Nonlabens tegetincola gen. nov., sp. nov., a novel member of the family *Flavobacteriaceae* isolated from a microbial mat in a subtropical estuary

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An orange-pigmented, Gram-negative, non-motile, rod-shaped, strictly aerobic bacterium (UST030701-324^T) was isolated from a microbial mat in an estuary in the Bahamas. The DNA G+C content was 33.6 mol%. Predominant fatty acids were i15:0, i16:0, i17:0 3-OH, and summed feature 3, comprising i15:0 2-OH and/or 16:1 ω 7c. MK-6 was the only respiratory quinone. Flexirubin-type pigments were not produced. Phylogenetic analysis based on 16S rRNA gene sequences placed UST030701-324^T in a distinct lineage in the family *Flavobacteriaceae* with less than 90.7% sequence similarity to the members of the nearest genus, *Psychroflexus*. UST030701-324^T can be distinguished from other members of *Flavobacteriaceae* by a number of chemotaxonomic and phenotypic characteristics. It is thus proposed that UST030701-324^T represents a novel taxon designated *Nonlabens tegetincola* gen. nov., sp. nov. The type strain is UST030701-324^T (=NRRL B-41136^T=JCM 12886^T).

The family *Flavobacteriaceae*, belonging to the phylum *Cytophaga–Flavobacterium–Bacteroides*, accommodates a large number of marine bacteria that are either psychrophilic or psychrotolerant (Bernardet *et al.*, 1996). Based on the data of the present study, we proposed the mesophilic bacterial strain UST030701-324^T of estuarine origin to represent a novel genus of the *Flavobacteriaceae*.

The bacterial strain UST030701-324^T was isolated from a microbial mat covering a polystyrene surface retrieved from an estuarine mangrove habitat in the Bahamas. After 48 h of cultivation at 30 °C on an agar medium composed of 5 g peptone l⁻¹, 3 g yeast extract l⁻¹ and 0.22 μ m-filtered-seawater (referred to as marine agar hereafter), UST030701-324^T appeared as orange, convex, circular colonies (2–4 mm diameter) with smooth surfaces and entire translucent margins. No diffusible pigment was observed. Unless otherwise specified, all characteristics described hereafter were based on cultures grown on marine agar for 48 h at 30 °C.

The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain UST030701-324^T is AY987349.

A scanning electron micrograph and detailed phenotypic characteristics of UST030701-324^T are available as supplementary material in IJSEM Online.

The optimum temperature for the growth of UST030701-324^T was 28–36 °C.

The nearly complete 16S rRNA gene sequence of UST030701-324^T (1462 bp) was obtained using a dye terminator method as described elsewhere (Lau *et al.*, 2004). Comparison of the nearly complete 16S rRNA gene sequence of UST030701-324^T to those available from GenBank revealed that UST030701-324^T was a member of the family *Flavobacteriaceae*. A neighbour-joining phylogenetic tree constructed using the ARB software package (Ludwig *et al.*, 2004) showed that UST030701-324^T formed a clade together with several uncharacterized bacterial strains (93.6–94.6% sequence similarity). This clade did not cluster robustly with any recognized species or genus (Fig. 1). UST030701-324^T was nearest to the members of the genera *Psychroflexus* and *Salegentibacter*, with 16S rRNA gene sequence similarity ranging from 88.5 to 90.7%. Trees based on maximum-parsimony and maximum-likelihood methods showed essentially the same topology (Fig. 1). The results of phylogenetic analysis suggest that UST030701-324^T represents a novel genus within the family *Flavobacteriaceae*.

The DNA G+C content of UST030701-324^T, determined by an HPLC method (Mesbah *et al.*, 1989), was

Fig. 1. Neighbour-joining dendrogram showing the estimated phylogenetic relationships among UST030701-324^T and related species on the basis of 16S rRNA gene sequences. Strains belonging to the genus *Flavobacterium* serve as outgroups. Lines in bold type indicate branches also found in maximum-likelihood and parsimony trees. Scale bar represents 1 nucleotide substitution per 10 nucleotides. Bootstrap values >50% (500 replicates) are indicated at nodes. GenBank accession numbers are shown in parentheses.

33.6 ± 0.3 mol% (three replicates). This value was similar to those for the members of *Psychroflexus* (32.0–36.0 mol%), but was lower than those for the members of *Salegentibacter* (36.8–38.0 mol%). The dominant cellular fatty acids of UST030701-324^T were i15:0, i15:0 3-OH, i16:0, i16:0 3-OH, i17:0 3-OH, summed feature 3 (comprising i15:0 2-OH and/or 16:1ω7c) and an unknown fatty acid with a carbon chain length equivalent to 13.6 (altogether representing 78.3 % of the total) as determined using the Sherlock Microbial Identification System according to the manufacturer's protocol (Table 1). This fatty acid profile differed from those described for *Psychroflexus* and *Salegentibacter* by, for instance, the absence of 15:0 and the presence of i17:1ω9c and an unknown fatty acid (Table 1). MK-6 was the only respiratory quinone as determined using an HPLC method according to Collins (1994). Menaquinones extracted from *Cellulophaga lytica* (Johansen *et al.*, 1999) and *Pedobacter heparinus* (Steyn *et al.*, 1998) served as references for MK-6 and MK-7, respectively.

The phenotypic characteristics of UST030701-324^T are given in the species description and in Supplementary Tables S1 and S2 available in IJSEM Online. Anaerobic growth was examined in the Oxoid Anaerobic System. The requirement for NaCl was tested in a medium containing (per litre) 5 g MgCl₂, 2 g MgSO₄, 0.5 g CaCl₂, 1 g KCl, 5 g peptone and various amounts of NaCl, adjusted to pH 7.5 using KOH (Isnansetyo & Kamei, 2003). Cell morphology

was examined using scanning electron microscopy (JEOL 7600F) according to the procedures in Neu *et al.* (2001) (see Supplementary Fig. S1). Reaction to Gram stain was determined using light microscopy according to Smibert & Krieg (1994). Gliding motility was determined using phase-contrast light microscopy after growth on quarter-strength marine 2216 medium solidified with 1 % agar according to Bowman (2000). Susceptibility to antibiotics was tested according to Acar (1980). Flexirubin-type pigment production and cellulose hydrolysis were determined according to Bowman (2000). Casein hydrolysis was determined according to Norris *et al.* (1985) and chitin and Tween 20, 40 and 80 hydrolysis was determined according to Baumann & Baumann (1988). Spore formation, oxidase and catalase activities and the hydrolysis of agar, DNA and starch were tested according to Smibert & Krieg (1994). Other enzyme activities, growth on carbon sources, acid production from carbon sources, nitrate reduction and the production of H₂S, indole and acetoin were tested using the commercial systems API 20E, API 20NE, API 50CH and API ZYM (bioMérieux). Cells for inoculation to the API systems were suspended in sterile solution of seawater mix at 22 ‰ salinity (MacDonell *et al.*, 1982).

Chemotaxonomic and phenotypic characteristics that distinguish UST030701-324^T from other genera of *Flavobacteriaceae* are given in Tables 1 and 2. UST030701-324^T differs from the members of *Psychroflexus* by (i) having a

Table 1. Comparison of major cellular fatty acids of UST030701-324^T and members of *Psychroflexus* and *Salegentibacter*

Taxa: 1, strain UST030701-324^T; 2, *Psychroflexus gondwanensis*; 3, *Psychroflexus torquis*; 4, *Psychroflexus tropicus*; 5, *Salegentibacter holothuriorum*; 6, *Salegentibacter mishustinae*; 7, *Salegentibacter salegens*. Values are percentages of total fatty acids; values for UST030701-324^T, *P. gondwanensis* and *P. torquis* are means $\pm$ SD. Growth conditions: column 1, 30 °C on marine agar (5 g peptone l⁻¹, 3 g yeast extract l⁻¹ in 0.22- μ m-filtered sea water) for 48 h; 2–4, 15 °C on marine agar 2216 (duration of cultivation not given); 5 and 6, 28 °C on marine agar 2216 for 48 h; 7, 20 °C on trypticase soy agar for 48 h. Data for members of *Psychroflexus* and *Salegentibacter* are from Bowman *et al.* (1998), McCammon & Bowman (2000), Donachie *et al.* (2004) and Nedashkovskaya *et al.* (2004, 2005b).

Fatty acid	1	2	3	4	5	6	7
Unknown 13.6	6.1 $\pm$ 1.8	—	—	—	—	—	—
i14:0	2.1 $\pm$ 0.8	4.8 $\pm$ 0.8	1.0 $\pm$ 0.2	2.7	—	—	—
15:0	—	1.9 $\pm$ 0.8	4.2 $\pm$ 0.6	0.6	9.6	6.7	4.5
a15:0	3.8 $\pm$ 2.3	23.0 $\pm$ 2.7	35.2 $\pm$ 4.4	19.3	—	7.9	11.6
i15:0	33.1 $\pm$ 6.4	2.1 $\pm$ 0.5	1.1 $\pm$ 0.3	16.7	26.3	7.5	23.7
i15:1	—	—	—	—	18.2	12.3	—
a15:1 ω 10c	—	18.4 $\pm$ 2.5	16.9 $\pm$ 1.8	12.9	—	—	—
i15:1 ω 10c	—	2.2 $\pm$ 1.0	0.4 $\pm$ 0.4	11.8	—	—	3.8
i15:0 3-OH	5.4 $\pm$ 3.0	0.9 $\pm$ 0.7	0.3 $\pm$ 0.2	2.9	—	—	—
i15:0 2-OH	7.5 $\pm$ 3.6*	—	—	—	7.9	7.9*	—
16:1 ω 7c	—	—	—	—	10.4	—	9.4
i16:0	6.8 $\pm$ 0.4	10.9 $\pm$ 0.3	6.0 $\pm$ 1.2	3.4	—	—	7.6
i16:0 3-OH	5.7 $\pm$ 3.1	18.5 $\pm$ 1.6	15.4 $\pm$ 1.0	10.1	—	—	0.3
17:1 ω 6c	2.2 $\pm$ 0.4	—	—	—	—	—	1.8
i17:1 ω 9c	3.5 $\pm$ 0.8	—	—	—	—	—	—
a17:0 3-OH	—	6.6 $\pm$ 0.8	10.9 $\pm$ 3.4	—	—	—	2
i17:0 3-OH	13.7 $\pm$ 5.5	0.9 $\pm$ 0.4	0.2 $\pm$ 0.1	10.0	—	8.6	3
18:0	2.5 $\pm$ 0.0	0.2 $\pm$ 0.2	0.1 $\pm$ 0.1	—	—	—	—

*Appeared as summed feature 3, comprising i15:0 2-OH and/or 16:1 ω 7c.

different fatty acid profile, (ii) the absence of filamentous cells, carbohydrate metabolism (except for sucrose) or α - and β -glucosidase activities, (iii) being able to hydrolyse gelatin and (iv) being less halo- and psychrotolerant. UST030701-324^T differs from the members of *Salegentibacter* by (i) having an orange pigmentation and a different fatty acid profile, (ii) being less halo- and psychrotolerant, (iii) being able to produce acetoin and (iv) the absence of carbohydrate metabolism (except for sucrose) or β -galactosidase activity. Additionally, UST030701-324^T can be distinguished from other closely related genera by traits detailed in Table 2. Molecular evidence together with chemotaxonomic and phenotypic characteristics suggests that UST030701-324^T constitutes a novel genus within the family *Flavobacteriaceae*.

Description of *Nonlabens* gen. nov.

Nonlabens (Non.la'bens. L. part. *non* not; L. part. adj. *labens* gliding; N.L. part. adj. *Nonlabens* non-gliding).

Gram-negative, short rod, non-motile and not forming spores. Strictly aerobic. MK-6 was the only respiratory quinone. Flexirubin-type pigments are not produced.

Catalase- and oxidase-positive. The genus contains one species, *Nonlabens tegetincola*, which is the type species.

Description of *Nonlabens tegetincola* sp. nov.

Nonlabens tegetincola (te.get.in'col.a. L. n. *teges* -etis mat; L. n. *incola* an inhabitant; N.L. n. *tegetincola* mat-inhabitant, pertaining to its microbial mat habitat).

Description is as for the genus plus the following. Colonies on marine agar are orange in colour, circular, 2.0–4.0 mm in diameter, convex with smooth surfaces and entire translucent margins. No diffusible pigment. Growth occurs between 12.0 and 44.0 °C (28.0–36.0 °C optimum), pH 5.0 and 10.0 and 2.0 and 4.0 % NaCl. Susceptible to ampicillin, chloramphenicol, penicillin, streptomycin and tetracycline, but not to kanamycin. DNA G + C content is 33.6 mol% and the dominant fatty acids are i15:0, i15:0 3-OH, i16:0, i16:0 3-OH, i17:0 3-OH, summed feature 3 (comprising i15:0 2-OH and/or 16:1 ω 7c) and an unknown fatty acid with a carbon chain length equivalent to 13.6 (altogether representing 78.3 % of the total). Produces acetoin, but not indole or H₂S. Nitrate is not reduced. Hydrolyses DNA, gelatin, starch and Tweens 20, 40 and 80, but not agar,

Table 2. Differentiation of strain UST030701-324^T from closely related genera

+, Positive; −, negative; ND, not determined; v, variable. Data for *Psychroflexus*, *Salegentibacter*, *Winogradskyella*, *Psychroserpens*, *Gelidibacter* and *Formosa* are from Bowman *et al.* (1997, 1998), McCammon & Bowman (2000), Macián *et al.* (2002), Donachie *et al.* (2004), Ivanova *et al.* (2004), Nedashkovskaya *et al.* (2004, 2005a, b) and Lau *et al.* (2005).

Characteristic	UST030701-324 ^T	<i>Psychroflexus</i>	<i>Salegentibacter</i>	<i>Winogradskyella</i>	<i>Psychroserpens</i>	<i>Gelidibacter</i>	<i>Formosa</i>
Growth:							
NaCl (%)	2.0–4.0	0.0–15.0	0.0–20.0	1.0–8.0	0.4–1.5 × seawater	2.0–6.0	0.0–6.0
Temperature (°C)	12.0–44.0	−16.0 to 43.0	4.0–36.0	4.0–44.0	0.0–15.0	0.0–37.0	5.0–37.0
Pigmentation	Orange	Orange	Yellow	Yellow	Yellow	Yellow	Yellow
Cell shape	Rod	Coccoid, rod, filament	Rod	Rod	Rod, ring, helical	Rod	Rod
Gliding motility	−	v	−	+	−	+	+
G + C content (mol%)	33.6	32.0–36.0	36.8–37.5	32.8–36.1	27.0–29.0	36.0–40.3	34.0–34.4
Gelatin hydrolysis	+	−	+	+	v	+	+
Acetoin production	+	ND	−	v	−	−	ND
Nitrate reduction	−	v	v	−	−	−	+
Metabolism of carbohydrates other than sucrose	−	+	+	+	+	+	+
Enzyme activities							
α- and β-Glucosidase	−	+	ND	−*	ND	ND	ND
β-Galactosidase	−	−	+	−	v	−	ND
Oxidase	+	+	+	+	−	−	−

*No data for *Winogradskyella epiphytica*, *Winogradskyella eximia* or *Winogradskyella thalassocola*.

casein, cellulose or chitin. Acid phosphatase, alkaline phosphatase, α-chymotrypsin, cystine arylamidase, leucine arylamidase, valine arylamidase, esterase (C4), esterase lipase (C8), lipase (C14), trypsin and naphthol-AS-BI-phosphohydrolase activities are positive. N-acetyl-β-glucosaminidase, arginine dihydrolase, α-fucosidase, α-galactosidase, β-galactosidase, α-glucosidase, β-glucosidase, β-glucuronidase, α-mannosidase, lysine decarboxylase, ornithine decarboxylase, tryptophan deaminase and urease activities are negative. Except for acid production from sucrose, no growth or acid production is observed from the carbon sources included in the API 50 CH, API 20 E and API 20 NE test systems. Except for growth on complex media containing yeast extract and peptone, the carbon and nitrogen sources supporting the growth of *Nonlabens tegetincola* are hitherto not known.

The type strain is UST030701-324^T (=NRRL B-41136^T=JCM 12886^T), isolated from a microbial mat in an estuarine mangrove habitat in the Bahamas.

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