Description of *Fabibacter halotolerans* gen. nov., sp. nov. and *Roseivirga spongicola* sp. nov., and reclassification of [*Marinicola*] *seohaensis* as *Roseivirga seohaensis* comb. nov.

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Bacterial strains UST030701-097^T and UST030701-084^T were isolated from a marine sponge in the Bahamas. Both strains were pink-pigmented, Gram-negative, strictly aerobic and chemo-organotrophic. Cells of strain UST030701-097^T were short, curved rods with fast-gliding motility, whereas those of strain UST030701-084^T were straight rods with a less rapid gliding motion. The two strains had MK-7 as the major respiratory quinone and did not produce flexirubin-type pigments. The DNA G+C contents of strains UST030701-097^T and UST030701-084^T were 42·5 and 43·7 mol%, respectively. Phylogenetic analysis based on 16S rRNA gene sequences indicated that the two strains belonged to the family '*Flexibacteraceae*' of the phylum *Bacteroidetes*. 16S rRNA gene sequence similarity between strains UST030701-097^T and UST030701-084^T was 95·0 %; their closest relative was [*Marinicola*] *seohaensis*, with 93·3 % and 96·0 % sequence similarity, respectively. Phylogenetic tree topology indicated that the two strains belonged to the same lineage, but were on separate branches. Whilst strain UST030701-084^T and [*Marinicola*] *seohaensis* were found on one branch, strain UST030701-097^T was in another branch that had no species with validly published names. Based on the polyphasic taxonomic data obtained in the present study, we propose that strain UST030701-097^T represents a novel genus and that strain UST030701-084^T represents a novel species in the phylum *Bacteroidetes*. The genus *Fabibacter* gen. nov. is proposed, with strain UST030701-097^T (=NRRL B-41220^T=JCM 13334^T) as the type strain of the type species, *Fabibacter halotolerans* sp. nov. Strain UST030701-084^T (=NRRL B-41219^T=JCM 13337^T) is proposed as the type strain of *Roseivirga spongicola* sp. nov. In an earlier study, it was suggested that the genus *Marinicola* is a later heterotypic synonym of the genus *Roseivirga*. However, a formal proposal to reclassify [*Marinicola*] *seohaensis*, the only member of the genus *Marinicola*, has not yet been made. The results of phylogenetic analyses in this study support the reclassification of [*Marinicola*] *seohaensis* as *Roseivirga seohaensis* comb. nov.

Many marine sponges harbour large quantities of live bacteria. Bacterial numbers in sponges have been estimated to be as high as 10^8 cells (g tissue)$^{-1}$ or up to 57 % of tissue volume (Hentschel *et al.*, 2003). These bacteria can be maternal in origin or captured from sea water as the sponges filter feed (Imhoff & Stohr, 2003). The bacteria associated with sponges are believed to play essential roles in their survival and fitness. For example, the bioactive metabolites

The GenBank/EMBL/DDBJ accession numbers for the 16S rRNA gene sequences of strains UST030701-097^T and UST030701-084^T are DQ080995 and DQ080996, respectively.

Tables detailing the results of API 20E, 20NE and 50CH tests and MicroLog 3 tests for strains UST030701-097^T and UST030701-084^T and scanning electron micrographs of cells of the two strains are available as supplementary material in IJSEM Online.

of bacteria may defend sponges against epibiosis (Chelossi *et al.*, 2004) and the extracellular enzymes of the bacteria may mobilize food resources that are otherwise indigestible by sponges (Wilkinson *et al.*, 1999). During the course of studying bacterial communities associated with the marine sponge *Tedania ignis* in the Bahamas, bacterial strains UST030701-097^T and UST030701-084^T were isolated. The strains appeared as pink-pigmented, circular, convex colonies (2–4 mm in diameter) with a smooth surface and an entire margin after 48 h of cultivation at 30 °C on an agar medium composed of 5 g peptone l^{-1}, 3 g yeast extract l^{-1} (both obtained from Oxoid) and 0·22 μm-filtered sea water. This agar medium is hereafter referred to as marine agar. Unless otherwise specified, all the characteristics described hereafter are based on cultures grown on marine agar at 30 °C for 48 h. Based on the polyphasic taxonomic data obtained in the present study, we propose that strain UST030701-097^T represents a novel genus and that strain UST030701-084^T represents a novel species within the family '*Flexibacteraceae*' of the phylum *Bacteroidetes*.

The nearly complete 16S rRNA gene sequences of strains UST030701-097^T (1412 bp) and UST030701-084^T (1387 bp) were obtained bidirectionally with replications ($n=3$) as described elsewhere (Lau *et al.*, 2004). Phylogenetic analysis based on nearly complete 16S rRNA gene sequences indicated that the two strains shared 95·0 % sequence similarity and were members of the family '*Flexibacteraceae*' in the phylum *Bacteroidetes*. Strain UST030701-084^T was most closely related to members of the genera *Marinicola* (Yoon *et al.*, 2005) and *Roseivirga* (Nedashkovskaya *et al.*, 2005a, b), with 95·8–96·0 % sequence similarity. Strain UST030701-097^T was most closely related to two uncharacterized bacteria (strains PM13 and DG1129), with 94·8–96·5 % sequence similarity, and to the members of the genera *Marinicola* and *Roseivirga*, with 93·1–93·3 % sequence similarity. A neighbour-joining phylogenetic tree constructed using the ARB software package (Ludwig *et al.*, 2004) indicated that strains UST030701-097^T and UST030701-084^T, the uncharacterized strains PM13 and DG1129 and members of the genera *Marinicola* and *Roseivirga* belonged to the same lineage. Within this lineage, strain UST030701-097^T and the two uncharacterized bacteria constituted one branch, whereas strain UST030701-084^T and the members of the genera *Marinicola* and *Roseivirga* constituted another (Fig. 1). This tree topology is supported by high bootstrap values within the lineage (>84 %, 500 replicates) and by its recurrence in maximum-parsimony and maximum-likelihood trees as determined using the ARB software package (Fig. 1).

Nedashkovskaya *et al.* (2005b) proposed that the genus *Marinicola* is a later heterotypic synonym of the genus *Roseivirga* due to many common genomic, chemotaxonomic and phenotypic features seen between members of

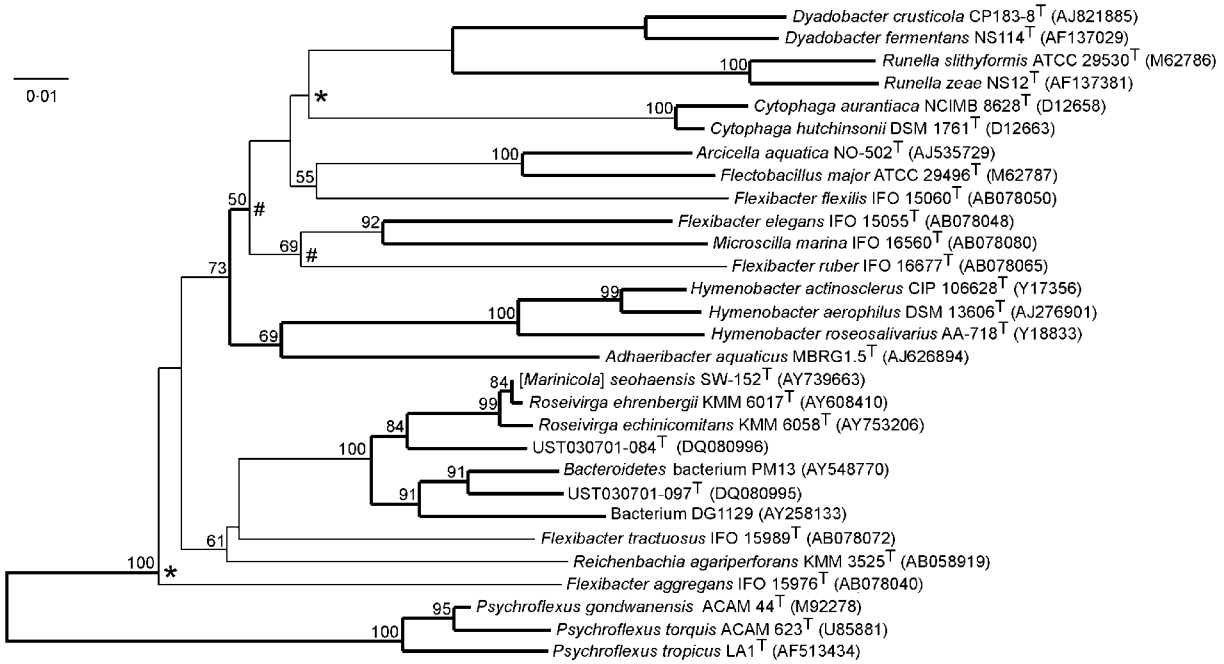

Fig. 1. Neighbour-joining dendrogram showing the estimated phylogenetic relationships between strains UST030701-097^T and UST030701-084^T and related species on the basis of 16S rRNA gene sequences. Strains belonging to the genus *Psychroflexus* serve as outgroups. Nodes also found in the maximum-likelihood tree are marked with #. Nodes also found in the maximum-parsimony tree are shown by *. Lines in bold type indicate branches found in both the maximum-likelihood and maximum-parsimony trees. Bootstrap values of ⩾50 % (500 replicates) are indicated at the nodes. GenBank accession numbers are shown in parentheses. Bar, 1 nucleotide substitution per 100 nucleotides.

the two genera. However, a formal proposal to reclassify [*Marinicola*] *seohaensis*, the only member of the genus *Marinicola*, has not yet been made. The results of the phylogenetic analysis in the study support the reclassification of [*Marinicola*] *seohaensis* to the genus *Roseivirga*. We thus propose that [*Marinicola*] *seohaensis* be renamed as *Roseivirga seohaensis* comb. nov.

The DNA G+C contents of strains UST030701-097^T and UST030701-084^T were 42·5±0·3 mol% (three replicates) and 43·7±0·6 mol% (three replicates), respectively, as determined by an HPLC method according to Mesbah *et al.* (1989). MK-7 was the major respiratory quinone in both strains as determined using an HPLC method described by Collins (1994). Menaquinones extracted from *Cellulophaga lytica* (Johansen *et al.*, 1999) and *Pedobacter heparinus* (Steyn *et al.*, 1998) were used as references for MK-6 and MK-7, respectively. Fatty acid contents of strains UST030701-097^T and UST030701-084^T were determined using the Sherlock Microbial Identification System (MIDI) according to the manufacturer's protocol and are given in Table 1. The fatty acid profile of the two strains differed mainly by the presence/absence of i14 : 0, i14 : 0 3-OH, 15 : 0 3-OH, 16 : 0 3-OH, i16 : 1 and i17 : 1ω9*c* and by the quantity of i15 : 0 3-OH, a15 : 0, i16 : 0 3-OH, 17 : 0 2-OH, i17 : 0 3-OH and summed feature 3 (SF3; comprising i15 : 0 2-OH and/or 16 : 1ω7*c*) (Table 1). The fatty acid profile of strain UST030701-097^T differed from those described for the members of the *Marinicola* and *Roseivirga* mainly by having larger quantities of i15 : 0 3-OH, i16 : 0 3-OH and SF3 and by the additional presence of i14 : 0 3-OH, 15 : 0 2-OH and 15 : 0 3-OH (Table 1). The fatty acid profile of strain UST030701-084^T could be distinguished from those of species of the genera *Marinicola* and *Roseivirga* mainly by having different quantities of i13 : 0, i15 : 1, i16 : 0 3-OH, 17 : 0 2-OH, i17 : 0 3-OH and i17 : 1ω9*c* and by the additional presence of 15 : 0 2-OH (Table 1).

Table 1. Comparison of major cellular fatty acids for strains UST030701-097^T and UST030701-084^T and recognized members of the genera *Marinicola* and *Roseivirga*

Strains/species: 1, UST030701-097^T; 2, UST030701-084^T; 3, [*Marinicola*] *seohaensis*; 4, *Roseivirga ehrenbergii*; 5, *Roseivirga echinicomitans*. The growth conditions for strains UST030701-097^T and UST030701-084^T were marine agar (as described earlier in this study) and incubation at 30 °C for 2 days. [*Marinicola*] *seohaensis* was grown in Marine agar 2216 at 30 °C for 3 days. The growth conditions for *R. ehrenbergii* and *R. echinicomitans* are not given. Values are percentages of total fatty acids. −, Not detected. Data for [*M.*] *seohaensis*, *R. ehrenbergii* and *R. echinicomitans* are from Yoon *et al.* (2005) and Nedashkovskaya *et al.* (2005a, b).

Fatty acid	1	2	3	4	5
i13 : 0	1·6	0·7	5·2	3·2	2·9
i14 : 0	4·7	−	−	−	1·9
i14 : 0 3-OH	1·1	−	−	−	−
15 : 0 2-OH	1·9	3·2	−	−	−
15 : 0 3-OH	1·3	−	−	−	−
i15 : 0 3-OH	12·5	4·9	5·6	3·0	4·1
a15 : 0	2·5	12·5	2·4	4·5	13·1
i15 : 0	18·3	18·6	33·5	24·0	20·2
a15 : 1	0·8	−	−	1·8	2·4
i15 : 1	14·2	12·5	20·5	34·2	20·2
16 : 0 3-OH	1·2	−	1·8	1·6	−
i16 : 0	1·2	2·0	1·2	1·1	1·8
i16 : 1	1·2	−	−	−	2·0
i16 : 0 3-OH	12·7	1·2	7·2	4·1	4·2
17 : 0 2-OH	1·3	10·1	−	−	2·0
i17 : 0	0·5	−	−	−	1·0
i17 : 0 3-OH	9·3	18·3	11·2	7·7	12·1
i17 : 1ω9*c*	−	10·8	−	−	1·1
SF3*	13·7	5·5	4·8	1·7	1·0

*Summed feature 3 comprises i15 : 0 2-OH and/or 16 : 1ω7*c*.

Anaerobic growth of the two novel strains was examined in the Oxoid Anaerobic System. The requirement for NaCl was tested in a medium containing (l^{-1}) 5 g $MgCl_2$, 2 g $MgSO_4$, 0·5 g $CaCl_2$, 1 g KCl, 5 g peptone and various amounts of NaCl, adjusted to pH 7·5 using KOH (Isnansetyo & Kamei, 2003). Cell morphology was examined using scanning electron microscopy (7600F; JEOL) according to the procedures described in Neu *et al.* (2001) (see Supplementary Fig. S1 in IJSEM Online). Reaction to Gram-stain was determined using light microscopy according to Smibert & Krieg (1994). Gliding motility was determined using phase-contrast light microscopy (Olympus) after growth on quarter-strength marine 2216 medium solidified with 1 % agar according to Bowman (2000). Susceptibility to antibiotics was tested by the routine disc-diffusion plate method according to Acar (1980). Flexirubin-type pigment production and carboxymethylcellulose hydrolysis were determined according to Bernardet *et al.* (2002). Casein hydrolysis was determined according to Norris *et al.* (1985). Hydrolysis of chitin and Tweens 20, 40 and 80 was performed by using the method of Baumann & Baumann (1988). Oxidase and catalase activities and the hydrolysis of agar, DNA and starch were tested according to Smibert & Krieg (1994). Other enzyme activities, growth on carbon sources, acid production from carbon sources, nitrate reduction and the production of H_2S, indole and acetoin were tested using the API 20E, API 20NE, API 50CH, API ZYM (bioMérieux) and MicroLog 3 (Biolog) commercial systems. Cells for inoculation into the API systems were suspended in a sterile solution of a seawater mixture at 22 ‰ salinity (MacDonell *et al.*, 1982). The phenotypic characteristics of strains UST030701-097^T and UST030701-084^T are given in the genus/species descriptions. Results obtained from the API and MicroLog 3 systems are detailed in Supplementary Tables S1–S3 in IJSEM Online.

Chemotaxonomic and phenotypic characteristics that distinguish strain UST030701-084^T from other members of the genera *Marinicola* and *Roseivirga* are given in Tables 1 and 2. Characteristics that distinguish strain UST030701-097^T

Table 2. Characteristics that differentiate strain UST030701-084^T from recognized species of the genera *Marinicola* and *Roseivirga*

Strains/species: 1, UST030701-084^T; 2, [*Marinicola*] *seohaensis*; 3, *Roseivirga ehrenbergii*; 4, *Roseivirga echinicomitans*. +, Positive; (+), weakly positive; −, negative; ND, not determined. Data for [*Marinicola*] *seohaensis*, *R. ehrenbergii* and *R. echinicomitans* are from Yoon *et al.* (2005) and Nedashkovskaya *et al.* (2005a, b).

Characteristic	1	2	3	4
DNA G+C content (mol%)	43·7	40·1	40·2	41·3
NaCl range for growth (%)	0–16·0	2·0–9·0	1·0–8·0	1·0–8·0
Temperature range for growth (°C)	12·0–44·0	4·0–40·0	4·0–39·0	4·0–31·0
Pigmentation	Pink	Orange	Pink	Pink
Flexirubin	−	+	−	−
Gliding motility	+	+	−	−
Hydrolysis of:				
DNA	+	ND	+	−
Gelatin	+	−	+	+
Tween 20	+	(+)	+	−
Tween 40	+	(+)	−	+
Tween 80	+	(+)	−	−
Reduction of nitrate	−	−	−	+
Enzyme activities:				
Cystine arylamidase	+	−	ND	+
β-Galactosidase	−	−	+	+
α-Glucosidase	+	−	ND	+
β-Glucosidase	+	−	ND	ND
Lipase	+	−	ND	ND
Trypsin	+	−	ND	+

from other genera in the phylum *Bacteroidetes* are detailed in Table 3. Most notably, strains UST030701-097^T and UST030701-084^T differ from their close relatives by being more halotolerant, but not requiring NaCl for growth. Moreover, strain UST030701-097^T has a distinctive curved cell shape and strain UST030701-084^T has a range of hydrolytic and enzyme activities not found in other members of the genera *Marinicola* and *Roseivirga*. Strains UST030701-097^T and UST030701-084^T differ from each other by: (i) cell shape, (ii) halo- and thermotolerance levels, (iii) gelatin hydrolysis and arginine dihydrolase, α-galactosidase, β-galactosidase and α-mannosidase activities and (iv) susceptibility to ampicillin, penicillin, streptomycin and tetracycline. Strain UST030701-097^T is able to utilize a variety of sole carbon sources in the API and MicroLog 3 systems, while strain UST030701-084^T can only utilize aesculin ferric citrate in the API 50CH system and α-ketovaleric acid in the MicroLog 3 system (see Supplementary Tables S2 and S3 in IJSEM Online). The small number of carbon sources utilized by strain UST030701-084^T is a feature also found in the members of the genus *Roseivirga*. Molecular evidence, together with chemotaxonomic and phenotypic characteristics, suggest that strain UST030701-097^T represents a novel genus and that strain UST030701-084^T represents a novel species within the phylum *Bacteroidetes*. The name *Fabibacter halotolerans* gen. nov., sp. nov., is proposed for strain UST030701-097^T. Strain UST030701-084^T is proposed as *Roseivirga spongicola* sp. nov.

Description of *Fabibacter* gen. nov.

Fabibacter [Fa.bi.bac′ter. L. fem. n. *faba* bean; N.L. masc. n. *bacter* rod; N.L. masc. n. *Fabibacter* bean(-like) rod].

Cells are Gram-negative, curved rods (1·5 μm long × 0·5 μm wide). Strictly aerobic and chemo-organotrophic. The major respiratory quinone is MK-7. Flexirubin-type pigments are not produced. Oxidase- and catalase-positive. Phylogenetic analysis based on 16S rRNA gene sequence indicates that the genus is a member of the family '*Flexibacteraceae*' in the phylum *Bacteroidetes*.

Currently, the genus contains one species, the type species *Fabibacter halotolerans*.

Description of *Fabibacter halotolerans* sp. nov.

Fabibacter halotolerans (ha.lo.to′le.rans. Gr. masc. n. *hals* salt; L. part. adj. *tolerans* tolerating; N.L. part. adj. *halotolerans* salt-tolerating).

Displays the following properties in addition to those given in the genus description. Colonies on marine agar are pink, circular, 2·0–4·0 mm in diameter, convex with a smooth surface and an entire margin. No diffusible pigment. Has

Table 3. Characteristics that differentiate strain UST030701-097^T from closely related genera

Taxa: 1, UST030701-097^T; 2, *Marinicola*; 3, *Roseivirga*; 4, *Reichenbachia*; 5, *Adhaeribacter*; 6, *Hymenobacter*. +, Positive; (+), weakly positive; −, negative; ND, not determined; V, variable. Data for *Roseivirga*, *Reichenbachia*, *Adhaeribacter* and *Hymenobacter* are from Hirsch *et al.* (1998), Collins *et al.* (2000), Buczolits *et al.* (2002), Nedashkovskaya *et al.* (2003, 2005a, b), Rickard *et al.* (2005) and Yoon *et al.* (2005).

Characteristic	1	2	3	4	5	6
DNA G+C content (mol%)	42·5	40·3	40·2–41·3	44·5	40·0	55·0–63·0
NaCl range for growth (%)	0–12·0	2·0–8·0	1·0–8·0	1·0–6·0	0–4·0	0–2·0
Temperature range for growth (°C)	12·0–36·0	4·0–40·0	4·0–39·0	4·0–35·0	4·0–37·0	0–42·0
Pigmentation	Pink	Orange	Pink	Orange	Pink	Pink/red
Flexirubin	−	+	−	+	ND	ND
Cell shape	Short curved rod	Rod	Rod	Rod	Rod	Rod/coccoid
Gliding motility	+	+	−	+	−	−
Hydrolysis of:						
Gelatin	−	−	+	+	ND	+
Tween 80	+	(+)	−	−	ND	+
Starch	(+)	−	−	+	−	+
Acid production from carbohydrates	+	−	−	−	−	−
Enzyme activities:						
Arginine dihydrolase	+	−	ND	ND	ND	ND
α-Galactosidase	+	−	V	ND	+	V
β-Galactosidase	+	−	V	ND	+	−
α-Glucosidase	+	−	+	ND	+	V
β-Glucosidase	+	−	V	ND	+	V
α-Mannosidase	+	−	V	ND	ND	−

fast-gliding motility. Growth occurs between 12 and 36 °C (optimum of 28–30 °C) and between pH 5·0 and 10·0. Does not require sodium for growth, but can tolerate up to 12 % NaCl. In disc-diffusion tests, susceptible to ampicillin (1 μg), chloramphenicol (1 μg), penicillin (1 μg), streptomycin (0·1 μg) and tetracycline (5 μg), but not to kanamycin (tested up to 100 μg). DNA G+C content is 42·5±0·3 mol%. Predominant fatty acids (>5 %) are i15 : 0, i15 : 1, i15 : 0 3-OH, i16 : 0 3-OH, i17 : 0 3-OH and SF 3(comprising i15 : 0 2-OH and/or 16 : 1ω7*c*). These fatty acids represent 80·7 % of the total. Produces acetoin, but not indole or H_2S. Nitrate is not reduced. DNA and Tweens 20, 40 and 80 are hydrolysed, but not agar, casein, carboxymethylcellulose, chitin or gelatin. Starch is weakly hydrolysed. *N*-Acetyl-β-glucosaminidase, acid phosphatase, alkaline phosphatase, arginine dihydrolase, α-galactosidase, β-galactosidase, α-glucosidase, β-glucosidase, α-chymotrypsin, cystine arylamidase, leucine arylamidase, valine arylamidase, esterase (C4), esterase lipase (C8), lipase (C14), α-mannosidase, trypsin and naphthol-AS-BI-phosphohydrolase activities are positive. No activities of α-fucosidase, β-glucuronidase, lysine decarboxylase, ornithine decarboxylase, tryptophan deaminase or urease. Growth occurs on the following sole carbon sources in the API 20E, 20NE and 50CH systems: D-cellobiose, D-lactose, D-maltose and starch. Acid is produced from the following sole carbon sources in the API 20E and 50CH systems: amygdalin, arbutin, D-cellobiose, aesculin ferric citrate, D-galactose, D-glucose, gentiobiose, maltose, methyl α-D-glucopyranoside, D-raffinose, salicin, sucrose, starch and D-trehalose. Utilizes the following carbon sources in the MicroLog 3 system: L-alaninamide, L-alanine, L-alanyl glycine, L-aspartic acid, D-cellobiose, dextrin, D-galacturonic acid, gentiobiose, α-D-glucose, D-glucose 6-phosphate, L-glutamic acid, glycogen, glycyl L-aspartic acid, glycyl L-glutamic acid, α-ketobutyric acid, α-ketoglutaric acid, α-ketovaleric acid, DL-lactic acid, α-D-lactose, lactulose, maltose, D-melibiose, methyl β-D-glucoside, L-ornithine, L-proline, L-pyroglutamic acid, D-raffinose, succinamic acid, sucrose, D-trehalose, turanose and L-threonine. A full list of carbon sources included in the API and MicroLog 3 systems is given in Supplementary Tables S2 and S3 in IJSEM Online.

The type strain, UST030701-097^T (=NRRL B-41220^T=JCM 13334^T), was isolated from the marine sponge *Tedania ignis* in the Bahamas.

Description of *Roseivirga spongicola* sp. nov.

Roseivirga spongicola [spon.gi′co.la. Late L. n. *spongos -i* sponge; L. masc./fem. suffix n. *-cola* (from *incola*) inhabitant; N.L. nom. n. (in apposition) *spongicola* inhabitant of sponges].

Cells are Gram-negative rods, 2·0 μm long ×0·5 μm wide, with gliding motility. Colonies on marine agar are pink, circular, 2·0–4·0 mm in diameter, convex with a smooth surface and an entire margin. No diffusible pigment. Strictly aerobic and chemo-organotrophic. Growth occurs between 12 and 44 °C (optimum is 20–30 °C) and between pH 5·0 and 10·0. Does not require sodium for growth, but can tolerate

up to 16 % NaCl. The major respiratory quinone is MK-7. In disc diffusion tests, susceptible to chloramphenicol (100 μg), but not to ampicillin, kanamycin, penicillin, streptomycin or tetracycline (each tested up to 100 μg). Flexirubin-type pigments are not produced. DNA G+C content is 43·7± 0·6 mol%. Predominant fatty acids (>5 %) are a15:0, i15:0, i15:1, 17:0 2-OH, i17:0 3-OH, i17:1ω9*c* and SF 3 (comprising i15:0 2-OH and/or 16:1ω7*c*). These fatty acids represent 88·3 % of the total. Produces acetoin, but not indole or H_2S. Nitrate is not reduced. DNA, gelatin and Tweens 20, 40 and 80 are hydrolysed, but not agar, casein, carboxymethylcellulose, chitin or starch. *N*-Acetyl-β-glucosaminidase, catalase, cystine arylamidase, leucine arylamidase, valine arylamidase, α-chymotrypsin, oxidase, α-glucosidase, β-glucosidase, esterase (C4), esterase lipase (C8), acid phosphatase, alkaline phosphatase, lipase (C14), naphthol-AS-BI-phosphohydrolase and trypsin activities are positive. No activities of arginine dihydrolase, α-fucosidase, α-galactosidase, β-galactosidase, β-glucuronidase, lysine decarboxylase, α-mannosidase, ornithine decarboxylase, tryptophan deaminase or urease. Utilizes only aesculin ferric citrate in the API 50CH system and α-ketovaleric acid in the MicroLog 3 system as sole carbon sources. No acid production from the sole carbon sources in the API 20E and 50CH systems. A full list of carbon sources included in the API and MicroLog 3 systems is provided in Supplementary Tables S2 and S3 in IJSEM Online.

The type strain, UST030701-084^T (=NRRL B-41219^T= JCM 13337^T), was isolated from the marine sponge *Tedania ignis* in the Bahamas.

Description of *Roseivirga seohaensis* comb. nov.

Roseivirga seohaensis (seo.ha.en′sis. N.L. fem. adj. *seohaensis* of Seohae, the Korean name for the Yellow Sea in Korea, from where the type strain was isolated).

Basonym: *Marinicola seohaensis* Yoon *et al.* 2005

The description is identical to that given for *Marinicola seohaensis* by Yoon *et al.* (2005). The type strain is SW-152^T (=KCTC 12312^T=JCM 12600^T).

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