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ORIGINAL PAPER

Aestuariisphingobium litorale gen. nov., sp. nov., a novel proteobacterium isolated from a water sample of Pearl River estuary

Xin Li · Jia-Ling Li · Xiao-Tong Zhang · Li Duan · Mipeshwaree Devi Asem · Min Xiao · Xiaozhen Mou · Nimaichand Salam · Wen-Jun Li

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Abstract Strain SYSU M10002^T was isolated from a water sample collected from the coastal region of Pearl River estuary, Guangdong Province, southern China. The taxonomic position of the isolate was investigated by polyphasic taxonomic approaches. The isolate was found to be Gram-negative, non-motile, short rods and aerobic. The strain was able to grow at 14–37 °C, pH 6.0–10.0 and in the presence of up to 0.5% (w/v) NaCl. Phylogenetic analysis based on 16S rRNA gene sequences indicated that strain SYSU M10002^T is a member of the family *Sphingomonadaceae*, with high sequence similarity to *Sphingorhabdus buctiana* T5^T (95.1%). Overall genomic related indices between the genome of strain SYSU M10002^T and those of related strains were low to moderate (AAI values $< 64.3\%$; POCP values $< 58\%$), indicating that strain SYSU M10002^T represents a novel lineage within the family *Sphingomonadaceae*. Strain SYSU M10002^T contained homospermidine as its polyamine. The major polar lipids were diphosphatidylglycerol, phosphatidylcholine, phosphatidylethanolamine, phosphatidylglycerol, sphingoglycolipid, two unidentified phospholipids and an unidentified aminolipid. Ubiquinone Q-9 (44.9%) and Q-10 (43.2%) were the dominant respiratory quinones, along with a minor amount of Q-8 (11.9%). The predominant cellular fatty acids ($> 10\%$) identified were summed feature 3 ($C_{16:1}$ ω7c and/or $C_{16:1}$ ω6c), summed feature 8 ($C_{18:1}$ ω7c) and $C_{14:0}$ 2-OH. The genomic DNA G+C content was 64.0%. Based on the analyses of the phenotypic, genotypic and phylogenetic characteristics, strain SYSU M10002^T is determined to represent a novel species of a novel genus, for which the name *Aestuariisphingobium litorale* gen. nov., sp. nov. is

Xin Li, Jia-Ling Li, and Xiao-Tong Zhang have contributed equally to this work.

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X. Li · J.-L. Li · X.-T. Zhang · L. Duan · M. D. Asem · M. Xiao · N. Salam (✉) · 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
e-mail: s.nimaichand@hotmail.com

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

X. Mou
Department of Biological Sciences, Kent State University, Kent, OH 44242, USA

W.-J. Li
College of Fisheries, Henan Normal University, Xinxiang 453007, People's Republic of China

proposed. The type strain of the species is SYSU M10002^T (= KCTC 52944^T = NBRC 112961^T).

Keywords *Aestuariisphingobium litorale* gen. nov., sp. nov. · Polyphasic taxonomy · Pearl River estuary

Introduction

The family *Sphingomonadaceae*, proposed by Kosako et al. (2000), belongs to the order *Sphingomonadales* of the *Alphaproteobacteria*. At the time of writing, the family *Sphingomonadaceae* comprises of 22 validly named genera (https://www.namesforlife.com/10.1601/tx.1165) that were isolated from various environments, such as freshwater, pristine or contaminated soils, the rhizosphere and clinical specimens (Balkwill et al. 2006; Gich and Overmann 2006; Glöckner et al. 2000; Kim et al. 2007; Takeuchi et al. 2001; Zwart et al. 2002). Members of the family *Sphingomonadaceae* are typically Gram-stain negative, non-spore-forming, ovoid to rod-shaped, non-motile or motile, aerobic [with the exception of the facultative anaerobe *Zymomonas* (Kalnenieks 2006)] and chemoorganotrophic. Members of the family contain sphingoglycolipid as a major polar lipid component, ubiquinone-10 as the main respiratory quinone, $C_{18:1}$ ω7c as the predominant fatty acid and homospermidine as the major polyamine. The DNA G+C content is in the range of 59–68.5 mol% (Kosako et al. 2000). In this study, we describe the taxonomic position of strain SYSU M10002^T by using a polyphasic taxonomic approach.

Materials and methods

Isolation and culture conditions

Water samples were collected from a conjunct point of freshwater and seawater, located along the coastal region of Pearl River estuary (113°35′42.00″E, 23°6′35.25″N), Guangdong Province, southern China. The sample was diluted 10^3-fold with sterile water and 0.2 ml aliquots spread on Reasoner's 2A (R2A; BD) agar plates adjusted to pH 7.0. The isolation plates were incubated at 28 °C for 14 days. Single colonies were picked, purified and cultivated on the same medium. The strain SYSU M10002^T was maintained on R2A agar and preserved as glycerol suspensions (20%, v/v) at −80 °C. The basal growth condition of the strain for all experiments was maintained at pH 7.0 and 28 °C, and the biomass for chemical and molecular studies were obtained by cultivating in R2A media, unless otherwise stated.

Phenotypic characterization

Cell morphology was observed using a light microscope (BH2; Olympus) and a transmission electron microscope (JEM-100CX-II; JEOL), on R2A agar at 28 °C after 3 days of incubation. Samples for transmission electron microscopy were prepared as described by Ming et al. (2012). Gram reaction was tested by the Gram Stain Solution kit (Shanghai Yeasen Biotechnology). Motility was determined by the development of turbidity in a tube containing semi-solid medium (Leifson 1960). Growth temperature range (4, 14, 20, 28, 37, 40, 45, 50, 55, and 60 °C) and NaCl tolerance (up to 5.0%, at intervals of 0.5%, w/v) were observed in R2A agar following 2 weeks of incubation. For pH tolerance, R2A agar was prepared between pH 4.0–10.0 (with an interval of 1.0 pH unit) using the buffer system described by Nie et al. (2012), and growth was observed after 2 weeks of incubation. Oxidase and catalase activities were determined by assessing the oxidation of 1% (w/v) tetramethyl-*p*-phenylenediamine (Kovacs 1956), and the production of gas bubbles on the addition of a drop of 3% H_2O_2 (v/v), respectively. Hydrolysis of cellulose, gelatin and starch, milk peptonization and coagulation, nitrate reduction, Tweens (20, 40, 60 and 80) degradation and activity of urease were examined as described previously (Gonzalez et al. 1978; Mac Faddin 1976; Tindall et al. 2007). H_2S production and indole formation were carried out as described by Cui et al. (2007). Additional physiological and biochemical tests were further performed using API 20NE (bioMérieux), API ZYM (bioMérieux), and GenIII MicroPlate systems (Biolog). All the commercial phenotypic tests were performed according to the manufacturer's recommendations.

Chemotaxonomy

Biomass for chemical and molecular studies of strain SYSU M10002^T were obtained from cultures grown in

R2A broth for 3 days. Extraction and analysis of polyamines were carried out as described earlier (Busse et al. 1997; Busse and Auling 1988). For this, cells were cultivated for 3 days, homogenized in 0.2 M perchloric acid ($HClO_4$) and centrifuged. Polyamines in the resultant supernatant were treated with dansyl chloride solution (7.5 μg ml^{-1} in acetone), and analyzed by HPLC, using UV–Vis detector L-7420. Polar lipids were extracted, separated and examined by a two-dimensional TLC procedure on silica gel G_{60} plates using the method of Minnikin et al. (1979). Respiratory quinones were extracted from lyophilized cells (Collins et al. 1977), purified and analyzed by HPLC (Groth et al. 1996). The fatty acid profile of strain SYSU M10002^T from cultures grown on R2A agar for 3 days (stationary phase) under optimal growth conditions [Note: Cells of strain SYSU M10002^T show no growth on tryptic soy agar (Difco)]. Cellular fatty acids were extracted, methylated and analyzed following the instructions of the Sherlock Microbial Identification System (MIDI) version 6.1 and the TSBA6 database (Sasser 2001).

Molecular characterization

Genomic DNA extraction, PCR amplification of the 16S rRNA gene and sequencing of the purified products from strain SYSU M10002^T were carried out as described by Li et al. (2007). The whole genome sequencing of strain SYSU M10002^T was performed using paired-end sequencing method with Hiseq X platform (Illumina, San Diego, CA, USA) at Magigene Company (Guangzhou, China). Reads of each data set were filtered, and high-quality paired-end reads were assembled using Spades (Harrison and Strulo 2000). Contigs with length greater than 500 bp were kept for gene prediction by applying Prodigal (Hyatt et al. 2010). The predicted coding sequences of the genome were translated and annotated in the COG, KEGG, GO and Pfam databases (Ashburner et al. 2000; Finn et al. 2016; Kanehisa et al. 2017; Tatusov et al. 2001). The phylogenetic relationship of strain SYSU M10002^T was determined after BLAST searches (Altschul et al. 1990) of the 16S rRNA gene sequences in NCBI and the EzBioCloud server (Yoon et al. 2017) databases. Analysis of the sequence data was performed by using the software package BioEdit (Hall 1999) and MEGA 7 (Kumar et al. 2016), after multiple alignments of the data by CLUSTAL X software package (Thompson et al. 1997). Phylogenetic analyses were carried out with three tree-making algorithms: neighbour-joining (NJ; Saitou and Nei 1987), maximum-likelihood (ML; Felsenstein 1981) and maximum-parsimony (MP; Fitch 1971) methods. Evolutionary distances in the NJ and ML dendrograms were calculated by the Kimura two-parameter model (Kimura 1983) and the topologies of the phylogenetic trees were evaluated by the bootstrap analysis of Felsenstein (1985) with 1000 replicates. Genome trees based on the concatenated sequences of 29 protein marker genes were generated using RAxML (Stamatakis 2014). Overall genomic relatedness indices between strain SYSU M10002^T and related strains in the family *Sphingomonadaceae* were calculated based on the percentage of conserved proteins (POCP; Qin et al. 2014) and Average amino acid identities (AAI; Hua et al. 2018).

Results and discussion

Phenotypic characteristics

Cells of strain SYSU M10002^T were Gram-stain negative, non-motile and aerobic. Colonies on R2A agar following incubation for 3 days were circular, opaque, convex and yellow. Cells of strain SYSU M10002^T were short rods, with size measuring approximately 0.8–1.8 μm in length and 0.4–0.6 μm in width (Fig. S1). Strain SYSU M10002^T grew at 14–37 °C, pH 6.0–10.0 and in the presence of up to 0.5% NaCl. Optimum growth was observed at 28 °C, pH 6.0–7.0 and in the absence of NaCl. The strain was positive for oxidase and catalase activities, but negative for H_2S production, indole formation, milk coagulation and peptonization, nitrate reduction and urease activity tests. Strain SYSU M10002^T could hydrolyse Tween 60, but not cellulose, gelatin, starch or Tweens 20, 40 or 80. The strain utilized D-turanose, *N*-acetyl-D-glucosamine, *N*-acetyl-*β*-D-mannosamine, L-fucose and glucuronamide as sole carbon source, but not L-alanine, D-fucose, D-galactose, D-galacturonic acid, D-glucose, stachyose, acetic acid, acetoacetic acid, *N*-acetyl-D-galactosamine, *N*-acetyl neuraminic acid, *γ*-amino-butyric acid, D-arabitol, L-arginine, D-aspartic acid, L-aspartic acid, bromosuccinic acid, D-cellobiose, citric acid, dextrin, formic acid, D-fructose, D-fructose-6-PO_4, L-galactonic acid lactone, gelatin,

Table 1 Key taxonomic characteristics differentiating strain SYSU M10002^T from its closely related phylogenetic neighbours of the family *Sphingomonadaceae*

Characteristic	1	2	3	4	5	6
Pigmentation (colony colour)	Yellow	Light-yellow	Cream	Yellow, orange, or brown	Whitish-brown, or yellow	Yellowish orange, transparent
Cell morphology	Short rod	Rod	Rod	Rod, or wedge	Rod	Rod
Motility	−	−	−	ND	+	−
Optimum growth temperature (°C)	28	25	30	30–35	ND	18–24
Optimum growth pH	6.0–7.0	9.0	6.0	7.0–7.5	ND	7.0–8.0
Nitrate reduction	−	+	+	−	ND	−
Hydrolysis of						
Aesculin	+	+	+	−	w	ND
Gelatin	−	−	−	+	ND	ND
Tween 20	−	+	−	ND	ND	ND
Tween 80	−	+	−	+	ND	ND
Enzyme activities						
Catalase	+	+	−	+	+	+
β-Glucosidase	−	−	+	ND	+	+
β-Galactosidase	−	+	−	ND	+	+
Assimilation of						
Glucose	+	−	−	−	+	+
L-Arabinose	−	−	+	−	+	−
D-Mannose	+	−	−	−	ND	−
Mannitol	−	−	−	ND	w	−
Maltose	+	−	−	+	+	−
Polyamine	Homospermidine	Spermidine	Spermidine, putrescine	Spermidine	Spermidine	Spermidine
Major fatty acids	Summed feature 3, summed feature, $C_{14:0}$ 2-OH	$C_{18:1}\omega7c$, $C_{16:1}\omega7c$	$C_{17:1}$ $\omega6c$, summed feature 3, $C_{18:1}$ $\omega7c$, $C_{15:0}$ 2-OH, $C_{17:1}$ $\omega8c$	$C_{18:1}$ $\omega7c$, $C_{17:1}$ $\omega6c$	Summed feature 3, summed feature 8	Summed feature 8, summed feature 3, $C_{14:0}$ 2-OH

Table 1 continued

Characteristic	1	2	3	4	5	6
Major ubiquinones	Q-9, Q-10	Q-10	Q-10	Q-10	Q-10	Q-10
Major phospholipids	DPG, PC, PE, PG, SGL	PE	PG, PE, DPG, PDE, SGL, PC	PG, PE, PDE, PC	ND	DPG, PG, PE, PMME, PDE, PC, SGL
DNA G+C content (mol%)	64.0	58.5	66.6	64.8	63.9	55.7

Taxa: 1, SYSU M10002^T (data from this study); 2, *Sphingorhabdus buctiana* T5^T (Chen et al. 2018); 3, *Novosphingobium fontis* BCRC 80924^T (Sheu et al. 2017); 4, *Blastomonas natatoria* LMG 17322^T (Sly and Cahill 1997); 5, *Sphingopyxis macrogoltabida* DSM 8826^T (Takeuchi et al. 1993); 6, *Sphingorhabdus planktonica* DSM 25081^T (Jogler et al. 2013)

+, positive; −, negative; w, weakly positive; ND, not determined or data not available at relevant literature

DPG, diphosphatidylglycerol; PC, phosphatidylcholine; PE, phosphatidylethanolamine; PG, phosphatidylglycerol; SGL, sphingoglycolipid; PDE, phosphatidyldimethylethanolamine; PMME, phosphatidylmonomethylethanolamine

Summed features represent two or three fatty acids that cannot be separated by GC with the MIDI system. Summed feature 3, $C_{16:1}$ ω7c and/or $C_{16:1}$ ω6c, Summed feature 8, $C_{18:1}$ ω7c and/or $C_{18:1}$ ω6c

gentiobiose, D-gluconic acid, D-glucuronic acid, D-glucose-6-PO_4, glycerol, glycyl-L-proline, L-glutamic acid, L-histidine, α-hydroxy-butyric acid, β-hydroxy-D,L-butyric acid, *p*-hydroxy-phenylacetic acid, α-keto-butyric acid, α-keto-glutaric acid, inosine, L-lactic acid, D-lactic acid methyl ester, α-D-lactose, D-malic acid, L-malic acid, D-maltose, D-mannitol, D-mannose, D-melibiose, 3-methyl glucose, β-methyl-D-glucoside, methyl pyruvate, *myo*-inositol, mucic acid, pectin, propionic acid, L-pyroglutamic acid, quinic acid, D-raffinose, L-rhamnose, D-saccharic acid, D-salicin, D-serine, L-serine, D-sorbitol, sucrose, D-trehalose, or Tween 40. In the API ZYM system, strain SYSU M10002^T was found to be positive for the activities of alkaline phosphatase, acid phosphatase, esterase (C4), esterase lipase (C8), leucine arylamidase, valine arylamidase, chymotrypsin, naphthol-AS-BI phosphohydrolase and α-glucosidase, but not cystine arylamidase, trypsin, β-glucosidase, β-fucosidase, α-galactosidase, β-galactosidase, β-glucuronidase, *N*-acetyl-β-glucosaminidase, lipase (C14) or α-mannosidase. In the API 20NE system, it could hydrolyse aesculin and assimilate glucose, arabinose, mannose, *N*-acetyl-D-glucosamine, maltose, gluconate, capric acid and malic acid. Differentiating characteristics of strain SYSU M10002^T from members of related genera of the family *Sphingomonadaceae* are listed in Table 1. The detailed physiological characteristics of strain SYSU M10002^T are given in the genus and species descriptions below.

Chemotaxonomic characteristics

The respiratory quinones of strain SYSU M10002^T were identified as ubiquinone Q-9 (44.9%), Q-10 (43.2%) and Q-8 (11.9%). Strain SYSU M10002^T contained homospermidine as its polyamine. The polar lipids of the strain comprised of diphosphatidylglycerol, phosphatidylcholine, phosphatidylethanolamine, phosphatidylglycerol, sphingoglycolipid, two unidentified phospholipids and an unidentified aminolipid (Fig. S2). The major cellular fatty acids (> 10%) detected for strain SYSU M10002^T were summed feature 3 ($C_{16:1}$ ω7c and/or $C_{16:1}$ ω6c, 37.4%), summed feature 8 ($C_{18:1}$ ω7c, 27.9%) and $C_{14:0}$ 2-OH (10.5%). A detailed fatty acid profile of strain SYSU M10002^T is provided in Table S1.

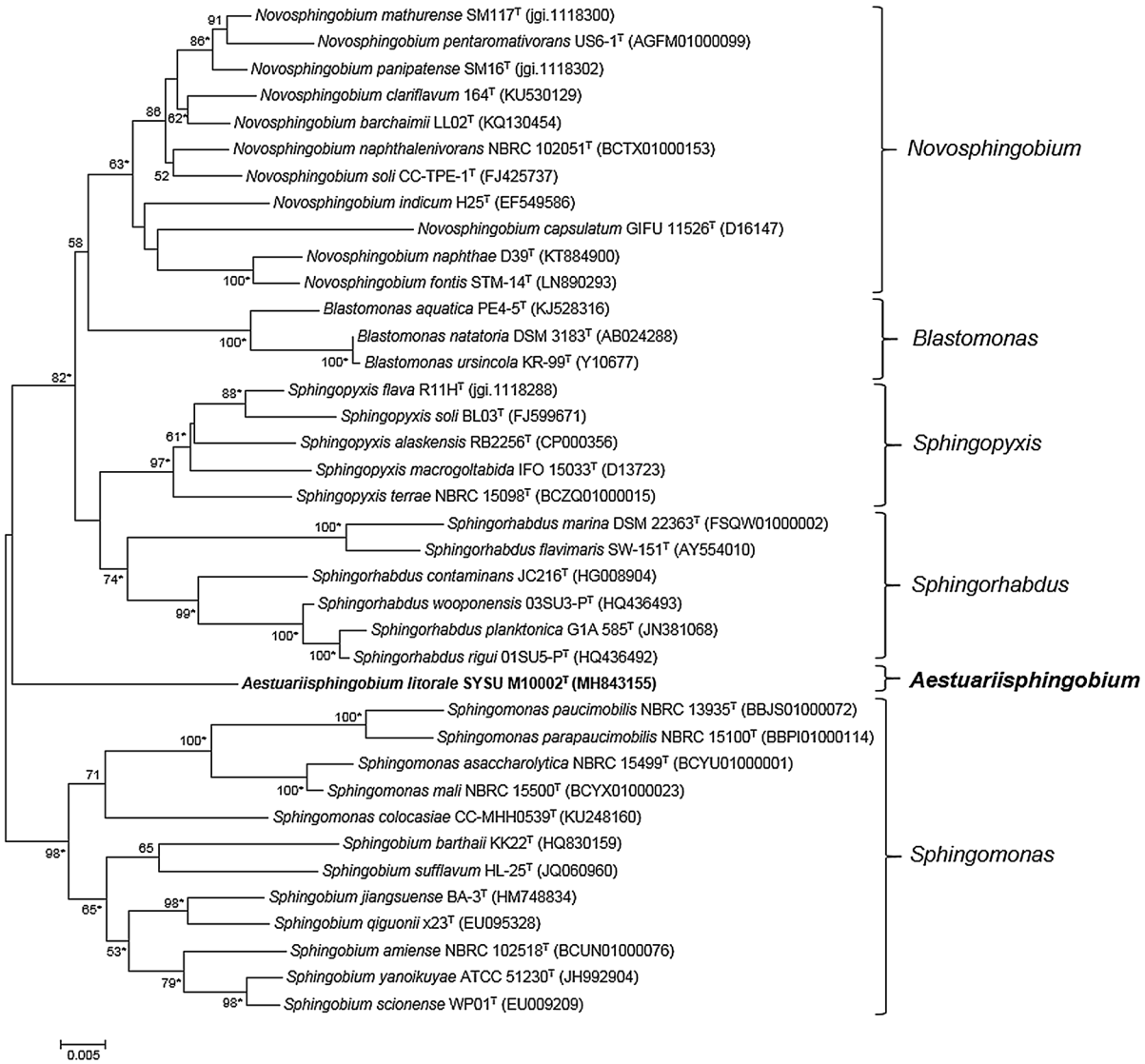

Fig. 1 Unrooted neighbour-joining phylogenetic tree based on 16S rRNA gene sequences showing the relationships between strain SYSU M10002^T and closely related members of the family *Sphingomonadaceae*. *Asterisks* indicate nodes that were supported in trees generated with maximum-likelihood and maximum-parsimony methods. Bootstrap values ($\geq$ 50%) based on 1000 resamplings are given at the nodes. Bar, 0.005 substitutions per nucleotide position

Molecular characteristics

The DNA G+C content of strain SYSU M10002^T was calculated at 64.0% (genome). Pairwise comparison with the almost-complete 16S rRNA gene sequence of strain SYSU M10002^T showed sequence similarities of less than 96% with members of the family *Sphingomonadaceae*. The highest 16S rRNA gene sequence identity of 95.1% is determined with *Sphingorhabdus buctiana* T5^T. Besides the low sequence identity, strain SYSU M10002^T also formed a separate clade distinct from the members of the genera *Novosphingobium*, *Blastomonas*, *Sphingopyxis*, *Sphingorhabdus* or *Sphingomonas* in all three phylogenetic trees (Fig. 1; Figs. S3 and S4). These findings indicated that the topology of the strain SYSU M10002^T is stable and that the strain should be affiliated to the family *Sphingomonadaceae*. A Similar finding was observed with the RAxML tree generated with related members of the family

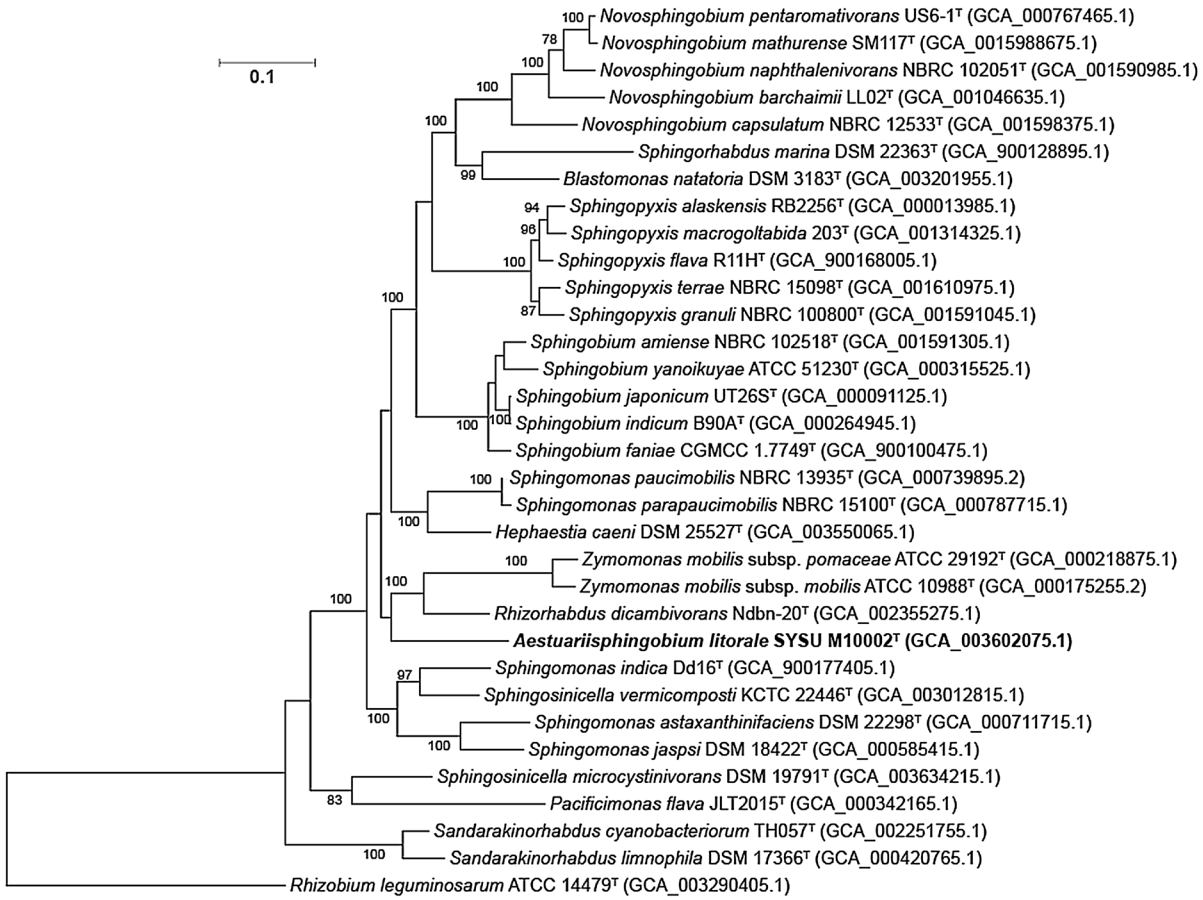

Fig. 2 RAxML phylogenomic tree showing the phylogenetic relationships between strain SYSU M10002^T and closely related members of the family *Sphingomonadaceae*. Bootstrap values ($\geq$ 70%) based on 1000 resamplings are given at the nodes. Bar, 0.1 substitutions per nucleotide position

Sphingomonadaceae (Fig. 2). Strain SYSU M10002^T showed low to moderately high POCP and AAI values with related members of the family *Sphingomonadaceae* (Table 2). Other general features of the genome of strain SYSU M10002^T are listed in Table S2.

Discussion

On the basis of 16S rRNA gene sequences identity and chemotaxonomic features, strain SYSU M10002^T can be affiliated to the family *Sphingomonadaceae*. While strain SYSU M10002^T exhibited many characteristics similar to members of the family *Sphingomonadaceae* in having ovoid to rod-shaped morphology, optimum growth temperature of about 30 °C, optimum growth pH of about 7 and DNA G+C content within the range of the family, it could, however, be differentiated physiologically and phenotypically from the other closely related genera (Table 1). For example, strain SYSU M10002^T could tolerate pH 10 which is obviously different from the other closely related genera. Unlike the other closely related genera, the major polyamine in strain SYSU M10002^T is homospermidine. Further, on pairwise comparison with the closely related phylogenetic neighbor *S. buctiana* T5^T, despite showing high 16S rRNA gene sequence similarity to *S. buctiana* T5^T, strain SYSU M10002^T differed from it on the basis of several distinct chemotaxonomic characteristics, such as (1) fatty acid profile [summed feature 3 ($C_{16:1}$ ω7c and/or $C_{16:1}$ ω6c), summed feature 8 ($C_{18:1}$ ω7c) and $C_{14:0}$ 2-OH for strain SYSU M10002^T, and $C_{18:1}$ ω7c and $C_{16:1}$ ω7c as major fatty acids for *Sphingorhabdus buctiana* T5^T]; and (2) respiratory quinone [ubiquinone Q-9

Table 2 Overall genome relatedness indices between strain SYSU M10002^T and related members of the family *Sphingomonadaceae*

Strains	Genome accession	POCP (%)	AAI (%)
Novosphingobium barchaimii LL02^T	GCA_001046635.1	43.1	61.2
Novosphingobium capsulatum NBRC 12533^T	GCA_001598375.1	48.6	62.1
Novosphingobium mathurense SM117^T	GCA_900168325.1	47.8	61.8
Novosphingobium naphthalenivorans NBRC 102051^T	GCA_001590985.1	43.4	61.2
Novosphingobium pentaromativorans US6-1^T	GCA_000767465.1	42.5	60.6
Blastomonas natatoria DSM 3183^T	GCA_003201955.1	52.7	62.6
Hephaestia caeni DSM 25527^T	GCA_003550065.1	49.4	63.9
Pacificimonas flava JLT2015^T	GCA_000342165.1	47.7	57.8
Rhizorhabdus dicambivorans Ndbn-20^T	GCA_002355275.1	46.0	62.6
Sandarakinorhabdus cyanobacteriorum TH057^T	GCA_002251755.1	50.9	59.4
Sandarakinorhabdus limnophila DSM 17366^T	GCA_000420765.1	52.3	59.3
Sphingobium amiense NBRC 102518^T	GCA_001591305.1	49.0	63.6
Sphingobium faniae CGMCC 1.7749^T	GCA_900100475.1	47.0	63.8
Sphingobium indicum B90A^T	GCA_000264945.2	50.4	64.2
Sphingobium japonicum UT26S^T	GCA_000091125.1	49.3	63.7
Sphingobium yanoikuyae ATCC 51230^T	GCA_000315525.1	46.3	62.9
Sphingomonas astaxanthinifaciens DSM 22298^T	GCA_000711715.1	50.2	61.6
Sphingomonas indica Dd16^T	GCA_900177405.1	51.9	63.7
Sphingomonas jaspsi DSM 18422^T	GCA_000585415.1	49.5	62.3
Sphingomonas paucimobilis NBRC 13935^T	GCA_000739895.2	47.1	63.2
Sphingomonas sanxanigenens DSM 19645^T	GCA_000512205.2	43.0	63.9
Sphingopyxis alaskensis RB2256^T	GCA_000013985.1	57.9	64.0
Sphingopyxis flava R11H^T	GCA_900168005.1	50.8	63.5
Sphingopyxis granuli NBRC 100800^T	GCA_001591045.1	52.8	63.5
Sphingopyxis macrogoltabida 203^T	GCA_001314325.1	48.6	64.1
Sphingopyxis terrae NBRC 100800^T	GCA_001610975.1	55.9	63.6
Sphingosinicella microcystinivorans DSM 19791^T	GCA_003634215.1	49.4	60.0
Sphingosinicella vermicomposti KCTC 22446^T	GCA_003012815.1	51.9	64.2
Zymomonas mobilis subsp. *mobilis* ATCC 10988^T	GCA_000175255.2	37.7	59.7
Zymomonas mobilis subsp. *pomaceae* ATCC 29192^T	GCA_000218875.1	38.4	60.0

(44.9%), Q-10 (43.2%) and Q-8 (11.9%) for SYSU M10002^T and ubiquinone Q-10 for *S. buctiana* T5^T], and genomic DNA G+C content (64.0% for strain SYSU M10002^T and 58.5 mol% for *S. buctiana* T5^T) (Table 1). Observation of the POCP and AAI also indicate that strain SYSU M10002^T was distinct from the related genera by low to moderate values ranging from 37 to 58 POCP values and 57–65 AAI values (Table 2). Based on the results of these differentiating characteristics (Tables 1 and 2) and phylogenetic analyses, strain SYSU M10002^T is considered to represent a novel species in a new genus of the family *Sphingomonadaceae*, for which the name *Aestuariisphingobium litorale* gen. nov., sp. nov. is proposed.

Description of *Aestuariisphingobium* gen. nov.

Aestuariisphingobium [Aes.tu.a.ri.i.sphin.go'bi.um. L. neut. n. *aestuarium* an estuary; N.L. neut. n. *Sphingobium*, a bacterial genus; N.L. neut. n. *Aestuariisphingobium*, a *Sphingobium*-like organism from an estuary].

Cells are Gram-negative, non-motile, strictly aerobic, and short rods. Colonies are irregular, opaque,

convex and yellow. No pigments are produced. Oxidase-positive and catalase-positive. The main respiratory isoprenologues are Q-9 and Q-10. Major polyamine is homospermidine. Major cellular fatty acids are summed feature 3, summed feature 8 and $C_{14:0}$ 2-OH. The known polar lipid profile comprises diphosphatidylglycerol, phosphatidylcholine, phosphatidylethanolamine, phosphatidylglycerol and sphingoglycolipid. The genomic DNA G+C content of the type strain of the type species is about 64.0 mol%. The type species is *Aestuariisphingobium litorale*.

Description of *Aestuariisphingobium litorale* sp. nov.

Aestuariisphingobium litorale (li.to.ra'le. L. neut. adj. *litorale*, of or belonging to the coast].

Displays the following properties in addition to those described for the genus. Cells measure 0.8–1.8 μm in length and 0.4–0.6 μm in width after 4 days of growth at 28 °C on R2A agar plates. Growth occurs at 14–37 °C (optimum, 28 °C), pH 6.0–10.0 (optimum, pH 6.0–7.0) and in the presence of up to 0.5% NaCl. Negative results for H_2S production, indole formation, nitrate reduction, milk coagulation and peptonization, and urease activity. Hydrolyses Tween 60, but not cellulose, gelatin, starch, or Tweens 20, 40 or 80.

The type strain SYSU M10002^T (= KCTC 52944^T = NBRC 112961^T) was isolated from a water sample collected along the coast of Pearl River estuary, Guangdong Province, southern China. The genomic DNA G+C content of the type strain is 64.0%. The GenBank accession number for the 16S rRNA gene sequence of strain SYSU M10002^T is MH843155. The draft genome has been deposited under accession number RAGX00000000.

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Authors' contribution N.S. and W.J.L. conceived the study. X.L., J.L.L, X.T.Z., N.S., L.D. and M.D.A. performed research. N.S., X.M. and M.X. analyzed data. X.L., N.S. and W.J.L. wrote the paper. All authors approved the manuscript.

Compliance with ethical standards

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

Ethical statement This article does not contain any studies with human participants or animals performed by any of the authors.

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