L-rhamnose, dulcitol, inositol, d-mannitol, d-sorbitol, methyl *α*-d-mannopyranoside, methyl *α*-d-glucopyranoside, *N*-acetylglucosamine, amygdalin, arbutin, salicin, d-cellobiose, d-maltose, d-lactose, d-melibiose, d-sucrose, d-trehalose, inulin, d-melezitose, d-raffinose, starch, glycogen, xylitol, gentiobiose, d-turanose, d-lyxose, d-tagatose, d-fucose, l-fucose, d-arabitol, l-arabitol, gluconate, 2-ketogluconate and 5-ketogluconate are observed. The major cellular fatty acids are Summed feature 8 ($C_{18:1}\omega7c$ and/or $C_{18:1}\omega6c$), $C_{17:1}\ \omega6c$ and summed feature 3 ($C_{16:1}\ \omega7c$ and/or $C_{16:1}\ \omega6c$). The polar lipids are composed of phosphatidylethanolamine, phosphatidylglycerol, two sphingoglycolipids, Diphosphatidylglycerol, five unidentified glycolipids and seven unidentified lipids. The major respiratory quinone is ubiquinone-10, whereas ubiquinone-11 is present in smaller amounts. The DNA G+C content of the type strain is 65.0 %.

The type strain SZY PN-1^T (KCTC 82150^T = NBRC 114675^T), was isolated from a skin sample of a Chinese. The GenBank accession number for 16S rRNA gene sequence of the strain SZY PN-1^T is MW135304. The GenBank/EMBL/DDBJ/PIR accession number for the Whole Genome Shotgun projects of the strains SZY PN-1^T is JADCUC000000000.

Ethical approval

All experiments involving human subjects were carried out according to the institutional review board protocols approved by Medical Ethics Committee of Guangdong Provincial Hospital of Chinese Medicine in China (BE2019-165). Informed consent was obtained from all subjects.

Declarations

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Author's contributions

YL and CC designed research and project outline. PHQ, HML, SL, LD, NP and YZM performed isolation, deposition and identification. PHQ, HML and JHF analysed the data. PHQ, HML and WJL drafted the manuscript. All authors read and approved the final manuscript.

Conflict of interest

All the authors have declared that there are no conflicts of interest

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"Erythromicrobium ursincola" as Erythromonas ursincola gen. nov., sp. nov. Int J Syst Bacteriol 47:1172–1178

Tables

Table 1. Phenotypic and biochemical characteristics that differentiate strain SZY PN-1^T from closely related species

Characteristics	1	2[a]	3[b]	4
Colour	Yellow	Yellow	Yellow-orange	Brown[c]
Motility	–	–	+	_[c]
Growth range:				
Oxygen requirement	Obligately aerobic	Facultatively anaerobic	Strictly aerobic	Obligately aerobic[c]
Temperature range (optimum) (°C)	10–37 (30)	4–37 (30)	(25–30)	4–35 (25)[c]
pH range (optimum)	6.0–8.0 (7.0)	6.0–8.0 (6.5–7.0)	(7.5–8.5)	7.0–10.0 (8.0)[c]
NaCl range (optimum) (%, w/v)	(0–1.0)	0–1.0 (0.5–1.0)	(0–1.0)	0–2.0[c]
Bacteriochlorophyll *a*	–	–	+	+[c]
Major carotenoid in *vivo* peaks (nm)	452, 478	450, 474	424, 450, 474	430, 455, 490[c]
Oxidase activity	–	+	+	–
Catalase activity	+	+	–	+
Gelatin	–	+	–	–
Hydrolysis of:				
Starch	+	+	–	–
Casein	+	+	nd	–
Tween 20	–	+	nd	–
Tween 80	–	+	nd	–
Enzyme activity (API ZYM):				
Esterase lipase (C8)	w	+	nd	+
Valine arylamidase	–	nd	nd	+
Cystine arylamidase	–	nd	nd	w
Trypsin	+	+	nd	–
α-chymotrypsin	w	+	nd	+
α-Galactosidase	–	–	nd	+

β-Galactosidase	–	+	nd	–
α-Glucosidase	+	+	nd	–
Assimilation of (API 20NE):				
Glucose	+	+	nd	–
Maltose	+	+	nd	–
Acid production (API 50CHB/E):				
Esculin ferric citrate	+	–	nd	+
d-Maltose	–	+	nd	–
Potassium 5-ketogluconate	–	+	nd	w
Main polar lipids	DPG, PE, PG, SGL1-2, GL1-4, L1-7	PG, PE, PL1–2, AL, GL, L	nd	PE, PG, PL, GL1–2, SGL[c]
Quinone(s)	Q-10 (major), Q-11 (small)	Q-10	Q-9, Q-10	Q-9 (small), Q-10 (major)[c]
DNA G+C content	65.0 %	65.3 %	68.5 mol%*	66.8 %
Genome Size (×10^6)	3.53	3.65	nd	3.37

Data from the original study: [a] Lee et al. (2020); [b] Yurkov et al. (1997), [c] Jia et al. (2015) respectively

Strains: 1, SZY PN-1^T; 2, *S. neustonicus* JCM 30734^T; 3, *S. sibiricus* RB16-17; 4, *P. fuscus* CGMCC 1.12714^T. Symbols: +, positive; –, negative; w, weakly positive; nd, not detected; * Thermal denaturation method (Yurkov et al. 1997). All data are from this study unless otherwise indicated.

All strains are positive for hydrolysis of Tweens 60, negative for gram staining. The following results of strain 3 are not detected. All strains except strain 3 are positive for hydrolysis of Tweens 40, alkaline phosphatase, esterase (C4), acidic phosphatase, naphthol-AS-BI-phosphohydrolase and *β*-galactosidase, negative for Voges-Proskauer reaction, H_2S production, *β*-glucuronidase, *β*-glucosidase, *N*-Acetyl-*β*-glucosaminidase, *α*-fucosidase, nitrate, nitrate reduction, indole production, acid production from glucose, arginine dihydrolase, urease activity, assimilation of caprate, malate, citrate, phenylacetate, glycerol, erythritol, d-arabinose, l-arabinose, d-ribose, d-xylose, l-xylose, d-adonitol, methyl *β*-d-xylopyranoside, d-galactose, d-glucose, d-fructose, d-mannose, l-sorbose, l-rhamnose, dulcitol, inositol, d-mannitol, d-sorbitol, methyl *α*-d-mannopyranoside, methyl *α*-d-glucopyranoside, *N*-acetylglucosamine, amygdalin, arbutin, salicin, d-cellobiose, d-lactose, d-melibiose, d-sucrose, d-trehalose, inulin, d-melezitose, d-raffinose, starch,

glycogen, xylitol, gentiobiose, d-turanose, d-lyxose, d-tagatose, d-fucose, l-fucose, d-arabitol, l-arabitol, potassium gluconate and potassium 2-ketogluconate.

Table 2. Cellular fatty acid compositions of strain SZY PN-1^{T} and its closely related species

Fatty acids (%)	1	2	3
Saturated straight-chain:			
$C_{12:0}$	5.1	–	1.0
$C_{16:0}$	4.7	7.9	5.3
$C_{17:0}$	1.1	2.2	tr
$C_{18:0}$	1.2	–	tr
Saturated branched-chain:			
Iso-$C_{10:0}$	2.3	–	tr
Anteiso-$C_{13:0}$	1.1	–	–
Anteiso-$C_{14:0}$	–	–	1.5
Anteiso-$C_{15:0}$	1.0	–	tr
Anteiso-$C_{17:0}$	1.1	–	tr
Iso-$C_{19:0}$	3.5	–	–
Hydroxy:			
$C_{14:0}$ 2-OH	–	–	14.9
$C_{15:0}$ 2-OH	–	–	2.3
$C_{16:0}$ 2-OH	6.6	6.8	tr
Unsaturated:			
$C_{14:1}$ $\omega 5c$	1.6	–	–
$C_{16:1}$ $\omega 5c$	1.2	2.9	1.0
$C_{17:1}$ $\omega 6c$	12.5	19.3	9.4
$C_{17:1}$ $\omega 8c$	–	1.3	tr
$C_{18:1}$ $\omega 5c$	–	1.2	tr
$C_{18:3}$ $\omega 6c$	2.4	–	tr
Summed feature:			
3	10.9	15.8	32.9

8	41.8	42.6	26.2

Taxa: 1, SZY PN-1^T; 2, *Sandaracinobacter neustonicus* JCM 30734^T (Lee et al. 2020); 3, *Polymorphobacter fuscus* CGMCC 1.12714^T. All data are from this study unless otherwise indicated. Values are the percentage of total fatty acids. Symbols: –, not detected; tr, trace (<0.8 %).

Summed features represent fatty acids that cannot be separated using gas-liquid chromatography with the Sherlock microbial identification (MIDI) system. Summed feature 3 contained $C_{16:1}$ *ω7c* and/or $C_{16:1}$ *ω6c*; Summed feature 8 contained $C_{18:1}$ *ω7c* and/or $C_{18:1}$ *ω6c*.

Figures

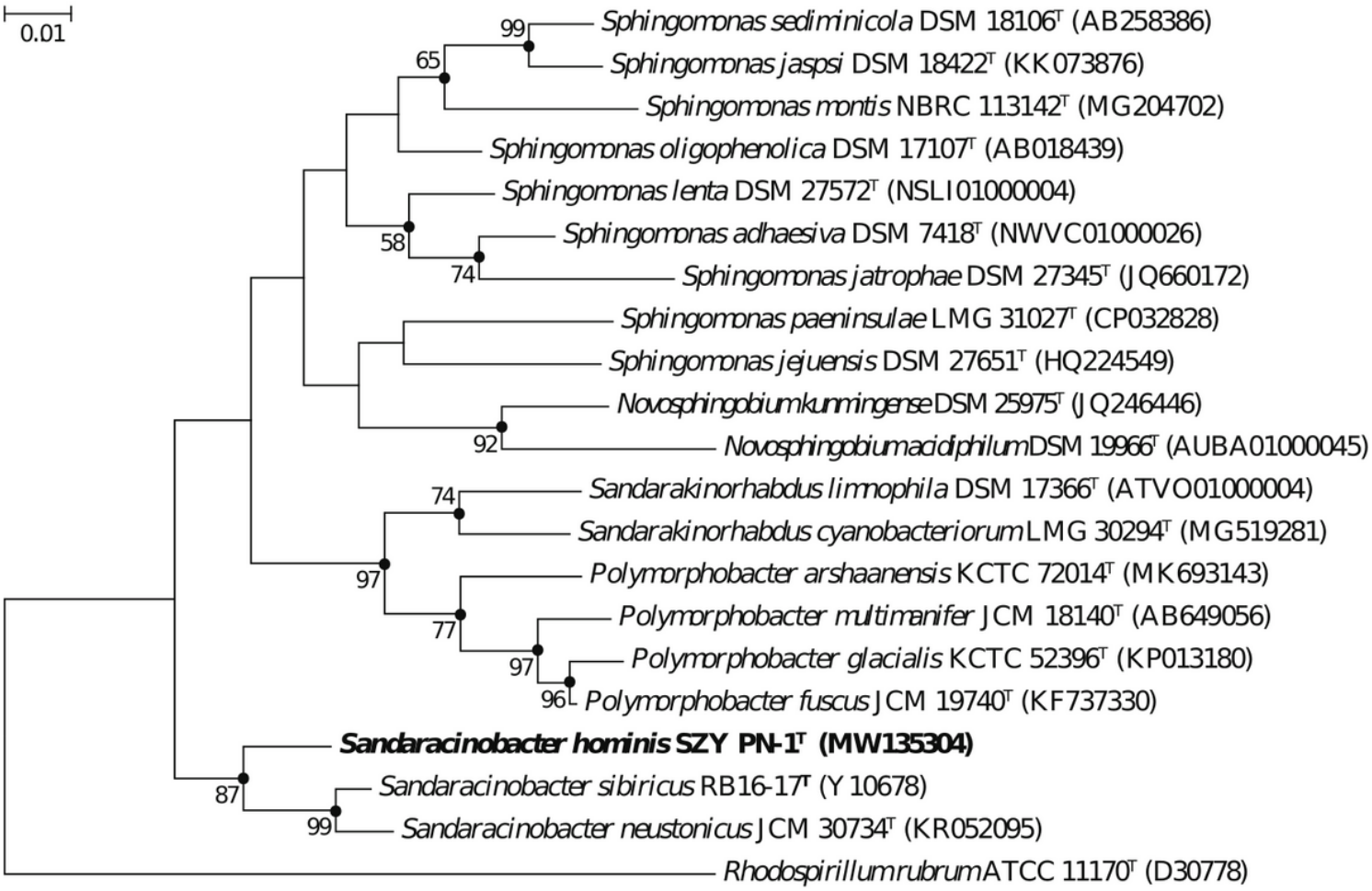

Figure 1

Maximum-likelihood tree of 16S rRNA gene sequences, showing relationships between strain SZY PN-1T and related taxa. Bootstrap values >50 % based on 1000 replications are shown at branch nodes. Rhodospirillum rubrum ATCC 11170T was used as an outgroup. Bar, 0.01 substitutions per nucleotide position.

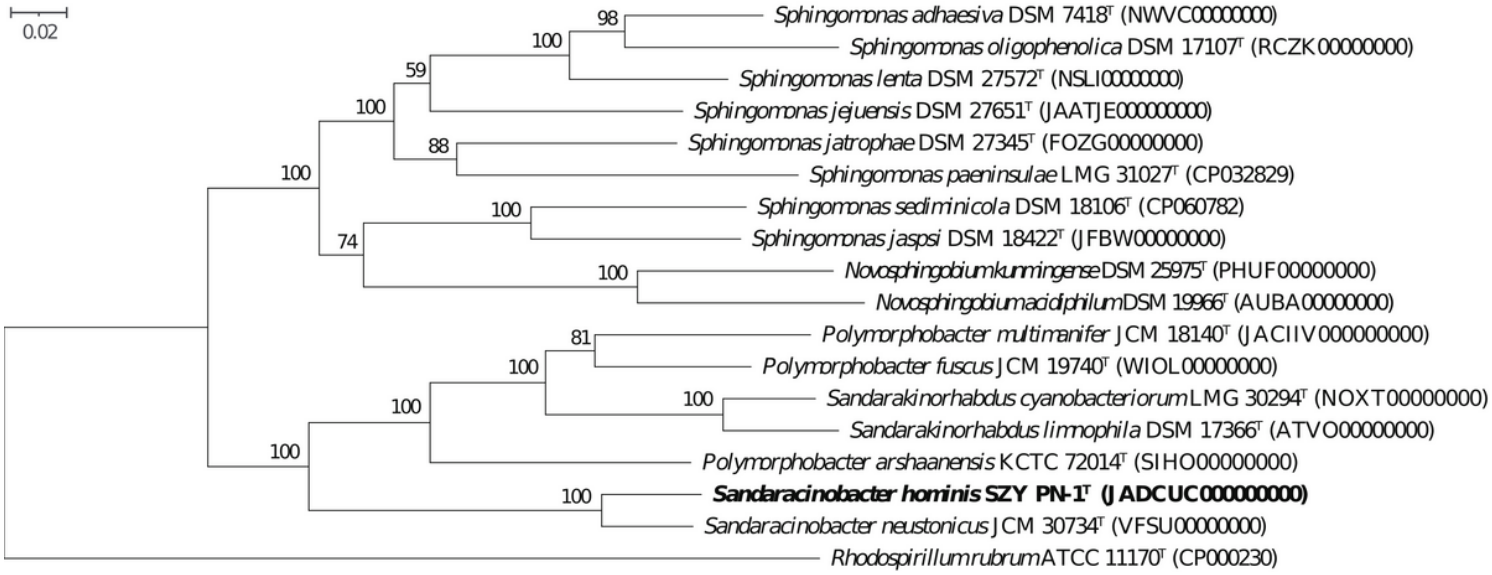

Figure 2

Protein-concatamer tree based on concatenation of 29 protein markers sequences retrieved from the genomic data showing the relationship of strain SZY PN-1T with closely related species within the family Sphingosinicellaceae. Bootstrap values (≥ 50 %) are given at the nodes. The genome of Rhodospirillum rubrum ATCC 11170T (CP000230) was used as an outgroup. Bar, 0.02 substitutions per nucleotide position.

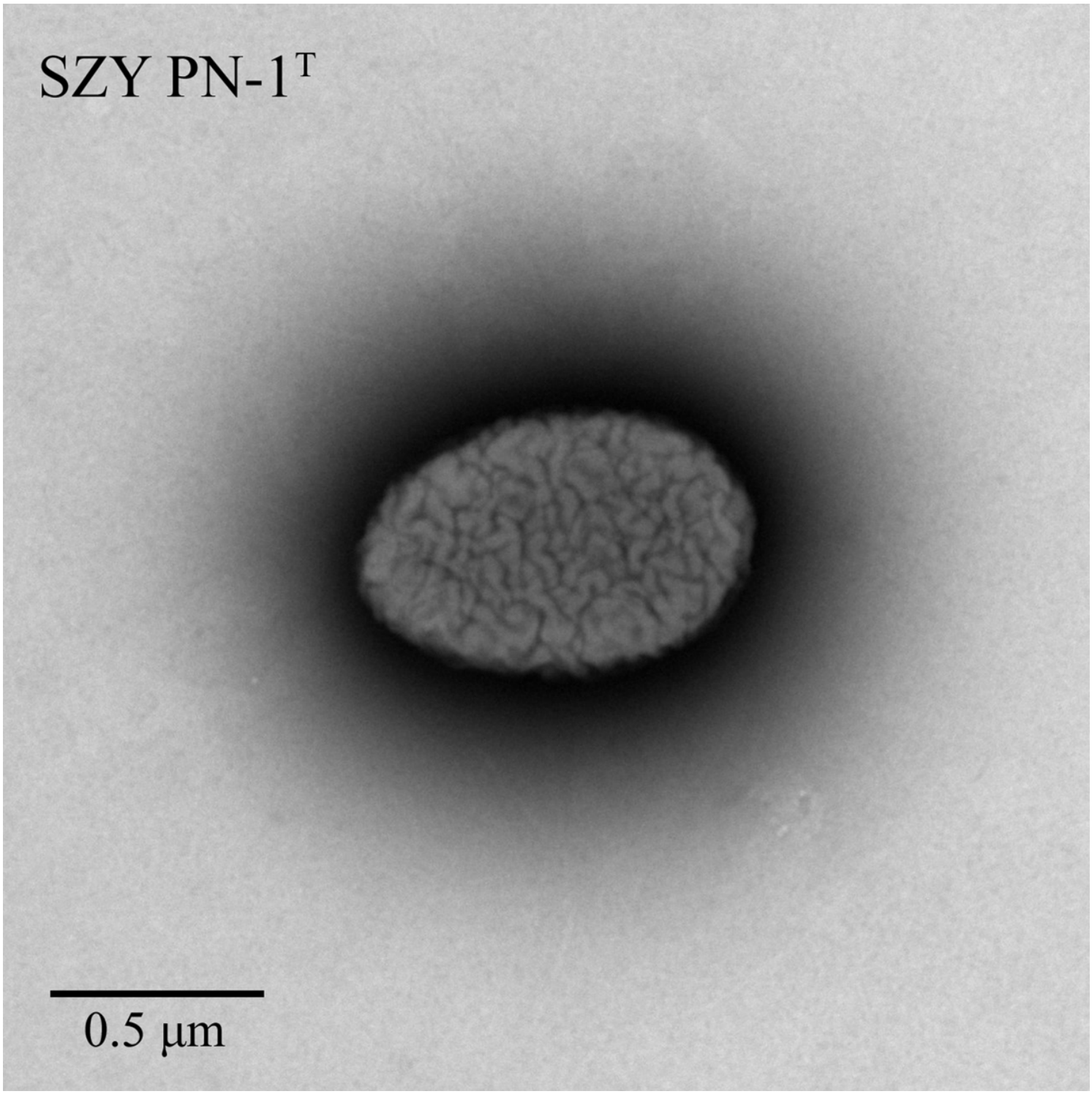

Figure 3

Transmission electron micrograph of strain SZY PN-1T from cultures grown on R2A agar for 2 days at 30 ºC. Bar, 0.5 μm.

Supplementary Files

This is a list of supplementary files associated with this preprint. Click to download.

- Supplementarymaterial.docx