Description of *Ancylomarina subtilis* gen. nov., sp. nov., isolated from coastal sediment, proposal of *Marinilabiliales* ord. nov. and transfer of *Marinilabiliaceae*, *Prolixibacteraceae* and *Marinifilaceae* to the order *Marinilabiliales*

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A Gram-stain-negative, facultatively anaerobic, moderately halophilic, filamentous, non-motile bacterium, designated FA102^T, was isolated from marine sediment from the coast of Weihai, PR China. Phylogenetic analysis based on 16S rRNA gene sequences showed that strain FA102^T formed a distinct evolutionary lineage within the family *Marinifilaceae* and its closest relative was *Marinifilum fragile* JCM 15579^T (93.2 % sequence similarity). The DNA G+C content of the novel strain was 36.5 mol%. The predominant cellular fatty acids and respiratory quinone were iso-$C_{15:0}$ and iso-$C_{15:0}$ 3-OH, and MK-7, respectively. On the basis of the phylogenetic, phenotypic and physiological data, strain FA102^T represents a novel genus and species, for which the name *Ancylomarina subtilis* gen. nov., sp. nov. is proposed. The type strain of *Ancylomarina subtilis* is FA102^T (=KCTC 42257^T=DSM 28825^T=CICC 10902^T). Furthermore, a new order named *Marinilabiliales* is proposed to accommodate three families previously classified in the order *Bacteroidales*. *Marinilabiliales* ord. nov. encompasses the families *Marinilabiliaceae*, *Prolixibacteraceae* and *Marinifilaceae*.

At the time of writing, the phylum *Bacteroidetes* consists of four classes, *Bacteroidia*, *Flavobacteria*, *Sphingobacteria* and *Cytophagia* (Krieg, 2011). The class *Bacteroidia* contains a single order, *Bacteroidales*, consisting of seven families: *Bacteroidaceae*, *Porphyromonadaceae*, *Prevotellaceae*, *Rikenellaceae*, *Prolixibacteraceae*, *Marinibiliaceae* and *Marinifilaceae*. Although the majority of members of the order *Bacteroidales* were identified as being strictly anaerobic, more and more facultatively anaerobic and even aerobic species have been reported recently. The family *Marinifilaceae* was first proposed by Iino *et al.* (2014) on the basis of phylogenetic analysis of 16S rRNA gene sequences. The family *Marinifilaceae* contains only one genus, *Marinifilum* (Na *et al.*, 2009), representing a group of Gram-stain-negative, filamentous and non-motile bacteria. *Marinifilum fragile* was isolated from tidal flat sediment (Na *et al.*, 2009), and *Marinifilum flexuosum was* isolated from surface seawater (Ruvira *et al.*, 2013). Here, we report on a novel species in a new genus within the family *Marinifilaceae*, for which the name *Ancylomarina subtilis* gen. nov., sp. nov. is proposed. A novel order within the class *Bacterioidia* is proposed on the basis of 16S rRNA gene-sequence-based phylogenetic clustering and physiological and chemotaxonomic characteristics.

Strain FA102^T was isolated from a marine sediment sample from the coast of Weihai, PR China (37°32′01.93″ N 122°03′44.01″ E) by using an enrichment culture technique described previously (Du *et al.*, 2014) with incubation at 25 °C for 5 days. A pure culture of FA102^T was obtained after several rounds of dilution streaking on 2216E agar. The isolate was routinely cultured on 2216E agar and stored at −80 °C in sterile 1 % (w/v) NaCl supplemented with 15 % (v/v) glycerol. *M. fragile* JCM 15579^T, *Carboxylicivirga mesophila* JCM 18290^T and *Carboxylicivirga taeanensis* JCM 19490^T, and *M. flexuosum* DSM 21950^T and *Saccharicrinis fermentans* DSM 9555^T, which were used in parallel as reference strains for physiological tests and determination of chemotaxonomic characteristics (except polar lipids analysis), were obtained from the Japan Collection of Microorganisms (JCM) and Deutsche Sammlung von Mikroorganismen und Zellkulturen (DSMZ), respectively.

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The GenBank accession number for the 16S rRNA gene sequence of strain FA102^T is KP214056.

Two supplementary tables and three supplementary figures are available with the online Supplementary Material.

Cell morphology, size and motility were examined by transmission electron microscope (Jem-1200; JEOL) and light microscopy (Ci-L; Nikon). Gram staining was performed following the standard procedure as described by Smibert & Krieg (1994). Gilding motility was examined as described by Bowman (2000). The temperature range for growth of the strain was examined on 2216E agar (Hopebio) at 4, 8, 13, 17, 24, 28, 30, 33, 37, 42 and 45 °C. The pH range for growth was examined in 2216E liquid medium (Hopebio) by using 20 mM MES (pH 5.5 and 6.0), PIPES (pH 6.5 and 7.0), HEPES (pH 7.5 and 8.0), Tricine (pH 8.5) and CAPSO (pH 9.0 and 9.5) buffers over a pH range from 5.5 to 9.5 and then measuring the OD_{600}. The salt tolerance of the strain was determined on marine agar 2216 and in marine broth 2216 made with artificial seawater [containing (w/v) 0.6 % $MgCl_2$, 0.32 % Na_2SO_4, 0.18 % $CaCl_2$, 0.06 % KCl, 0.02 % Na_2CO_3 and traces of Na_2SiO_3 and NaF], with various concentrations of NaCl (0, 0.5 and 1.0−8.0 %, at 1 % intervals). Catalase and oxidase activities were examined as described by Wang *et al.*(2014). Growth on 2216E agar (Hopebio) with or without 0.1 % (w/v) $NaNO_3$ under anaerobic conditions was checked in an anaerobic chamber. Reduction of nitrate and hydrolysis of agar, starch, CM-cellulose, alginate and Tween 80 were examined as described by Dong & Cai (2001). Additional enzyme activities were determined using API ZYM strips, and acid production from carbon sources was assessed by using API 50CHB strips (both from bioMérieux) according to the manufacturer's instructions, with 2 % (w/v) NaCl. Other biochemical tests were performed using API 20E strips and API 20NE strips (bioMérieux). Substrate oxidation was examined by using GEN III MicroPlates (Biolog) according to the manufacturer's instructions. Antibiotic susceptibility tests were performed by the disc diffusion method on 2216E agar (Hopebio) (since FA102^T showed poor growth on Iso-Sensitest agar or Mueller–Hinton agar plates) according to the protocol of Du *et al.* (2014).

Cells of FA102^T at the late-exponential phase of growth in 2216E liquid medium (Hopebio) at 28 °C were used for characterization of isoprenoid quinones, cellular fatty acids and polar lipids. Analysis of isoprenoid quinone content was carried out by HPLC according to the method of Komagata & Suzuki (1987). The fatty acids of FA102^T, *M. fragile* JCM 15579^T and *M. flexuosum* DSM 21950^T were analysed by extraction and methylation according to the protocol of the Microbial Identification System (MIDI; Sasser, 1990). Analysis of the polar lipids of FA102^T was carried out by the Identification Service, Leibniz-Institut DSMZ (Braunschweig, Germany).

Genomic DNA was extracted and purified by using a genomic DNA extraction kit (TaKaRa). The DNA G+C content was determined by HPLC (Mesbah *et al.*, 1989). The almost-complete 16S rRNA gene sequence (1450 bp) of FA102^T was obtained by the method described by Wu *et al.* (2015). To identify the related taxa, sequences obtained were assembled by using the GenBank database and the EzTaxon server (Kim *et al.*, 2012). The latest version of the ARB-Silva reference database 123 (Yarza *et al.*, 2008) was also used to find phylogenetic relatives of FA102^T. Phylogenetic analysis was performed using the ARB software package (Ludwig *et al.*, 2004). Alignments were retrieved from SINA online (Pruesse *et al.*, 2012) and improved manually. Phylogenetic trees were reconstructed using the neighbour-joining (NJ) method with Jukes–Cantor correction, the maximum-likelihood (ML) method using RAxML8 with GTR-GAMMA model, and the maximum-parsimony (MP) method using DNAPARS version 3.6 in ARB. Sequences from almost all members of the class *Bacteroidia* available in the database were included. Furthermore, the arithmetical average distance between any two folded groups (sequences which clustered in a phyletic clade were folded as a group) visible in the ARB NJ tree shown was calculated using the 'Calculate Compressed Matrix' function in ARB.

FA102^T was a facultatively anaerobic bacterium. Cells were filamentous, approximately 0.3–0.4 μm wide and 2.9–30 μm long (Fig. S1, available in the online Supplementary Material). Non-motile and non-spore forming. Catalase and oxidase reactions were negative. Growth occurred at temperatures of 8–33 °C (optimum, 28–30 °C) and at pH 6.0–8.5 (optimum, pH 7.5). Growth occurred in the presence of 0.5–5.0 % (w/v) NaCl, with an optimum of 2.0 % (w/v) NaCl. FA102^T was susceptible to (μg per disc): erythromycin (15), chloramphenicol (30), rifampicin (5) and lincomycin (2), but resistant to ofloxacin (5), tobramycin (10), trimethoprim (5), nalidixic acid (30), norfloxacin (10), kanamycin (30) and neomycin (30).

The G+C content of genomic DNA of FA102^T was 36.5 mol %. The major respiratory quinone was MK-7, as has also been reported for members of the genus *Marinifilum*. The major cellular fatty acids (>5 %) of FA102^T were iso-$C_{15:0}$ (43.8 %), iso-$C_{15:0}$ 3-OH (14.5 %), iso-$C_{15:1}$F (8.8 %), iso-$C_{13:0}$ (6.0 %) and anteiso-$C_{15:0}$ (5.2 %), which differentiated FA102^T from species of the genus *Marinifilum* on the basis of the proportions of some cellular fatty acids (Table S1). The major polar lipids of FA102^T were phosphatidylethanolamine and two unidentified aminolipids. In addition, two unidentified phospholipids, three unidentified lipids and an unidentified phosphoaminolipid were present in moderate to minor amounts (Fig. S2). The polar lipid profile of FA102^T contained phosphoaminolipid but lacked aminophosphoglycolipid, which distinguished it clearly from that of *M. flexuosum* DSM 21950^T.

Comparative 16S rRNA gene sequence analysis using the EzTaxon server indicated that FA102^T shared the highest (93.2 %) 16S rRNA gene sequence similarity with *M. fragile* JCM 15579^T (Na *et al.*, 2009) and 92.8 % similarity with *M. flexuosum* DSM 21950^T (Ruvira *et al.*, 2013); it showed less than 89 % similarity with other members of the class *Bacteroidia*. Phylogenetic analysis showed that FA102^T formed a distinct evolutionary lineage within the family *Marinifilaceae* in the NJ (Fig. 1), ML and MP trees (Fig. S3a, b) and placed it in a phylogenetic position most closely related to the members of the genus *Marinifilum*, with high bootstrap values (100 %,

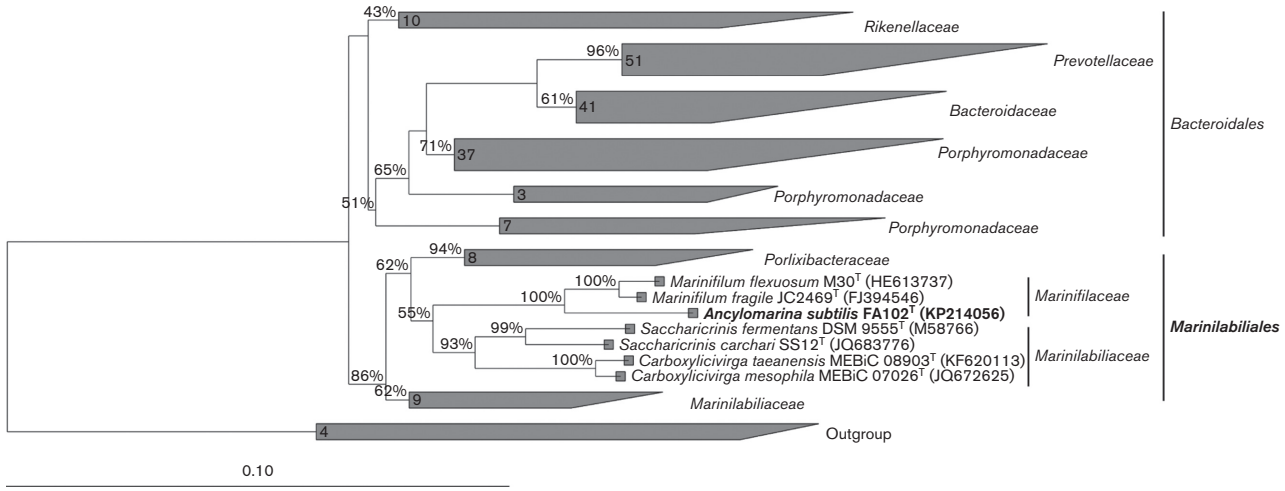

Fig. 1. Phylogenetic tree based on 16S rRNA gene sequences using the neighbour-joining method, showing the positions of FA102^T and members of the class *Bacteroidia*. The database of LTP release 123 was used. Four different sequences (*Lentisphaera araneosa* HTCC2155^T, *Lentisphaera marina* IMCC11369^T, *Victivallis vadensis* ATCC BAA-548^T and *Oligosphaera ethanolica* 8KG-4^T) within the *Lentisphaerae* were used as the outgroup. Bootstrap values (>40 %) based on 1000 replications are shown at nodes. Bar, 0.1 substitutions per nucleotide position.

98 %, 100 %, respectively). These relatively low levels of 16S rRNA gene sequence similarity with closely related neighbours suggested that FA102^T represents a novel species of a new genus in the family *Marinifilaceae*.

Detailed morphological and biochemical data for FA102^T are given in the genus and species descriptions. FA102^T was filamentous, lacked gliding motility and was catalase-negative, similar to members of the genus *Marinifilum*, while species of the genera *Saccharicrinis* and *Carboxylicivirga* are rods, show gliding motility and are catalase-positive. FA102^T could grow at 15 °C and hydrolyse alginate, whereas members of the genus *Marinifilum* do not. FA102^T differed from the members of the genus *Marinifilum* as the latter have activity of oxidase and trypsin, but not esterase or chymotrypsin, whereas FA102^T showed opposite results. The phenotypic characteristics that differentiate FA102^T from its closest phylogenetic neighbours are given in Table 1. Therefore, on the basis of the above morphological, physiological and phylogenetic evidence, strain FA102^T represents a novel genus and species, for which the name *Ancylomarina subtilis* gen. nov., sp. nov. is proposed.

The average 16S rRNA gene sequence similarities between any two groups of families of the class *Bacteroidia*, based on the 'Calculate Compressed Matrix' function implemented in the ARB program, are shown in Table S2. The sequence similarities (90.3 %, 90.5 % and 91.1 %, respectively) of the members of families *Marinilabiliaceae*, *Prolixibacteraceae* and *Marinifilaceae* indicated that the three families were more closely related to each other than to the other four families (83.7–88.6 %). In the NJ tree (Fig. 1), members of these three families, *Marinilabiliaceae*, *Prolixibacteraceae* and *Marinifilaceae*, were found to form a separate branch within the class *Bacteroidia* with a bootstrap percentage of 86 %. In the ML and MP trees (Fig. S3a, b), the three families *Marinilabiliaceae*, *Prolixibacteraceae* and *Marinifilaceae* formed a subgroup, the families *Bacteroidaceae*, *Prevotellaceae* and *Porphyromonadaceae* formed another subgroup, while the family *Rikenellaceae* was found to form a clade with the families *Marinilabiliaceae*, *Prolixibacteraceae* and *Marinifilaceae* with low bootstrap support. Because members of the family *Rikenellaceae* are strictly anaerobes, mostly isolated from human and animal clinical specimens, and the major respiratory quinone is MK-8, the family *Rikenellaceae* should be retained in the order *Bacteroidales*. Furthermore, members of these families *Marinilabiliaceae*, *Prolixibacteraceae* and *Marinifilaceae* have been isolated mainly from aquatic environments, while members of these families *Bacteroidaceae*, *Prevotellaceae*, *Porphyromonadaceae* and *Rikenellaceae* were recovered mainly from various terrestrial environments, such as human and animal clinical specimens. Most members of the families *Bacteroidaceae*, *Prevotellaceae*, *Porphyromonadaceae* and *Rikenellaceae* are strictly anaerobic bacteria, whereas most members of the families *Marinilabiliaceae*, *Prolixibacteraceae* and *Marinifilaceae* are facultatively anaerobic or even aerobic. The major respiratory quinone present in members of the families *Marinilabiliaceae*, *Prolixibacteraceae* and *Marinifilaceae* is MK-7, while those of members of the families *Bacteroidaceae*, *Porphyromonadaceae*, *Prevotellaceae* and *Rikenellaceae* are MK-8, MK-9, MK-10, MK-11, MK-12 and MK-13. The differential characteristics which characterize the seven families in the class *Bacteroidia* are shown in Table 2. The above characteristics justify the creation of a new order, *Marinilabiliales* ord. nov., to accommodate the families *Marinilabiliaceae*, *Prolixibacteraceae* and *Marinifilaceae*. The revised order *Bacteroidales* contains four families: *Bacteroidaceae*,

Table 1. Comparison of major features of strain FA102^T with its phylogenetically related neighbours

Strains: 1, FA102^T; 2, *Marinifilum fragile* JCM 15579^T; 3, *Marinifilum flexuosum* DSM 21950^T; 4, *Saccharicrinis carchari* SS12^T; 5, *Saccharicrinis fermentans* DSM 9555^T; 6. *Carboxylicivirga mesophila* JCM 18290^T; 7, *Carboxylicivirga taeanensis* JCM 19490^T. All data were obtained as part of this study unless indicated otherwise. All strains are facultatively anaerobic and are positive for alkaline phosphatases and acid phosphatase activities. +, Positive; −, negative; V, variable; W, weak; ND, no data available.

Characteristic	1	2	3	4	5	6	7
Cell form	Filamentous	Filamentous	Filamentous	Rods	Rods	Rods	Rods
Gliding motility	−	−	−	+	+	−	+
Growth at 15 °C	+	−	−	+	−	−	+
Optimal temperature (°C)	28–30	33	25–30†	28–30	30	30	30
Oxidase activity	−	+	W	−	−	−	−
Catalase activity	−	−	−	+	+	+	+
Nitrate reduction	−	+	−	+	−	−	+
Indole production	+	+	+	+	−	V	−
Hydrolysis of gelatin	+	+	+	−	−	+	−
Enzymatic activities							
Esterase	+	−	−	W	+	−	+
Trypsin	−	+	+	+	−	+	+
Chymotrypsin	+	−	−	−	−	−	+
Acid production from:							
Aesculin	−	−	+	+	+	+	+
Cellobiose	−	−	+	+	+	+	−
Polar lipids*	PE, ALs, PL, Ls, PN	ND	PE, Ls, PLs, AL, PNGL‡	PE, Ls, GL, PLs§	PE, Ls‖	PE, Ls‖	PE, Ls‖

*PE, phosphatidylethanolamine; AL, unidentified aminolipid; PL, unidentified phospholipid; GL, unknown glycolipid; L, unidentified lipid; PN, Phosphoaminolipid; PNGL, unidentified aminophosphoglycolipid.
†Result not consistent with the original report.
Data taken from ‡, Ruvira *et al.* (2013); §, Liu *et al.* (2014a); ‖, Yang *et al.* (2014).

Prevotellaceae, *Porphyromonadaceae* and *Rikenellaceae*. Thus, we propose the novel order *Marinilabiliales* ord. nov., named after its oldest standing genus.

Description of *Ancylomarina* gen. nov.

Ancylomarina (An.cy.lo.ma.ri′na. Gr. adj. *ankulos* crooked, curved; L. fem. adj. *marina* of the sea, marine; N.L. fem. n. *Ancylomarina* crooked bacterium isolated from seawater).

Cells are Gram-stain-negative, filamentous and non-motile. Oxidase- and catalase-negative. Facultatively anaerobic and moderately halophilic. NaCl is required for growth. The predominant fatty acids are iso-$C_{15:0}$ and iso-$C_{15:0}$ 3-OH. The major respiratory quinone is MK-7. As determined by 16S rRNA gene sequence analysis, the genus is affiliated to the family *Marinifilaceae*. The type species is *Ancylomarina subtilis*.

Description of *Ancylomarina subtilis* sp. nov.

Ancylomarina subtilis (sub′ti.lis. L. fem. adj. *subtilis* slender, referring to the slender cells).

Displays the following characteristics in addition to those given in the genus description. Cells are 0.3–0.4 μm in width by 2.9–30 μm in length (Fig. S1). Colonies on 2216E agar (Hopebio) are circular, in some cases with erose edges and beige colour, 1–1.5 mm in diameter after 2–3 days of incubation at 28 °C. Grows at temperatures of 8–33 °C (optimum, 28–30 °C) and at pH 6.0–8.5 (optimum, pH 7.5). Grows in the presence of 0.5–5.0 % (w/v) NaCl (optimum, 2.0 %). Nitrate is not reduced. Alginate is hydrolysed, agar is slightly hydrolysed, but starch, CM-cellulose and Tween 80 are not hydrolysed. The results of ONPG, indole production and gelatinase tests are positive, but arginine dihydrolase, lysine decarboxylase, ornithine decarboxylase, Simmons' citrate utilization, H_2S production, urease, tryptophan deaminase and Voges–Proskauer reaction are negative. Positive responses for aesculin and PNPG, as well as hydrolysis of gelatin. Glucuronamide and L-malic acid are oxidized. Acid is produced from D-galactose, D-glucose, *N*-acetylglucosamine and potassium 5-ketogluconate. Positive for alkaline phosphatase, esterase (C4), chymotrypsin, acid phosphatase, naphthol-AS-BI-phosphohydrolase and *N*-acetyl-β-glucosaminidase, but negative for esterase lipase (C8), lipase (C14), leucine arylamidase, valine arylamidase, cystine arylamidase, trypsin, α-galactosidase, β-galactosidase, β-glucosidase, β-glucuronidase, α-glucosidase, α-mannosidase and β-fucosidase. Principal fatty acids (above 5 %) are iso-$C_{15:0}$, iso-$C_{15:0}$ 3-OH, iso-$C_{15:1}$F, iso-$C_{13:0}$ and anteiso-$C_{15:0}$. The major polar lipids are phosphatidylethanolamine and two unidentified aminolipids. In addition, two unidentified phospholipids, three unidentified lipids and

Table 2. Differential characteristics of the two orders and seven families in the class *Bacteroidia*

Families: 1, *Bacteroidaceae* [four genera (*n*=4); Krieg, 2011; Bouanane-Darenfed *et al.*, 2015; Hania *et al.*, 2016]; 2, *Porphyromonadaceae* (*n*=15; Sakamoto & Benno, 2006; Hardham *et al.*, 2008; Sakamoto *et al.*, 2009; Krieg, 2011; Jabari *et al.*, 2012; Shkoporov *et al.*, 2013; Sánchez-Andrea *et al.*, 2014; Wagener *et al.*, 2014); 3, *Prevotellaceae* (*n*=3; Moore & Moore, 1994; Morotomi *et al.*, 2009; Krieg, 2011; Downes *et al.*, 2013); 4, *Rikenellaceae* (*n*=5; Krieg, 2011; Abe *et al.*, 2012; Su *et al.*, 2014; Nelson *et al.*, 2015); 5, *Marinilabiliaceae* (*n*=10; Krieg, 2011; Sorokin *et al.*, 2011; Miyazaki *et al.*, 2012; Zhao *et al.*, 2012; Zhao & Chen, 2012; Gao *et al.*, 2013; Yang *et al.*, 2014); 6, *Prolixibacteraceae* (*n*=8; Irgens, 1977; Holmes *et al.*, 2007; Qu *et al.*, 2011; Takai *et al.*, 2013; Du *et al.*, 2014; Huang *et al.*, 2014; Iino *et al.*, 2014; Liu *et al.*, 2014b; Wu *et al.*, 2015); 7, *Marinifilaceae* (*n*=1; Na *et al.*, 2009; Ruvira *et al.*, 2013; present study). Members of all families are Gram-stain-negative and non-spore-forming. +, Positive; −, negative; $+^{-}$, >60 % positive; $-^{+}$, >60 % negative, ND, no data available.

Characteristic	*Bacteroidales*				*Marinilabiliales*		
	1	2	3	4	5	6	7
Isolation source	Human and animal clinical specimens, sewage sludge	Human and animal clinical specimens, waste water, soil environment	Human and animal clinical specimens, soil environment	Human and animal clinical specimens, reed swamp	Marine sediment, soda lake, hot spring, oilfield	Marine sediment, seawater	Marine sediment, seawater, tidal flat
Oxygenic metabolism*	AN	AN†	AN	AN	FAN/AN	A/FAN	FAN
Motility	−	−‡	−	−	+§	−‖	−
Catalase	$-^{+}$	$-^{+}$	−	$-^{+}$	$+^{-}$	$+^{-}$	−
Nitrate reduction	−	$-^{+}$	−	−	$-^{+}$	$-^{+}$	$-^{+}$
Gelatin hydrolysis	$-^{+}$	$-^{+}$	$+^{-}$	$+^{-}$	$+^{-}$	$+^{-}$	$-^{+}$
Indole production	$-^{+}$	$+^{-}$	$-^{+}$	$+^{-}$	$-^{+}$	$+^{-}$	+
DNA G+C content (mol%)	34–62	37–58	39–60	32–61	37–44	37–47	35–37
Major fatty acids	anteiso-$C_{15:0}$, iso-$C_{15:0}$	anteiso-$C_{15:0}$, iso-$C_{15:0}$	anteiso-$C_{15:0}$, $C_{18:1}\omega 9c$	iso-$C_{15:0}$	iso-$C_{15:0}$, anteiso-$C_{15:0}$	iso-$C_{15:0}$, anteiso-$C_{15:0}$, iso-$C_{17:0}$ 3-OH	iso-$C_{15:0}$, anteiso-$C_{15:0}$
Major respiratory menaquinone(s)	MK-10, MK-11	MK-8, MK9, MK-10, MK-11, MK-12	MK-8, MK9, MK-10, MK-11, MK-12, MK-13	MK-8	MK-7	MK-7	MK-7
Polar lipids¶	ND	PE, PL, APL (L, PG, AL, GL, PGL)	ND	PE, PL, APL, L	PE, L, PL (AL, GL, APL, DPG)	PE, L, PL, GL (AL, APL, DPG)	PE, AL, PL, L (PN, PNGL)

*A, Aerobic; AN, anaerobic; FAN, facultatively anaerobic.
†Unlike the members of the genus *Dysgonomonas* which are facultatively anaerobic.
‡Unlike *Proteiniphilum acetatigenes*, the strain is motile by means of lateral flagella.
§Strains of the family *Marinilabiliaceae* have gliding motility.
‖Unlike *Sunxiuqinia faeciviva*, the strain has gliding motility.
¶Polar lipids in parentheses were observed in <50 % of genera for which data are available in each family. PE, phosphatidylethanolamine; PG, phosphatidylglycerol; APL, unidentified aminophospholipid; PL, unidentified phospholipid; GL, unidentified glycolipid; L, unidentified lipid; AL, unidentified aminolipid; DPG, diphosphatidylglycerol; PN, Phosphoaminolipid; PGL, phosphoglycolipid; PNGL, unidentified aminophosphoglycolipid.

another unidentified phosphoaminolipid are present in moderate to minor amounts.

The type strain, FA102^{T} (=KCTC 42257^{T}=DSM 28825^{T}=CICC 10902^{T}), was isolated from marine sediment of the coast of Weihai, China. The DNA G+C content of the type strain of the type species is 36.5 mol%.

Description of *Marinilabiliales* ord. nov.

Marinilabiliales (Ma.ri.ni.la.bi.li.a'les. N.L. fem. n. *Marinilabilia* type genus of the order; suff. *-ales* ending to denote an order; N.L. fem. pl. n. *Marinilabiliales* the *Marinilabiliales* order).

Cells are Gram-stain-negative. Straight or curved rods or filamentous. Mesophilic. Non-endospore-forming. Mostly facultatively anaerobic. Non-motile or motile by gliding. The major respiratory quinone is MK-7. The major polar lipid include phosphatidylethanolamine. The order includes the families *Marinilabiliaceae*, *Prolixibacteraceae* and *Marinifilaceae*. *Marinilabilia* is the type genus.

Acknowledgements

This work was supported by the National Natural Science Foundation of China (31370057) and 2013 Shandong Provincial Second Group Projects on Resource Platforms for Marine Economic and Innovative

Development Regions: Marine Microorganisms Preservation Platform (2150299).

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