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Shewanella affinis sp. nov., isolated from marine invertebrates

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Four marine bacterial strains, designated KMM 3587^T, KMM 3586, KMM 3821 and KMM 3822, were isolated from the sipuncula *Phascolosoma japonicum*, a common inhabitant of Troitza Bay in the Gulf of Peter the Great (Sea of Japan region), and from an unidentified hydrocoral species collected in Makarov Bay (Iturup Islands), Kuril Islands, North-West Pacific Ocean. The strains were characterized to clarify their taxonomic position. 16S rRNA gene sequences of KMM 3587^T and KMM 3586 indicated 99 % similarity to *Shewanella colwelliana*. Despite such a high level of 16S rRNA gene sequence similarity, DNA–DNA hybridization experiments demonstrated only 45–52 % binding with DNA of *S. colwelliana* ATCC 39565^T. The DNA G + C contents of the novel strains were 45 mol% and the shared level of DNA hybridization was conspecific (81–97 %), indicating that they represent a single genospecies. The novel strains were mesophilic (able to grow at 10–34 °C), neutrophilic and haemolytic, and able to degrade gelatin, casein and Tween 20, 40 and 80, but not starch, agar, elastin, alginate or chitin. The major fatty acids were i13 : 0, i15 : 0, 16 : 0, 16 : 1ω7 and 17 : 1ω8 (68·9 % of total). The major isoprenoid quinones were Q7 (47–62 %) and Q8 (26–47 %). Eicosapentaenoic acid was produced in minor amounts. Based on these data, the strains are assigned to a novel species, *Shewanella affinis* sp. nov. (type strain KMM 3587^T = CIP 107703^T = ATCC BAA-642^T).

The genus *Shewanella* MacDonell and Colwell 1986 comprises an ubiquitous group of Gram-negative, aerobic and facultatively anaerobic γ-*Proteobacteria* (MacDonell & Colwell, 1985; Gauthier *et al.*, 1995; Venkateswaran *et al.*, 1999; Garrity & Holt, 2001; Satomi *et al.*, 2003). This study involved the characterization of four *Shewanella*-like bacteria that shared high levels of 16S rRNA gene sequence similarity (99 %) with *Shewanella colwelliana* (Ivanova *et al.*, 2003b). One strain, KMM 3587^T, was isolated from the benthic marine 'peanut worm' (*Phascolosoma japonicum*; phylum *Sipuncula*), collected in 1997 from a depth of 3–5 m (salinity 32 ‰; temperature 18 °C) at the Pacific Institute of Bio-organic Chemistry Marine Experimental Station, in Troitza Bay, Gulf of Peter the Great (Sea of Japan region). Three other strains (KMM 3586, KMM 3821 and KMM 3822) were isolated from an unidentified hydrocoral collected from Makarov Bay, Iturup Islands (Kuril Islands), North-West Pacific Ocean from a depth of 120 m (salinity 33 ‰; temperature 6 °C). The procedures for invertebrate handling and strain isolation have been described elsewhere (Ivanova *et al.*, 1996, 2003a, b). All

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The GenBank/EMBL/DDBJ accession numbers for the 16S rRNA gene sequences of strains KMM 3587^T and KMM 3586 are AY351983 and AF500080, respectively.

Tables showing the cellular fatty acid composition and isoprenoid quinone composition of *Shewanella affinis* are available in IJSEM Online.

strains were incubated on marine agar 2216 (Difco) or medium B, which contained: 0·2 % (w/v) Bacto peptone (Difco); 0·2 % (w/v) casein hydrolysate (Merck); 0·2 % (w/v) Bacto yeast extract (Difco); 0·1 % (w/v) glucose; 0·02 % (w/v) KH_2PO_4; 0·005 % (w/v) $MgSO_4.7H_2O$; 1·5 % (w/v) Bacto agar (Difco); 50 % (v/v) natural sea water; and 50 % (v/v) distilled water at pH 7·8. Agar plates were incubated aerobically at room temperature (about 22–25 °C) for 5–10 days. The strains were stored at −80 °C in marine broth 2216 (Difco) supplemented with 20 % (v/v) glycerol.

Unless otherwise indicated, the phenotypic characteristics were studied using standard procedures (Baumann *et al.*, 1972; Smibert & Krieg, 1994) as described elsewhere (Ivanova *et al.*, 1996, 1998, 2003a; Sawabe *et al.*, 1998). The following physiological and biochemical properties were examined: oxidation/fermentation of glucose, denitrification, catalase and oxidase activities, gelatin liquefaction, arginine dihydrolase, lysine decarboxylase, ornithine decarboxylase, indole and H_2S production, and the ability to hydrolyse starch, alginate, chitin, elastin, Tween 20, 40 and 80, and casein. The requirement for Na^+ ions was studied on a medium containing (w/v): 0·25 % yeast extract; 0·1 % glucose; 0·02 % K_2HPO_4; and 0·005 % $MgSO_4.7H_2O$ (pH 7·8). Salt tolerance tests were performed on trypticase soy agar (TSA; Difco) with NaCl concentrations of 0·6–20·0 % (w/v). Dissimilatory iron reduction was tested on LM medium [0·02 % (w/v) yeast extract, 0·01 % (w/v) peptone, 0·6 % (w/v) NaCl, 10 mM sodium bicarbonate and 10 mM HEPES] supplemented with carbon substrates as appropriate (5 mM lactate, 5 mM succinate, 5 mM glycerol, 1 mM acetate), 50 mM ferric citrate, 5 mM sodium molybdate and the colour reagent ferrozine [3-(2-pyridyl)-5,6-bis(4-phenylsulfonic acid)-1,2,4 triazine, pH 7·2] in distilled water. Plates were inoculated and incubated anaerobically at room temperature (for approx. 7 days) with positive and negative controls. Colonies displaying cleared zones were scored as positive for iron reduction. Haemolytic activity of the strains studied was detected on blood agar (40 g TSA in 50 ml sheep blood and 950 ml water). Haemolytic activity on mouse erythrocytes and cytotoxicity on Ehrlich cells were tested on butanol extracts of the strains as described earlier (Ivanova *et al.*, 2001). Antimicrobial activity was assessed by the agar diffusion assay, based on the method described by Barry (1980). Cultures (0·1 ml) of indicator test strains were spread onto TSA plates in which circular wells (10 mm diameter) had been cut. Samples (0·1 ml) of butanol extracts of the isolates were added to the wells and areas of inhibited bacterial growth were measured after incubation for 48 h at 28 °C. Zones of inhibited growth of the indicator strains surrounding the wells were observed. Mean diameters were measured and 10 mm was subtracted (representing the diameter of the well). Indicator test strains used were *Staphylococcus aureus* CIP 103594, *Escherichia coli* ATCC 15034, *Proteus vulgaris* IFO 3851^T, *Enterococcus faecium* CIP 104105, *Bacillus subtilis* ATCC 6051^T and the yeast *Candida albicans* KMM 455. Susceptibility to antibiotics was tested by the conventional diffusion plate technique using medium B agar and discs impregnated with the following antibiotics: kanamycin (10 μg), ampicillin (10 μg), benzylpenicillin (10 μg), streptomycin (10 μg), erythromycin (15 μg), gentamicin (10 μg), oxacillin (20 μg), lincomycin (15 μg), carbenicillin (25 μg), vancomycin (30 μg), tetracycline (30 μg), oleandomycin (15 μg) and O/129 (150 μg). Phenotypic analysis showed that all isolates were essentially identical to each other, exhibited haemolytic, but not cytotoxic or antimicrobial activities, and differed only in their ability to produce acid from arabinose and maltose and their susceptibility to some antibiotics: KMM 3587^T, KMM 3821 and KMM 3822 were susceptible to oleandomycin, whereas KMM 3586 was not; and KMM 3586 and KMM 3821 were also susceptible to carbenicillin, whereas the rest of the strains were not. The results of analysis of morphological and physiological properties are given in Table 1 and in the species description.

Table 1. Characteristics that differentiate *Shewanella affinis* from phylogenetically related species

Species: 1, *Shewanella affinis*; 2, *Shewanella colwelliana*; 3, *Shewanella fidelis*; 4, *Shewanella pealeana*; 5, *Shewanella marinintestina*; 6, *Shewanella schlegeliana*; 7, *Shewanella sairae*; 8, *Shewanella gelidimarina*; 9, *Shewanella waksmanii*; 10, *Shewanella frigidimarina*. All strains are Gram-negative, motile, rod-shaped organisms that are oxidase- and catalase-positive and can reduce nitrate to nitrite. V, Variable reaction depending on the strain; ND, data not available. Data from this study, Weiner *et al.* (1988), Bowman *et al.* (1997), Nogi *et al.* (1998), Venkateswaran *et al.* (1999), Skerratt *et al.* (2002), Satomi *et al.* (2003) and Ivanova *et al.* (2003a).

Characteristic	1	2	3	4	5	6	7	8	9	10
G+C content (mol%)	45	46	45	45	43	45	43	48	43	40–43
Pigments	−	−	−	−	−	−	−	−	+	−
Growth at:										
4 °C	−	+	+	+	−	−	−	+	+	+
32 °C	+	−	+	+	−	+	−	−	+	−
0 % NaCl	−	−	+	−	−	−	−	−	−	+
6 % NaCl	+	−	+	+	−	−	−	+	+	+
Haemolysis	+	−	+	−	ND	ND	ND	−	+	ND
Production of:										
Lipase	+	+	V	+	+	−	+	+	+	+
Amylase	−	+	−	−	−	−	−	−	−	−
Gelatinase	+	+	+	−	+	+	+	+	+	+
Chitinase	−	−	−	−	−	−	−	+	−	−
Utilization of:										
D-Galactose	−	−	−	+	−	−	−	−	−	+
DL-Lactate	−	−	−	+	−	−	−	+	−	+
Succinate	−	−	−	+	−	−	−	−	−	−
Citrate	−	−	−	+	−	−	−	−	−	−

Analysis of fatty acid methyl esters was performed by GLC as described previously by Svetashev *et al.* (1995). Isoprenoid quinones were extracted from lyophilized cells and analysed as described by Moule & Wilkinson (1987) and elsewhere (Ivanova *et al.*, 2003b). The cellular fatty acid profile was typical for *Shewanella* and included saturated, monoenoic, monounsaturated, straight-chain and iso-branched components, namely (%±SD): i13 : 0 (6·7±3·4); i15 : 0 (20·1±10·0); 15 : 0 (6·8±1·6); 16 : 0 (6·9±4·3); 16 : 1ω7 (21·5±5·6); and 17 : 1ω8 (14·1±4·6) (see supplementary material in IJSEM Online). The strains produced up to 2·1 % of their total fatty acids as 20 : 5ω3 (eicosapentaenoic fatty acid) when grown at 28 °C.

The almost-complete 16S rRNA gene sequences for KMM 3587^{T}and KMM 3586 were amplified and sequenced as described elsewhere (Ivanova *et al.*, 2001, 2003a, b) and compared to the GenBank nucleotide database using online BLAST searches. 16S rRNA gene sequences of *Shewanella* species (if available) were aligned and analysed in the program BIOEDIT using PHYLIP version 3.57c (Felsenstein, 1993). DNADIST was used to determine sequence similarities using the maximum-likelihood algorithm option. Phylogenetic trees were constructed with the neighbour-joining method using the program NEIGHBOR. The outgroup on the *Shewanella* trees was *Psychromonas antarctica* DSM 10704^{T} (GenBank accession no. Y14697). According to phylogenetic analysis, strains KMM 3587^{T} and KMM 3586 formed a cluster with *S. colwelliana* ATCC 33888 and shared high (99 %) 16S rRNA gene sequence similarity (Fig. 1).

DNA was extracted from cells grown overnight on medium B following the method of Marmur (1961). DNA–DNA hybridization was performed spectrophotometrically and initial renaturation rates were recorded as described elsewhere (Marmur & Doty, 1962; De Ley *et al.*, 1970; Bowman *et al.*, 1998). The G+C content of the DNA ranged from 45·2±0·5 to 45·4±0·3 mol%. DNA–DNA hybridization data revealed high intraspecies levels of DNA relatedness among the four strains (81–97 %). *S. colwelliana* ATCC 39565^{T} was obtained from the American Type Culture Collection. DNA hybridization analysis indicated that hybridization between DNA of *S. colwelliana* ATCC 39565^{T} and the novel isolates was 45–52 %. This clearly indicates that the strains investigated in this study belong to the same genospecies, but are separate (Wayne *et al.*, 1987; Stackebrandt & Goebel, 1994) from *S. colwelliana*, which is also derived from an invertebrate, the eastern oyster (*Crassostrea virginica*) (Coyne *et al.*, 1989). Thus, levels of genetic relatedness according to DNA–DNA hybridization experiments were less than 70 %, which leads to the conclusion that the isolates represent a novel and distinct species. Strains of the novel species can be phenotypically, chemotaxonomically and genetically distinguished from other species, in particular from *S. colwelliana*, by a combination of phenotypic traits listed in Table 1, including

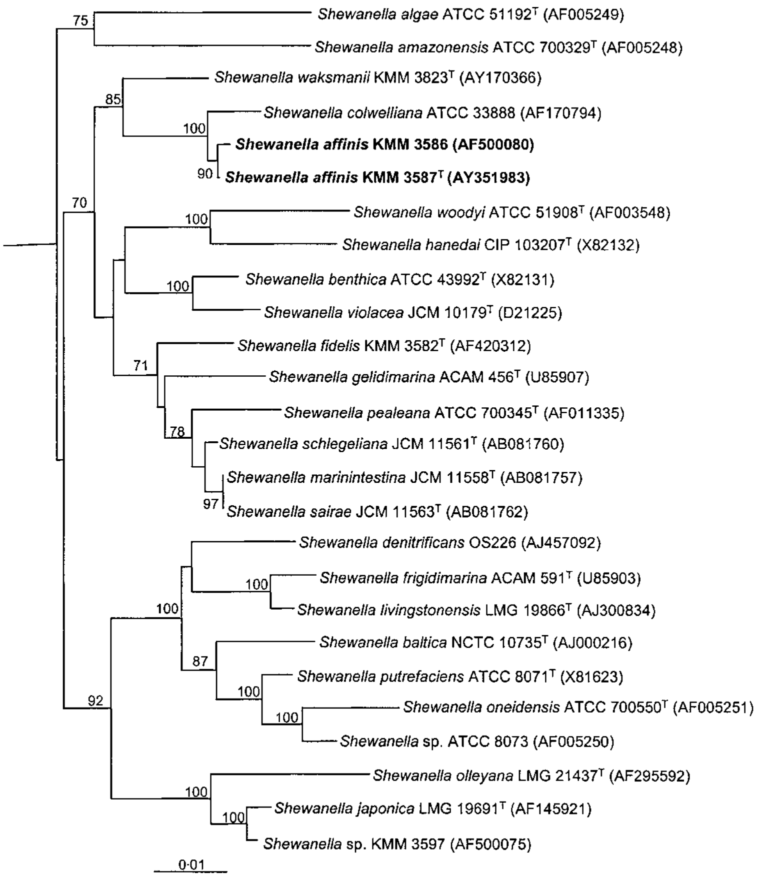

Fig. 1. Phylogenetic position of *Shewanella affinis* according to 16S rRNA gene sequence analysis. The tree was generated from maximum-likelihood distances clustered by the neighbour-joining method. Bootstrap values, expressed as a percentage of 1000 replications, are given at branching points.

pigmentation, different growth temperatures, tolerance to 6 % NaCl, haemolytic ability, lack of amylase activity, different Biolog substrate utilization pattern and cellular fatty acid profile.

Description of *Shewanella affinis* sp. nov.

Shewanella affinis (af.fi′nis. L. fem. adj. *affinis* adjoining, a novel bacterium that has joined the genus *Shewanella*).

Cells are rod-shaped, 1·0–2·0 × 0·6–0·8 μm and polarly flagellated, although some strains are non-flagellated. Gram-negative, facultatively anaerobic heterotroph. Anaerobic growth occurs by fermentation of D-glucose by anaerobic respiration of nitrate. No endospores are formed. Colonies on marine agar 2216 are circular, smooth, convex with an entire edge and slightly pinkish. Organic growth factors are not required. Has an absolute requirement for Na^+ ions and grows in 0·5–6·0 % NaCl; some strains (KMM 3821 and KMM 3822) grow in 8 % NaCl. Temperature of growth is 10–34 °C; optimum growth occurs at 20–25 °C and no growth is detected at 37 °C. Oxidase- and catalase-positive. Reduces nitrate to nitrite. Arginine dihydrolase and lysine decarboxylase are not detected. Haemolytic. Has esterase (Tween 20, 40, 80) and proteinase (caseinase, gelatinase) activities, whereas amylase, alginase, elastinase, agarase and chitinase activities are not found. H_2S is formed from thiosulfate anaerobically. Indole is not formed from L-tryptophan. Voges–Proskauer test is negative. D-Glucose is utilized as sole source of carbon. Susceptible to gentamicin; some strains susceptible to oleandomycin, kanamycin and streptomycin (see text). Utilizes limited range of carbon sources according to Biolog: DL-lactic acid and L-asparagine. Weakly utilizes methyl β-D-glucoside, D-psicose, D-raffinose, sucrose, turanose, succinic acid monomethyl ester, acetic acid, *cis*-aconitic acid, L-ornithine, L-serine, 2-aminoethanol, 2,3-butanediol, DL-α-glycerol phosphate and D-glucose 6-phosphate. The major cellular fatty acids are i13 : 0, i15 : 0, 16 : 0, 16 : 1ω7 and 17 : 1ω8 (68·9 % of total). The major isoprenoid quinones are Q7 (47–62 %) and Q8 (26–47 %). Eicosapentaenoic fatty acid (20 : 5ω3) is produced in minor amounts. Isolated from benthic marine worms of the species *Phascolosoma japonicum* collected in Troitza Bay, Gulf of Peter the Great (Sea of Japan region) and from a hydrocoral species collected in the Kuril Islands (Makarov Bay, Iturup Islands) North-West Pacific Ocean. DNA G + C content is 45·2 ± 0·5 to 45·4 ± 0·3 mol%.

Type strain is KMM 3587^T (= CIP 107703^T = ATCC BAA-642^T).

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