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ORIGINAL PAPER

Flavisericum labens gen. nov., sp. nov., a novel member of the family *Flavobacteriaceae* isolated from the seawater of Dongshan Bay

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Abstract A Gram-negative, aerobic, non-motile and rod-shaped bacterial strain, designated DST062^T, was isolated from the seawater of Dongshan Bay in Fujian, China. Growth occurred with 0.5–6% (w/v) NaCl (optimum, 3%), at 4–40 °C (optimum, 28 °C) and at pH 7.0–8.0 (optimum, 7.0), displaying positive reactions for both catalase and oxidase activities. Comparative 16S rRNA gene sequence studies showed that strain DST062^T formed a distinct lineage within the family *Flavobacteriaceae*. It exhibited the highest 16S rRNA gene sequence similarity value to *Confluentibacter sediminis* DSL-48^T (95.35%). This low similarity value enabled clear differentiation of strain DST062^T from strains of related genera such as *Confluentibacter*, *Snuella*, *Jejuia*, and *Tamlana* through 16S rRNA gene sequence analysis. The G+C content of the genomic DNA was 35.92%. The estimated Average Nucleotide Identity and digital DNA-DNA Hybridization values between strain DST062^T and the reference species ranged from 73.7 to 76.0% and from 18.5 to 20.0%, respectively. The major fatty acid profile comprised iso-$C_{15:0}$, summed feature 3 ($C_{16:1}\omega6c$/$C_{16:1}\omega7c$), iso-$C_{15:1}$ G and iso-$C_{17:0}$ 3-OH. The respiratory quinone was identified as menaquinone 6. The major polar lipids of strain DST062^T included two aminolipids phosphatidylethanolamine, and two unknown polar lipids. Based on phylogenetic, chemotaxonomic and genomic analysis, strain DST062^T represents a novel species from a novel genus of the family *Flavobacteriaceae*, for which the name *Flavisericum labens* gen. nov. sp. nov. is proposed. The type strain is DST062^T (=MCCC 1K08936^T=KCTC 102361^T).

Keywords *Flavisericum labens* · Dongshan Bay · *Flavobacteriaceae* · Polyphasic taxonomic approach

Introduction

The family *Flavobacteriaceae* was described by Reichenbach (Reichenbach 1989) and its description was subsequently emended by Bernardet (Bernardet et al. 1996). At the time of writing, this family is currently the largest family belonging to the phylum *Bacteroidetes*, containing 161 genera with the validly published and correct name (https://lpsn.dsmz.de/family/favobacteriaceae). Members of the family *Flavobacteriaceae* are ubiquitous in marine habitats, such as tidal fat sediment (Wei et al. 2019), hydrothermal zone (Chen et al. 2023), and mangrove estuary (Yoon et al. 2015), surface of starfish, sponges

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and seaweed (Kawano et al. 2020; Yoon et al. 2017; Yin et al. 2019). Characteristically, these bacteria are rod-shaped, Gram-negative, chemoheterotrophic, and aerobic, with menaquinone-6 (MK-6) being their predominant respiratory quinone (Choi et al. 2018). In the course of investigating novel bacteria, strain DST062^T was isolated from seawater of Dongshan Bay of China. Polyphasic taxonomic analyses (phenotypic, chemotaxonomic, and genotypic) demonstrate that strain DST062^T constitutes a novel species and genus within the *Flavobacteriaceae* family.

Materials and methods

Bacterial isolation and culture conditions

Strain DST062^T was isolated from a seawater sample collected in July 2023 at Dongshan Bay (23 °38′N, 117° 22′E), Fujian, China (sampling site DS04; in situ temperature: 28 °C). Following tenfold dilution, the sample was plated on Marine Agar 2216 (Hopebio, China) and incubated at 28 °C for 5 days. A yellow colony was isolated and purified, with relatively low 16S rRNA gene sequence similarity to other species. The isolate was preserved at −80 °C with 15% (v/v) glycerol for long-term preservation. For comparative analyses, the reference strains *Confluentibacter sediminis* DSL-48 ^{T} (=MCCC 1K03537^T), *Snuella sedimenti* CAU 1569 ^{T} (=MCCC 1K05670^T), *Jejuia pallidilutea* EM39^T (=KCTC 22298 ^{T}), *Flaviramulus aquimarinus* KYW499^T (=KCTC 23924 ^{T}), *Tamlana nanhaiensis* FHC16^T (=MCCC 1A06648^T) and *Gelatiniphilus marinus* GYP-24 ^{T} (=MCCC 1K01730^T) were cultured under identical conditions.

Physiological and biochemical characterization

The cell morphology and dimensions of strain DST062^T were examined using transmission electron microscopy (Tecnai G2 Spirit BioTwin, Netherlands) with exponentially growing cells. Growth parameters were assessed through 4-day cultures monitored by photometric measurement at 600 nm. Temperature adaptation (4, 12, 20, 25, 28, 30, 35, 40, 42, 45 °C) was evaluated in 2216E Liquid Medium (Hopebio, China) (pH 7.0) with incubation for 4 days. Salt tolerance was investigated in rich organic (RO) medium at 28 °C for 4 days, with NaCl concentrations ranging from 0.5 to 12% (intervals of 1%, w/v). The pH range determination (pH 2–11, at 1-pH-unit intervals) was assessed in RO medium at 28 °C for 4 days, using appropriate buffer systems: Na_2HPO_4/citric acid (pH 2.0–8.0), NaOH/glycine (pH 9.0–10.0), Na_2HPO_4/NaOH (pH 11.0) for pH adjustment.

Motility testing was performed by stab inoculation into 0.5% semi-solid agar followed by 5-day incubation at 28 °C. Gram reaction was determined using the Gram stain kit (AG1060, Acmec, Shanghai, China). Activities of catalase and oxidase were tested according to the methods described of Smibert and Krieg (Gerhardt 1994). API 20 NE and API ZYM kits (bioMérieux, France) were used following the manufacturer's instructions to analyze biochemical characteristics and enzyme activities of strain DST062^T. For incubation, a single colony of DST062^T was aseptically transferred from 48-h cultures grown on Marine Agar (Hopebio, China) into 2 mL of sterile 0.85% (w/v) NaCl solution.

16S rRNA gene sequencing and phylogenetic analysis

The 16S rRNA gene sequence of strain DST062^T was amplified by polymerase chain reactionusing universal primers 27F and 1492R (Frank et al.2008), followed by full-length 16S rRNA gene sequence assembly by the tool ContEst16S (https://www.ezbiocloud.net/tools/contest16s) (Lee et al. 2017). To identify phylogenetic relatives, the 16S rRNA gene sequence of strain DST062^T was uploaded and compared with sequences in the EzBioCloud (https://www.ezbiocloud.net/)and NCBI database (https://www.ncbi.nlm.nih.gov/). Based on the alignment results, type strains with high similarity were selected, and their 16S rRNA gene sequences were subsequently downloaded from the NCBI database. Phylogenetic trees based on 16S rRNA gene sequences were constructed using MEGA version 11 (Tamura et al. 2021) with two methods: the neighbor-joining (NJ) algorithm with Kimura's two-parameter model (Saitou & Nei 1987), and the maximum-likelihood (ML) method with the K2+G+I substitution model (Felsenstein 1981). Bootstrap analysis was replicated 1000 times to ensure the confidence of the phylogenetic tree (Felsenstein 1985). *Salibacter halophilus* JZ3C34^T

(family *Cryomorphaceae*) was selected as the outgroup for phylogenetic analysis.

Genomic analysis

Genomic DNA sequencing of strain DST062^T was conducted on the Hiseq Nova sequencing platform (Illumina, USA). The sequencing raw data were assembled de novo using both A5-MiSeq (Coil et al. 2015) and SPAdes (Bankevich et al. 2012) software. Protein-coding genes were predicted with higher accuracy by GeneMarkS-2 (http://exon.gatech.edu/GeneMark/genemarks2.cgi) (Lomsadze et al. 2018). Gene functional annotation was performed using the EggNOG 5.0 database (Huerta-Cepas et al. 2019) and eggNOG-mapper v2 (Cantalapiedra et al. 2021), followed by KEGG pathway extraction using TBtools (Chen et al. 2023). For genomic relatedness assessment between strain DST062^T and its closely related strains, the average nucleotide identity (ANI) values and digital DNA-DNA hybridization (dDDH) values were calculated using the EzBioCloud platform (www.ezbiocloud.net/tools/ani) (Yoon et al. 2017), and Genome-to-Genome Distance Calculator (GGDC 3.0)online service (https://ggdc.dsmz.de/distcalc2.php) (Meier-Kolthoff et al. 2022), respectively. The phylogenetic tree was constructed based on 120 conserved bacterial single-copy conserved genes by Genome Taxonomy Database Toolkit GTDB-Tk v2.1.1 (Chaumeil et al. 2022).

Chemotaxonomic profiling

Strain DST062^T and reference strains were cultured on Marine Agar (MA) at 28 °C (pH 7.0) for 48 h to exponential phase. Then, their colonies were harvested and the cellular fatty acids were saponified, methylated and extractedusing the method outlined by Komagata and Suzuki (Komagata and Suzuki 1988). The fatty acids were identified by utilizing the TSBA6 database within the Microbial Identification System (MIDI, Sherlock version 6.0). Respiratory quinones were extracted from freeze-dried cells and separated into their different classes by thin-layer chromatography (TLC) on silica gel (Tindall 1990), then analyzed by high-performance liquid chromatography (HPLC), using mass spectrometry to measure the molecular weight. Polar lipids were extracted using a chloroform/methanol system and analyzed using one- & two-dimensional TLC, as described previously (Kates 1986; Minnikin et al. 1984).

Results and discussion

Physiological and biochemical characterization of strain DST062^T

After 4 days of cultivation on MA at 28 °C under aerobic conditions, strain DST062^T formed small, round, smooth, convex, and slightly yellow colonies. Electron microscopy revealed rod-shaped cells measuring approximately 0.8–1.7 µm in length and 0.3–0.6 µm in width (Fig. 1). Strain DST062^T exhibited a growth temperature range of 4–40 °C (optimum, 28 °C), pH 7.0–8.0 (optimum, 7.0), and salinity tolerance of 0.5–6% (w/v) NaCl (optimally, 3% (w/v) NaCl). Additional physiological tests revealed that strain DST062^T is a Gram-negative, aerobic, and non-motile rod-shaped bacterium, displaying positive reactions for both catalase and oxidase activities. API ZYM revealed that strain DST062^T exhibited activities for alkaline phosphatase, leucine arylamidase, valine arylamidase, acid phosphatase, naphthol-AS-BI-phosphohydrolase, β-galactosidase, and α-glucosidase.

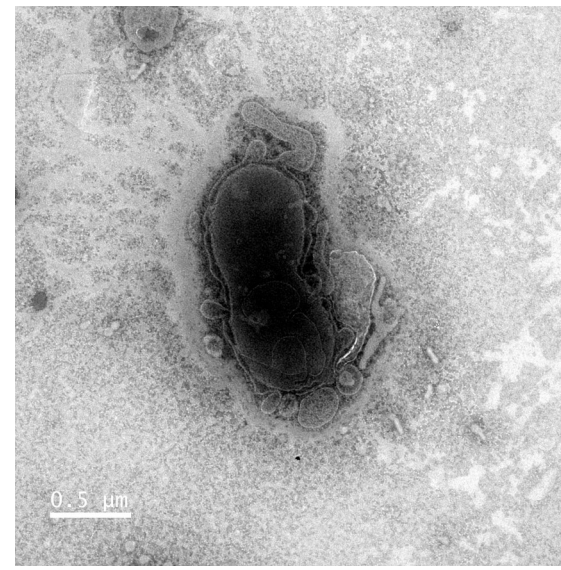


Fig. 1 Transmission electron micrograph of strain DST062^T cells harvested from marine agar 2216 after 4-days incubation at 28 °C. (Bars 0.5 µm)

Esterase (C4) and esterase lipase (C8) showed weak positive results. In API 20NE test, D-glucose fermentation and 4-nitrophenyl-*β*-D-galactopyranoside were positive. Detailed physiological and biochemical properties of strain DST062^T are listed in Table 1.

Table 1 Differential characteristics of strain DST062^T and its closely related genera in the family *Flavobacteriaceae*

Characteristic	1	2	3	4	5	6	7
Isolation source	Seawater	tidal flat sediment[a]	Marine sediment[b]	Seawater[c]	Seawater[d]	Seawater[e]	Seawater[f]
Cells (μm)	0.3–0.6×0.8–1.7	0.4–0.6×1.9–4.0[a]	0.6–0.8×1.8–2.5[b]	0.5–0.7×1.8–2.6[c]	0.3–0.4×1.0–3.0[d]	0.3–0.7×1.5–5.3[e]	0.3–1.1×1.1–3.4[f]
Growth conditions							
Temperature (optimum) (°C)	28	35[a]	30[b]	25–30[c]	25–30[d]	25–30[e]	30–33[f]
NaCl (%, w/v)	3	4[a]	2[b]	2–4[c]	3[d]	3[e]	2–3[f]
pH (optimum)	7.0	6.0[a]	7.0[b]	7.0–8.5[c]	7.0[d]	7.0[e]	7.0–8.0[f]
Enzyme activities (API ZYM)							
Esterase (C4)	w	w	+	+	–	+	w
Esterase lipase (C8)	w	w	w	+	–	+	w
Cystine arylamidase	–	+	+	+	–	+	–
Acid phosphatase	+	+	–	+	+	+	+
N-acetyl-*β*-glucosaminidase	–	+	+	+	–	+	+
β-Galactosidase	+	+	+	–	–	+	+
α-Glucosidase	+	–	+	+	–	+	w
β-Glucosidase	–	–	+	–	–	+	–
API 20NE							
Nitrate reduction	–	–	–	–	–	–	+
D-glucose fermentation	+	+	–	–	+	+	+
Esculin	–	+	–	–	+	+	+
Urease	–	+	–	–	–	–	+
Hydrolysis of gelatin	–	+	–	–	+	+	+
4-nitrophenyl-β-D-galactopyranoside	+	+	+	+	–	+	+
Glucose	–	+	–	–	–	–	+
Malate	–	+	–	+	–	+	+
Maltose	–	–	–	–	–	–	–
Gluconate	–	–	–	–	–	–	+
DNA G+C content (mol%)	35.9	33.3	35.7	34.6	31.7	34.2	36.9
Major polar lipids	PE, AL1-2, L1-2	PE	DPG, AGL, AL, L1-3	ND	PE, PL, AL1-2, L1-2	PE, PN1, AL1-2, L1-7	PE, PL, AL1-3, L1-3
Major respiratory quinone	MK-6	MK-6	MK-6	MK-6	MK-6	MK-6	MK-6

Strains: 1, DST062^T; 2, *Confluentibacter sediminis* DSL-48^T ([a]Wei et al. 2019); 3, *Snuella sedimenti* CAU 1569^T ([b]Kim et al. 2021); 4, *Jejuia pallidilutea* EM39^T ([c]Lee et al. 2009); 5, *Flaviramulus aquimarinus* KYW499^T ([d]Lee et al. 2015); 6, *Tamlana nanhaiensis* FHC16^T ([e]Liu et al. 2015); 7, *Gelatiniphilus marinus* GYP-24^T ([f]Tang et al. 2016). Characteristics are scored as: +, Positive; –, negative; w, weakly positive; ND, no data available

Phylogenetic analysis

The amplified 16S rRNA gene sequence of strain DST062^T was 1422 bp. 16S rRNA gene sequence comparisons showed that strain DST062^T shared the highest similarities with *Confluentibacter sediminis* DSL-48^T (95.35%), followed by *Algibacter marinivivus* ZY111^T (95.06%), *Snuella sedimenti* CAU 1569^T (95.05%), *Confluentibacter flavum* 3B^T (94.98%), *Flaviramulus ichthyoenteri* Th78^T (94.94%), *Jejuia pallidilutea* EM39^T (94.74%) and *Flaviramulus aquimarinus* KYW499^T (94.55%). Two reference stains, *Tamlana nanhaiensis* FHC16^T and *Gelatiniphilus marinus* GYP-24^T, which are close to strain DST062^T in the NJ tree (Fig. 2), shares 94.16% and 93.55% similarity with strain DST062^T, relatively. All of these values are clearly below the species' threshold limit of 98.65% (Kim et al. 2014). Phylogenetic analyses based on the NJ tree (Fig. 2) and the ML tree (Fig. S2) revealed the same results that strain DST062^T formed a deep novel branch within the family *Flavobacteriaceae*. It clustered with three different genera *Gelatiniphilus*, *Hwangdonia* and *Thalassorhabdus* with a bootstrap value of 40%, and their similarities (Fig. 2) are under the threshold of 94.50% for defining a novel genus (Yarza et al. 2014). These results suggest that strain DST062^T represents a novel genus of the family *Flavobacteriaceae.*

Genomic analysis

Strain DST062^T has a draft genome sequence of 3,806,689 bp with 35 scaffolds. The genome scaffolds exhibited a range of 529 to 798,496 bp, with an N50 size of 327,721 bp. The DNA G+C content of the draft genome was 35.9%, which is higher than that of other reference bacteria, except *Gelatiniphilus marinus* GYP-24^T (36.9%). The genome contained 3,334 predicted protein-coding genes, 3 rRNA genes, 40 tRNA genes, and 22 additional non-coding RNA genes. Functional annotation assigned 2,989 genes to the Clusters of Orthologous

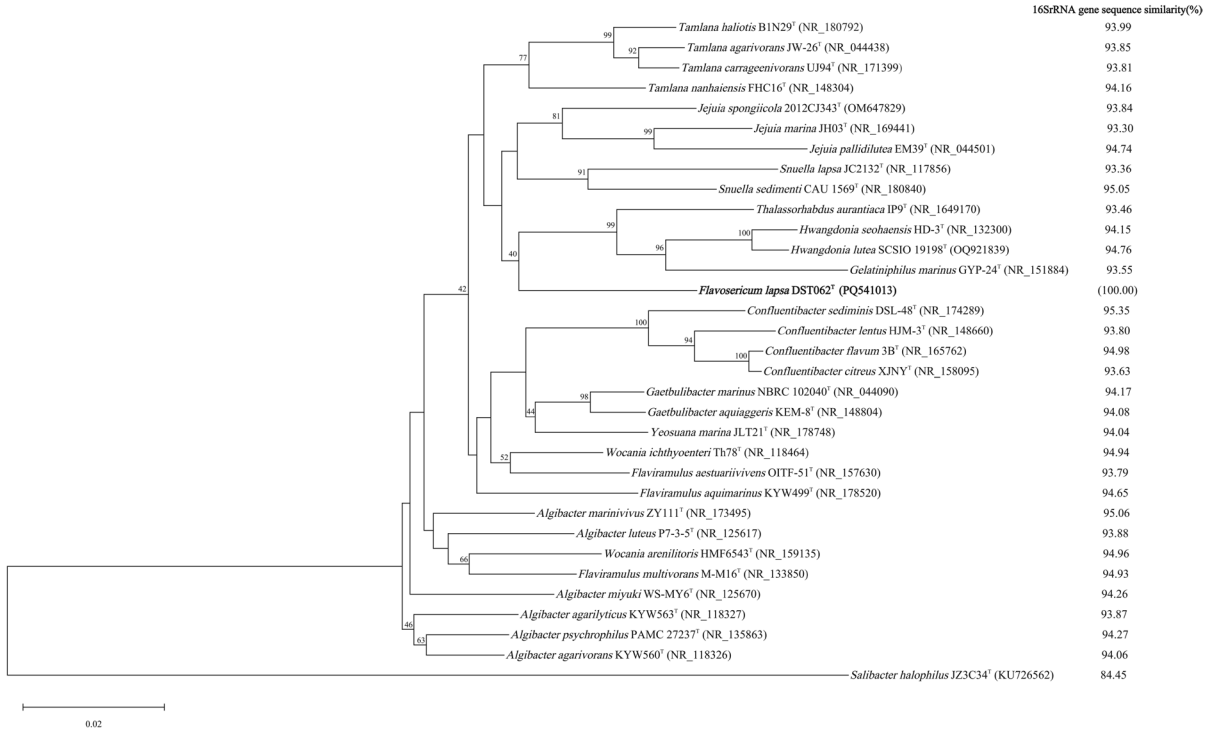


Fig. 2 Neighbour-joining phylogenetic tree based on 16S rRNA gene sequences showing the position of strain DST062^T within the family *Flavobacteriaceae*. *Salibacte rhalophilus* JZ3C34^T was used as an out group. Numbers at branch points indicate bootstrap percentages (based on 1000 replicates); only values ≥ 40% are indicated. Bar, 0.01 substitutions per nucleotide position

Groups (COG) database, distributed across 19 functional categories. With 36.3% of the COG category having an unknown function, followed by inorganic ion transport and metabolism (M, 6.2%), carbohydrate transport and metabolism (G, 5.7%), amino acid transport and metabolism (E, 5.5%) (Fig. 3). The comparison of COG category distribution patterns between strain DST062^T and its closely related species showed a general consistency (Fig. S4).

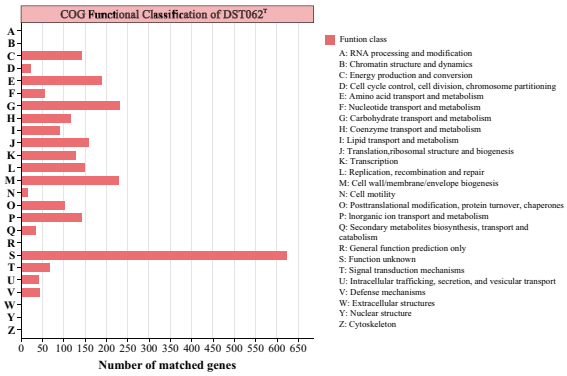


Fig. 3 COG functional classification of strain DST062^T genome

A total of 2859 genes (assigned to six major functional categories) were revealed by KEGG pathway analysis. Metabolic pathways constituted the predominant functional category, accounting for 80.9% of the total annotated genes in the KEGG database, encompassing carbohydrate, amino acid, energy, cofactor/vitamin, and nucleotide metabolism (Fig. 4). Specifically, 55 genes were associated with purine metabolism (ko00230) and 44 genes with pyrimidine metabolism (ko00240) which account for a large proportion. Additionally, strain DST062^T contains 27 genes involved in homologous recombination (ko03440), a process that is a key mechanism of DNA repair. Genomic analysis has shown that strain DST062^T has a complete *Uvr* gene cluster composed of *uvrA*, *uvrB* and *uvrC* genes. The UvrA protein, characterized by its ATPase and DNA-binding activities, synergistically associates with the UvrB protein to constitute a damage recognition complex capable of scanning and identifying abnormalities in DNA (Jaciuk et al. 2020). The UvrC protein is a DNA endonuclease involved in further processing of the damage site. The UvrABC repair system can catalyze the recognition and repair of DNA damage, thereby maintaining genome stability. Furthermore, strain

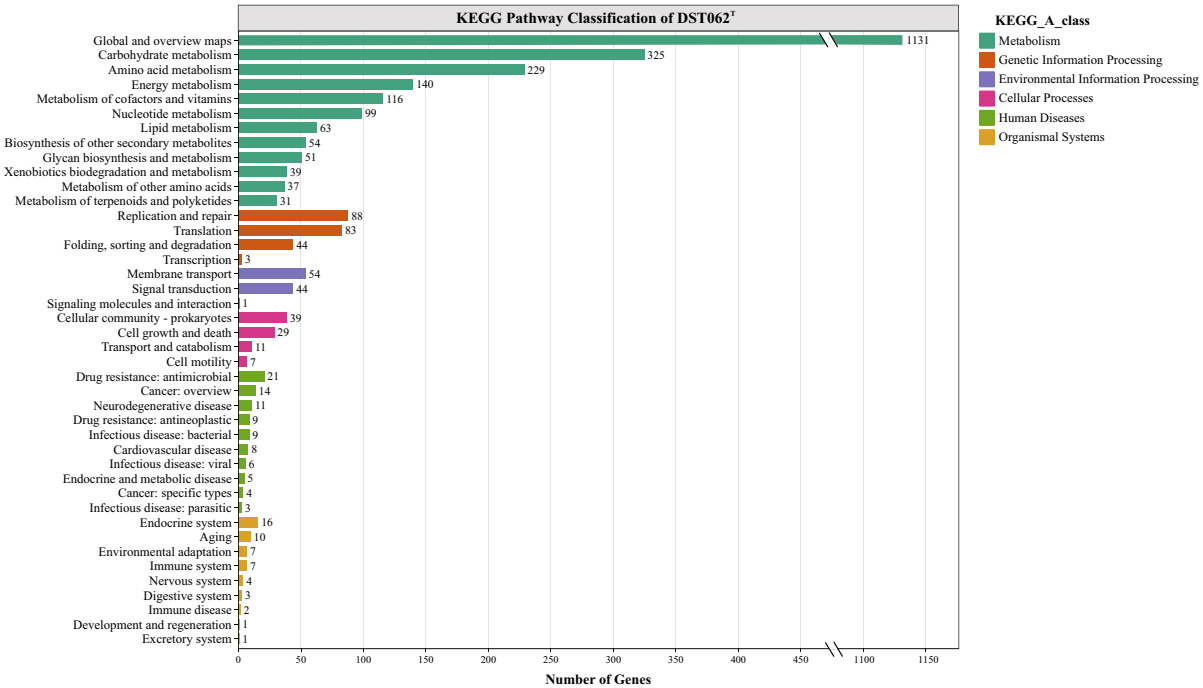


Fig. 4 KEGG pathway classification of strain DST062^T

DST062^T is implicated in numerous pathways associated with carbohydrate metabolism. For instance, the genome of strain DST062^T encompasses a suite of genes dedicated to galactose metabolism including *galE*, *galK*, and *galT* responsible for converting and utilizing galactose. The presence of up to 29 genes related to this metabolic pathway underscores the strain's capacity to metabolize carbohydrates effectively. In *Saccharomyces cerevisiae*, the *Gal* gene cluster includes *gal1*, *gal7* and *gal10* genes, which are involved in galactose catabolic metabolism through the Leloir pathway (Peri et al.2024). There are also genes related to other carbohydrate metabolism pathways such as amino sugar and nucleotide sugar metabolism (34 genes), galactose metabolism (29 genes), pentose and glucuronate interconversions (25 genes), starch and sucrose metabolism (25 genes). In addition, strain DST062^T possesses the *Gld* gene clusters, which are responsible for encoding some proteins related to gliding motility protein, gliding motility-associated lipoprotein, gliding motility-associated ABC transporter permease protein and gliding motility-associated ABC transporter ATP-binding subunit. The abundance of these genes in strain DST062^T suggests that it can efficiently repair DNA during rapid proliferation or nucleic acid damage. Besides, strain DST062^T also has diverse carbohydrate metabolism for energy and synthesis, supporting life-sustaining activities and adaptability. This ensures accurate genetic transmission, especially under environmental stress or genotoxic exposure.

The estimated Average Nucleotide Identity (ANI) and digital DNA-DNA Hybridization (dDDH) values between strain DST062^T and the reference species ranged from 73.7 to 76.0% and from 18.5 to 20.0%, respectively (Table S2). These values are significantly lower than the ANI threshold (95–96%) and dDDH threshold (70%) for species delimitation (Meier-Kolthoff et al. 2013; Chun et al. 2018; Barco et al. 2020). Strain DST062^T exhibited the highest ANI value (76.02%) and the highest dDDH value with *Tamlana nanhaiensis* FHC16^T (20.00%). However, *Tamlana nanhaiensis* FHC16^T exhibits low 16S rRNA gene sequence similarities with strain DST062^T (Fig. 2) and also possesses distinct major polar lipids compared to strain DST062^T (Table 1). In the phylogenomic tree (Fig. S3), strain DST062^T was also found to form a novel branch, consistent with the results of the NJ tree and the ML tree.

Chemotaxonomic characteristics

The fatty acid profile of strain DST062^T cells was dominated (> 10%) by iso-$C_{15:0}$ (20.0%), summed feature 3 ($C_{16:1}\omega6c$ and/or $C_{16:1}\omega7c$) (14.9%), iso-$C_{15:1}$ G (12.6%) and iso-$C_{17:0}$ 3-OH (11.8%) (Table S1). Although the fatty acid profile was similar to that of the reference strains, the distinct content for each fatty acid could distinguish strain DST062^T from these strains. For instance, the proportions of $C_{15:1}$ $\omega6c$, iso-$C_{16:0}$, $C_{16:0}$ and summed feature 3 ($C_{16:1}$ $\omega6c$ and/or $C_{16:1}$ $\omega7c$) in strain DST062^T were the highest compared with those of the reference bacteria. Moreover, iso-$C_{16:1}$ H is only detected in strain DST062^T. The respiratory quinone was identified as menaquinone 6 (MK-6), which is known as a common feature of bacteria in the *Flavobacteriaceae* family. The major polar lipids of strain DST062^T included two aminolipids (AL1 & AL2), phosphatidylethanolamine (PE), and two unknown polar lipids (L1 & L2) (Fig.S1).

Polyphasic taxonomic conclusion

Results of phylogenetic, phenotypic and chemotaxonomic characteristics analysis, such as low 16S rRNA gene similarity, large difference in genomic DNA G + C content, and cellular fatty acid and polar lipid profiles, indicated that a novel genus and species should be established to accommodate strain DST062^T. Thus, *Flavisericum labens* gen. nov., sp. nov. is proposed.

Description of *Flavisericum* gen. nov.

Flavisericum (Fla.vi.se'ri.cum. L. masc. adj. *flavus*, yellow; L. neut. n. *sericum*, silk; N.L. neut. n. *Flavisericum*, yellow silk, referring to the shape of bacteria in liquid medium).

Cells are Gram-stain-negative, rod-shaped, non-motile and strictly aerobic. Oxidase and catalaseare positive. The major polar lipids are two amino lipids, phosphatidylethanolamine (PE), and two unknown polar lipids. The major respiratory quinone is MK-6. The DNA G + C content of the type strain of the type species is 35.9 mol%. The predominant fatty acids are iso-$C_{15:0}$, summed feature 3 ($C_{16:1}$ $\omega6c$/$C_{16:1}$ $\omega7$c), iso-$C_{15:1}$ G and iso-$C_{17:0}$ 3-OH. Member of the family

Flavobacteriaceae, order *Flavobacteriales*. The type species is *Flavisericum labens*.

Description of *Flavisericum labens* sp. nov.

Flavisericum labens (la'bens. L. neut. adj. *labens*, gliding).

Cells are rod-shaped, approximately 0.3–0.6 μm in width and 0.8–1.7 μm in length. After 4–5 days of incubation on marine agar 2216 at 28 °C, the strain formed yellow-pigmented, round, smooth, and convex colonies. Strain DST062^T could grow at 4–40 °C (optimum, 28 °C), pH 7.0–8.0 (optimum, 7.0), and salinity tolerance of 0.5–6% (w/v) NaCl (optimally, 3% (w/v)). Alkaline phosphatase, leucine arylamidase, valine arylamidase, acid phosphatase, naphthol-AS-BI-phosphohydrolase, β-galactosidase, α-glucosidase, D-glucose fermentation, 4-nitrophenyl-β-D-galactopyranosidewere positive. Esterase (C4) and esterase lipase (C8) were weakly positive. The dominated fatty acids (> 10%) in cells are iso-$C_{15:0}$, summed feature 3($C_{16:1}$ $\omega 6c$/$C_{16:1}$ $\omega 7c$), iso-$C_{15:1}$ G and iso-$C_{17:0}$ 3-OH. MK-6 is the major respiratory quinone. The major polar lipids are two aminolipids, phosphatidylethanolamine, and two unknown polar lipids.

The type strain, DST062^T (= MCCC 1K08936^T = KCTC 102361 ^{T}), was isolated from seawater of Dongshan Bay (23° 38′N, 117° 22′E), Fujian, China. The DNA G + C content of strain DST062^T is 35.92 mol%. The GenBank accession numbers for the 16S rRNA gene sequence and the complete genome sequence of strain DST062^T are PQ541013 and PRJNA1180476, respectively.

Author contributions JL, ZX, ZS, YX and JY designed and performed the experiments. JL, ZX, GL, DL and KT analyzed the data. JL, KT, ZX, ZS and DL wrote the manuscript. All authors read and approved the final manuscript. Additionally, we would like to express our sincere gratitude to Junqing Tian from Ocean University of China, who originally isolated the novel strain DST062^T and made significant contributions to this study.

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Data availability The 16S rRNA gene sequence and the genome sequence of strain DST062^T have been deposited in GenBank with accession numbers PQ541013 and PRJNA1180476, respectively.

Declarations

Conflict of interest The authors declare no competing interests.

References

Bankevich A, Nurk S, Antipov D et al (2012) SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. J Comput Biol 19:455–477. https://doi.org/10.1089/cmb.2012.0021

Barco RA, Garrity GM, Scott JJ et al (2020) A genus definition for *Bacteria* and *Archaea* based on a standard genome relatedness index. Mbio 11:e02475-e2519. https://doi.org/10.1128/mBio.02475-19

Bernardet JF, Segers P, Vancanneyt M et al (1996) Cutting a Gordian knot: emended classification and description of the genus *Flavobacterium*, emended description of the family Flavobacteriaceae, and proposal of *Flavobacterium hydatis* nom. nov. (basonym, *Cytophaga aquatilis* Strohl and Tait 1978). Int J Syst Bacteriol 46:128–148. https://doi.org/10.1099/00207713-46-1-128

Cantalapiedra CP, Hernández-Plaza A, Letunic I et al (2021) EggNOG-mapper v2: functional annotation, orthology assignments, and domain prediction at the metagenomic scale. Mol Biol Evol 38:5825–5829. https://doi.org/10.1093/molbev/msab293

Chaumeil PA, Mussig AJ, Hugenholtz P et al (2022) GTDB-Tk v2: memory friendly classification with the genome taxonomy database. Bioinformatics 38:5315–5316. https://doi.org/10.1093/bioinformatics/btac672

Chen C, Wu Y, Li J et al (2023) TBtools-II: a "one for all, all for one" bioinformatics platform for biological big-data mining. Mol Plant 16:1733–1742. https://doi.org/10.1016/j.molp.2023.09.010

Choi J, Jang JH, Cha S et al (2018) *Thalassorhabdus aurantiaca* gen. nov., sp. nov., a new member of the family *Flavobacteriaceae* isolated from seawater in South Korea. Antonie Van Leeuwenhoek 111:2185–2193. https://doi.org/10.1007/s10482-018-1111-z

Chun J, Oren A, Ventosa A et al (2018) Proposed minimal standards for the use of genome data for the taxonomy of prokaryotes. Int J Syst Evol Microbiol 68:461–466. https://doi.org/10.1099/ijsem.0.002516

Coil D, Jospin G, Darling AE (2015) A5-miseq: an updated pipeline to assemble microbial genomes from Illumina MiSeq data. Bioinformatics 31:587–589. https://doi.org/10.1093/bioinformatics/btu661

Felsenstein J (1981) Evolutionary trees from DNA sequences: a maximum likelihood approach. J Mol Evol 17:368–376. https://doi.org/10.1007/BF01734359

Felsenstein J (1985) Confidence limits on phylogenies: an approach using the bootstrap. Evolution 39:783–791. https://doi.org/10.1111/j.1558-5646.1985.tb00420.x

Frank JA, Reich CI, Sharma S et al (2008) Critical evaluation of two primers commonly used for amplification of bacterial 16S rRNA genes. Appl Environ Microbiol 74:2461–2470. https://doi.org/10.1128/AEM.02272-07

Gerhardt, P. et al (1994) Methods for general and molecular bacteriology. American Society for Microbiology.

Huerta-Cepas J, Szklarczyk D, Heller D et al (2019) eggNOG 5.0: a hierarchical, functionally and phylogenetically annotated orthology resource based on 5090 organisms and 2502 viruses. Nucleic Acids Res 47:D309–D314. https://doi.org/10.1093/nar/gky1085

Jaciuk M, Swuec P, Gaur V et al (2020) A combined structural and biochemical approach reveals translocation and stalling of UvrB on the DNA lesion as a mechanism of damage verification in bacterial nucleotide excision repair. DNA Repair 85:102746. https://doi.org/10.1016/j.dnarep.2019.102746

Kates M (1986) Techniques of lipidology: isolation, analysis, and identification of lipids (2nd rev. ed). Elsevier ; Sole distributors for the U.S.A. and Canada, Elsevier Science Pub. Co.

Kawano K, Ushijima N, Kihara M et al (2020) *Patiriisocius marinistellae* gen. nov., sp. nov., isolated from the starfish *Patiria pectinifera*, and reclassification of *Ulvibacter marinus* as a member of the genus *Patiriisocius* comb. nov. Int J Syst Evol Microbiol 70:4119–4129. https://doi.org/10.1099/ijsem.0.004254

Kim M, Oh HS, Park SC et al (2014) Towards a taxonomic coherence between average nucleotide identity and 16S rRNA gene sequence similarity for species demarcation of prokaryotes. Int J Syst Evol Microbiol 64:346–351. https://doi.org/10.1099/ijs.0.059774-0

Kim JH, Weerawongwiwat V, Yoon JH et al (2021) *Snuella sedimenti* sp. nov., isolated from marine sediment. Arch Microbiol 203:5437–5443. https://doi.org/10.1007/s00203-021-02528-8

Komagata K and Suzuki KI (1988) 4 Lipid and Cell-Wall Analysis in Bacterial Systematics. In Methods in Microbiology (Vol. 19, pp. 161–207). Elsevier. https://doi.org/10.1016/S0580-9517(08)70410-0

Lee DH, Kahng HY, Lee YS et al (2009) *Jejuia pallidilutea* gen. nov., sp. nov., a new member of the family *Flavobacteriaceae* isolated from seawater. Int J Syst Evol Microbiol 59:2148–2152. https://doi.org/10.1099/ijs.0.007625-0

Lee JH, Baik KS, Seong CN (2015) *Flaviramulus aquimarinus* sp. nov., isolated from seawater. Int J Syst Evol Microbiol 65:644–649. https://doi.org/10.1099/ijs.0.066126-0

Lee I, Chalita M, Ha SM et al (2017) ContEst16S: an algorithm that identifies contaminated prokaryotic genomes using 16S RNA gene sequences. Int J Syst Evol Microbiol 67:2053–2057. https://doi.org/10.1099/ijsem.0.001872

Liu X, Lai Q, Du Y et al (2015) *Tamlana nanhaiensis* sp. nov., isolated from surface seawater collected from the South China Sea. Antonie Van Leeuwenhoek 107:1189–1196. https://doi.org/10.1007/s10482-015-0410-x

Lomsadze A, Gemayel K, Tang S et al (2018) Modeling leaderless transcription and atypical genes results in more accurate gene prediction in prokaryotes. Genome Res 28:1079–1089. https://doi.org/10.1101/gr.230615.117

Meier-Kolthoff JP, Auch AF, Klenk H-P et al (2013) Genome sequence-based species delimitation with confidence intervals and improved distance functions. BMC Bioinformatics 14:60. https://doi.org/10.1186/1471-2105-14-60

Meier-Kolthoff JP, Carbasse JS, Peinado-Olarte RL et al (2022) TYGS and LPSN: a database tandem for fast and reliable genome-based classification and nomenclature of prokaryotes. Nucleic Acids Res 50:D801–D807. https://doi.org/10.1093/nar/gkab902

Minnikin DE, O'Donnell AG, Goodfellow M et al (1984) An integrated procedure for the extraction of bacterial isoprenoid quinones and polar lipids. J Microbiol Methods 2:233–241. https://doi.org/10.1016/0167-7012(84)90018-6

Peri KVR, Yuan L, Faria Oliveira F et al (2024) A unique metabolic gene cluster regulates lactose and galactose metabolism in the yeast *Candida intermedia*. Appl Environ Microbiol 90:e01135-e1224. https://doi.org/10.1128/aem.01135-24

Reichenbach H (1989). Order I. Cytophagales Leadbetter 1974. In Bergey's Manual of Systematic Bacteriology, vol. 3. Williams & Wilkins. pp: 2011–2013.

Saitou N, Nei M (1987) The neighbor-joining method: a new method for reconstructing phylogenetic trees. Mol Biol Evol. https://doi.org/10.1093/oxfordjournals.molbev.a040454

Tamura K, Stecher G, Kumar S et al (2021) MEGA11: molecular evolutionary genetics analysis version 11. Mol Biol Evol 7:3022–3027. https://doi.org/10.1093/molbev/msab120

Tang M, Tan L, Wu H et al (2016) *Gelatiniphilus marinus* gen. nov., sp. nov., a bacterium from the culture broth of a microalga, *Picochlorum* sp. 122, and emended description of the genus *Hwangdonia*. Int J Syst Evol Microbiol 66:2893–2898. https://doi.org/10.1099/ijsem.0.001074

Tindall BJ (1990) A comparative study of the lipid composition of *Halobacterium saccharovorum* from various sources. Syst Appl Microbiol 13:128–130. https://doi.org/10.1016/S0723-2020(11)80158-X

Walker BJ, Abeel T, Shea T et al (2014) Pilon: an integrated tool for comprehensive microbial variant detection and genome assembly improvement. PLoS ONE 9:e112963. https://doi.org/10.1371/journal.pone.0112963

Wei Y, Wang K, Pei J et al (2019) *Confluentibacter sediminis* sp. nov., isolated from the junction between the ocean and a freshwater lake and emended description of the genus *Confluentibacter*. Int J Syst Evol Microbiol 69:3581–3585. https://doi.org/10.1099/ijsem.0.003665

Yarza P, Yilmaz P, Pruesse E et al (2014) Uniting the classification of cultured and uncultured bacteria and archaea using 16S rRNA gene sequences. Nat Rev Microbiol 12:635–645. https://doi.org/10.1038/nrmicro3330

Yin R, Yi YJ, Chen Z et al (2019) Flavihalobacter algicola gen. nov. sp. nov., a member of the family Flavobacteriaceae with alginate-degradation activity, isolated from marine alga Saccharina japonica. Int J Syst Evolut Microbiol. https://doi.org/10.1099/ijsem.0.004701

Yoon J, Adachi K, Kasai H (2015) Isolation and classification of a novel marine *Bacteroidetes* as *Frondibacter aureus* gen. nov., sp. nov. Antonie Van Leeuwenhoek 107:321–328. https://doi.org/10.1007/s10482-014-0330-1

Yoon SH, Ha S, Lim J et al (2017) A large-scale evaluation of algorithms to calculate average nucleotide identity.

Antonie Van Leeuwenhoek 110:1281–1286. https://doi.org/10.1007/s10482-017-0844-4

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