Fulvibacter tottoriensis gen. nov., sp. nov., a member of the family *Flavobacteriaceae* isolated from marine sediment

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A novel bacterium, MTT-39^T, was isolated from a sample of marine sediment collected at Tottori on the coast of the Sea of Japan. Cells were Gram-negative, rod-shaped and non-motile. The bacterium formed yellowish brown colonies on marine agar 2216. Although the 16S rRNA gene sequence of strain MTT-39^T classified this strain as a member of the family *Flavobacteriaceae*, the maximum sequence similarity obtained was only 91.5 % (with *Kordia algicida* OT-1^T). In the maximum-likelihood tree based on 16S rRNA gene sequences, the novel bacterium clustered with the type strains of *Kordia algicida*, *Lutibacter litoralis*, *Tenacibaculum maritimum* and *Polaribacter filamentus*. The novel strain exhibited the following characteristics: the predominant fatty acids in cells grown on artificial seawater-based tryptic soya agar were iso-C_{15:1}, iso-C_{15:0} and iso-C_{15:0} 3-OH, the major respiratory quinone was MK-6 and the DNA G + C content was 35 mol%. On the basis of its distinct phenotypic traits and the phylogenetic distance between this marine isolate and other recognized taxa, strain MTT-39^T represents a novel genus and species of the family *Flavobacteriaceae*, for which the name *Fulvibacter tottoriensis* gen. nov., sp. nov. is proposed. The type strain of the type species is MTT-39^T (=NBRC 102624^T=KCTC 22214^T=CGMCC 1.7058^T).

Members of the phylum *Bacteroidetes* may constitute a large proportion of the bacterial community in marine environments, as detected by fluorescence *in situ* hybridization and analysis of 16S rRNA gene libraries (Glöckner *et al.*, 1999; Alonso *et al.*, 2007). Many *Bacteroidetes* strains belong to the family *Flavobacteriaceae*, in which they form a distinct 'marine clade' (Bowman, 2006). They are known for their capacity to degrade macromolecules such as proteins, chitin and other polysaccharides (Cottrell & Kirchman, 2000) and thus may be important in carbon cycling in marine ecosystems. The family *Flavobacteriaceae* is rapidly expanding: 47 novel genera and many novel species have been described over the last five years, most of which are marine organisms (Bernardet & Nakagawa, 2006).

The polyphasic characterization of a novel marine strain, MTT-39^T, isolated from a sediment sample is described here. The sample was collected with a scoop, from a depth of 2–10 cm, from the beach of Tottori (134° 5' E 35° 31' N) in Japan. The strain was isolated using the dilution plating method on half-strength marine agar 2216 (HSMA; Difco). After 3–4 days incubation at 25 °C, the colonies that formed

were yellowish brown, smooth, circular with regular edges and 1–2 mm in diameter. Slants and plates of the same medium were used for routine cultivation at 25 °C, while 20 % (v/v) glycerol in artificial seawater (ASW; Naigai Chemicals) was used for long-term preservation at –80 °C.

Isolation of DNA from strain MTT-39^T, sequencing of the 16S rRNA gene and phylogenetic analysis based on the 16S rRNA gene sequence were performed as described previously (Khan *et al.*, 2007). The results from the BLAST search suggested that strain MTT-39^T is a member of the family *Flavobacteriaceae*, sharing the highest 16S rRNA gene sequence similarity (93 %) with an unpublished marine bacterium (GenBank accession no. EF100858). Pairwise sequence similarities between the 16S rRNA gene of strain MTT-39^T and those of recognized members of the family *Flavobacteriaceae* were also checked using the dynamic programming algorithm (Needleman & Wunsch, 1970; <http://www.ebi.ac.uk/emboss/align/>). The highest sequence similarity was only 91.5 %, obtained with *Kordia algicida* OT-1^T. In a phylogenetic tree based on 16S rRNA gene sequences and constructed by using the maximum-likelihood method (Fig. 1), strain MTT-39^T formed a stable cluster with *K. algicida* OT-1^T, *Lutibacter litoralis* CL-TF09^T, *Tenacibaculum maritimum* ATCC

The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain MTT-39^T is AB294107.

Fig. 1. Dendrogram inferred from maximum-likelihood analysis and based on almost-complete 16S rRNA gene sequences of strain MTT-39^T and related members of the family *Flavobacteriaceae*. Numbers at nodes represent bootstrap percentages calculated from 100 resamplings. *Flexibacter flexilis* (GenBank accession no. AB078054) was used as an outgroup (not shown). Bar, 0.02 K_{nuc} .

43398^T and *Polaribacter filamentus* 215^T. Similar results were obtained using a neighbour-joining analysis (data not shown).

Microscopic observations (Khan *et al.*, 2007), Gram-staining (Cowan & Steel, 1993; Buck, 1982) and gliding motility tests (Perry, 1973; Bernardet *et al.*, 2002) were carried out as described previously. The absorption spectrum (260–700 nm) of an acetone extract of bacterial cells was obtained with a Shimadzu UV-visible spectrophotometer (UV-1650 PC) to assess the presence of carotenoid pigment(s). The bathochromic shift test with 20% KOH (w/v) was performed for the detection of flexirubin-type pigments (Fautz & Reichenbach, 1980). Anaerobic growth was assessed on HSMA plates incubated in air-tight jars containing an AnaeroPack (Mitsubishi Gas Chemical Co.). Growth at 4, 10, 20, 25, 30, 35, 37, 40, 42 and 45 °C was assessed on HSMA plates. Salt tolerance was tested in marine broth 2216 (Difco) with final NaCl concentrations adjusted to 3, 4, 5, 6, 7, 8, 9 and 10% (w/v). Growth was also tested in 1/5-strength Luria–Bertani medium [2 g Bacto tryptone (Difco) and 1 g Bacto yeast extract (Difco) dissolved in a final volume of 1 l] prepared with ASW (0, 30, 50 and 70%, v/v) and NaCl (0, 1 and 2%, w/v). Growth requirements for divalent cations (Mg^{2+} and Ca^{2+}) were assessed in 1/5-strength Luria–Bertani medium with 2.8% (w/v) NaCl and one of the following: 0.6% (w/v) magnesium sulphate or 0.14% (w/v) calcium chloride. Utilization of different nitrogen sources [sodium nitrate (7.8 g l⁻¹), ammonium sulphate (7.8 g l⁻¹), sodium glutamate (20 g l⁻¹), Casamino acids (10 g l⁻¹) and peptone (10 g l⁻¹)] was tested in medium SN (1.0 g glucose and 1.0 g Tris-base dissolved in 1 l ASW, pH 7.0) to which 1 ml filter-sterilized vitamin solution was added. The vitamin solution consisted of the following (l⁻¹ distilled water): 2.0 mg biotin, 2.0 mg folic acid, 10.0 mg pyridoxine hydrochloride, 5.0 mg thiamine hydrochloride, 5.0 mg riboflavin, 5.0 mg nicotinic acid, 5.0 mg DL-calcium pantothenic acid, 0.1 mg vitamin B₁₂, 5.0 mg *p*-aminobenzoic acid and 5.0 mg lipoic acid. Cells from a 2 day-old culture on HSMA were spotted onto a glass slide and flooded with 3% (v/v) hydrogen peroxide to check for the presence of catalase. The presence of oxidase was tested by spotting a cell suspension (in sterile water) onto a cytochrome oxidase strip (Nissui Pharmaceuticals). Marine

broth 2216 solidified with 1.5% (w/v) carrageenan (Type I; Sigma) or agar was used to test the ability of the strain to liquefy these compounds. The degradation of cellulose was assessed by immersing cellulose strips (No. 1 paper; Whatman) in a culture of strain MTT-39^T in 1/5-strength LB medium prepared with ASW at 25 °C for 1 month. The degradation of carboxymethylcellulose was tested by observing the liquefaction of 1/5-strength LB medium solidified with 3% (w/v) carboxymethylcellulose (High Viscosity; Sigma), while the degradation of casein, chitin, DNA, gelatin and starch was assessed using methods described in detail elsewhere (Cowan & Steel, 1993; Lewin & Lounsbury, 1969; Smibert & Krieg, 1981). The novel isolate was tested using an API 20NE strip according to the instructions of the manufacturer (bioMérieux) except that inocula were prepared by suspending cells in sterile ASW. The GN2 MicroPlate system (Biolog) was used to test the utilization of 95 different carbon sources. The MicroPlate was inoculated by using the protocol of Rüger & Krambeck (1994) before being incubated at 25 °C for 3 days. Acidification of the carbon sources included in the API 50 CH strip was tested according to the manufacturer's instructions (bioMérieux), using inocula prepared in a mixture (1:1) of ASW and commercially available CHB medium (bioMérieux). Results were recorded after incubation of the two commercial systems for 3 days at 25 °C. No utilization or acidification occurred for any of the carbon sources included in the Biolog GN2 microplate or the API 50 CH strip, respectively. The poor growth of strain MTT-39^T observed in these systems could be related to a requirement for cofactors. Therefore, the utilization of different carbon sources (adonitol, D-arabinose, D-galactose, D-glucose, D-mannose, glycerol, L-aspartic acid, L-glutamic acid, L-rhamnose, maltose, *meso*-erythritol, peptone, pyruvic acid, raffinose, sucrose, xylitol and yeast extract) was also tested using a basal medium containing either 1 ml vitamin solution or 0.2 g each of peptone and yeast extract (Lewin & Lounsbury, 1969) per litre ASW. The properties of strain MTT-39^T are given in the genus and species descriptions and in Table 1.

To compare the fatty acid content of strain MTT-39^T with those of its closest neighbours, *K. algicida* OT-1^T and *L. litoralis* CL-TF09^T, the novel strain was grown for 3 days at 25 °C on the media that were used to grow these strains for

Table 1. Characteristics that differentiate *Fulvibacter* gen. nov. from related genera

Genera: 1, *Fulvibacter* (this study); 2, *Kordia* (Sohn *et al.*, 2004); 3, *Lutibacter* (Choi & Cho, 2006); 4, *Polaribacter* (Gosink *et al.*, 1998; Nedashkovskaya *et al.*, 2005); 5, *Tenacibaculum* (Suzuki *et al.*, 2001; Yoon *et al.*, 2005, 2006; Choi *et al.*, 2006; Jung *et al.*, 2006; Sheu *et al.*, 2007). +, Positive; –, negative; (+), weakly positive; YB, yellowish brown; Y, yellow; V, variable; S/O, salmon or orange; NG, no growth; NA, not available.

Characteristic	1	2	3	4	5
Catalase/oxidase	–/+	–/+	+/-	V/V*	+/+*
Colony colour	YB	Y	Y	S/O	Y
Degradation of casein	+	+	NA	+/NG	+/NA
β -Glucosidase	+	–	+	V	NA
β -Galactosidase	(+)	–	+	V	NA
Growth temperature range (°C)	10–37	4–40	5–30	4–33	4–41
Salinity range (% NaCl, w/v)	1–5	1–5	1–5	1–6	1–10
Nitrate reduction	–	+	–	V	V
DNA G+C content (mol%)	35	34	34	30–33	30–35

*Data for some species are not available.

fatty acid analyses, i.e. tryptic soy agar (TSA) prepared with 75 % (v/v) ASW, and marine agar 2216 (Difco), respectively (Sohn *et al.*, 2004; Choi & Cho, 2006). Fatty acid analysis was performed by using the Sherlock Microbial Identification System (MIDI). Only slight differences were noticed between the fatty acid contents of strain MTT-39^T grown on the two different media: the presence of two minor fatty acids (C_{14:0} and C_{16:0}) and the proportions of iso-C_{15:0} were medium-dependent (Table 2). The two profiles also differed significantly from those of *K. algicida* OT-1^T and *L. litoralis* CL-TF 09^T. Respiratory quinones were analysed according to the protocol of Nakagawa & Yamasato (1993). DNA was extracted from exponentially growing cells in marine broth 2216 (at 25 °C) using the protocol of Minamisawa (1990). The HPLC method of Mesbah *et al.* (1989) was used to determine the G+C content of the extracted DNA.

Phylogenetic distances (≤ 91.5 % 16S rRNA gene sequence similarity) and differences in phenotypic characteristics (Tables 1 and 2) between strain MTT-39^T and related members of the family *Flavobacteriaceae* clearly indicated that this strain should be classified as a novel genus and species, for which the name *Fulvibacter tottoriensis* gen. nov., sp. nov. is proposed.

Description of *Fulvibacter* gen. nov.

Fulvibacter (Ful.vi.bac'ter. L. adj. *fulvus* yellowish brown; N.L. masc. n. *bacter* a rod; N.L. masc. n. *Fulvibacter* a rod that produces yellowish brown pigment).

Table 2. Fatty acid contents (%) of strain MTT-39^T and related species

Strains: 1, MTT-39^T (MA; this study); 2, MTT-39^T (TSA in 75 % ASW; this study); 3, *K. algicida* OT-1^T (TSA in 75 % aged seawater; Sohn *et al.*, 2004); 4, *L. litoralis* CL-TF09^T (MA; Choi & Cho, 2006). The following fatty acids occur as traces (i.e. <1 %) in strain MTT-39^T: C_{10:0}, C_{11:0}, C_{12:0}, C_{13:0}, iso-C_{11:0}, iso-C_{12:0}, anteiso-C_{13:0}, iso-C_{14:0}, C_{13:1}, C_{12:0} 3-OH, iso-C_{13:0} 3-OH, C_{14:0} 2-OH, iso-C_{14:0} 3-OH and iso-C_{16:0} 3-OH. Collectively, these fatty acids represent 4–7 % of the total fatty acid content.

Fatty acid	1	2	3	4
Straight-chain fatty acids				
C _{14:0}		2		
C _{15:0}			1	2
C _{16:0}	1			
C _{18:0}				1
Branched fatty acids				
iso-C _{13:0}	2	3		
anteiso-C _{13:0}				1
iso-C _{14:0}				2
iso-C _{15:0}	8	20	41	17
anteiso-C _{15:0}	2	3	3	15
Saturated fatty acids				
C _{15:1} ω6c				2
iso-C _{15:1}	32	33		4
anteiso-C _{15:1}	4	3		2
iso-C _{16:1} H				1
C _{17:1} ω6c				1
iso-C _{17:1} ω9c			2	
Hydroxy fatty acids				
C _{15:0} 2-OH	2	1		2
C _{15:0} 3-OH	3	2	14	2
iso-C _{15:0} 3-OH	7	11		17
C _{16:0} 3-OH	11	6	4	
iso-C _{16:0} 3-OH				13
C _{17:0} 2-OH				4
iso-C _{17:0} 3-OH	7	5	22	4
Summed features*				
1				1
2	2	2		
3	6	4	3	1
Unknown fatty acid			9	

*Summed features are groups of two or three fatty acids that cannot be separated by GLC using the MIDI system. Summed feature 1 contains iso-C_{15:1} I and/or C_{13:0} 3-OH, summed feature 2 contains C_{14:0} 3-OH and/or iso-C_{16:1} I; summed feature 3 contains iso-C_{15:0} 2-OH and/or C_{16:1}ω7c.

Gram-negative, aerobic, non-motile, rod-shaped bacteria. Oxidase-positive and catalase-negative. Carotenoid-type pigments (absorption maxima at 425, 452 and 478 nm) are produced but flexirubin-type pigments are not produced (negative KOH test). Sodium and magnesium ions are essential for growth but calcium ions are not. The major cellular fatty acids of cells grown on TSA are iso-C_{15:1},

iso-C_{15:0} and iso-C_{15:0} 3-OH. MK-6 is the major respiratory quinone. The type species is *Fulvibacter tottoriensis*.

Description of *Fulvibacter tottoriensis* sp. nov.

Fulvibacter tottoriensis (tot.to.ri.en'sis. N.L. masc. adj. *tottoriensis* pertaining to Tottori, from where the type strain was isolated).

Displays the following properties in addition to those given in the genus description. Cells are 0.5–0.7 µm wide and 5–14 µm long. Three-day-old colonies on HSMA are yellowish brown in colour, circular with entire edges and 1–2 mm in diameter. Growth occurs at 10–37 °C (optimally at 25–30 °C) and at pH 6.0–10.0 (optimally at pH 7.0–9.0). Growth is not observed at 4, 40, 42 or 45 °C or at pH 5.0. Growth occurs in the presence of 1–5 % (w/v) NaCl. Growth does not occur in the absence of NaCl, or with more than 5 % (w/v) NaCl. Casein, aesculin, gelatin, starch and Tweens 20, 40 and 80 are degraded. Agar, DNA, carrageenan, carboxymethylcellulose, cellulose (filter paper) and chitin are not degraded. Weakly positive for β-galactosidase. Negative for reduction of nitrate and nitrite, production of indole from tryptophan, acidification of glucose and for arginine dihydrolase and urease activities. Peptone, Casamino acids and glutamate are utilized as nitrogen sources but ammonium sulphate and sodium nitrate are not utilized. No utilization or oxidation of carbon sources occurs in GN2 MicroPlates or API 50 CH strips, but L-glutamic acid, pyruvic acid, peptone and yeast extract are utilized with a conventional method. Adonitol, D-arabinose, D-galactose, D-glucose, D-mannose, glycerol, L-aspartic acid, L-rhamnose, maltose, meso-erythritol, raffinose and sucrose are not utilized. The detailed fatty acid content is given in Table 2. The G+C content of the chromosomal DNA is 35 mol%.

The type strain, MTT-39^T (=NBRC 102624^T=KCTC 22214^T=CGMCC 1.7058^T), was isolated from sediment from Tottori on the coast of the Sea of Japan.

Acknowledgements

This work was supported by the New Energy and Industrial Technology Development Organization (NEDO grant no. 04000182-0). The authors would like to thank Mr Motoyuki Ohuchi for his technical assistance.

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