Thermohalobaculum Xanthum Gen. Nov., Sp. Nov., A Novel Moderately Thermophilic Bacterium Isolated From Mangrove Sediment

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Abstract

A novel moderately thermophilic and halophilic bacterium, designated strain M0105^T, was isolated from mangrove sediment collected in the Beibu Gulf, south China. The isolate is Gram-negative, non-motile and rod-shaped bacterium with smooth colonies of pale-yellow appearance. Growth occurs at 15-46°C (optimum 37-40°C) and pH range of 6.0-10.0 (optimum pH 8.0-9.0). It required 1-7% NaCl (optimum 3-5%) for growth. Strain M0105^T was affiliated to the family '*Rhodobacteraceae*', sharing the highest 16S rRNA gene sequence similarity with *Limibaculum halophilum* CAU 1123^T (96.8%). The major menaquinone Q-10 and the dominant unsaturated fatty acid (C_{18:1} ω7) in this family were also detected in the strain M0105^T. The genome sequence possesses a circular 4.1 Mb chromosome with a G+C content of 67.9%. Strain M0105^T encoded many genes for cellular stress resistance and nutrient utilization, which could improve its adaptive capacity to the mangrove environment. Values of conserved proteins (POCP), average nucleotide identity (ANI), average amino acid identity (AAI) and DNA-DNA hybridization (dDDH) between the isolate and closely related species were below the proposed threshold for species discrimination. Information from phenotypic, chemotaxonomic and phylogenetic analyses proposed that strain M0105^T should be assigned to a novel genus within the family '*Rhodobacteraceae*'. Thus, we suggested that the strain M0105^T represents a novel species in a new genus, for which the name *Thermohalobaculum xanthum* gen. nov., sp. nov. is proposed. The type strain of the type species is M0105^T (=BGMRC 2019^T=KCTC 52118^T=MCCC 1K03767^T=NBRC 112057^T).

Six supplementary figures and two supplementary tables are available with the online version of this article.

Introduction

Mangrove ecosystems located at the land-sea interface that play vital roles in coastlines protection, marine environment purification and organic carbon fixation [Giri et al. 2015; Nagelkerken et al. 2008]. Accumulating reports confirmed that a wide range of element and nutrient cycles processes in mangrove ecosystems are assisted by microorganisms, such as carbohydrate degradation, phosphate solubilization, sulfur metabolism and nitrogen fixation [Kathiresan and Selvam, 2006; Priya et al. 2018]. Additionally, genes involved in carbohydrate, energy and amino acid metabolisms are enrich in mangrove sediments [Zhao et al. 2019]. In recent decades, bacteria possess different nutrient utilization characteristics, including chitinolytic, lignocellulolytic, cellulose and organic compound degradation, were isolated from worldwide mangrove ecosystems using classical culture methods [Marcon et al. 2014; Lam et al. 2020; Aziz et al. 2018].

The family '*Rhodobacteraceae*' belonging to the class *Alphaproteobacteria* contains more than hundreds validly named species with diverse physiologies [González et al. 2000]. Most of members originate from marine, but only a few from terrestrial. At the time of writing, there are approximately 186 genera with validly name in the family (<https://lpsn.dsmz.de/family/rhodobacteraceae>). In an attempt to investigate

the diversity of culturable bacteria from the mangrove sediment in Beibu Gulf, 45 *Rhodobacteraceae*-like species were isolated and characterized taxonomically. Among them, strain M0105^T shared less than 97% 16S rRNA gene sequences similarities with other published known species in the EzBioCloud database. Thus, the aim of the present work was to determine the taxonomic position of strain M0105^T by using a polyphasic approach.

Material And Methods

Strain isolation and cultivation

Mangrove soil were collected from the Beibu Gulf in Beihai, Guangxi province, China (21°55'25" N, 108°50'42" E). A 1 g of air-dried soil sample was suspended in distilled water to prepare 10^{-2} - 10^{-3} soil solution. Subsequently, a 100 μ L of solution was spread onto modified international *Streptomyces* project 7 agar (ISP7, L-tyrosine 0.05% w/v, aspartic acid 0.1% w/v, glycerol 0.5% v/v, agar 1.5% w/v, water 1 L) and incubated at 28°C for 14 days. Single colonies were selected based on their morphological features and carefully inoculated onto modified ISP7 agar. A single round colony named M0105^T, appearing pale-yellow color on ISP7 agar, was isolated with the preceding method. For further phenotypic and genotypic characteristic investigation, the isolate was maintained in ISP2 (yeast extract 0.2% w/v, maltol 0.2% w/v, glucose 0.2% w/v, sea water 1 L, agar 1.5% w/v) or Reasoner's 2A (R2A) media.

Genotypic analysis

Genomic DNA of strain M0105^T was extracted using a bacterial genomic DNA extraction kit (Bio-Teke). The 16S rRNA gene was amplified from the genomic DNA by PCR with a universal primer pair 27F and 1492R [Lane, 1991]. The PCR product was purified using the gel extraction kit and ligated with PMD 19-T vector (TaKaRa). The extracted plasmid was transformed into *Escherichia coli* DH 5 α competent cells and then send to Sangon Biotech (Shanghai) Co., Ltd for sequencing. For species classification, the 16S rRNA gene sequence of strain M0105^T was aligned with published sequences of closely related type species on the EzBioCloud server (<https://www.ezbiocloud.net/dashboard>) [Yoon et al. 2017]. Phylogenetic trees were reconstructed in the MEGA 7 platform using the maximum-likelihood, neighbor-joining and maximum-parsimony with the kimura's two-parameter or subtree-pruning-regrafting algorithms [Kumar et al. 2016]. The topologies of all phylogenetic trees were evaluated based on the 1000 replications of bootstrap analyses.

The genome of strain M0105^T was sequenced by Majorbio Bio-pharm Technology Co., Ltd (Shanghai, PR China) using an Illumina HiSeq 2500-PE150 platform. The assembly of draft genome was conducted by SOAP denovo software (v2.04) [Luo et al. 2012]. The prediction of coding sequences was achieved with Glimmer (v3.02), and gene functions were annotated through the comparison of protein sequences in (Non-Redundant Protein Sequence) NR database, (Gene Ontology) GO database, Pfam database, Swiss-Prot database, (Clusters of Orthologous Groups) COG database and (Kyoto encyclopedia of genes and genomes) KEGG database. Secondary metabolites gene clusters were predicted by using antiSMASH

[Blin et al. 2019]. Genome completeness was evaluated using BUSCO (v3.0.2) [Seppey et al. 2019]. Values of dDDH, ANI, AAI and POCP were utilized to assess the genetic relatedness between strain M0105^T and closely related species within the family '*Rhodobacteraceae*'. Values of dDDH and ANI were determined using the Genome-to-Genome Distance Calculator (GGDC) web server [Meier-Kolthoff et al. 2013] (<http://ggdc.dsmz.de/ggdc.php#>) and ANI calculator in the EzBioCloud [Yoon et al. 2017] platform, respectively. A command line version of the AAI software (<http://enve-omics.ce.gatech.edu/aai/>) was used to evaluate the average amino acid identity between two genomes [Rodriguez-R and Konstantinidis, 2014]. Conserved proteins shared between two strains were estimated based on the percentage of conserved proteins (POCP), which were calculated as the algorithm $[(C_1 + C_2)/(T_1 + T_2)] \times 100\%$ [Qin et al. 2014]. The phylogenomic analysis of whole genome nucleotide sequences of the isolate and type species within the family '*Rhodobacteraceae*' were achieved on the Type (Strain) Genome Server (<https://tygs.dsmz.de/>) with default parameters.

The genomic feature of strain M0105^T was analyzed in comparison with five species (*Meinhardsimonia xiamenensis* YBY-7^T, *Oceanicella actignis* PRQ-67^T, *Amaricoccus solimangrovi* HB172011^T, *Rhodobacter vinaykumarii* DSM 18714^T and *Alkalilacustris brevis* 34079^T), which were selected based on their high genetic relatedness with the isolate. Whole genome sequences of these bacteria were obtained from NCBI database. A heatmap represented the distribution of functional genes was generated using "pheatmap" package in R software.

Phenotypic characterization

The type strains of type species of the most closely genera, *A. brevis* 34079^T, *M. xiamenense* YBY-7^T, *Defluviimonas nitratireducens* 25810_4^T and *L. halophilum* CAU 1123^T were obtained from Marine Culture Collection of China (MCCC) and selected as reference strains for polar lipid, fatty acid and biochemical analyses. Cell morphology was observed from a five-day-old culture on R2A agar medium under a scanning electron microscopy (HITACHI SU8010). A 10 µL of bacteria suspension was placed on a coverslip and then enclosed with petroleum jelly to keep out the air. To observe the motility of strain M0105^T under microscopy (Leica DM1000), the coverslip was inverted over the well of a depression slide. The pH range (pH 4.0–12.0, at increments of 0.5 pH-values) for growth was examined in R2A liquid medium at 28°C, 180 rpm. The ability of salt tolerance was assessed on R2A agar medium supplemented with 0–10% NaCl (at intervals of 1% units, w/v). Oxidase activity was examined by using *p*-aminodimethylaniline oxalate solution to observe the chemistry of the color change. Catalase activity was determined by the bubble production in 3% (v/v) H₂O₂. Hydrolysis of starch, urea, cellulose, gelatin and Tweens (20, 40, 60 and 80) were also examined on R2A agar using the method described by Cowan and Steel [Barrow and Feltham, 1993]. Enzyme activities and carbon source utilization were tested using the API ZYM and API 50CH systems according to the manufacturer's instructions.

The fatty acid methyl esters of all strains were extracted, methylated and sonificated using the protocol of the Sherlock Microbial Identification (MIDI) system. Fatty acid profile was subsequently analyzed using Aglient 6890N gas chromatography [Sasser, 2006]. Isoprenoid quinones were extracted according

to the method described by Minnikin *et al.* [Minnikin et al, 1984], and analyzed by HPLC equipped an C18 column using an isocratic solvent system (methanol/isopropanol, 67:33) and a flow rate of 1 mL min⁻¹. Polar lipids were extracted from 20 mg of freeze-dried material and then were separated by two-dimensional thin-layer chromatography (TLC) on silica gel 60 F254 plates (Merck) [Minnikin et al. 1977] using chloroform/methanol/water (64:25:5, by vol) for the first dimension and chloroform/methanol/acetic acid/water (80:12:18:5, by vol) for the second dimension. Lipids were detected by using five different reagents included phosphomolybdic acid hydrate, molybdenum blue, α -naphthol/sulphuric acid, ninhydrin and Dragendorff.

Effect of temperature on growth of strain M0105^T

The optimal growth temperature was tested at 4, 10, 15, 20, 25, 28, 30, 32, 33, 34, 35, 37, 40, 41, 46 and 50°C on R2A agar medium. Since the optimal growth temperature of *M. xiamenense* YBY-7^T was much higher than other bacteria used in this study, it is difficult to evaluate their thermal tolerance ability at the same culture conditions. We are therefore, choosing *L. halophilum* CAU 1123^T, *A. brevis* 34079^T and *D. nitratireducens* 25810_4^T to examine the temperature effects on the growth of four strains. All strains were firstly cultivated in ISP2 medium at 28°C on a rotatory shaker at 180 rpm until reached the stationary phase. At this point, cells were harvested by centrifugation (8,500 rpm, 5 min) and suspended in ISP2 medium to yield a final concentrations of about 1×10⁶ cells mL⁻¹. Two milliliters of this suspension were evenly inoculated in 100 mL ISP2 medium and maintained at different temperatures for few days. The influence of temperature on bacterial growth was determined based on the statistical relationship between temperature and bacterial concentration in cultures. For this, optical density (OD) measurement was carried out in this test using an ultraviolet-visible spectrophotometer and absorbance was measured at a wavelength of 600 nm.

Results And Discussion

Phylogeny

The 16S rRNA gene sequence of strain M0105^T (1423 bp) shared the highest relatedness to *L. halophilum* CAU 1123^T (96.8%) and less than 94% of identities with other type strains of type species within the family 'Rhodobacteraceae'. Phylogenetic analyses based on 16S rRNA gene sequences revealed that the isolate formed a distinct phylogenetic lineage, and was adjacent to a clade with *L. halophilum* CAU 1123^T and *Rubrimonas cliftonensis* OCh 317^T (Fig. 1 and Fig. S4). However, it was located at a clade with *L. halophilum* CAU 1123^T in the neighbor-joining tree with a bootstrap value of 76% (Fig. S3). In the genome-based phylogenetic tree, strain M0105^T and *R. cliftonensis* OCh 317^T formed a distinct phylogenetic clade with a bootstrap value of 81% (Fig. S5). The ANI and dDDH values between strain M0105^T and *R. cliftonensis* OCh 317^T were 73.4% and 19.5%, respectively (Table 1), both were well below the thresholds for species delineation cutoffs of 95–96% for ANI values [Richter and Rosselló-Móra, 2009; Kim et al. 2014] and 70% for dDDH values [Goris et al. 2007]. The highest values of

ANI, dDDH, AAI and POCP were obtained from *O. actignis* PRQ-67^T, although it only shared 93.2% 16S rRNA gene sequence similarity with strain M0105^T. Besides, values of AAI and POCP between strain M0105^T and other type strains derived from proteomes comparison were less than the established cut-off values for genus delineation of 60% and 50% [Rodriguez-R and Konstantinidis, 2014; Qin et al. 2014], respectively. Combined data from 16S rRNA gene sequence analysis and genome-scale investigations suggested that strain M0105^T should be classified in the family '*Rhodobacteraceae*' and represented as a new genus.

Table 1

Genomic similarities of ANI, AAI, dDDH and POCP between strain M0105^T and 18 type species within the class *Alphaproteobacteria*.

Strains	Size Mb	AAI (%)	dDDH (%)	ANI (%)	POCP (%)	Accession number
<i>Rhodobacter vinaykumarii</i> JA123 ^T	3.5	55.8	19.3	72.4	41.8	OBMN000000000
<i>Meinhardsimonia xiamenensis</i> YBY-7 ^T	3.1	57.6	19.3	72.4	49.8	FNFV000000000
<i>Oceanicella actignis</i> PRQ-67 ^T	3.4	60.8	19.8	74.1	53.4	FOHL000000000
<i>Alkalilacustris brevis</i> 34079 ^T	3.5	55.9	18.8	71.6	43.3	QNVJ000000000
<i>Rubrimonas cliftonensis</i> OCh 317 ^T	4.9	58.4	19.5	73.4	47.9	FNQM000000000
<i>Sinirhodobacter hankyongi</i> BO-81 ^T	3.8	54.6	18.8	72	42.4	RCHI000000000
<i>Thioclava marina</i> 11.10-0-13 ^T	4.1	54.2	18.8	71.3	42.3	JACIZB000000000
<i>Ruegeria pomeroyi</i> HF-Din03 ^T	4.1	56.1	18.9	71.4	47.9	JABXIY000000000
<i>Phaeovulum veldkampii</i> DSM 11550 ^T	3.3	56.1	19	70.1	42.3	SNYP000000000
<i>Rhodovulum visakhapatnamense</i> JA 181 ^T	4.4	56.1	19.1	71.9	43.4	SOEB000000000
<i>Thioclava nitratreducens</i> 25810_4 ^T	3.9	54.1	19.2	71.7	41.6	CP019437
<i>Rhodovulum euryhalinum</i> DSM 4868 ^T	3.8	57.1	19	72	47.7	SLWW000000000
<i>Rhodobacter sediminicola</i> JA983 ^T	4.2	55.7	18.9	72.5	42.6	VDEK000000000
<i>Rhodovulum viride</i> JA756 ^T	4.5	56.0	19	72.1	43.1	MUAV000000000
<i>Pseudoruegeria aquimaris</i> CECT 7680 ^T	3.7	56.9	18.9	72	46.9	FWFQ000000000
<i>Thioclava sediminum</i> TAW-CT134 ^T	4.1	53.8	18.7	71.3	42.2	MPZV000000000
<i>Acidimangrovimonas indica</i> CGMCC 1.10859 ^T	4.3	55.5	19.3	71.9	43.0	BNAB000000000
<i>Rhodovulum kholense</i> DSM 19783 ^T	4.5	56	19	72.1	44.0	QAYC000000000

Morphological and phenotypical properties

Strain M0105^T exhibits some common morphological properties with *L. halophilum* CAU 1123^T, such as irregular rod-shaped, non-motile and non-spore forming. Cells of strain M0105^T were 0.3–0.5 µm in width and 1-1.7 µm in length (Fig. S1). Growth occurs on R2A agar supplemented with 1–7% NaCl (optimum 3–5%), at the temperature of 15–46°C (optimum 37–40°C, Fig. S2). It could grow at a pH range of 6.0 to 10.0 (optimum pH 8.0–9.0). The phylogenetically closely related species are positive for oxidase and catalase, whereas strain M0105^T is negative for oxidase. All different phenotypic characteristics between strain M0105^T and other type strains were listed in Table 2.

Table 2. Different phenotypic characteristics between strain M0105^T and four type species.

Strains: 1, M0105^T; 2, *A. brevis* 34079^T; 3, *M. xiamenense* YBY-7^T; 4, *D. nitratreducens* 25810_4^T; 5, *L. halophilum* CAU 1123^T. Data were obtained in this study. *data from [Shin et al. 2017; Yin et al. 2012]. +, Positive; -, negative; w, weakly positive.

Characteristics	1	2	3	4	5
Growth conditions					
Growth temperature range (°C)	15-46 (37-40)	10-50 (35)	28-65 (50-58)*	8-40 (28-30)	20-40 (37)
NaCl tolerance (optimum %, w/v)	1-7 (3-5)	2-10 (5-6)	1-6 (3)	2-7 (4-5)	1-10 (5-6)
pH range (optimum)	6-10 (8-9)	7-10 (8)	6-9 (8)	6-9 (7)	6-9 (7)
Oxidase	-	+	+	w	+
Carbon source utilization					
D-arabinose	+	-	-	-	-
L-arabinose	+	-	-	-	-
D-ribose	+	-	+	-	+
D-xylose	-	-	w	+	-
L-xylose	+	-	-	-	-
D-glucose	-	-	-	+	-
D-mannitol	-	-	-	+	-
D-cellobiose	-	-	w	-	-
D-maltose	-	-	-	+	-
sucrose	-	-	-	+	-
D-trehalose	-	-	-	+	-
glycogen	+	-	-	-	-
D-arabinitol	-	-	-	+	-
2-ketogluconate	+	-	-	-	-
Turanose	-	-	-	+	-
D-lyxose	+	-	-	-	-
Enzyme activities					
α -chymotrypsin	+	-	-	w	-
acid phosphatase	+	-	+	+	+
naphthol-AS-BI-	-	w	-	w	w

phosphohydrolase					
α -galactosidase	-	-	+	-	-
β -galactosidase	-	-	+	-	-
β -glucuronidase	-	w	-	w	-
α -glucosidase	-	-	+	w	-
β -glucosidase	-	-	+	-	-
N-acetyl- β -glucosaminidase	+	-	-	-	-
Cystine arylamidase	-	-	w	w	-
Alkaline phosphatase	+	-	+	+	+
Lipase (C14)	-	-	w	w	w
Polar lipids	DPG, PG, PC, PGL, PL, L, AL	DPG, PG, PC, PGL, PL, L, AL	DPG, PG, PC, PGL, PL, L	DPG, PG, PC, PGL, PL, L	PG, PE, PL, L, AL*

The polar lipid profile pattern on thin-layer chromatography of strain M0105^T (Fig. S6) was similar with *A. brevis* 34079^T, containing unidentified aminolipid (AL), phosphoglycolipids (PGL), diphosphatidylglycerol (DPG), phosphatidylglycerol (PG), unidentified phospholipids (PL), unknown lipid (L) and phosphatidylcholine (PC). The sole respiratory quinone Q-10 is frequently found in the family ‘*Rhodobacteraceae*’ that was also detected as the major respiratory quinone in the isolate. The major fatty acids were C_{18:1} ω 7c and C_{16:0} DMA in strain M0105^T, which were in accordance with the closely related species *A. brevis* 34079^T, *D. nitratireducens* 25810_4^T and *L. halophilum* CAU 1123^T. Other main cellular fatty acids (> 5%) of the isolate were C_{16:0} DMA (12.5%), C_{16:0} (8.6%) and C_{18:1} ω 7c 10-methyl (6.0%).

Genome characteristics

Genome sequencing revealed a genome of 4,055,176 bp and an N50 contig length of 318,302 bp with a DNA G + C content of 67.9 mol%. A total of 3808 protein-coding genes, 45 tRNA genes and 3 rRNA genes were consisted in the sequence. The genome of strain M0105^T comprised 99 genes associated with carbohydrate-active enzymes, including auxiliary activities (12), carbohydrate esterases (17), glycosyl transferases (46), polysaccharide lyases (1), carbohydrate-binding modules (5) and glycoside hydrolases (18). Functional gene category analysis revealed that most of genes involved in Global and overview maps (249), amino acid metabolism (265) and energy metabolism (200), Three putative secondary metabolite biosynthetic gene clusters involving in biosynthesis of terpene, type I PKS and arylpolyene were identified.

As compared with other non-mangrove dwelling bacteria, the genes associated with “Replication and repair”, “Protein families: metabolism”, “Energy metabolism” “Metabolism of cofactors and vitamins”, “Transport and catabolism”, “Metabolism of other amino acids”, “Cellular community” and “Amino acid metabolism” were abundance in the mangrove-derived bacteria strain M0105^T and *A. solimangrovi* HB172011^T (Fig. 3). Mangrove sediments are known to be rich in various organic substrates such as amino acids, carbohydrates, polysaccharides, phenolics and other related compounds. Microbe in mangrove sediment involved in carbon and energy process by the degradation and utilization of organic matter, thus implying genes associated with carbohydrate metabolism, energy metabolism and amino acid metabolism were abundant in the mangrove-dwelling bacteria [Zhao et al. 2019; Lin et al. 2019]. The abundance of “carbohydrate metabolism” genes in *A. solimangrovi* HB172011^T were higher than strain M0105^T. This might be caused by the distribution of carbon source, which was influenced by tidal flow and estuary water flow. The high abundance of DNA-repaired-related genes and heat-shock-related genes (Table S2) were detected in strain M0105^T that were highly responsive to cellular stress, such as salt stress, heat stress, radiation and oxidative stresses.

Description of *Thermohalobaculum* gen. nov.

Thermohalobaculum (Ther.mo.ha.lo.ba'cu.lum Gr. fem. n. *therme*, heat; Gr. masc. n. *hals*, salt; L. neut. n. *baculum*, small rod; N.L. neut. n. *Thermohalobaculum*, a thermophilic, halophilic rod). A moderately thermophilic, halophilic and Gram-negative bacterium. The major fatty acids are C_{18:1} ω7c and C_{16:0} DMA. The major menaquinone is Q-10. The type species is *Thermohalobaculum xanthum*.

Description of *Thermohalobaculum xanthum* sp. nov.

Thermohalobaculum xanthum (xan.thum. N.L. neut. adj. *xanthum* yellow. *xanthum*, a yellow-colony-forming organism).

Cells are non-motile, rod shaped with width of 0.3–0.5 μm and length of 1-1.7 μm. Test for catalase is positive, but for oxidase is negative. Negative for hydrolysis of cellulose, starch, Tweens (20, 40, 60 and 80), urea and gelatin, as well as for H₂S production. It can utilize D-tagatose, 5-ketogluconate, D-arabinose, L-arabinose, D-ribose, L-xylose, glycogen, 2-ketogluconate and D-lyxose, but cannot use glycerol, meso-erythritol, D-xylose, D-adonitol, methyl beta-D-xylopyranoside, D-galactose, D-glucose, D-fructose, D-mannose, L-sorbose, L-rhamnose, dulcitol, Myo-inositol, D-mannitol, sorbitol, methyl α-D-mannopyranoside, methyl α-D-glucopyranoside, N-acetyl-D-glucosamine, amygdalin, arbutin, salicin, D-cellobiose, D-maltose, D-lactose, D-melibiose, sucrose, D-trehalose, inulin, D-melezitose, D-raffinose, starch, xylitol, gentiobiose, turanose, D-fucose, L-fucose, D-arabinitol, L-arabinitol and potassium gluconate. Negative for catalase. Shows positive reactions for α-chymotrypsin, acid phosphatase, alkaline phosphatase, esterase (C4), esterase lipase (C8), leucine arylamidase, N-acetyl-β-glucosaminidase and valine arylamidase, but negative reactions for lipase (C14), cystine arylamidase, trypsin, naphthol-ASBI-phosphohydrolase, α-galactosidase, β-galactosidase, β-glucuronidase, α-glucosidase, β-glucosidase, α-mannosidase, β-fucosidase. Colonies are pale-yellow. Temperature range

for growth is 15–46°C, with an optimum of 37–40°C. Growth occurs at pH 6.0–10.0, with an optimum of pH 8.0–9.0. NaCl concentration range for growth is 1–7% (optimum, 3–5%, w/v). The DNA G + C content of the type species is 67.9%.

The type strain, M0105^T (= BGMRC 2019^T = KCTC 52118^T = MCCC 1K03767^T = NBRC 112057^T) was isolated from the mangrove sediments, which were collected from Beibu Gulf in Beihai, Guangxi province. The GenBank accession numbers for the 16S rRNA gene sequence of strain M0105^T is MT613384 and the genome sequence is JAEHHL000000000.

Declarations

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Authors' contributions

XP: characterized the bacterium and prepare the manuscript; FL, ZHL, YH, QZH performed the phenotypic and biochemical characterization; SHH helped the analysis of taxonomic data; WH supervised the study and edited the original draft.

Conflicts of interest

The authors declare that there are no conflicts of interest.

Ethical standards

This study does not describe any experimental work related to human.

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Figures

Figure 1

Maximum-likelihood phylogenetic tree based on the 16S RNA gene sequences revealing the phylogenetic position of strain M0105^T within the family 'Rhodobacteraceae'. Numbers on the branched refer to percentage values (> 50%) of 1000 bootstrap. Bar, 0.02 substitutions per nucleotide. Strain *Methylobacillus methanolivorans* ZT (NR156096) was served as an outgroup.

Figure 2

Distribution pattern of functional genes in *A. solimangrovi* HB172011T (1), strain M0105T (2), *R. vinaykumarii* JA123T (3), *O. actignis* PRQ-67T (4), *M. xiamenensis* YBY-7T (5) and *A. brevis* 34079T (6).

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