Psychroserpens Luteus Sp. Nov., Isolated fFrom Red Algae

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Research Article

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Abstract

A Gram-stain-negative, gliding-motile, positive for catalase, facultative anaerobic, designated strain XSD401^T, was isolated from the red algae of Xiaoshi Island, Shandong Province, China. Growth occurred at 20–37 °C (optimum, 33 °C), pH 5.5–9.5 (optimum, pH 6.5–7.5), and with 0.5–5% (w/v) NaCl (optimum, 3%). The main fatty acids are iso-C_{15:0}, iso-C_{15:1} G, iso-C_{17:0} 3-OH, iso-C_{15:0} 3-OH, C_{16:0}. Phosphatidylethanolamine (PE), three unidentified aminolipids (AL1, AL2, AL3) and one unidentified lipid (L) were the major polar lipids. The G+C content of the genomic DNA was 33.9 mol%. Strain XSD401^T had the highest sequence similarity (96.88%) to the 16S rRNA gene of *Psychroserpens damuponensis* KCTC 23539^T. The similarities with *Psychroserpens burtonensis* DSM 12212^T was 96.31%. The dDDH values between strain XSD401^T and *P. damuponensis* KCTC 23539^T, *P. burtonensis* DSM 12212^T, were 20.40% and 20.30%, respectively. The average nucleotide identity (ANI) values between strain XSD401^T and *P. damuponensis* KCTC 23539^T, *P. burtonensis* DSM 12212^T were 76.91%, 76.88%, respectively. The differences in morphology, physiology and genotype from the previously described taxa support the classification of strain XSD401^T as a representative of a novel species of the genus *Psychroserpens*, for which the name *Psychroserpens luteus* sp. nov. is proposed. The type strain is XSD401^T (= MCCC 1H00396^T = KCTC 72684^T = JCM 33931^T).

Introduction

The genus *Psychroserpens* is a member of the family *Flavobacteriaceae* in the phylum *Bacteroidetes*. *Flavobacteriaceae* is the largest family of *Bacteroidetes* in the class *Flavobacterium*, comprising at least 140 genera and several hundred species (Zhang et al. 2019). The diversity of *Flavobacteraceae* is closely related to the diversity of its living environment. Members of *Flavobacteraceae* are found in freshwater, marine and terrestrial environments. In aquatic environments it is usually associated with algae cells, fish or organic matter. Most members of the *Flavobacteraceae* family can digest large molecules of organic polymers such as proteins and polysaccharides and exhibit gliding motion (McBride 2014). *P. burtonensis*, isolated from the Antarctic ice at Lake Burton (Bowman et al. 1997), is the first member of the genus. So far, there are only four recognized members of the genus, *P. burtonensis*, *P. damuponensis* (Lee et al. 2013), *P. jangbogonensis* (Baek et al. 2015), *P. mesophilus* (Kown et al. 2006). In winter, *Psychroserpens* helps reduce N and P in marine wastewater, thereby reducing the harmful algal blooms in marine coastal regions (Kim et al. 2020). The genus *Psychroserpens* comprises Gram-negative, obligately aerobic, rod-shaped, oxidase-positive, yellow-to yellowish-orange-pigmented bacteria. The predominant isoprenoid quinone is Menaquinone-6 (MK-6). DNA G + C contents were in the range of 27–33.9 mol%. Phosphatidylethanolamine (PE), three unidentified aminolipids (AL1, AL2, AL3) and one unidentified lipid (L) were the major polar lipids.

In the present study, strain XSD401^T was isolated in the red algae from Xiaoshi Island. The Xiaoshi Island, located in the west of Weihai city, north of Shandong Province, is a national marine special protection zone. As an offshore wetland reserve, it participates in many kinds of element cycle, such as nitrogen

cycle and sulfur cycle. In previous studies, we have isolated many bacteria belonging to *Bacteroidetes* from sea water and sediment samples from the Xiaoshi Island (Mu et al. 2018, 2021).

Strain XSD401^T was found to resemble members of the genus *Psychroserpens* and was subjected to further taxonomic investigation. As a result, we report the genotypic, chemotaxonomic and phenotypic characteristics of strain XSD401^T, in order to establish its phylogenetic affiliation.

Materials And Methods

Isolation, cultivation and maintenance

The red algae were collected at the Xiaoshi Island, Weihai, China (GPS position: 37°32'N 122°0'E) and the red algae samples were crushed and spread on marine agar 2216 (MA, Becton Dickinson) with a standard dilution-plating method. Then, the isolated colonies were subsequently purified by plating three times on MA and incubated at 28 °C for 2 days.

The purified strains were stored at –80 °C in sea water supplemented with 20% (v/v) glycerol. Strain XSD401^T has been deposited at the MCCC (Marine Culture Collection of China, MCCC 1H00396^T), JCM (Japan Collection of Microorganisms, JCM 33931^T) and KCTC (Korean Collection for Type Cultures, KCTC 72684^T). To identify strain XSD401^T, *P. damuponensis* KCTC 23539^T and *P. burtonensis* DSM 12212^T were used as reference strains for the analysis of phenotypic characters. *P. damuponensis* KCTC 23539^T was ordered from the Korean Collection for Type Cultures (KCTC). *P. burtonensis* DSM 12212^T was ordered from the Deutsche Sammlung von Mikroorganismen und Zellkulturen (DSMZ).

Phenotypic and biochemical tests

Morphological properties (cell shape, cell size, and motility) were observed by light microscopy (E600, Nikon), semi-solid agar (Bowman 2000) and hanging drop methods, transmission electron micrograph (JEOL 1100). Temperature-dependent growth was tested at 0, 4, 15, 20, 25, 28, 30, 33, 35, 37, 40 °C on MA. Physiological tests such as growth at different pH (using appropriate buffers: MES buffer for pH 5.5–6.0, PIPES buffer for pH 6.5–7.0, HEPES buffer for pH 7.5–8.0, Tricine buffer for pH 8.5 and CAPSO buffer for pH 9.0–9.5) and NaCl concentrations (0–7 % in increments of 1 %, 9 %, 11 % (w/v)) were performed in marine broth 2216 (MB, BD) made with artificial seawater (0.32 % MgSO₄, 0.22 % MgCl₂, 0.12 % CaCl₂, 0.07 % KCl, 0.02 % NaHCO₃, w/v) and growth was observed after 2 days. Gram-stain, catalase and oxidase activities, reduction of nitrate, hydrolysis of Tweens 20, 40, 60, 80, starch, casein, alginate and CM-cellulose were studied as previously described (Wang et al. 2018). Anaerobic growth was examined on MA with or without 0.1 % (w/v) KNO₃ incubated in a jar (N₂: H₂: CO₂ at 85:10:5, by vol.). Susceptibility to antibiotics was investigated on MA plates at 33 °C for up to 2 days (0.5 McFarland standard) using the disc diffusion method as described previously (Wayne 2014). Tests for other physiological or biochemical characteristics were performed by using API 20E, API ZYM and API 50CHB strips (all from bioMérieux) and GEN III MicroPlates (Biolog), according to the manufacturers' instructions

except that salinity was adjusted to 3 %. All the API tests and Biolog tests were performed in duplicate, with closely related strains. Susceptibility to antibiotics was tested on MA plates using antibiotic discs containing the following (μg per disc unless otherwise stated): erythromycin (15), tobramycin (10), vancomycin (30), streptomycin (10), penicillin (10), chloramphenicol (30), rifampicin (5), tetracycline (30), norfloxacin (10), neomycin (30), cefotaxime sodium (30), gentamicin (10), ofloxacin (5), lincomycin (2), kanamycin (30), ceftriaxone (30), carbenicillin (100), polymixin B (300 IU) and clarithromycin (15). CLSI standards were strictly followed for cultivation and inhibition zone diameter reading (CLSI 2012).

16S rRNA gene sequencing and phylogenetic analysis

The taxonomic position of strain XSD401^T was first determined by sequential analysis of the 16S rRNA gene. Genomic DNA of the strain XSD401^T was extracted and purified using a bacterial genomic DNA isolation kit (Takara). The 16S rRNA gene was amplified using the bacterial universal primers 27F and 1492R (Liu et al. 2014). Purified PCR products were cloned into the pMD18-T vector (Takara) and recombinant plasmids were reproduced in *Escherichia coli* DH5a cells. The positive clones were selected and sequenced at BGI Co. Ltd (Qingdao, China) using the ABI 3730XL system. Sequence similarities of the 16S rRNA genes were determined using the EzTaxon-e server (www.ezbiocloud.net/) (Kim et al. 2012) and the BLAST algorithm in NCBI database (www.ncbi.nlm.nih.gov/). Based on the available sequences, we performed phylogenetic analysis. A phylogenetic tree was constructed with the neighbor-joining algorithm implemented in the software package MEGA (version 7.0) (Kumar et al. 2016). Phylogenetic trees were also generated with the maximum-likelihood and maximum-parsimony algorithms. Bootstrap analysis was performed with 1000 replications (Felsenstein 1985) to provide confidence estimates for tree topologies.

Genomic analysis

The draft genome of strain XSD401^T was obtained using Illumina HiSeq platform (Illumina) by the Beijing Novogene Bioinformatics Technology (Beijing, PR China). All good quality paired reads were assembled using the SOAP denovo software (version 2.04) into a number of scaffolds (Li et al. 2010). The genes of strain XSD401^T were identified by NCBI Prokaryotic Genome Annotation Pipeline server online (Angiuoli et al. 2008). The genes involved in metabolic pathways were then subjected to functional annotation with the KEGG database (Kanehisa et al. 2016a) using BlastKOALA (Kanehisa et al. 2016b).

The G+C content of chromosomal DNA was calculated using genome sequence. For analysis of genomic relatedness, the average nucleotide identity (ANI) values between strain XSD401^T, *P. damuponensis* KCTC 23539^T and *P. burtonensis* DSM 12212^T were calculated using the OrthoANlu algorithm from the EzGenome web service (Yoon et al. 2017). Meanwhile, the dDDH values were obtained using the Genome-to-Genome Distance Calculator (GGDC) website (<http://ggdc.dsmz.de/distcalc2.php>).

Chemotaxonomic analysis

For the analysis of respiratory quinones, fatty acid and polar lipids, strain XSD401^T and the reference bacteria were incubated in MB medium to reach the exponential phase. The cells were harvested at the late-exponential growth phase and subjected to freeze-drying. Respiratory quinones were analysed by HPLC after extraction with a chloroform/methanol (2:1, v/v) mixture and separated by TLC (Kroppenstedt 1982). For two-dimensional TLC of polar lipid analysis, TLC on silica gel 60 F254 plates (Merck) were developed with chloroform/methanol/water (65:25:4, by vol.) for the first dimension and chloroform/acetic acid/methanol/water (80:15:12:4, by vol.) for the second dimension. Total lipid material was detected using molybdotophosphoric acid and the functional groups were determined using spray reagents specific for each one. Complete details are provided by Fang *et al.* (Fang et al. 2017). The fatty acids were extracted according to a standard protocol of MIDI (Sherlock Microbial Identification System, version 6.3B) and then analysed by gas chromatography using an Agilent 6890N gas chromatograph and identified using the TSBA40 database of the microbial identification system.

Results And Discussion

Morphological and phenotypical characteristics

Cells of strain XSD401^T were facultative anaerobic, Gram-stain-negative, no flagella, coccus to rod shaped, 0.35–0.5 µm in diameter and 1.2–3 µm in length (Fig. S1). The motility was not detected under the microscope by hanging drop methods. The gliding motility was detected under the microscope and was also confirmed using semi-solid agar. The shape of the cells and the color of the colonies are the same as most *Psychroserpens* strains. Growth occurs at 20–37 °C (optimal 33 °C), pH 5.5–9.5 (optimal pH 6.5–7.5) and 0.5–5% (w/v) NaCl (optimal NaCl 3.0%). Strain XSD401^T was positive for catalase and hydrolysis of Tween 20, 40 and 80, casein, sodium alginate, but negative for the hydrolysis of oxidase, agar, starch, CM-cellulose, DNase and Tween 60. Strain XSD401^T is susceptible to ampicillin (10), rifampin, but resistant to tobramycin (10), tetracycline (30), norfloxacin (30), neomycin (30), gentamycin (10), ofloxacin (30), kanamycin (30). All of them contain esterase (C4), leucine arylamidase, valine arylamidase, cystine arylamidase, trypsin, α-chymotrypsin, acid phosphatase, naphthol-AS-BI-phosphohydrolase activity. Comprehensive morphological, biochemical and physiological traits of strain XSD401^T are summarized in the species description. The test results distinguishing strain XSD401^T from the related strains are shown in Table 1.

Phylogenetic analysis of 16S rRNA sequences

The 16S rRNA gene of strain XSD401^T was amplified by PCR using universal primers (27F and 1492R). 16S rRNA (1488 bp) was basically complete and stored in the NCBI GenBank database. The 16S rRNA accession number of strain XSD401^T was MN330029. The results showed that strain XSD401^T had the highest similarity (96.88%) to the 16S rRNA gene of *P. damuponensis* KCTC 23539^T.

Only one 16S rRNA gene sequence (1524 bp) was extracted from the draft genome, shared 99.9 % similarity with the nearly complete (1488 bp) 16S rRNA gene sequence obtained by conventional Sanger

sequencing. The complete sequence (1524 bp) matched with a counterpart of PCR amplification (1483 bp).

The results of phylogenetic analysis also indicated that strain XSD401^T was affiliated to the genus *Psychroserpens*, but formed a unique clade separated from other species, indicating that this strain represents a novel species (Fig. 1). The results showed that the strain XSD401^T was located in *Psychroserpens*, and was associated with *P. damuponensis* KCTC 23539^T and *P. burtonensis* DSM 12212^T. The phylogenetic tree was constructed based on maximum likelihood and maximum parsimony. The phylogenetic data indicated that the strain XSD401^T was a new species of *Psychroserpens*.

Genomic analysis

Draft genome sequencing of strain XSD401^T yielded a genome of 3.7 Mb in length after assembly, producing 60 contigs, and the N50 value was 706,489 bp, with the largest being 1,282,496 bp and the smallest 298 bp. The genomic DNA G+C content of strain XSD401^T is 33.9 mol%. The ANI values between strain XSD401^T and *P. damuponensis* KCTC 23539^T, *P. burtonensis* DSM 12212^T were 76.91%, 76.88%, respectively. The dDDH values between strain XSD401^T and *P. damuponensis* KCTC 23539^T–*P. burtonensis* DSM 12212^T, were 20.40% and 20.30%, respectively.

Further, we focused on the genes of XSD401^T that were predicted by KEGG pathway annotation (<https://www.kegg.jp>). Among the 3512 protein-coding genes, strain XSD401^T pathway modules showed that thirty-nine of them were complete, including carbohydrate metabolism, energy metabolism, lipid metabolism, nucleotide metabolism, amino acid metabolism, glycan metabolism, metabolism of cofactors and vitamins, biosynthesis of terpenoids and polyketides. To be specific, the genome of strain XSD401^T contains a complete set of genes of the citrate cycle (TCA) pathway that transform acetyl-CoA to oxaloacetate. Known as *pilE*, *pilB*, that encode protein *pilB* and protein *pilE* in the genome for the synthesis of type IV Pilus. Several sugar transporters were tagged in the genome, providing additional support for the sugar-dependent growth of strain XSD401^T. The Embden-Meyerhof pathway and the Semi-phosphorylative Entner-Doudoroff pathway are incomplete because they lack the necessary genes. The formaldehyde assimilation, dissimilatory nitrate reduction and assimilatory sulfate reduction are incomplete due to the lack of the necessary genes.

After annotating with KEGG, the results showed the strain XSD401^T has 39 complete metabolic pathways, *P. burtonensis* DSM 12212^T has 44, and *P. damuponensis* KCTC 23539^T has 41 (Fig. 2). In these three strains, 37 of the metabolic pathways are shared, strain XSD401^T and *P. damuponensis* KCTC 23539^T each have 2 distinct metabolic pathways, and *P. burtonensis* DSM 12212^T has 5 distinct metabolic pathways. For example, it is found that strain XSD401^T lacks the assimilatory sulfate reduction pathway, and *P. burtonensis* DSM 12212^T lacks a block, but the assimilatory sulfate reduction pathway of *P. damuponensis* KCTC 23539^T is complete. Strain XSD401^T and *P. burtonensis* DSM 12212^T have no glycogen biosynthesis pathway, but *P. damuponensis* KCTC 23539^T has a complete glycogen

biosynthesis pathway. Strain XSD401^T lacks the polyamine biosynthesis pathway, while *P. burtonensis* DSM 12212^T and *P. damuponensis* KCTC 23539^T all have a complete polyamine biosynthesis pathway.

Chemotaxonomic characteristics

The respiratory quinone of strain XSD401^T was Menaquinone-6 (MK-6), which is typical of the genus *Psychroserpens*. The major polar lipids of strain XSD401^T consist of phosphatidylethanolamine (PE) (Fig. S2), which also was typical of the genus *Psychroserpens*. Minor amounts of three unidentified aminolipids (AL1, AL2, AL3) and one unidentified lipid (L) were also detected. Strain XSD401^T differed from *P. damuponensis* KCTC 23539^T by the absence of AL4 and L2-L3. Strain XSD401^T differed from *P. burtonensis* DSM 12212^T by the absence of L4.

The predominant cellular fatty acids found in strain XSD401^T were iso-C_{15:0} (26.73%), iso-C_{15:1} G (18.4%), iso-C_{17:0} 3-OH (14.51%), iso-C_{15:0} 3-OH (11.35%), C_{16:0} (6.99%), along with the lesser amounts of summed feature 3 (C_{16:1} ω 7c and/or C_{16:1} ω 6c) (4.38%), C_{18:1} ω 9c (3.19%), C_{16:0} 3-OH (2.09%), C_{16:1} ω 9c (1.3%), anteiso-C_{15:0} (1.26%), C_{18:0} (1.25%), iso-C_{16:0} 3-OH (1.19%).

Taxonomic conclusion

The respiratory quinone of strain XSD401^T was Menaquinone-6 (MK-6), which is typical of the genus *Psychroserpens*. The major polar lipids of strain XSD401^T consist of phosphatidylethanolamine (PE), which also was typical of the genus *Psychroserpens*. Strain XSD401^T contained iso-C_{15:0} (26.73%) as predominant fatty acids (≥ 10.0 %) in common with closely related strains. The fatty acids composition of strain XSD401^T were somewhat different from *P. damuponensis* KCTC 23539^T and *P. burtonensis* DSM 12212^T. The fatty acid differences could be observed between strain XSD401^T and its closely strains (Table 2). These findings suggest that strain XSD401^T is most closely related to *P. damuponensis* KCTC 23539^T, rather than *P. burtonensis* DSM 12212^T.

Based on the phenotypic, chemotaxonomic and phylogenetic results, strain XSD401^T represents a novel species within the genus *Psychroserpens*, for which the name *Psychroserpens luteus* sp. nov. is proposed.

Description of *Psychroserpens luteus* sp. nov.

Psychroserpens luteus *lu*'te.us L. masc. adj. *luteus*, orange-coloured.

Cells are facultative anaerobic, Gram-stain-negative, non-motile, no flagella, but gliding motility is present, coccus to rod shaped, 0.35–0.5 μ m in diameter and 1.2–3 μ m in length. After 2 days of incubation on MA at 33 °C, the colonies were circular, smooth, yellow, with diameters of 1.0–2.0 mm. Growth occurs at 20–37 °C (optimal 33 °C), pH 5.5–9.5 (optimal pH 6.5–7.5) and 0.5–5% (w/v) NaCl (optimally 3.0%). Positive for catalase and nitrate reduction, negative for oxidase

activities. Hydrolysis of Tween 20, 40 and 80, casein, sodium alginate, but not starch, agar, CM-cellulose, DNase and Tween 60. The reaction of tryptophan deaminase(TDA), Voges-Proskauer reaction(VP), gelatinase (GEL) are positive, while the other reactions are negative. Activities of alkaline phosphatase, esterase (C4), leucine arylamidase, valine arylamidase, cystine arylamidase, trypsin, α -chymotrypsin, acid phosphatase, naphthol-AS-BI-phosphohydrolase were positive, and the others were negative. Acids are produced from d-ribose, esculin ferric citrate, d-tagatose, and potassium 5-ketogluconate. Positive for the oxidation of dextrin, d-maltose, d-trehalose, d-cellobiose, gentiobiose, sucrose, d-turanose, stachyose, d-raffinose, d-lactose, d-melibiose, β -methyl-d-glucoside, d-salicin, α -d-glucose, d-mannose, d-fructose, d-galactose, 3-methyl glucose, d-sorbitol, d-mannitol, d-gluconic acid, and l-lactic acid can all be assimilated by carbon sources. Sensitive to ampicillin, rifampin, but resistant to tobramycin, tetracycline, norfloxacin, neomycin, gentamycin, ofloxacin, kanamycin. The main fatty acids are iso-C_{15:0}, iso-C_{15:1} G, iso-C_{17:0} 3-OH, iso-C_{15:0} 3-OH, C_{16:0}. Phosphatidylethanolamine (PE), three unidentified aminolipids (AL1, AL2, AL3) and one unidentified lipid (L) were the major polar lipids. The major respiratory quinone is MK-6.

The type strain, XSD401^T (=MCCC 1H00396^T =KCTC 72684^T =JCM 33931^T), was isolated from red algae in the Xiaoshi Island, Weihai, China. The DNA G+C content of the type strain is 33.91 mol%.

Abbreviations

KCTC, Korean Collection for Type Cultures; JCM, Japan Collection of Microorganisms; MCCC, Marine Culture Collection of China; MEGA, Molecular Evolutionary Genetics Analysis; dDDH, the digital DNA-DNA hybridisation; ANI, average nucleotide identity; HPLC, high performance liquid chromatography; TLC, thin layer chromatography.

Declarations

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Conflicts of interests and ethical statements

The authors declare that they have no conflict of interest.

This article does not contain any studies with animals performed by any of the authors.

The GenBank accession number for the 16S rRNA gene sequence of strain XSD401^T is MN330029. The whole-genome shotgun project of strain XSD401^T has been deposited at GenBank under the accession number JAHVXI000000000.

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Tables

Table 1. Phenotypic characteristics differentiating strain XSD401^T and its closest phylogenetic relatives.

Strains: 1, XSD401^T, 2, *P. damuponensis* KCTC 23539^T, 3, *P. burtonensis* DSM 12212^T. All data are from this study unless otherwise indicated. +, Positive, -, negative, w, weakly positive, R, resistant, S, susceptible.

Characteristic	1	2	3
Cell diameter (μm)	0.35-1	0.5 ^a	0.5-0.6 ^b
Cell length (μm)	1.2-3	2 ^a	2-6 ^b
Gliding motility	+	₋ ^a	₋ ^b
Range for growth:			
NaCl range (optimum) (%)	0.5-5(3)	1–6(3) ^a	1–5 ^a
Temperature range (optimum) (°C)	20-37(33)	4–30 (25) ^a	0–20 (10–12) ^b
pH range (optimum)	5.5-9.5(6.5-7.5)	6.0–9.0(7-8) ^a	6.5–9.0 ^b
Oxidase activity	-	+ ^a	₋ ^b
Hydrolysis of:			
Tween 80	+	+ ^a	₋ ^b
API 20E results:			
Citrate utilization	-	+	+
Tryptophan deaminase	+	-	-
Voges–Proskauer reaction	+	+	-
API ZYM results:			
Esterase (C4)	+	-	+
Esterase lipase (C8)	-	W	-
Susceptibility to:			
Rifampin (5 μg)	S	S ^a	R ^c
Tetracycline (30 μg)	R	R ^a	S ^a
DNA G+C content (mol%)	33.9	33.5 ^a	27–29 ^b

*Data from: a, (Lee et al. 2013), b, (Bowman et al. 1997), c, (Baek et al. 2015).

Table 2. Cellular fatty acid contents (%) of strain XSD401^T and its closest phylogenetic relatives.

Strains 1, XSD401^T, 2, *P. damuponensis* KCTC 23539^T, 3, *P. burtonensis* DSM 12212^T. All data from the present study. Major components (≥ 10 %) are highlighted in bold. Fatty acids that represented <1.0 % in both strains are omitted. TR, Traces (<1.0 %), -, not detected.

Fatty acid	1	2	3
Straight-chain			
C _{14:0}	-	1.1	TR
C _{16:0}	6.99	4.38	2.37
C _{18:0}	1.25	1.61	-
Branched			
anteiso C _{13:0}	-	1.38	TR
anteiso C _{15:0}	1.26	10.84	12.77
iso C _{15:1} G	18.4	8.31	20.31
iso C _{16:1} G	TR	-	2.35
anteiso C _{15:1} A	-	1.11	7.72
iso C _{15:0}	26.73	30.21	12.12
iso C _{16:0}	-	1.3	1.48
Unsaturated			
C _{15:1} ω 6 <i>c</i>	-	-	2.65
C _{16:1} ω 9 <i>c</i>	1.3	-	-
C _{18:1} ω 9 <i>c</i>	3.19	1.41	TR
Hydroxy			
C _{15:0} 2-OH	-	1.47	5.67
C _{17:0} 2-OH	-	3	2.19
C _{15:0} 3-OH	-	-	2.34
C _{16:0} 3-OH	2.09	-	6.02
iso C _{15:0} 3-OH	11.35	8.1	6.40
iso C _{16:0} 3-OH	1.19	3.12	6.02
iso C _{17:0} 3-OH	14.51	9.8	5.36
Summed feature 3	4.38	1.72	1.65

* Summed feature 3 comprises C_{16:1} ω 6c and/or C_{16:1} ω 7c, summed feature 9 comprises iso-C_{17:1} ω 9c and/or C_{16:0} 10-methyl.

Figures

Figure 1

Neighbor-joining phylogenetic tree reconstructed from a comparative analysis of 16S rRNA gene sequences showing the relationships between strain XSD401^T and related taxa. Filled circles indicate nodes also obtained in both maximum-likelihood and maximum-parsimony trees. Bootstrap values (expressed as percentages of 1000 replications) of ≥ 50.0 % are shown at branch points (NJ/ML/MP). Bar, 1.0 % sequence divergence. *Lutimonas vermicola* IMCC 1616^T (EF108218) was used as an outgroup.

Figure 2

Comparison of pathway modules between strain XSD401T and its closest phylogenetic relatives.

Supplementary Files

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