Ulvibacter litoralis gen. nov., sp. nov., a novel member of the family *Flavobacteriaceae* isolated from the green alga *Ulva fenestrata*

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Two heterotrophic, aerobic, Gram-negative, pigmented and non-motile marine bacteria that were isolated from the green alga *Ulva fenestrata* were studied by polyphasic taxonomic methods. 16S rDNA sequence analysis indicated that strain KMM 3912^T formed a distinct lineage within the family *Flavobacteriaceae*. On the basis of phenotypic, chemotaxonomic, genotypic and phylogenetic analyses, the novel bacteria were classified as *Ulvibacter litoralis* gen. nov., sp. nov. The type strain is KMM 3912^T (=KCTC 12104^T=CCUG 47093^T).

Pigmented bacteria that belong to the phylum *Cytophaga-Flavobacterium-Bacteroides* (CFB) are one of the dominant groups of the many microbial populations that inhabit different marine environments (Glöckner *et al.*, 1999; Bano & Hollibaugh, 2002; Kirchman, 2002). Despite broad application of molecular techniques to bacterial identification, study of the phenotypic properties of micro-organisms is essential for species discrimination (Vandamme *et al.*, 1996). For example, the presence of cell-bound flexirubin-type pigments is considered to be an important phenotypic characteristic for differentiation of the bacteria of the CFB phylum from each other and from other Gram-negative, non-motile micro-organisms (Fautz & Reichenbach, 1980). Six species of marine representatives of the CFB phylum, namely *Chryseobacterium indoltheticum*, *Chryseobacterium*

scophthalmum, *Zobellia galactanivorans*, *Zobellia uliginosa*, *Reichenbachia agariperforans* and *Vitellibacter vladivostokensis*, are currently known to be flexirubin-type pigment producers; they demonstrate a colony colour shift from yellow or orange to red, brown or purple after addition of 20 % KOH (Reichenbach, 1989; Vandamme *et al.*, 1994; Barbeyron *et al.*, 2001; Nedashkovskaya *et al.*, 2003a, b). During the investigation of taxonomic diversity of the microbial population of the common green alga *Ulva fenestrata* from the Sea of Japan, novel flexirubin-producing bacteria were isolated. Phylogenetic analysis based on 16S rDNA sequencing revealed that strain KMM 3912^T forms a cluster with representatives of the genera *Cellulophaga*, *Arenibacter*, *Zobellia*, *Muricauda*, *Aequorivita* and *Vitellibacter* and with [*Cytophaga*] *marinoflava*, in which it occupies a distinct lineage.

The polyphasic taxonomic study presented in this work, which includes characterization of the phenotypic, chemotaxonomic and genotypic characteristics of strains KMM 3912^T and KMM 3976 in combination with phylogenetic differences, supports the creation of a novel genus; we therefore describe a novel member of the family *Flavobacteriaceae*, designated *Ulvibacter litoralis* gen. nov., sp. nov.

Strains KMM 3912^T and KMM 3976 were isolated from samples of the green alga *Ulva fenestrata* that were collected

Published online ahead of print on 4 July 2003 as DOI 10.1099/ijs.0.02757-0.

Abbreviations: CCUG, Culture Collection University of Göteborg, Göteborg, Sweden; CFB, *Cytophaga-Flavobacterium-Bacteroides* group; KCTC, Korean Collection for Type Cultures, Korea Research Institute of Bioscience and Biotechnology, Daejeon, Republic of Korea; KMM, Collection of Marine Microorganisms of the Pacific Institute of Bioorganic Chemistry of the Far-Eastern Branch of the Russian Academy of Sciences, Vladivostok, Russia.

The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of *Ulvibacter litoralis* KMM 3912^T is AY243096.

in Troitsa Bay, Gulf of Peter the Great, Sea of Japan, during June 2000. For strain isolation, 0.1 ml homogenates of algal fronds were transferred onto plates of marine agar 2216 (Difco). After primary isolation and purification, strains were cultivated at 28 °C on the same medium and stored at -80 °C in marine broth (Difco) supplemented with 20 % (v/v) glycerol.

Oxidative or fermentative utilization of glucose was determined by using the medium of Hugh & Leifson, modified for marine bacteria (Lemos *et al.*, 1985). Catalase activity was tested by addition of 3 % (v/v) H₂O₂ solution to a bacterial colony and observation for the appearance of gas. Flexirubin pigments were detected by using the method of Fautz & Reichenbach (1980). Gram-staining reaction, degradation of alginic acids (1 %, w/v) and agar (1.5 %, w/v), oxidase, urease, alkaline phosphatase and β -galactosidase activities, production of acid from carbohydrates, hydrolysis of starch, casein, gelatin, cellulose (filter paper and CM-cellulose), chitin, Tweens 20, 40 and 80 and DNA, nitrate reduction and production of hydrogen sulphide and indole were carried out according to methods described by Smibert & Krieg (1994). To examine carbon source utilization, commercial API 20NE identification strips (bioMérieux) were used, following the instructions of the manufacturers, with a medium that contained 0.2 g NaNO₃, 0.2 g NH₄Cl, 0.05 g yeast extract (Difco) and 0.4 % (w/v) carbon source in 1000 ml artificial sea water. In order to study the temperature range for growth, bacteria were cultivated on medium A, which consisted of (l⁻¹): 5 g Bacto peptone (Difco), 2 g Bacto yeast extract (Difco), 1 g glucose, 0.02 g KH₂PO₄ and 0.05 g MgSO₄·7H₂O in 50 % (v/v) natural sea water and 50 % (v/v) distilled water. Bacterial growth at different concentrations of NaCl was checked on medium A that was prepared with distilled water and contained 0, 1, 2, 3, 5, 6, 8, 10 or 12 % (w/v) NaCl. Spreading growth was observed by cultivation on medium B, which contained (l⁻¹): 1 g Bacto peptone (Difco), 1 g yeast extract (Difco), 15 g agar and half-strength natural sea water under conditions of high moisture. Gliding motility was determined as described by Bowman (2000). Cell movement at colony edges was verified by using phase-contrast microscopy. Susceptibility to antibiotics was examined by the routine diffusion plate method. Discs were impregnated with the following antibiotics: ampicillin (10 µg), benzylpenicillin (10 µg), carbenicillin (100 µg), gentamicin (10 µg), kanamycin (30 µg), lincomycin (15 µg), neomycin (30 µg), oleandomycin (15 µg), polymyxin B (300 U), streptomycin (10 µg) and tetracycline (30 µg).

The organisms isolated in this study were Gram-negative, chemo-organotrophic with respiratory-type metabolism, non-motile, single, flexible rods that were 0.4–0.5 µm in diameter and 2.5–7.3 µm in length. Optimal growth was observed at 1.5–2 % NaCl. Temperature range for growth was 4–34 °C for KMM 3912^T and 4–36 °C for KMM 3976, with optimum growth occurring at 21–23 °C. pH range for growth was 5.5–10.0, with optimum growth occurring

between pH 7.1 and 8.3. Both strains were susceptible to carbenicillin and lincomycin and strain KMM 3912^T was also susceptible to oleandomycin and tetracycline. Other physiological and biochemical findings are listed in Table 1 and the species description.

Analysis of fatty acid methyl esters was carried out according to the standard protocol of the Microbial Identification system (Microbial ID). Cellular fatty acids of KMM 3912^T were as follows: i-C_{14:0} (1.9 %), i-C_{15:0} (21.3 %), a-C_{15:0} (2.3 %), i-C_{15:1} (12.5 %), C_{15:0} (3.9 %), C_{15:1}ω6c (1.2 %), i-C_{16:0} (2.8 %), i-C_{16:1} (4.2 %), C_{16:1}ω7/i-C_{15:0} 2-OH (5.7 %), i-C_{17:1}ω9c (3.7 %), C_{17:1}ω6c (1.5 %), C_{15:0} 2-OH (1.2 %), i-C_{15:0} 3-OH (3.3 %), C_{15:0} 3-OH (1.3 %), i-C_{16:0} 3-OH (8.7 %), i-C_{17:0} 3-OH (17.2 %), C_{17:0} 2-OH (1.7 %) and unidentified fatty acids (3.2 %). The predominant fatty acids were straight- and branched-chain unsaturated, namely, i-C_{15:0}, i-C_{15:1}, i-C_{16:0} 3-OH and i-C_{17:0} 3-OH, which represented 59.7 % of the total fatty acids. It should be noted that the whole-cell fatty acid profile of strain KMM 3912^T was characterized by the presence of 79.3 % branched fatty acids. These results are consistent with data reported for other representatives of the family *Flavobacteriaceae* (Bruns *et al.*, 2001; Nedashkovskaya *et al.*, 2003b). Isoprenoid quinones were extracted from lyophilized cells and analysed as described by Akagawa-Matsushita *et al.* (1992). Isoprenoid quinone composition was characterized by HPLC (Shimadzu), using a reverse-phase type Zorbax ODS column (250 × 4.6 mm) and acetonitrile/propan-2-ol (65:35, v/v) as the mobile phase at a flow rate of 0.5 ml min⁻¹. The column was kept at 40 °C. Menaquinones were detected by monitoring A₂₇₀ and were identified by comparison with known quinones from reference strain *Salegentibacter salegens* DSM 5424^T. The main lipoquinone was MK-6.

DNA was isolated following the method of Marmur (1961) and its G+C content was determined by the thermal denaturation method (Marmur & Doty, 1962). DNA–DNA hybridization was performed spectrophotometrically and initial renaturation rates were recorded as described by De Ley *et al.* (1970). The DNA G+C content was 36.7–38.0 mol% as determined by the thermal denaturation method. DNA–DNA relatedness between KMM 3912^T and KMM 3976 was 85 %.

DNA extraction, PCR and sequencing of 16S rDNA followed previous procedures (Kim *et al.*, 1998). The obtained sequence data were aligned with those of representative members of selected genera of the family *Flavobacteriaceae* by using PHYDIT version 3.2 (<http://plaza.snu.ac.kr/~jchun/phydit/>). Phylogenetic trees were inferred by using suitable programs of the PHYLIP package (Felsenstein, 1993). Phylogenetic distances were calculated from the models of Kimura (1980) and trees were constructed on the basis of the neighbour-joining (Saitou & Nei, 1987), least-squares (Fitch & Margoliash, 1967) and maximum-likelihood (Felsenstein, 1993) algorithms. Bootstrap analysis was performed with 1000 resampled datasets by using the SEQBOOT and CONSENSE programs of the PHYLIP package.

Table 1. Differential characteristics of *Ulvibacter litoralis* and allied genera of the family *Flavobacteriaceae*

Species/taxon: 1, *Ulvibacter litoralis*; 2, *Cellulophaga*; 3, [*Cytophaga*] *marinoflava*; 4, *Aequorivita*; 5, *Arenibacter*; 6, *Zobellia*; 7, *Muricauda*; 8, *Vitellibacter*. Data from Reichenbach (1989), Johansen *et al.* (1999), Bowman (2000), Barbeyron *et al.* (2001), Bruns *et al.* (2001), Ivanova *et al.* (2001), Bowman & Nichols (2002), Nedashkovskaya *et al.* (2003b, c) and this study. Abbreviations: –, negative; +, positive; V, variable; ND, not determined.

Characteristic	1	2	3	4	5	6	7	8
Anaerobic growth	–	–	–	–	–	–	+	–
Gliding motility	+	+	+	–	–	+	+	–
Oxidase/catalase	+ / +	+ / +	+ / +	– / +	+ / +	+ / +	+ / –	+ / +
Flexirubin pigments	+	–	–	–	–	+	–	+
Requirement for Na ⁺ for growth	+	+	–	V	+	+	+	+
Acid formation from carbohydrates	–	+	+	–	+	+	ND	–
Growth at:								
37 °C	–	V	–	–	+	+	+	+
42 °C	–	–	–	–	+	+	–	+
Hydrolysis of:								
Agar	–	+	–	–	–	+	–	–
Casein	–	V	–	V	–	+	ND	+
Gelatin	+	+	ND	+	V	+	–	+
Starch	–	+	+	–	–	+	–	–
DNA	–	+	ND	–	V	+	ND	+
Urea	–	V	ND	V	V	–	ND	–
Nitrate reduction	+	V	+	–	+	+	–	–
H ₂ S production	–	–	–	–	V	–	–	–
DNA G + C content (mol%)	36–38	33–38	37	33–39	37–40	42–43	41	41

Phylogenetic analysis of almost-complete 16S rDNA sequence (1385 nucleotide positions) revealed that strain KMM 3912^T forms a distinct lineage in a cluster that includes members of the family *Flavobacteriaceae* (Bernardet *et al.*, 2002), such as *Cellulophaga*, *Arenibacter*, *Zobellia*, *Muricauda*, *Aequorivita*, *Vitellibacter* and [*Cytophaga*] *marinoflava* (Fig. 1). 16S rDNA sequence similarity values of strain KMM 3912^T to its closest relatives, *Cellulophaga lytica*, *Cellulophaga fucicola* and [*Cytophaga*] *marinoflava*, were 92.2, 92.1 and 91.7 %, respectively. The low sequence similarity levels of the strain tested to other members of the CFB phylum that have been described to date (86.2–91.5 %) clearly demonstrate that the bacteria isolated in this study represent a novel genus. Results of phenotypic analysis, including production of flexirubin pigments and inability to oxidize carbohydrates or hydrolyse starch, in combination with phylogenetic distinctiveness, allow the differentiation of strains KMM 3912^T and KMM 3976 from their nearest neighbours, including *Cellulophaga lytica*, *Cellulophaga fucicola* and [*Cytophaga*] *marinoflava*. Phenotypic features that separate the strains studied from other members of the family *Flavobacteriaceae* are shown in Table 1.

The results of the polyphasic analysis presented in this work demonstrate that the bacteria studied could not be assigned to any currently described taxon of the family *Flavobacteriaceae* and support the placement of strains KMM 3912^T and KMM 3976 in a novel genus, *Ulvibacter* gen. nov., as *Ulvibacter litoralis* sp. nov.

Description of *Ulvibacter* gen. nov.

Ulvibacter (Ul.vi.bac'ter. N.L. fem. n. *Ulva* generic name of the green alga *Ulva fenestrata*; N.L. masc. n. *bacter* from Gr. n. *bakterion* rod; N.L. masc. n. *Ulvibacter* rod isolated from the green alga *Ulva fenestrata*).

Rod-shaped, non-motile cells. Gram-negative. Endospores are not formed. Na⁺ ions are required for growth. Strictly aerobic. Non-diffusible, yellow–orange pigments are produced. Flexirubins are formed. Chemo-organotrophic. Cytochrome oxidase-, catalase- and alkaline phosphatase-positive. Major respiratory quinone is MK-6. Main cellular fatty acids are the straight- and branched-chain unsaturated fatty acids i-C_{15:0}, i-C_{15:1}, i-C_{16:0} 3-OH and i-C_{17:0} 3-OH. As determined by 16S rDNA sequence analysis, the genus *Ulvibacter* is a member of the family *Flavobacteriaceae* within the phylum *Cytophaga–Flavobacterium–Bacteroides*. The type species is *Ulvibacter litoralis*.

Description of *Ulvibacter litoralis* sp. nov.

Ulvibacter litoralis (li.to.ra'lis. L. masc. adj. *litoralis* of the shore, a shallow-water dweller).

Main characteristics are as given for the genus. In addition, cells range from 0.4 to 0.5 µm in width and from 2.5 to 7.3 µm in length. On marine agar, colonies are 2–4 mm in diameter, circular, convex, shiny with entire edges, viscous and yellow–orange in colour. Growth is observed at 4–36 °C.

Fig. 1. Phylogenetic tree based on 16S rDNA sequences of strain KMM 3912^T and representative members of related genera in the family *Flavobacteriaceae*. The tree was generated by the neighbour-joining method (Saitou & Nei, 1987). Numbers at nodes indicate bootstrap values (%) and asterisks indicate branches that were also recovered in Fitch-Margoliash and maximum-likelihood trees. Bar, 0.01 substitutions per nucleotide position.

Optimal temperature for growth is 21–23 °C. Growth occurs at 1–6 % NaCl. Gelatin, Tweens 20 and 40 and DNA are decomposed. Agar, casein, alginate, starch, Tween 80, cellulose (CM-cellulose and filter paper) and chitin are not hydrolysed. No acid is formed from cellobiose, fucose, galactose, melibiose, raffinose, rhamnose, xylose, adonitol, dulcitol or glycerol. Arabinose, glucose, lactose, mannose, maltose, sucrose, mannitol, inositol, sorbitol, malonate, citrate, *N*-acetylglucosamine, gluconate, caprate, adipate, malate and phenylacetate are not utilized. Nitrate is reduced. Production of indole, H₂S and acetoin (Voges-Proskauer reaction) is negative. DNA G+C content is 36.7–38.0 mol%.

Type strain is KMM 3912^T (=KCTC 12104^T=CCUG 47093^T). Reference strain is KMM 3976. Isolated from the green alga *Ulva fenestrata*.

Acknowledgements

This research was supported by grant no. 95-02/03-19 from the Ministry for Industry and Science of the Russian Federation (MIS RF), the Biodiversity Programme of the Russian Academy of Science and MIS RF and grant no. 02-04-49517 from the Russian Foundation for Basic Research. K. S. B., S. K. H. and S. B. K. are also grateful for support from the Korea Research Council of Fundamental Science and Technology (grant no. KBM1000212).

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