Description of *Mariniphaga anaerophila* gen. nov., sp. nov., a facultatively aerobic marine bacterium isolated from tidal flat sediment, reclassification of the *Draconibacteriaceae* as a later heterotypic synonym of the *Prolixibacteraceae* and description of the family *Marinifilaceae* fam. nov.

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A mesophilic, chemoheterotrophic bacterium, strain Fu11-5T, was isolated from tidal-flat sediment from Tokyo Bay, Chiba, Japan. Cells of strain Fu11-5T were facultatively aerobic, Gram-negative, non-sporulating, non-motile and rod-shaped (1.9–6.9 μm long). Strain Fu11-5T grew optimally at 35–37 °C and pH 6.5–7.0 and with 1–2 % (w/v) NaCl. Oxygen and L-cysteine were used as an alternative electron acceptor and donor, respectively. Strain Fu11-5T also grew fermentatively on some pentoses, hexoses and disaccharides and soluble starch. Succinic acid was the major end product from D-glucose. Phylogenetic analysis based on the 16S rRNA gene sequence revealed that strain Fu11-5T was affiliated with the order *Bacteroidales*, and its nearest neighbours were members of the genera *Meniscus*, *Prolixibacter*, *Sunxiuqinia*, *Mangrovibacterium* and *Draconibacterium*, with 87–91 % sequence similarity. Cell morphology, optimum growth temperature and utilization of sugars of strain Fu11-5T distinguished the strain from phylogenetically related bacteria. On the basis of its phenotypic features and phylogenetic position, a novel genus and species are proposed to accommodate strain Fu11-5T, with the name *Mariniphaga anaerophila* gen. nov., sp. nov. The type strain of *Mariniphaga anaerophila* is strain Fu11-5T (=JCM 18693T=NBRC 109408T=DSM 26910T). We also propose to combine the family *Draconibacteriaceae* into the family *Prolixibacteraceae* as a later heterotypic synonym and to place the distinct sublineage of the genus *Marinifilum* in the family *Marinifilaceae* fam. nov.

Microbial diversity in nature has been investigated phylogenetically by both culture-dependent and -independent approaches, and it is obvious that the majority of micro-organisms have not yet been cultivated in synthetic laboratory media (Amann et al., 1995; DeLong & Pace, 2001; Olsen et al., 1986; Pace et al., 1986; Ward et al., 1990; Whitman et al., 1998). In particular, isolation of novel marine micro-organisms has lagged behind that of enterobacteria and terrestrial micro-organisms as a result of their oligotrophic habitats and the difficulty in accessing sampling sites.

In our previous studies, some rare and/or unique micro-organisms have been isolated from marine sediment and the alimentary tracts of marine organisms collected from the coast and tidal flats in Japan, for example ‘*Methanoseta pelagica*’, an acetoclastic and NaCl-requiring methanogen (Mori et al., 2012), *Oscillibacter valericigenes*, a strictly anaerobic, fermentative species that is phylogenetically related to a representative uncultured bacterium *Oscillospira guilliermondii* (Iino et al., 2007), *Ferrimonas futtsuensis* and *Ferrimonas kyonanensis*, facultatively anaerobic, selenite-reducing species (Nakagawa et al., 2006), and others (Hamada et al., 2009, 2010; Muramatsu et al., 2010). These findings suggest that diverse novel micro-organisms are still cultivable from the shallow sea and tidal-flat environments of Japan. Recognition of their diversity and development of cultivation methods for unknown marine
micro-organisms are thus important in understanding the marine ecosystem and functional diversity in marine environments.

This paper describes the isolation of a heterotrophic marine bacterium from sediment of a tidal flat in Tokyo Bay. On the basis of a polyphasic taxonomic approach, a novel genus and species are proposed for this bacterium.

Blackening sediment was collected on 10 September 2003 at a depth of approximately 100 cm using a peat sampler (model DIIK-105A; Daiki Rika Kogyo) on the Futtsu tidal flat in Tokyo Bay, Chiba Prefecture, Japan, as reported previously (Mori et al., 2012). The soil sample was kept in a sealed nylon bag with an O2-absorbing and CO2-generating agent (Anaero-Pack; Mitsubishi Gas Chemical) until it was inoculated into a fresh medium.

The basal medium used in this study, designated Sw medium, contained (l−1) 0.54 g NH4Cl, 0.14 g KH2PO4, 0.15 g CaCl2.2H2O, 4.0 g MgCl2.6H2O, 18.0 g NaCl, 2.5 g NaHCO3 and 1.0 ml trace elements solution (Touzel & Albagnac, 1983), containing 4.0 mg Na2WO4, H2O and with NaCl omitted. The medium was adjusted to pH 7.0 with 6 M HCl, and 20 ml medium was dispensed in 50 ml serum bottles. Dissolved air was removed by flushing with N2/CO2 (4:1, v/v), and the bottles were sealed with butyl rubber stoppers. Prior to inoculation, 0.2 ml vitamin solution (Wolin et al., 1963) and 0.2 ml reductant solution containing 0.5 g Na2S and 0.5 g L-cysteine hydrochloride 1−1 were added to each bottle with filtration through a 0.2 μm-pore membrane filter. For enrichment, 1.0 g sediment was inoculated into 20 ml HXSw medium supplemented with 0.2 % (w/v) each yeast extract (Becton Dickinson) and Polypepton (Nihon Pharmaceutical) in the Sw medium with filtration and with a headspace of H2/CO2 (4:1, v/v; approx. 150 kPa) instead of N2/CO2. The culture was incubated at 25 °C for 3 weeks and then transferred to fresh HXSw medium. After several transfers, the culture was spread on slants of HXSw medium solidified with 1.5 % (w/v) agar and colonies that appeared were picked and streaked on fresh HXSw medium. The purification procedure was repeated several times until the culture was deemed pure, and a culture with uniformly shaped cells was obtained, which was designated Fu11-5T. After purification, the isolate was maintained in HXSw medium, and cultivated routinely in GXSm medium with the addition of 0.2 % (w/v) yeast extract, 0.2 % (w/v) Polypepton and 10 mM D-glucose in Sw medium with filtration for the following study.

The isolate was cultivated in 10 ml medium dispensed in screw-capped tubes (18 × 180 mm, Sanshin Industrial Co.) with inoculation of a 1/100 dilution of the preculture. Bacterial growth was followed by the increase in turbidity at 660 nm determined with a spectrophotometer. Utilization of electron acceptors and donors was determined in Sw medium without NH4Cl after adding 10 mM pyruvate and 0.01 % (w/v) yeast extract. Concentrations of electron acceptors and donors and the product in the cultures were quantified by HPLC equipped with a conductivity detector model CDD-10ADsp, a Shim-Pack Cation column IC-C4 and a Shim-Pack Anion column IC-SA2 (Shimadzu). Utilization of sugars was examined using GXSsw medium with the addition of each sugar in place of D-glucose. Concentrations of organic acids in cultures were quantified by HPLC equipped with a diode array detector model SPD-M20A (Shimadzu) and Rezex ROA-Organic acid H+ (8 %) column (Phenomenex).

Cells of strain Fu11-5T were rods, approximately 1.9–6.9 μm long and 0.5–0.6 μm wide (Fig. 1). Cells usually occurred singly or in pairs. Motility and spore formation were not observed under a phase-contrast microscope. Flagellation was also not observed by electron microscopy. The colony consistency of strain Fu11-5T was butyrous. Cells stained Gram-negative by conventional Gram staining.

Strain Fu11-5T was a facultatively aerobic bacterium that grew better under anaerobic conditions comprising a N2/CO2 (4:1, v/v) atmosphere than under aerobic conditions in air. Catalase and oxidase reactions were negative. The growth temperature of strain Fu11-5T was 20–40 °C, with an optimum at 35–37 °C. No growth was observed at 15 or 45 °C. The pH range for growth was 6.0–8.5, with an optimum at pH 6.5–7.0. No growth was observed at pH 5.5 or 9.0. Growth occurred in media containing 9 % (w/v) NaCl or below, with the optimum being 1–2 % (w/v) NaCl. No growth was observed at 10 % (w/v) NaCl. Strain Fu11-5T grew using oxygen (5 %, w/v) as the electron acceptor in the presence of L-cysteine as the electron donor. Sulfate (10 mM), sulfite (2 mM), thiosulfate (5 mM), elemental sulfur (1 %, w/v), nitrite (10 mM), nitrate (2 mM) and iron(III) oxide (2 mM) were not utilized as alternative electron acceptors in the presence of L-cysteine. Strain Fu11-5T grew using L-cysteine (2 mM) as the electron donor in the presence of oxygen (5 %, w/v). H2/CO2 (4:1, v/v), sulfide (2 mM), elemental sulfur (1 %, w/v), thiosulfate (5 mM), sulfate (2 mM), ammonium (10 mM) and nitrite (2 mM) were not utilized as alternative electron donors in the presence of oxygen (5 %, w/v). Strain Fu11-5T grew...
fermentatively on L-arabinose, D-ribose, D-xyllose, D-glucose, D-mannose, cellobiose, lactose, maltose, sucrose, trehalose (all at 10 mM) and soluble starch (0.2 %, w/v). No growth occurred on D-fructose, D-sorbitose, D-mannitol or D-sorbitol (all at 10 mM). Succinic acid (91.3 %) was the major end product from D-glucose. Acetic acid (8.7 %) was also produced as a minor end product. Strain Fu11-5T was susceptible to ampicillin, chloramphenicol, rifampicin, tetracycline and vancomycin (all at 100 µg ml⁻¹), but resistant to bacitracin, gentamicin, kanamycin and streptomycin (all at 100 µg ml⁻¹).

The major cellular fatty acids of strain Fu11-5T were iso-C₁₅:0 (26.7 %) and anteiso-C₁₅:0 (18.5 %), as determined by using the MIDI microbial identification system (Microbial ID; Agilent Technologies) based on the method described by Sasser (1990). C₁₆:0 (7.7 %) was also detected as a minor component. The major isoprenoid quinone was identified as menaquinone 7 (MK-7), determined using the HPLC method described by Komagata & Suzuki (1987). The polar lipid pattern of strain Fu11-5T comprised only phosphatidylethanolamine, as determined by using two-dimensional TLC with spraying with 5 % ethanolic molybdophosphoric acid, ninhydrin, Dittmer & Lester reagent, anisaldehyde reagent and Dragendorff reagent, as described by Lechevalier et al. (1977) and Minnikin et al. (1984). The genomic DNA G+C content of strain Fu11-5T was 41.7 mol%, determined by the HPLC method described by Tamaoka & Komagata (1984).

A 16S rRNA gene of strain Fu11-5T was amplified by PCR with the universal primers U27F (5'-AGAGTTTGTATCCTGGGCTAG-3'; positions 8–27 in the Escherichia coli numbering system) and U1492R (5'-GGTTACCTTGT-TAGCAGTT-3'; positions 1510–1492), and the almost-complete sequence (1443 bp) was determined using primers U27F, U1492R, U520F (5'-AACCTCAAGGAGATTGC-3'), U920F (5'-AACTCAAGAGATTGC-3'), U520R (5'-ACCGCGCTGCGTGGC-3') and U920R (5'-GCTCAATTCC-TTTGAGTTT-3'). After alignment with the ARB software (Ludwig et al., 2004), phylogenetic trees were reconstructed by the neighbour-joining (NJ) method with the CLUSTAL_X program (Saitou & Nei, 1987; Thompson et al., 1997) and the maximum-likelihood (ML) method with the MOLPHY software version 2.3b3 (Felsenstein, 1981; Hasegawa et al., 1985). In addition, the posterior probabilities of branching points were estimated by Bayesian inference (BI) using MrBayes 3.1 (Huelsenbeck & Ronquist, 2001; Ronquist & Huelsenbeck, 2003), referring to the method and parameters described by Mori et al. (2008). The topologies of the trees determined by the three methods were almost identical. In the phylogenetic trees of the 16S rRNA gene sequences reconstructed using the NJ, ML and BI methods, strain Fu11-5T was located near Draconibacterium orientale FH5T (Du et al., 2014) and formed a distinct sublineage with the genera Meniscus (Irgens, 1977), Prolixibacter (Holmes et al., 2007), Sunxiuqinia (Qu et al., 2011), Mangrovibacterium (Huang et al., 2014) and Draconibacterium (Du et al., 2014) (Fig. 2). The branching at the base of this group was supported by a bootstrap percentage of 99–100 %. The 16S rRNA gene sequence of strain Fu11-5T showed 87.6–91.3 % sequence similarity to those of members of the five above-mentioned genera.

Morphological, biochemical and physiological properties of strain Fu11-5T, along with those of members of phylogenetically related genera, are summarized in Table 1. Some morphological, biochemical and physiological traits of strain Fu11-5T such as the rod-shaped cells, lack of motility, facultatively aerobic metabolism, mesophyly and neutrophility, were similar to those of the single species in the four related monospecific genera, namely Meniscus glaucopis (Irgens, 1977), Prolixibacter bellarivorans (Holmes et al., 2007), Mangrovibacterium diazotrophicum (Huang et al., 2014) and D. orientale (Du et al., 2014). However, the optimum temperature of strain Fu11-5T was slightly higher than those of these four species. Moreover, strain Fu11-5T differed from these taxa in the utilization of L-arabinose, D-ribose, D-fructose, D-glucose and D-mannose. Strain Fu11-5T was also different from Sunxiuqinia elliptica (Qu et al., 2011) and Sunxiuqinia faeciviva (Takah et al., 2013) in morphological and physiological properties, e.g. cell morphology, optimum growth temperature and utilization of sugars, as shown in Table 1.

On the basis of its distinct phylogenetic position, morphology and biochemical and physiological properties, strain Fu11-5T was distinguished from members of the five related genera Draconibacterium, Mangrovibacterium, Meniscus, Prolixibacter and Sunxiuqinia. Consequently, a novel species in a new genus, Mariniphaga anaerophila gen. nov., sp. nov., is proposed to accommodate strain Fu11-5T. Recently, the two families Prolixibacteraceae and Draconibacteriaceae have been proposed for two sublineages: the former accommodates Prolixibacter, Mangrovibacterium and Sunxiuqinia (Huang et al., 2014) and the latter accommodates Draconibacterium (Du et al., 2014). In the phylogenetic tree reconstructed by Du et al. (2014), the genus Draconibacterium was indicated to form a distinct sublineage that branched at the periphery of the five known families in the order Bacteroidales with the genera Mangrovibacterium, Marinifilum, Prolixibacter and Sunxiuqinia by a bootstrap percentage of 91 %, but the phylogenetic independence of the genus Draconibacterium from the genus Marinifilum and other related genera in this sublineage was not well supported, as shown by the low bootstrap percentage of 63 %. This implies that the family Draconibacteriaceae should not be retained for the single genus Draconibacterium and the species D. orientale. In our study, 16S rRNA gene sequence analysis revealed that the genera Meniscus (Irgens, 1977), Prolixibacter (Holmes et al., 2007), Sunxiuqinia (Qu et al., 2011), Mangrovibacterium (Huang et al., 2014), Draconibacterium (Du et al., 2014) and Mariniphaga gen. nov. formed a distinct phylogenetic lineage adjacent to the families Bacteroidaceae, Porphyromonadaceae, Prevotellaceae, Marinilablaceae and Rikenellaceae and the genus Marinifilum in the order

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**Bacteroidales** (Fig. 2). This lineage was strongly supported with high bootstrap values by the three phylogenetic analysis methods (99–100%). The cell morphology, oxygenic metabolism, major respiratory quinones and DNA G+C contents of these six genera are similar (Table 2). Therefore, the two lineages named *Prolixibacteraceae* and *Draconibacteriaceae* should be combined, and the name *Prolixibacteraceae* should be retained according to Rule 38 of the Bacteriological Code to avoid taxonomic complication and to keep priority of publication (Lapage et al., 1992). Fundamentally, the genus *Meniscus* (Irgens, 1977) should be assigned as the type genus of the taxon named *Prolixibacteraceae* rather than *Prolixibacter* (Holmes et al., 2007) according to Principle 8 of the Bacteriological Code.

However, the name *Prolixibacteraceae* is retained because this name is not illegitimate since the preceding proposal was based on a phylogenetic analysis without *Meniscus glaucopus* (Huang et al., 2014). Consequently, we propose to combine the family *Draconibacteriaceae* into the family *Prolixibacteraceae*. The name *Draconibacteriaceae* Du et al. 2014 would be regarded as a later heterotypic synonym of *Prolixibacteraceae* Huang et al. 2014. On the other hand, the genus *Marinifilum* was completely separated from all known families in the order *Bacteroidales* in the phylogenetic trees reconstructed by three methods (Fig. 2). We therefore propose a novel family for the distinct lineage accommodating the genus *Marinifilum*, to be named *Marinifilaceae* fam. nov.

![Phylogenetic tree of strain Fu11-5T and strains of related species based on 16S rRNA gene sequences.](image_url)

**Fig. 2.** Phylogenetic tree of strain Fu11-5T and strains of related species based on 16S rRNA gene sequences. The tree was based on an alignment of 1296 bp of the 16S rRNA gene sequence and reconstructed by using the NJ method. Open circles at branching nodes indicate supporting probabilities above 95% by all the phylogenetic analysis methods (NJ, ML and BI), and solid circles indicate probabilities above 85% by two or more analyses. Bootstrap probabilities at nodes A, B and C are as follows (NJ/ML/BI): A, 68/−/−; B, 99/99/100; C, 100/100/100. Lineage 1 represents the *Prolixibacteraceae* as defined in this study, and lineage 2 represents the *Marinifilaceae* fam. nov. Bar, 0.02 substitutions per nucleotide position.
Table 1. Morphological, biochemical and physiological properties of strain Fu11-5T and phylogenetic relatives

<table>
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<tr>
<th>Characteristic</th>
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<th>4</th>
<th>5</th>
<th>6</th>
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<tbody>
<tr>
<td>Cell form</td>
<td>Rods</td>
<td>Rods</td>
<td>Rods</td>
<td>Rods</td>
<td>Rods</td>
<td>Elliptical and rods</td>
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<tr>
<td>Cell length (μm)</td>
<td>2–7</td>
<td>1–2</td>
<td>5–6</td>
<td>2–3</td>
<td>10–12</td>
<td>0.8–28</td>
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<tr>
<td>Growth optima</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
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<tr>
<td>Temperature (°C)</td>
<td>35–37</td>
<td>28–32</td>
<td>25–30</td>
<td>30</td>
<td>22</td>
<td>30</td>
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<td>pH</td>
<td>6.5–7.0</td>
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<td>7–8</td>
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<td>0.5</td>
<td>ND</td>
<td>2</td>
<td>2–3</td>
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<td>Substrates for growth</td>
<td></td>
<td></td>
<td></td>
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<tr>
<td>l-Arabinose</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>D-Ribose</td>
<td>+</td>
<td>+</td>
<td>ND</td>
<td>ND</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>D-Xylose</td>
<td>–</td>
<td>+</td>
<td>ND</td>
<td>+</td>
<td>–</td>
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<tr>
<td>D-Fructose</td>
<td>–</td>
<td>+</td>
<td>ND</td>
<td>+</td>
<td>–</td>
<td>+</td>
</tr>
<tr>
<td>D-Glucose</td>
<td>+</td>
<td>+</td>
<td>–</td>
<td>+</td>
<td>+</td>
<td>–</td>
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<tr>
<td>D-Mannose</td>
<td>+</td>
<td>ND</td>
<td>+</td>
<td>–</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Lactose</td>
<td>+</td>
<td>ND</td>
<td>ND</td>
<td>+</td>
<td>–</td>
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<td>Maltose</td>
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<td>ND</td>
<td>+</td>
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<td>Sucrose</td>
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</tr>
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<td>D-Sorbitol</td>
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<td>ND</td>
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<td>–</td>
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<td>Soluble starch</td>
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<td>+</td>
<td>ND</td>
<td>ND</td>
<td>+</td>
<td>–</td>
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<tr>
<td>DNA G+C content (mol%)</td>
<td>41.7</td>
<td>42.0</td>
<td>43</td>
<td>44.9</td>
<td>44.9</td>
<td>43.5</td>
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</table>

*Values indicate NaCl concentrations added to the basal medium.

Description of Mariniphaga gen. nov.

Mariniphaga (Ma.ri.ni.pha’ga. L. adj. marinus marine; Gr. v. phagein to devour, to eat; N.L. fem. n. Mariniphaga a marine eater).

Facultatively aerobic, mesophilic, neutrophilic, moderately halophilic and chemo-organoheterotrophic bacteria. Gram-staining negative, non-sporulating and non-motile. Cells form rods. Catalase-negative and oxidase-negative. The major cellular fatty acids are iso-C15 : 0 and anteiso-C15 : 0. The major respiratory quinone is MK-7. The major polar lipid is phosphatidylethanolamine. The genomic DNA G+C content of the type strain of the type species is 41.7 mol%. The genus represents a distinct phylogenetic lineage in the family Prolibacteraceae based on 16S rRNA gene sequence analysis. The type species is Mariniphaga anaerophila.

Table 2. Taxonomic properties of the seven families of the order Bacteroidales

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<th>Characteristic</th>
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<tbody>
<tr>
<td>Cell form</td>
<td>Rods</td>
<td>Filamentous</td>
<td>Rods</td>
<td>Rods</td>
<td>Rods</td>
<td>Rods</td>
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<tr>
<td>Oxidogenic metabolism*</td>
<td>AN</td>
<td>FAN</td>
<td>FAN–AN</td>
<td>FAN–AN</td>
<td>AN</td>
<td>A–FAN</td>
</tr>
<tr>
<td>Major respiratory menaquinone(s)</td>
<td>10, 11</td>
<td>7</td>
<td>7</td>
<td>8, 9, 10, 11, 12</td>
<td>8, 9, 10, 11, 12, 13</td>
<td>7</td>
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</tbody>
</table>

*AN, Aerobic; AN, anaerobic; FAN, facultatively anaerobic.
Description of *Mariniphaga anaerophila* sp. nov.

*Mariniphaga anaerophila* (an.aer.o’phi.la. Gr pref. an-., not; Gr. n. aer, aeris air; N.L. fem. adj. philé friend to, loving; N.L. fem. adj. anaerophila not air-loving).

The following properties are given in addition to the genus description. Cells are 0.5–0.6 x 1.9–6.9 μm. Growth occurs at 20–40 °C with an optimum at 35–37 °C. The pH range for growth is 6.0–8.5 with an optimum around pH 6.5–7.0. Growth occurs below 9 % (w/v) NaCl, with an optimum at 1–2 % (w/v) NaCl. Oxygen [5 % (v/v) in N₂] is used as an alternative electron acceptor. Sulfate, sulfite, thiosulfate, elemental sulfur, nitrate, nitrite and iron(III) oxide are not used as alternative electron acceptors. L-Cysteine is used as an alternative electron donor. H₂/CO₂ (4 : 1, v/v), sulfide, elemental sulfur, sulfite, sulfate, ammonium and nitrate are not used as alternative electron donors. Fermentative growth occurs on L-arabinose, D-ribose, D-xylose, D-fructose, D-sorbose, D-mannitol or D-sorbitol.

The type strain is Fu11-5 T (DSM 26910 T), which was isolated from sediment of a tidal flat in Futsu, Chiba, Japan.

Emended description of *Prolixibacteraceae*  

*Prolixibacteraceae* Du et al. 2014

Later heterotypic synonym: *Draconibacteriaceae* Du et al. 2014.

The following properties are given in addition to those described by Huang et al. (2014). The family is defined on the basis of a phylogenetic tree reconstructed by phylogenetic analysis of the 16S rRNA gene sequence. The family accommodates the genera *Draconibacterium*, *Mangrovibacterium*, *Mariniphaga*, *Meniscus*, *Prolixibacter* and *Sunxiuqinia*. Gram-staining negative rods, non-sporulating, non-motile, aerobic to facultatively aerobic and chemo-organoheterotrophic. The major respiratory quinone is MK-7. The type genus is *Prolixibacter*.

Description of *Marinifilaceae* fam. nov.

*Marinifilaceae* (Ma.rin.i.fi.la’ceae. N.L. neut. n. Marinifila type genus of the family; L. suff. -aceae ending to denote a family; N.L. fem. pl. n. Marinifilaceae family of the genus Marinifilum).

The family is defined on the basis of a phylogenetic tree reconstructed by phylogenetic analysis of the 16S rRNA gene sequence. The family accommodates the genus *Marinifilum*. Gram-staining-negative, filamentous, non-sporulating, non-motile, facultatively anaerobic and chemo-organoheterotrophic. The major respiratory quinone is MK-7. The type genus is *Marinifilum*.

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References


