Shewanella corallii sp. nov., a marine bacterium isolated from a Red Sea coral

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A marine bacterial strain, designated fav-2-10-05^T, was isolated from the mucus layer of a coral of the genus *Favia*, collected from the coral reef in the Gulf of Eilat, Israel (29.51° N 34.94° E). On the basis of 16S rRNA gene sequence comparisons, strain fav-2-10-05^T was affiliated with the family *Shewanellaceae*. The closest relatives of strain fav-2-10-05^T were *Shewanella marisflavi* SW-117^T (96.0 % 16S rRNA gene sequence similarity) and *Shewanella haliotis* DW-1^T (95.9 %). Strain fav-2-10-05^T was Gram-negative, rod-shaped and motile by means of a single polar flagellum and formed yellow–brownish colonies within 2 days of incubation at 26 °C. Strain fav-2-10-05^T demonstrated antibacterial activity against indicator strains and grew in the presence of 0.5–8.0 % (w/v) NaCl and at 10–37 °C. The major fatty acids were C_{17:1ω8c} (21.6 %), iso-C_{15:0} (18.6 %), C_{15:0} (9.1 %) and iso-C_{13:0} (8.9 %). The DNA G + C content was 49.1 mol%. The phylogenetic and phenotypic analyses of strain fav-2-10-05^T suggested that it belongs to a novel species of the genus *Shewanella*, for which the name *Shewanella corallii* sp. nov. is proposed. The type strain is fav-2-10-05^T (=LMG 24563^T =DSM 21332^T).

The genus *Shewanella* (family *Shewanellaceae*, order *Alteromonadales*, class *Gammaproteobacteria*) was first described by MacDonell & Colwell (1985) to accommodate Gram-negative, rod-shaped, facultatively anaerobic gamma-proteobacteria. Members of this genus are frequently isolated from aquatic environments and the genus comprises mesophilic and psychrotolerant species (Miyazaki *et al.*, 2006). To date, at least 50 *Shewanella* species have been recognized (Euzéby, 2007).

Although the genus *Shewanella* has been studied over the last three decades, little is known of the antibacterial properties of its members. Indeed, only a few taxonomic studies have included tests of antimicrobial activity. Among strains of the genus *Shewanella* that have been found to possess antimicrobial activity, *Shewanella algae* OK-1^T produced tetrodotoxin, a strong neurotoxin (Simidu *et al.*, 1990), and five *Shewanella* strains isolated from a fish farm tank wall were antagonistic against two larval-pathogenic strains (Hjelm *et al.*, 2004). The *Shewanella* strains studied by Ivanova *et al.* (2003) demonstrated weak antimicrobial and antifungal activities and, similarly, Barbieri *et al.* (1997) reported weak antimicrobial activity for *Shewanella pealeana*

(Leonardo *et al.*, 1999). Moreover, it has been hypothesized that tetrodotoxin-producing *Shewanella* strains may serve a protective role in the marine environment, such as benefiting the eggs of squids of the genus *Loligo* (Barbieri *et al.*, 2001; Hau & Gralnick, 2007). In a recent study, coral mucus-associated bacteria were isolated and screened for antibacterial activity (Shnit-Orland & Kushmaro, 2009). Strain fav-2-10-05^T originated from a scleractinian coral of the genus *Favia* and demonstrated antibacterial activity against a Gram-positive indicator strain (Shnit-Orland & Kushmaro, 2009). According to 16S rRNA gene sequence similarity, strain fav-2-10-05^T was found to belong to the genus *Shewanella*. This study further describes its taxonomic position.

Coral mucus samples were collected as described by Barneah *et al.* (2007) from the reef adjacent to the Inter-University Institute for Marine Science in the Gulf of Eilat, Red Sea, Israel (29.51° N 34.94° E), in March 2005. After serial dilution and plating, strain fav-2-10-05^T was isolated on 10 % marine agar 2216 (MA; HiMedia Laboratories) prepared with artificial seawater after 2–5 weeks of incubation at room temperature. A pure culture was obtained by subcultivation under the same conditions. Screening for antibacterial activity was performed using the drop technique, as detailed by Shnit-Orland & Kushmaro

The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain fav-2-10-05^T is FJ041083.

(2009). Further subcultivation was performed on 50 % MA prepared with artificial seawater at 26 °C. The strain was maintained as viable cultures on plates at room temperature and stored as 20 % (v/v) glycerol suspensions at –80 °C.

Gram-staining of strain fav-2-10-05^T was performed using a Gram-stain kit (Sigma Diagnostics). For scanning electron microscopy, cells were placed on 300-mesh copper grids coated with Formvar and carbon and left to be absorbed for 3 min. Negative staining was achieved with 2 % (w/v) ammonium molybdate (Riedel-deHaen) for 1 min, with no washing during the staining process and removal of excess liquid with filter paper placed close to the grid. Negatively stained cells were examined using a JEM-1230 scanning electron microscope (JEOL) with an acceleration voltage of 120 kV. Strain fav-2-10-05^T was characterized biochemically using the API 20NE and API ZYM systems (bioMérieux), according to the manufacturer's instructions. Haemolytic activity was tested on tryptic soy blood agar containing 5 % defibrinated sheep blood (Hy-Laboratories) and anaerobic growth was tested on 50 % MA in an anaerobic cell (Gas Pak EZ; BD).

Cells of strain fav-2-10-05^T were Gram-negative, non-sporulating rods, approximately 0.8–1 µm wide and 2 µm long, and motile by means of a single polar flagellum (Fig. 1). Strain fav-2-10-05^T formed yellow–brownish colonies within 2 days of incubation at 26 °C on 50 % MA. Strain fav-2-10-05^T grew under aerobic conditions and grew slowly under anaerobic conditions. The strain was also able to grow in marine broth and Luria-Bertani broth (Hy-Laboratories) and grew weakly in nutrient broth (HiMedia Laboratories). Growth with 0.5, 3, 6, 8, 10 and 15 % NaCl was tested in nutrient broth. Strain fav-2-10-05^T grew with 0.5–6 % NaCl, grew weakly with 8 % NaCl and did not grow at all with 10 % NaCl. Cells after growth

with 0.5 and 8 % NaCl appeared yellow and did not display the yellow–orange pigment that was observed after growth in liquid medium made with artificial seawater. Strain fav-2-10-05^T grew at 10–37 °C (weakly at 37 °C, optimally at 26 °C), but no growth was observed after a week of incubation at 4 or 42 °C.

The profile of enzyme activities was obtained from API ZYM strips after incubation at 26 °C for 4.5 and 24 h and at 37 °C for 4.5 h. Strain fav-2-10-05^T showed positive reactions for alkaline phosphatase and α -chymotrypsin and weak reactions for esterase (C4), esterase lipase (C8), naphthol-AS-BI-phosphohydrolase and *N*-acetyl- β -glucosaminidase. All other enzyme tests were negative. Data from API 20 NE strips were obtained after incubation at 26 °C for 24 and 48 h. Strain fav-2-10-05^T was positive for catalase, oxidase, arginine dihydrolase, fermentation of D-glucose, hydrolysis with β -glucosidase and protease (gelatinase), reduction of nitrates to nitrites and assimilation of *N*-acetylglucosamine and maltose. Haemolytic activity was not detected after 48 h of incubation but was detected after 4 days, after which haemolysis proceeded to form clear zones that surrounded the colonies. Phenotypic characteristics that differentiate strain fav-2-10-05^T from its closest phylogenetic relatives *Shewanella marisflavi* SW-117^T, *Shewanella haliotis* DW01^T, *Shewanella amazonensis* SB2B^T and *Shewanella pneumatophori* SCRC-2738^T are shown in Table 1.

Antibiotic resistance was determined by the disc diffusion method using commercial antibiotic discs (Oxoid). The inhibition zone of each antibiotic was measured on MA plates incubated at 26 °C for 48 h. Strain fav-2-10-05^T was sensitive to ampicillin, chloramphenicol, erythromycin, nalidixic acid, tetracycline and sulphamethoxazole plus trimethoprim and was slightly sensitive to meticcillin.

For analysis of cellular fatty acid content, cells of strain fav-2-10-05^T were prepared on MA plates at 26 °C and the fatty acid methyl esters were analysed using the MIDI/Hewlett Packard microbial identification system (Analytical Services, Plant Protection and Inspection Services, Beit-Dagan, Israel). Strain fav-2-10-05^T exhibited a cellular fatty acid profile that contained large amounts of straight-chain, branched, unsaturated and hydroxy fatty acids (Table 2). The major cellular fatty acids were C_{17:1} ω 8c (21.6 %), iso-C_{15:0} (18.6 %), C_{15:0} (9.1 %) and iso-C_{13:0} (8.9 %). The proportions of the major fatty acids of *S. marisflavi* SW-117^T and *S. haliotis* DW01^T, the strains most closely related to strain fav-2-10-05^T, were largely similar to those of strain fav-2-10-05^T (Table 2).

Genomic DNA was extracted from strain fav-2-10-05^T using an UltraClean Microbial DNA Isolation kit (MoBio Laboratories), according to the manufacturer's instructions. The 16S rRNA gene was amplified by PCR with a gradient thermocycler (Mastercycler; Eppendorf) using bacterial 16S rRNA gene primers taken from Felske *et al.* (1997) with the modification that the forward primer was shortened at the 5' end [forward primer 8F,

Fig. 1. Scanning electron micrograph of a negatively stained cell of strain fav-2-10-05^T. Bar, 1 µm.

Table 1. Phenotypic characteristics that differentiate strain fav-2-10-05^T from its closest phylogenetic neighbours

Strains: 1, *Shewanella corallii* sp. nov. fav-2-10-05^T; 2, *S. marisflavi* SW-117^T (data from Yoon *et al.*, 2004); 3, *S. haliotis* DW01^T (Kim *et al.*, 2007); 4, *S. amazonensis* SB2B^T (Venkateswaran *et al.*, 1998); 5, *S. pneumatophori* SCRC-2738^T (Hirota *et al.*, 2005). All strains were Gram-negative, rod-shaped, motile and catalase- and oxidase-positive, hydrolysed gelatin and grew under anaerobic conditions and at 10–32 °C. None of the strains assimilated D-mannose or D-mannitol. +, Positive; –, negative; ND, no data available.

Characteristic	1	2	3	4	5
Growth at/with:					
4 °C	–	+	–	+	+
37 °C	+	+	+	+	–
42 °C	–	+	+	+	–
6 % NaCl	+	+	+	–	+
10 % NaCl	–	–	+	–	ND
Reduction of nitrates	+	+	+	+	–
Fermentation of D-glucose	+	ND	–	–	+
Hydrolysis with β-glucosidase	+	–	–	ND	–
Arginine dihydrolase	+	ND	–	–	ND
Assimilation of:					
D-Glucose	–	+	–	ND	+
Maltose	+	+	–	–	–
D-Mannose	–	–	–	+	–
Capric acid	–	ND	+	ND	ND
Malic acid	–	+	+	–	ND
Resistance to ampicillin (10 µg per disc)	–	ND	+	ND	ND
DNA G + C content (mol%)	49.1	51	53.7	51.7	42.8

5'-GGATCCAGACTTTTGAT(C/T)(A/C)TGGCTCAG-3'; reverse primer 1512R, 5'-GTGAAGCTTACGG(C/T)TAGCT-TGTTACGACTT-3']. The resulting 16S rRNA gene sequences were compared with those in the GenBank database using the BLAST tool (<http://www.ncbi.nlm.nih.gov/blast/blast.cgi>) and aligned with sequences of representative strains of the genus *Shewanella* using CLUSTAL W in the MEGA package (Kumar *et al.*, 2004). A phylogenetic tree was constructed with the neighbour-joining method (Saitou & Nei, 1987) using the MEGA package. Bootstrap resampling analysis (Felsenstein, 1985) based on 100 replications was performed to estimate the confidence levels of the tree topology.

An almost-complete 16S rRNA gene sequence (1481 bases) was obtained and sequence database searches revealed that strain fav-2-10-05^T was most closely related to the family *Shewanellaceae* and exhibited the highest 16S rRNA gene sequence similarities with type strains of species of the genus *Shewanella*, notably *S. marisflavi* SW-117^T (96.0%), isolated from seawater of the Yellow Sea in Korea (Yoon *et al.*, 2004), and *S. haliotis* DW01^T (95.9%), isolated from the gut microflora of abalone collected from the South Sea, Republic of Korea (Kim *et al.*, 2007). Strain fav-2-10-05^T did not exhibit 16S rRNA gene sequence similarities above 97% with any type strain of the genus *Shewanella*. The

Table 2. Cellular fatty acid composition of strain fav-2-10-05^T and its closest phylogenetic neighbours

Strains: 1, *Shewanella corallii* sp. nov. fav-2-10-05^T; 2, *S. marisflavi* SW-117^T (data from Yoon *et al.*, 2004); 3, *S. haliotis* DW01^T (Kim *et al.*, 2007). tr, Trace amount (<1%); –, not present; NR, not reported.

Fatty acid (%)	1	2	3
Straight-chain saturated			
C _{12:0}	1.5	1.6	2.2
C _{13:0}	3.7	0.5	NR
C _{14:0}	0.7	1.5	1.9
C _{15:0}	9.1	4.1	2.8
C _{16:0}	3.5	14.5	13.4
C _{17:0}	3.6	1.9	2.5
C _{18:0}	0.1	NR	6.5
Branched saturated			
iso-C _{11:0}	0.1	2.0	NR
iso-C _{13:0}	8.9	5.9	4.1
iso-C _{14:0}	0.9	0.7	1.1
iso-C _{15:0}	18.6	22.9	17.7
iso-C _{16:0}	0.2	0.2	tr
iso-C _{17:0}	1.1	1.6	1.6
Monounsaturated			
C _{15:1} ω8c	1.7	NR	NR
C _{16:1} ω9c	0.8	0.7	1.1
C _{17:1} ω6c	1.9	0.6	tr
C _{17:1} ω8c	21.6	5.3	10.7
C _{18:1} ω7c	2.7	4.1	5.4
C _{18:1} ω9c	1.1	1.7	4.5
Hydroxy			
C _{11:0} 3-OH	1.0	NR	NR
C _{12:0} 3-OH	1.0	1.3	2.0
iso-C _{13:0} 3-OH	3.5	4.5	–
iso-C _{15:0} 3-OH	1.1	NR	NR
Summed features*			
1	3.3	0.5	1.5
2	1.0	0.9	1.1
3	4.8	18.6	12.5

*Summed features represent two or three fatty acids that cannot be separated by the Microbial Identification System. Summed feature 1 consisted of one or more of C_{13:0} 3-OH, iso-C_{15:1} I and iso-C_{15:1} H. Summed feature 2 consisted of C_{14:0} 3-OH and/or iso-C_{16:1} I. Summed feature 3 consisted of C_{16:1}ω7c and/or iso-C_{15:0} 2-OH.

phylogenetic tree (Fig. 2), based on a comparison of 1169 bp of the 16S rRNA gene sequence, showed that strain fav-2-10-05^T clustered with *S. amazonensis* SB2B^T, *Shewanella spongiae* HJ039^T and *Shewanella irciniae* UST040317-058^T (bootstrap value of 53%) and *S. haliotis* DW01^T and *S. algae* ATCC 51192^T. The topology of the phylogenetic tree and the sequence divergence values supported the findings of the phenotypic and chemotaxonomic analysis that strain fav-2-10-05^T represents a novel species of the genus *Shewanella*.

For the determination of DNA G+C content, genomic DNA of strain fav-2-10-05^T was prepared according to a

Fig. 2. Neighbour-joining 16S rRNA gene sequence phylogeny, based on a comparison of 1169 bases, showing the relationships between strain fav-2-10-05^T and the type strains of 50 species of the genus *Shewanella*. Bootstrap values (>50 %) based on 100 replications are shown at branch nodes. Bar, 1 substitution per 100 nucleotide positions.

modification of the procedure of Wilson (1987). The G + C content was determined in three independent analyses using the HPLC technique (Mesbah *et al.*, 1989) by the BCCM/LMG Bacteria Collection Identification Service. The DNA G + C content of strain fav-2-10-05^T was 49.1 mol%.

On the basis of phenotypic characterization and phylogenetic analysis, strain fav-2-10-05^T should be classified in a novel species of the genus *Shewanella*, for which the name *Shewanella corallii* sp. nov. is proposed.

Description of *Shewanella corallii* sp. nov.

Shewanella corallii (co.ral'li.i. L. gen. n. *corallii* of a coral, from which the type strain was isolated).

Cells are Gram-negative, non-spore-forming rods, approximately 0.8–1 µm wide and 2 µm long, motile by means of a single polar flagellum. Aerobic and catalase- and oxidase-positive, but capable of slow growth under anaerobic

conditions. Colonies are yellow-brownish, circular, smooth, opaque and small (approximately 1 mm in diameter after 24 h at 26 °C). Slightly haemolytic. Grows with 0.5–8.0 % NaCl and at 10–37 °C. With API ZYM, positive for alkaline phosphatase and α-chymotrypsin activities, weakly positive for esterase (C4), esterase lipase (C8), naphthol-AS-BI-phosphohydrolase and N-acetyl-β-glucosaminidase activities, but negative for lipase (C14), cystine arylamidase, leucine arylamidase, valine arylamidase, trypsin, acid phosphatase, α- and β-galactosidase, β-glucuronidase, α- and β-glucosidase, α-mannosidase and α-fucosidase activities. Positive for arginine dihydrolase, fermentation of D-glucose, hydrolysis with β-glucosidase and protease (gelatinase), reduction of nitrates to nitrites and assimilation of N-acetylglucosamine and maltose. Negative for indole production, urease, β-galactosidase and assimilation of D-glucose, L-arabinose, D-mannose, D-mannitol, potassium gluconate, capric acid, adipic acid, malic acid, trisodium citrate and phenylacetic acid. The

major fatty acids (>5%) are C_{17:1ω8c}, iso-C_{15:0}, C_{15:0} and iso-C_{13:0}. Demonstrates antibacterial activity against *Bacillus cereus*. Sensitive to (μg per disc) ampicillin (10), chloramphenicol, (30), erythromycin (15), meticillin (5), nalidixic acid (30), tetracycline (30) and sulphamethoxazole plus trimethoprim (25). The G+C content of the type strain is 49.1 mol%.

The type strain, fav-2-10-05^T (=LMG 24563^T =DSM 21332^T), was isolated from the mucus layer of a specimen of the coral genus *Favia* from the Gulf of Eilat, Red Sea.

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