Vibrio azureus sp. nov., a luminous marine bacterium isolated from seawater

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Two luminous marine bacterial strains, LC2-005^T and LC2-102, were isolated from seawater at Kuroshio Region and Sagami Bay in Japan, respectively. These bacteria were Gram-negative, oxidase-positive, catalase-positive, motile and rod-shaped. On the basis of 16S rRNA gene sequence analysis, strains LC2-005^T and LC2-102 formed a cluster within the *Vibrio harveyi* species group. However, multilocus sequence analysis using five loci (*pyrH*, *ftsZ*, *mreB*, *gyrB* and *gapA*) and DNA–DNA hybridization experiments indicated that these strains were distinct from the currently known *Vibrio* species. Additionally, these strains differ from related *Vibrio* species in utilization of glucose, mannitol, inositol, sorbitol, rhamnose, sucrose, melibiose and arabinose, production of lysine decarboxylase, ornithine decarboxylase, tryptophan deaminase, esterase (C4), lipase (C4), chymotrypsin, acid phosphatase, α -glucosidase, β -glucosidase and *N*-acetyl- β -glucosaminidase and the ability to reduce nitrate to nitrite. The major fatty acids were C_{15:0} iso 2-OH and/or C_{16:1} ω 7c, C_{16:0}, C_{18:1} ω 7c and C_{14:0}. The DNA G+C contents of strains LC2-005^T and LC2-102 were 45.2 and 45.5 mol%, respectively. On the basis of the polyphasic taxonomic evidence presented in this study, it can be concluded that strains LC2-005^T and LC2-102 belong to the same genospecies and represent a novel species of the genus *Vibrio*, for which the name *Vibrio azureus* sp. nov. is proposed. The type strain is LC2-005^T (=NBRC 104587^T =KCTC 22352^T).

The family *Vibrionaceae* includes six genera: *Vibrio* (Baumann & Schubert, 1984), *Photobacterium* (Baumann & Baumann, 1984), *Salinivibrio* (Mellado *et al.*, 1996), *Grimontia* (Thompson *et al.*, 2003), *Enterovibrio* (Thompson *et al.*, 2002) and *Aliivibrio* (Urbanczyk *et al.*, 2007). Several species of the genus *Vibrio* are ubiquitous in aquatic environments, especially the ocean, and are often isolated from various organisms ranging from plankton to fish (Thompson *et al.*, 2004). Seven species in this genus contain luminous strains: *Vibrio cholerae* (Palmer & Colwell, 1991), *Vibrio harveyi* (Reichelt & Baumann, 1973), *Vibrio campbellii* (Gomez-Gil *et al.*, 2004), *Vibrio mediterranei* (Pujalte & Garay, 1986), *Vibrio orientalis*

(Yang *et al.*, 1983), *Vibrio splendidus* (biotype I) (Nealson *et al.*, 1993) and *Vibrio vulnificus* (Oliver *et al.*, 1986).

Two luminescent bacterial strains, LC2-005^T and LC2-102, were isolated from seawater. To determine their taxonomic position, the 16S rRNA gene and the genes encoding uridylyl transferase (*pyrH*), a cell-division protein (*ftsZ*), a rod-shaping protein (*mreB*), DNA gyrase B subunit (*gyrB*) and glyceraldehyde-3-phosphate dehydrogenase (*gapA*) were analysed (Thompson *et al.*, 2007). Based on the phylogenetic analysis, these strains formed a tight cluster in which no type strain of a known *Vibrio* species is grouped. This suggests that the isolates represent a novel species of the genus *Vibrio*. Therefore, we conducted a series of analyses to identify these isolates.

Strains LC2-005^T and LC2-102 were isolated from seawater samples obtained from Kuroshio Region (32° 30' N 138° 00' E; depth, 200 m) and Sagami Bay (35° 00' N 139° 20' E; depth, 30 m) during cruises KT-05-16 (13–21 July 2005) and KT-05-31 (30 November–5 December 2005) of RV 'Tansei Maru' [Ocean Research Institute, University of Tokyo, and Japan Agency for Marine-Earth Science and

Abbreviation: MLSA, multilocus sequence analysis.

The GenBank/EMBL/DDBJ accession numbers for the 16S rRNA, *gyrB*, *pyrH*, *ftsZ*, *mreB* and *gapA* gene sequences of strains NBRC 104587^T and NBRC 104588 determined in this study are AB428897–AB428908 (see Supplementary Table S1, available with the online version of this paper).

Two supplementary tables and eight supplementary figures are available with the online version of this paper.

Technology (JAMSTEC)], respectively. The samples were filtered through a polycarbonate filter (pore size of 0.2 µm) (Whatman), which was then placed on half-strength marine agar 2216E (Difco) and kept at 20 °C. Luminous colonies grown on the agar plate were isolated with sterile toothpicks, utilizing a CCD camera (Atto Bioscience and Technology), and transferred to new marine agar 2216E plates for reisolation. Bacterial cultures of the isolates and reference strains were stored at –80 °C in marine broth containing 20 % (v/v) glycerol.

Cell morphology and flagella were observed by using atomic force microscopy (model SPM-9500 J2; Shimadzu) as described previously (Nishino *et al.*, 2004). The temperature range for growth was determined by incubating the isolates on marine agar 2216E (Difco). Growth at different NaCl concentrations [0.5–10.0 % (w/v)] was determined on tryptone soya agar (Difco). Catalase activity was determined by bubble formation in a 3 % H₂O₂ solution. Oxidase activity was determined by using cytochrome oxidase paper (Nissui Pharmaceutical). API 20E and API ZYM strips (bioMérieux) were used to determine physiological and biochemical characteristics, and were read after 48 and 6 h incubation at 20 °C, respectively. All suspension media for API test strips were supplemented with 2 % (w/v) NaCl solution. Cellular fatty acid composition (MIDI system) was determined as described previously (Xie & Yokota, 2003). The cells were grown for 48 h at 20 °C on plates of marine agar 2216E.

DNA was prepared according to the method of Marmur (1961) from cells grown on marine agar 2216E and the DNA base composition was determined by using HPLC (Mesbah *et al.*, 1989). DNA–DNA hybridizations were carried out with photobiotin-labelled probes in microplate wells as described by Ezaki *et al.* (1989). Quality and quantity of DNA were determined by measuring A₂₆₀ and A₂₈₀. Only high-quality DNA with an A₂₆₀/A₂₈₀ ratio of 1.8–2.0 was used. The hybridization temperature was set at 43 °C. Hybridizations were performed, using five replications for each. The highest and lowest values obtained were excluded and the mean of the remaining three values was quoted as the DNA–DNA relatedness value.

A fragment (approx. 1500 bp) of the 16S rRNA gene was amplified from the extracted DNA by using bacterial universal primers specific to the 16S rRNA gene (27F and 1492R) (Lane, 1991). The *pyrH*, *ftsZ*, *mreB*, *gyrB* and *gapA* genes were used for multilocus sequence analysis (MLSA) (Thompson *et al.*, 2007). PCR primers for the five genetic loci and reaction conditions were used according to Sawabe *et al.* (2007). To test the evolutionary relationships of the genus *Vibrio*, phylogenetic analysis was performed with the program MEGA 3.1 (Kumar *et al.*, 2004) and PHYLIP 3.67 software, developed by Dr Joe Felsenstein (<http://evolution.genetics.washington.edu/phylip.html>). Multiple alignments of the sequences were performed using CLUSTAL W (version 1.6) (Thompson *et al.*, 1994). Distances were calculated by using the Kimura two-parameter model

(Kimura, 1980). Clustering based on the neighbour-joining (Saitou & Nei, 1987), maximum-parsimony and maximum-likelihood methods was determined by using bootstrap values based on 1000 replications (Felsenstein, 1985). Sequence data of other *Vibrio* species from the online taxonomic scheme for vibrios (<http://www.taxvibrio.lncc.br>) and GenBank were used in this study.

16S rRNA gene sequence analysis using the neighbour-joining, maximum-parsimony and maximum-likelihood methods indicated that strains LC2-005^T and LC2-102 belong to the genus *Vibrio* and are included in the *V. harveyi* clade (Sawabe *et al.*, 2007) (Fig. 1; Supplementary Fig. S1 in IJSEM Online). The closest phylogenetic neighbours were *Vibrio parahaemolyticus* ATCC 17802^T (16S rRNA gene sequence similarity, 99.8 %), *Vibrio natriegens* ATCC 14048^T (99.8 %) and *Vibrio alginolyticus* LMG 4409^T (99.7 %) and the closest neighbours belonging to luminous species were *V. campbellii* ATCC 25920^T (99.7 %) and *V. harveyi* ATCC 14126^T (99.6 %). DNA–DNA hybridization values between strain LC2-005^T and other *Vibrio* species were 23.2 % (*V. parahaemolyticus* NBRC 12711^T), 23.0 % (*V. natriegens* ATCC 14048^T), 24.2 % (*V. alginolyticus* ATCC 17749^T), 20.0 % (*V. campbellii* ATCC 25920^T) and 21.4 % (*V. harveyi* NBRC 15634^T). The DNA–DNA hybridization value between strains LC2-005^T and LC2-102 was 85.2 %.

The phylogenetic trees based on *pyrH*, *ftsZ*, *mreB*, *gyrB* and *gapA* gene sequences confirmed the clustering of strains LC2-005^T and LC2-102, with a bootstrap value of 100 %, and their distinction from their closest phylogenetic neighbours *V. parahaemolyticus*, *V. natriegens*, *V. alginolyticus*, *V. campbellii*, *V. harveyi* and *Vibrio rotiferianus*. Similarities between *pyrH* gene sequences ranged between 90 % (LC2-005^T and *V. rotiferianus* LMG 21460^T) and 85 % (LC2-005^T and *V. parahaemolyticus* LMG 2850^T). Similarities between *ftsZ* gene sequences ranged between 84 % (LC2-005^T and *V. parahaemolyticus* LMG 2850^T) and 81 % (LC2-005^T and *V. alginolyticus* LMG 4409^T). Similarities between *mreB* gene sequences ranged between 79 % (LC2-005^T and *V. campbellii* LMG 11216^T) and 77 % (LC2-005^T and *V. alginolyticus* LMG 4409^T). Similarities between *gyrB* gene sequences ranged between 92 % (LC2-005^T and *V. rotiferianus* LMG 21460^T) and 83 % (LC2-005^T and *V. alginolyticus* LMG 4409^T). Similarities between *gapA* gene sequences ranged between 92 % (LC2-005^T and *V. parahaemolyticus* LMG 2850^T) and 90 % (LC2-005^T and *V. alginolyticus* LMG 4409^T). All phylogenetic trees are shown in Supplementary Figs S2–S6 in IJSEM Online. Phylogenetic analysis using MLSA (*pyrH*, *ftsZ*, *mreB*, *gyrB* and *gapA* genes) revealed that the two strains belong to a novel species in this genus (Fig. 2). A further phylogenetic tree using MLSA (16S rRNA, *pyrH*, *ftsZ*, *mreB*, *gyrB* and *gapA* genes) is shown in Supplementary Fig. S7 in IJSEM Online. These results demonstrate that strain LC2-005^T is distinct from any recognized species of the genus *Vibrio*. The DNA G + C contents of strains LC2-005^T and LC2-102 were 45.2 and 45.5 mol%, respectively.

Fig. 1. Phylogenetic tree based on the neighbour-joining method, using partial 16S rRNA gene sequences. Bootstrap values are expressed as percentages of 1000 replications; only values >50 % are shown. *Alteromonas macleodii* was used as an outgroup. Bar, 1 % estimated sequence divergence.

Both isolates are luminous, and form green colonies on thiosulfate–citrate–bile–sucrose (TCBS) agar and unpigmented, translucent colonies on marine agar. On the basis of the API 20E and API ZYM tests, the two strains can be discriminated from other *Vibrio* species. In contrast to most of their phylogenetic neighbours, these strains cannot reduce nitrates to nitrites, cannot produce lysine decarboxylase, ornithine decarboxylase, tryptophan deaminase, esterase (C4), lipase (C4), chymotrypsin, acid phosphatase, α -glucosidase, β -glucosidase or *N*-acetyl- β -glucosaminidase and cannot utilize mannitol, inositol, sorbitol or sucrose (Table 1).

The predominant cellular fatty acids of strains LC2-005^T and LC2-102 are C_{15:0} iso 2-OH and/or C_{16:1} ω 7c (37.7 and 41.3 %, respectively), C_{18:1} ω 7c (18.5 and 8.4 %), C_{16:0} (15.8 and 16.8 %) and C_{14:0} (6.1 and 9.3 %). For other fatty acids, see Supplementary Table S2 in IJSEM Online and the species description, but no clear differences from type strains of related species in the genus *Vibrio* were observed.

Morphological, cultural, physiological and biochemical characteristics of strain LC2-005^T are given in the species description or are shown in Table 1 and Supplementary Fig. S8 (available in IJSEM Online). These results show that strain LC2-005^T is related closely to the *V. harveyi* clade, but can be differentiated from closely related species based on phylogenetic analysis, DNA–DNA similarity and several phenotypic traits. The new strains can also be differentiated from all known *Vibrio* species based on a combination of physiological characteristics: luminescence, production of

protease and decarboxylase, and nitrate reduction. Therefore, strains LC2-005^T and LC2-102 should be identified as members of a novel species in the genus *Vibrio*, for which the name *Vibrio azureus* sp. nov. is proposed.

Description of *Vibrio azureus* sp. nov.

Vibrio azureus (a.zur'e.us. N.L. masc. adj. *azureus* azure blue, referring to the colour of emitted light).

Gram-negative, oxidase-positive, catalase-positive and motile by means of more than one polar flagellum. Non-pigmented, translucent, luminescent colonies with weak swarming are formed on marine agar. Round, 5–7 mm green colonies are formed on TCBS agar. Growth occurs in the presence of 0.5, 2.0, 3.5 and 6.0 % NaCl (w/v), but not at 8.0 or 10.0 % NaCl; growth occurs at 10–37 °C, but not at 4 °C. Positive for indole production and fermentation of glucose and amygdalin. Positive enzyme activities are seen for protease, alkaline phosphatase, esterase lipase (C8), leucine arylamidase, naphthol-AS-BI-phosphohydrolase and *N*-acetyl- β -glucosaminidase. Major fatty acids are C_{15:0} iso 2-OH and/or C_{16:1} ω 7c, C_{18:1} ω 7c, C_{16:0}, C_{14:0}, C_{12:0}, C_{17:1} ω 8c, C_{16:1} iso I and/or C_{14:0} 3-OH, C_{15:0}, C_{18:0}, C_{17:0}, C_{16:0} ω 7c alcohol and C_{12:0} 3-OH. The DNA G + C content of the type strain is 45.2 mol%.

The type strain is LC2-005^T (=NBRC 104587^T =KCTC 22352^T), isolated from seawater of Kuroshio Region, Japan. Reference strain is LC2-102 (=NBRC 104588 =KCTC 22353).

Fig. 2. Phylogenetic tree based on the concatenated gene sequences of the five loci (2452 bp). This tree combines the results of both the neighbour-joining (NJ) and maximum-parsimony (MP) methods. The topology shown was obtained by using the NJ method. Numbers at nodes denote the level of bootstrap support (%) based on 1000 replicates (NJ/MP). *Photobacterium leiognathi* was used as an outgroup. Bar, 2% sequence divergence.

Table 1. Differential phenotypic characteristics of *Vibrio azureus* sp. nov. and related species of the genus *Vibrio*

Taxa: 1, strain LC2-005^T; 2, strain LC2-102; 3, *V. parahaemolyticus* NBRC 12711^T; 4, *V. alginolyticus* ATCC 17749^T; 5, *V. harveyi* NBRC 15634^T; 6, *V. campbellii* ATCC 25920^T; 7, *V. natriegens* ATCC 14048^T. +, Positive; w, weakly positive; –, negative; G, green; Y, yellow.

Characteristic	1	2	3	4	5	6	7
Luminescence	+	+	–	–	+	–	–
Production of:							
Lysine decarboxylase	–	–	–	+	+	–	–
Ornithine decarboxylase	–	–	+	–	–	–	–
Tryptophan deaminase	–	–	–	+	w	w	+
Esterase (C4)	–	–	w	–	–	w	–
Lipase (C4)	–	–	–	w	–	w	–
Chymotrypsin	–	–	–	–	–	+	–
Acid phosphatase	–	–	+	+	+	–	+
α -Glucosidase	–	–	w	w	w	–	+
<i>N</i> -Acetyl- β -glucosaminidase	+	w	–	w	–	–	–
Citrate utilization	–	–	–	+	–	–	–
Indole production	w	+	+	+	+	+	–
Reduction of nitrate to nitrite	–	–	+	+	+	–	+
Fermentation of:							
Glucose	w	w	+	+	w	–	w
Mannitol	–	–	+	+	+	+	+
Inositol	–	–	w	w	w	w	w
Sorbitol	–	–	w	w	–	w	w
Rhamnose	–	–	–	–	–	–	+
Sucrose	–	–	w	+	+	+	+
Melibiose	–	–	–	–	w	w	w
Arabinose	–	–	–	w	–	–	+
Growth in NaCl (% w/v):							
8	–	–	w	+	–	–	+
10	–	–	–	w	–	–	–
Colony colour on TCBS agar	G	G	G	Y	Y	–*	Y
DNA G + C content (mol%)	45.2	45.5	46–47†	45–47†	46–48†	46–48†	45.1–47.0†

**V. campbellii* could not grow on TCBS agar.

†Data were described by Farmer *et al.* (2005).

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