Marinithermofilum abyssi gen. nov., sp. nov. and Desmospora profundinema sp. nov., isolated from a deep-sea sediment, and emended description of the genus Desmospora Yassin et al. 2009

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Two novel filamentous bacteria, strains SCSIO 11157T and SCSIO 11154T, were isolated from a deep-sea sediment sample. Strain SCSIO 11157T grew optimally at 55–60°C, while strain SCSIO 11154T grew optimally at 40°C. Both strains produced aerial and substrate mycelia. Phylogenetic analysis of the 16S rRNA gene sequences of strains SCSIO 11157T and SCSIO 11154T showed that the isolates were affiliated to the family Thermoaetinomycetaceae. The two isolates contained LLL-diaminopimelic acid as the cell-wall diamino acid, and did not have diagnostic sugars. The major polar lipids of strain SCSIO 11157T were diphasphatidylglycerol, phosphatidylphosphatidylethanolamine, phosphatidylethanolamine and phosphatidylglycerol, and the major polar lipids of SCSIO 11154T were diphasphatidylglycerol, phosphatidylglycerol and phosphatidylethanolamine. The predominant menaquinone of both strains was MK-7. The major cellular fatty acids of strain SCSIO 11157T were iso-C15:0, C18:1ω9c and iso-C17:0, and strain SCSIO 11154T contained iso-C15:0 and iso-C17:0 as major fatty acids. The DNA G+C contents of strains SCSIO 11157T and SCSIO 11154T were 54.2 and 51.8 mol %, respectively. On the basis of its phenotypic and phylogenetic properties, strain SCSIO 11157T represents a novel species in the new genus, for which we propose the name Marinithermofilum abyssi gen. nov., sp. nov. The type strain of Marinithermofilum abyssi is SCSIO 11157T (=CGMCC 1.15179T=NBRC 109939T). Strain SCSIO 11154T represents a novel species of the genus Desmospora, for which we propose the name Desmospora profundinema sp. nov. The type strain is SCSIO 11154T (=DSM 45903T=NBRC 109626T).

On the basis of phylogenetic analysis and chemotaxonomic characteristics, the genus Thermoaetinomycetes (Tsilinsky, 1899) was reclassified in a new family, Thermoaetinomycetaceae (Matsuo et al., 2006), which consisted of six genera: Thermoaetinomyces, Laceyella, Thermoflavimicrobium, Seinonella (Yoon et al., 2005), Planifilum (Hatayama et al., 2005) and Mechercharimyces (Matsuo et al., 2006). At the time of writing, 16 genera and 29 recognized species have been described in the family Thermoaetinomycetaceae. The genera Shimazuella (Park et al., 2007), Desmospora (Yassin et al., 2009), Kropkenstedtia (von Jan et al., 2011), Melghirimyces (Addou et al., 2012), Lihuaxuella (Yu et al., 2012), Marininema (Li et al., 2012), Polyclaydomyces (Tsubouchi et al., 2013), Hazenella (Buss et al., 2013), Geothermamicrobium (Zhou et al., 2014) and Salinitrix (Zarparvar et al., 2014) have been found in succession and assigned to this family. Strains of this family have been isolated from various environmental samples, such as marine sediments, salt lakes, sugar cane, mushroom compost and clinical samples. We noticed that some members of the Thermoaetinomycetaceae were isolated recently from deep-sea environments (Li et al., 2012, 2013; Tsubouchi et al., 2013). During an investigation of micro-organism populations from marine sediments, two new members of the family Thermoaetinomycetaceae were isolated. In the present study, the aim

Abbreviation: DAP, dianaminopimelic acid.

The GenBank/EMBL/DDBJ accession numbers for the 16S rRNA gene sequences of strains SCSIO 11157T and SCSIO 11154T are KM368341 and KM368342, respectively.

Five supplementary figures and a supplementary table are available with the online Supplementary Material.
was to determine the taxonomic positions of strains SCSIO 11157<sup>T</sup> and SCSIO 11154<sup>T</sup> by using a polyphasic approach.

With the serial dilution technique, strains SCSIO 11157<sup>T</sup> and SCSIO 11154<sup>T</sup> were isolated using R2A medium (BD) (per litre distilled water: 0.5 g yeast extract, 0.5 g proteose peptone no. 3, 0.5 g Casamino acids, 0.5 g glucose, 0.5 g soluble starch, 0.3 g sodium pyruvate, 0.3 g dipotassium phosphate, 0.05 g magnesium sulfate, 15.0 g agar) from a sediment sample collected from the Indian Ocean (1° 03.300' N80° 03.099' E) at a depth of 4593 m (pH 7.8; salinity 15 p.p.t.). Isolates SCSIO 11157<sup>T</sup> and SCSIO 11154<sup>T</sup> were routinely cultivated on modified nutrient agar (per litre distilled water: 10 g soya peptone, 3 g beef extract desiccant, 12 g agar, pH 7.2–7.4) at 60 and 40 °C, respectively, and stored as aqueous glycerol suspensions (20 %, v/v) at −80 °C.

Cultural characteristics, including the growth and colour of substrate and aerial mycelia and the production of diffusible pigments, were observed on yeast extract-malt extract agar (ISP medium 2), oatmeal agar (ISP medium 3), inorganic salts-starch agar (ISP medium 4) and glycerol-asparagine agar (ISP medium 5) (Shirling & Gottlieb, 1966), Ćzapek’s agar (Dong & Cai, 2001) and modified nutrient agar for 3, 8 and 15 days at 60 and 40 °C for strains SCSIO 11157<sup>T</sup> and SCSIO 11154<sup>T</sup>, respectively. All media were prepared with distilled water. The colour of both substrate and aerial mycelia and any soluble pigments produced were determined by comparing with chips from the colour charts of the Inter-Society Color Council (Kelly, 1964). Strain SCSIO 11157<sup>T</sup> was incubated on modified nutrient agar at 60 °C for 1 day and strain SCSIO 11154<sup>T</sup> for 15 days at 40 °C, and morphological characteristics were then observed by using a light microscope (BH-2; Olympus) and a scanning electron microscope (S-3000N; Hitachi).

Gram staining was tested by using a Gram stain kit (Guangdong HuanKai Microbial Sci. & Tech. Co.), Growth at 20–70 °C (at intervals of 5 °C) and 0, 1, 3, 5, 7 and 10 % (w/v) NaCl was tested using modified nutrient agar as the basal medium. Growth at pH 4, 5, 6, 7, 8, 9 and 10, generated using the buffer system described by Xu et al. (2005), was tested by culturing the strains in tryptic soy broth (TSB) for 3 days. Degradation of various specific substrates was determined as described by Gordon (1966) and Dong & Cai (2001). Hydrolysis of gelatin was tested by incubating strains SCSIO 11157<sup>T</sup> and SCSIO 11154<sup>T</sup> on peptone-gelatin medium (per litre distilled water: 5 g peptone and 120 g gelatin, pH 7.2–7.4), and the tubes were held at 4 °C for 30 min before the observation of results. Degradation of starch was determined on modified nutrient agar supplemented with 1 % (w/v) starch, with a positive result indicated by the presence of an unstained zone around the colonies after iodine solution was added to the cultures. Coagulation and peptonization of milk were determined by incubating with 20 % (w/v) skimmed milk as the medium. Degradation of casein was determined on plates containing 5 % (w/v) milk powder, 0.5 % (w/v) NaCl and 1.5 % (w/v) agar; positive results were indicated by clear zones around the colonies. Urease activity was determined on peptone-glucose agar comprising (per litre distilled water) 1 g peptone, 1 g glucose, 5 g NaCl and 2 g KH₂PO₄, supplemented with 2 % (w/v) urea and 0.001 % (w/v) phenol red, pH 6.8–6.9. Catalase activity was detected by observing the production of bubbles after the addition of a drop of 3 % (v/v) H₂O₂. Oxidase activity was determined by the oxidation of tetramethyl p-phenylenediamine. Nitrate reduction was performed as described by Lányi (1987). The Voges–Proskauer test was determined by using a test kit (Guangdong HuanKai Microbial Sci. & Tech. Co.). ISP medium 9 (Shirling & Gottlieb, 1966) was used as basal medium for sole carbon source utilization tests. More biochemical characteristics were investigated using API ZYM test kits (bioMérieux) according to the manufacturer’s instructions.

Biomass for analyses of polar lipids, isoprenoid quinones and DNA G+C contents of strains SCSIO 11157<sup>T</sup> and SCSIO 11154<sup>T</sup> was obtained using cells cultured in modified nutrient broth on a rotary shaker (about 200 r.p.m.) and harvested at the exponential growth phase. Polar lipids were examined by two-dimensional TLC and identified as described previously (Minnikin et al., 1979; Collins & Jones, 1980). Menaquinones were extracted according to Collins et al. (1977) and separated by HPLC (Tamaoka et al., 1983). Cell-wall samples were prepared according to the method described by Uchida & Aida (1977), and the diaminopimelic acid (DAP) isomer was then analysed by TLC as described by Staneck & Roberts (1974). The acyl type of the cell wall was examined according to Uchida & Aida (1977). Diagnostic sugars of whole-cell hydrolysates were analysed according to the procedures described by Lechevalier & Lechevalier (1980). The G+C content of the genomic DNA was analysed by using the HPLC method (Mesbah et al., 1989). For cellular fatty acid analysis, cell mass was obtained from cultures grown in TSB on a rotary shaker (200 r.p.m.) at the late-exponential growth phase. Cellular fatty acids were extracted, methylated and analysed by using the Sherlock Microbial Identification System (MIDI) according to the manufacturer’s instructions. Fatty acid methyl esters were identified by using the Microbial Identification Software package (Sherlock version 4.5; MIDI database, TSBA40).

Extraction of genomic DNA, PCR amplification and sequencing of the 16S rRNA gene were performed as described previously (Li et al., 2007). The 16S rRNA gene sequences of strains SCSIO 11157<sup>T</sup> and SCSIO 11154<sup>T</sup> were compared with available 16S rRNA gene sequences from GenBank using the BLAST program (http://blast.ncbi.nlm.nih.gov/Blast.cgi) and the EzTaxon server (http://www.ezbiolab.org/etaxon; Kim et al., 2012). Multiple alignments with sequences of the most closely related strains were tested by CLUSTAL_X (Thompson et al., 1997). Phylogenetic trees were reconstructed with the software package MEGA version 5.0 (Tamura et al., 2011) using the neighbour-joining (Saitou & Nei, 1987), maximum-parsimony (Fitch, 1971)
and maximum-likelihood (Felsenstein, 1981) tree-making algorithms. Besides strains SCSIO 11157T and SCSIO 11154T, all type strains in the family Thermoactinomycetaceae were included in the phylogenetic trees. Topologies of the phylogenetic trees were evaluated by using the bootstrap resampling method of Felsenstein (1985) based on 1000 resamplings.

Strain SCSIO 11157T grew well on modified nutrient agar and Czapek’s agar and grew weakly on ISP media 3 and 5, and formed pale-yellow substrate mycelium with radial crumpled colonies on these four media. No growth occurred on ISP medium 2 or 4. Strain SCSIO 11154T grew well on modified nutrient agar and Czapek’s agar, and formed yellow–white substrate mycelium with radial crumpled colonies. It grew weakly and formed pale-yellow substrate mycelium with radial crumpled colonies on ISP media 3, 4 and 5; no growth occurred on ISP medium 2. Neither strain produced soluble pigments on any of the tested media, and aerial mycelium could not be observed with the naked eye. Microscope observation revealed that strain SCSIO 11157T produced endospores on the substrate mycelium, and formed chains of arthrospores on the aerial mycelium (Fig. S1, available in the online Supplementary Material). Strain SCSIO 11154T produced single endospores with unbranched sporophores on the substrate mycelium and produced short chains of arthrospores on the aerial mycelium (Fig. S2).

Growth of strain SCSIO 11157T was observed at 35–65 °C (optimum 55–60 °C), at pH 6.0–8.0 (optimum pH 7.0) and in the presence of 0–1% (w/v) NaCl. Strain SCSIO 11154T grew at 25–50 °C (optimum 40 °C), at pH 7.0–9.0 (optimum pH 8.0) and in the presence of 0–7% (w/v) NaCl. The results of other physiological and biochemical tests are shown in Table 1 and in the species descriptions.

Both strains SCSIO 11157T and SCSIO 11154T contained LL-DAP as the cell-wall diamino acid, and their cell-wall acyl type was N-glycolyl. No characteristic sugars were detected in whole-cell hydrolysates. The polar lipids of strain SCSIO 11157T consisted of diphosphatidylglycerol, phosphatidylmethylethanolamine, phosphatidylyethanolamine, phosphatidylglycerol, five unknown phospholipids and one unknown polar lipid (Fig. S3a, b). The polar lipids of strain SCSIO 11154T consisted of diphosphatidylglycerol, phosphatidylglycerol, phosphatidylyethanolamine, three unknown phospholipids and one unknown polar lipid (Fig. S3c, d). The predominant menaquinone of both strains was MK-7, and no other menaquinones were detected. The major fatty acids (>10% of the total fatty acids) of strain SCSIO 11157T were iso-C15:0 (40.52%), C18:1ω9c (11.89%) and iso-C17:0 (10.04%), and those of strain SCSIO 11154T were iso-C15:0 (66.03%) and iso-C17:0 (14.53%). Detailed fatty acid profiles are given in Table S1. The genomic DNA G+C contents of strains SCSIO 11157T and SCSIO 11154T were 54.2 and 51.8 mol%, respectively.

The almost-complete 16S rRNA gene sequences of strains SCSIO 11157T (1523 bp) and SCSIO 11154T (1511 bp) were determined in this study. The similarity of the 16S rRNA gene sequences of strains SCSIO 11157T and SCSIO 11154T was 95.79%. The highest 16S rRNA gene sequence similarity between strain SCSIO 11157T and other type strains, determined using EzTaxon (http://www.ezbiocloud.net/eztaxon; Kim et al., 2012), was to Melghirimyces profundicolus SCSIO 11153T (96.49%), Polycladomyces abyssicola JIR-001T (95.96%), Melghirimyces algeriensis NariEXT (95.63%), Salinithrix halophila R4S8T (95.29%) and Desmospora activa IMMIB L-1269T (94.94%). Strain SCSIO 11157T formed a separate branch in a clade that included the genera Melghirimyces, Kroppenstedtia, Polycladomyces and Planilimum (Fig. 1); this topology was also supported by using the maximum-parsimony (Fig. S4) and maximum-likelihood (Fig. S5) tree-making algorithms. The level of DNA–DNA relatedness between strain SCSIO 11154T and other type strains was to Desmospora activa IMMIB L-1269T (96.56%), Salinithrix halophila R4S8T (95.96%), Mariniinema mesophilum SCSIO 10219T (94.74%), Melghirimyces algeriensis NariEXT (94.68%), Kroppenstedtia guangzhouensis GD02T (94.22%) and Kroppenstedtia eburnea JFMB-ATET (94.08%). In the neighbour-joining tree, strain SCSIO 11154T formed a distinct clade with Desmospora activa IMMIB L-1269T (Fig. 1); this topology was also supported by using the maximum-parsimony (Fig. S4) and maximum-likelihood (Fig. S5) tree-making algorithms. The phylogenetic analysis showed that strains SCSIO 11157T and SCSIO 11154T were members of the family Thermoactinomycetaceae.

Besides the phylogenetic evidence, the phenotypic characteristics of strains SCSIO 11157T and SCSIO 11154T, such as being Gram-positive, showing filamentous growth and producing endospores, are typical of the family Thermoactinomycetaceae. Strains SCSIO 11157T and SCSIO 11154T can be distinguished easily from each other by differences in phenotypic characteristics as well as the phylogenetic evidence. Growth temperature range and NaCl tolerance clearly differentiate strain SCSIO 11157T from SCSIO 11154T (Table 1). In addition, strain SCSIO 11157T contains phosphatidymethylethanolamine, which is absent from strain SCSIO 11154T. The phylogenetic and phenotypic evidence supports the conclusion that strains SCSIO 11157T and SCSIO 11154T are representatives of different species.

In the phylogenetic tree, strain SCSIO 11157T formed a distinct branch in a clade including the genera Melghirimyces, Kroppenstedtia, Polycladomyces and Planilimum. DNA–DNA hybridization results showed relatively high genomic divergence between strain SCSIO 11157T and the type strain of Melghirimyces profundicolus. In addition, strain SCSIO...
Table 1. Differential phenotypic characteristics of strains SCSIO 11157<sup>T</sup> and SCSIO 11154<sup>T</sup> and their closest relatives in the family Thermoactinomycetaceae

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
<th>5</th>
<th>6</th>
<th>7</th>
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<tr>
<td>Aerial mycelium</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>-</td>
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<td>Degradation of:</td>
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<tr>
<td>Gelatin</td>
<td>–</td>
<td>–</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>–</td>
<td>+</td>
<td>+&lt;sup&gt;a&lt;/sup&gt;</td>
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<tr>
<td>Starch</td>
<td>+</td>
<td>+</td>
<td>–</td>
<td>+</td>
<td>+</td>
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<td>–</td>
<td>+</td>
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<td>Optimal temperature for growth (°C)</td>
<td>55–60</td>
<td>40</td>
<td>40–55</td>
<td>30–50</td>
<td>55–60</td>
<td>40</td>
<td>45</td>
<td>55–63</td>
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<tr>
<td>NaCl concentration for growth (%, w/v)</td>
<td>0–7</td>
<td>0–21</td>
<td>NO</td>
<td>1–2</td>
<td>1–15</td>
<td>NO</td>
<td>0–20&lt;sup&gt;b&lt;/sup&gt;</td>
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<tr>
<td>Predominant menaquinone</td>
<td>MK-7</td>
<td>MK-7</td>
<td>MK-7</td>
<td>MK-7</td>
<td>MK-7</td>
<td>MK-6</td>
<td>MK-7</td>
<td>MK-7</td>
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<tr>
<td>Other menaquinones</td>
<td>NO</td>
<td>NO</td>
<td>MK-6, MK-8</td>
<td>NO&lt;sup&gt;a&lt;/sup&gt;</td>
<td>MK-7</td>
<td>MK-7</td>
<td>MK-7</td>
<td>MK-8</td>
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<tr>
<td>Major cellular fatty acids (&gt;10 %)†</td>
<td>i-C&lt;sub&gt;15:0&lt;/sub&gt;, i-C&lt;sub&gt;15:0&lt;/sub&gt;, i-C&lt;sub&gt;17:0&lt;/sub&gt;</td>
<td>i-C&lt;sub&gt;15:0&lt;/sub&gt;, i-C&lt;sub&gt;15:0&lt;/sub&gt;, i-C&lt;sub&gt;17:0&lt;/sub&gt;</td>
<td>i-C&lt;sub&gt;15:0&lt;/sub&gt;, ai-C&lt;sub&gt;15:0&lt;/sub&gt;</td>
<td>i-C&lt;sub&gt;15:0&lt;/sub&gt;, i-C&lt;sub&gt;15:0&lt;/sub&gt;, ai-C&lt;sub&gt;15:0&lt;/sub&gt;</td>
<td>i-C&lt;sub&gt;15:0&lt;/sub&gt;, ai-C&lt;sub&gt;15:0&lt;/sub&gt;, i-C&lt;sub&gt;15:0&lt;/sub&gt;</td>
<td>i-C&lt;sub&gt;15:0&lt;/sub&gt;, ai-C&lt;sub&gt;15:0&lt;/sub&gt;, i-C&lt;sub&gt;15:0&lt;/sub&gt;</td>
<td>i-C&lt;sub&gt;15:0&lt;/sub&gt;, ai-C&lt;sub&gt;15:0&lt;/sub&gt;, i-C&lt;sub&gt;15:0&lt;/sub&gt;</td>
<td>i-C&lt;sub&gt;15:0&lt;/sub&gt;, ai-C&lt;sub&gt;15:0&lt;/sub&gt;, i-C&lt;sub&gt;15:0&lt;/sub&gt;</td>
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<tr>
<td>DAP isomer</td>
<td>LL</td>
<td>LL</td>
<td>meso</td>
<td>meso</td>
<td>meso</td>
<td>meso</td>
<td>LL</td>
<td>meso</td>
</tr>
<tr>
<td>DNA G + C content (mol%)</td>
<td>54.2</td>
<td>51.8</td>
<td>47.3</td>
<td>49.3</td>
<td>55.1</td>
<td>52.6</td>
<td>54.6</td>
<td>58.7–60.3</td>
</tr>
<tr>
<td>Major polar lipids‡</td>
<td>DPG, PG, PE</td>
<td>DPG, PG, PE</td>
<td>DPG, PG, PE</td>
<td>DPG, PG, PE</td>
<td>DPG, PG, PE</td>
<td>DPG, PG, PE</td>
<td>DPG, PG, PE</td>
<td>DPG, PG, PE</td>
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</table>

*a* Data taken from: a, von Jan et al. (2011); b, Tsubouchi et al. (2013); c, Addou et al. (2013) and Li et al. (2013).

†ai, anteiso; i, iso.

‡DPG, Diphosphatidylglycerol; PE, phosphatidylethanolamine; PG, phosphatidylycerol; PME, phosphatidylmethyl ethanolamine; PS, phosphatidylserine.
11157T is clearly differentiated from members of the genus *Melghirimyces* by phenotypic evidence, including its relatively narrow NaCl range for growth, higher optimal growth temperature and the inability to hydrolyse gelatin or starch (Table 1). Moreover, the phenotypic characteristics of strain SCSIO 11157T are different from those of other closely related genera (Table 1). The optimum growth temperature of strain SCSIO 11157T is 55–60°C, but members of the genera *Salinithrix* and *Kroppenstedtia* grow well at 40 and 45°C, respectively. The NaCl tolerance of SCSIO 11157T is clearly different from that of members of the genera *Salinithrix* and *Planifilum*. The inability to hydrolyse gelatin distinguishes strain SCSIO 11157T from members of closely related genera except *Salinithrix*. Unlike strain SCSIO 11157T, members of *Planifilum* do not show aerial mycelium. The presence of LL-DAP in the cell-wall peptidoglycan of strain SCSIO 11157T rather than the meso isomer distinguishes the strain from all other closely related genera except *Kroppenstedtia*. The predominant menaquinone of SCSIO 11157T is MK-7, but MK-6 is the predominant menaquinone in the genus *Salinithrix*. On the basis of the results of this study, strain SCSIO 11157T should be assigned to a novel species in a new genus of the family *Thermoactinomycetaceae*, for which the name *Marinithermofilum abyssi* gen. nov., sp. nov. is proposed.

The results of the phylogenetic analysis based on 16S rRNA gene sequences show that strain SCSIO 11154T forms a distinct clade with *Desmospora actica* IMIB L-1269T (AM940019) in the family *Thermoactinomycetaceae*. Bootstrap values (expressed as percentages of 1000 replications) above 50% are shown at branch points. Asterisks denote nodes that were also recovered using the maximum-parsimony and maximum-likelihood methods. Bar, 0.01 substitutions per nucleotide position.
phylogenetic tree (Fig. 1). However, strain SCSIO 11154\textsuperscript{T} can be distinguished from Desmospora activa IMMIB L-1269\textsuperscript{T} by phenotypic characteristics, such as the inability to hydrolyse gelatin, having lL-DAP as the cell-wall diaminoc acid (meso-DAP in Desmospora activa IMMIB L-1269\textsuperscript{T}) and the absence of phosphatidylmethylethanolamine. Therefore, the results of phylogenetic analysis and the phenotypic characteristics support the conclusion that strain SCSIO 11154\textsuperscript{T} represents a novel species in the genus Desmospora, for which the name Desmospora profundinema sp. nov. is proposed. The description of this novel species also necessitates an emended description of the genus Desmospora.

**Description of Marinithermofilum gen. nov**

*Marinithermofilum* [Ma.ri’ni.ther.mo.fi’lum. L. adj. marin-us of the sea, marine; Gr. adj. thermos hot; L. neut. n. filum thread, filament; N.L. neut. n. *Marinithermofilum* heat (loving) filament existing in marine environment].

Cells are aerobic, Gram-stain-positive, thermophilic and form pale-yellow substrate mycelium on modified nutrient agar. Grow at 35–65 °C. Produce chains of arthrospores on aerial mycelium and endospores on substrate mycelium. Cell-wall acyl type is N-glycolyl. Cell wall contains lL-DAP as the diaminoc acid. No characteristic sugars. The major polar lipids are diphosphatidylglycerol, phosphatidylglycerol, phosphatidylethanolamine and phosphatidylglycerol. The predominant menaquinone is MK-7. Major cellular fatty acids (> 10%) are iso-C\textsubscript{15:0} C\textsubscript{18:1}ω9c and iso-C\textsubscript{17:0}. The DNA G+C content of the type strain of the type species is 54.2 mol%. The type species is *Marinithermofilum abyssi*.

**Description of Marinithermofilum abyssi sp. nov**


Grows well on modified nutrient agar and Czapek’s agar, but weakly on ISP media 3 and 5, forming radial crumpled colonies. No growth on ISP medium 2 or 4. Soluble pigment is not produced on any tested medium. Optimum growth at 60 °C and pH 7.0. Starch and Tweens 40 and 80, coagulation and peptonization of milk, degradation of casein, cellulose and Tween 20 and nitrate reduction. Catalase test is positive. Oxidase test is negative. Tests for acid phosphatase, alkaline phosphatase and naphthol-AS-BI-phosphohydrolase are positive, but tests for ß-chymotrypsin, cystine aminopeptidase, esterase, esterase lipase, ß-fucosidase, ß-galactosidase, ß-glucuronidase, ß-glucosidase, ß-glucoisidase, leucine aminopeptidase, lipase (C14), ß-mannosidase, N-acetyl-ß-glucosaminidase, trypsin and valine aminopeptidase are negative. D-Arabinose, fructose, D-galactose, D-ribose and D-xylene are utilized as sole carbon sources for growth, but L-arabinose, cellobiose, D-glucose, glycerol, lactose, maltose, D-mannitol, D-mannose, *myo*-inositol, raffinose, L-rhamnose, sodium pyruvate, D-sorbitol, sucrose, trehalose and xylitol are not used. Urea is degraded, whereas adenine, ascinul, arbutin, guanine, hypoxanthine and xanthine are not degraded. The result of the Voges–Proskauer test is negative. The species shares the traits listed in the genus description. In addition, five unknown phospholipids and one unknown polar lipid are present. The type strain is SCSIO 11157\textsuperscript{T} (=CGMCC 1.15179\textsuperscript{T} = NBRC 109939\textsuperscript{T}), isolated from a sediment sample collected from the Indian Ocean (1° 03.300′ N 80° 03.099′ E) at a depth of 4593 m.

**Emended description of the genus Desmospora Yassin et al. 2009**

The description of the genus *Desmospora* is as given by Yassin et al. (2009), with the following amendment. The peptidoglycan contains meso-DAP or lL-DAP.

**Description of Desmospora profundinema sp. nov**

*Desmospora profundinema* (pro.fun.di.ne’m.a. L. n. profundum the depths of the sea; Gr. neut. n. nema a filament; N.L. neut. n. *profundinema* a filament from the depths of the sea).

Grows well on modified nutrient agar and Czapek’s agar, but weakly on ISP media 3, 4 and 5, forming radial crumpled colonies. No growth on ISP medium 2. Soluble pigment is not produced on any tested medium. Single endospores with unbranched sporophores are produced on the substrate mycelium, and short chains of arthrospores are formed on the aerial mycelium. Optimum growth occurs at 40 °C and pH 8.0. NaCl is tolerated up to 7% (w/v). Starch is degraded, but negative for hydrolysis of gelatin and Tweens 20, 40 and 80, coagulation and peptonization of milk, degradation of casein and cellulose and nitrate reduction. Catalase test is positive. Oxidase test is negative. Tests for alkaline phosphatase, esterase and naphthol-AS-BI-phosphohydrolase are positive, but results for acid phosphatase, ß-chymotrypsin, cystine aminopeptidase, esterase lipase, ß-fucosidase, ß-galactosidase, ß-galactosidase, ß-glucuronidase, ß-glucoisidase, ß-glucoisidase, leucine aminopeptidase, lipase (C14), ß-mannosidase, N-acetyl-ß-glucosaminidase, trypsin and valine aminopeptidase are negative. D-Galactose, D-ribose and D-xylene are used as sole carbon sources, but D- and l-arabinose, cellobiose, fructose, D-glucose, glycerol, lactose, maltose, D-mannitol, D-mannose, *myo*-inositol, L-rhamnose, raffinose, sodium pyruvate, D-sorbitol, sucrose, trehalose and xylitol are not used. Adenine, ascinul, arbutin, guanine, hypoxanthine, urea and xanthine are not degraded. The result of the Voges–Proskauer test is negative. The cell-wall contains LL-DAP as the diaminoc acid. Cell-wall acyl type is N-glycolyl. No characteristic sugars. The polar lipids are diphosphatidylglycerol, phosphatidylglycerol, phosphatidylethanolamine, three unknown phospholipids and one unknown polar lipid are present.
unknown polar lipid. The predominant menaquinone is MK-7. Major cellular fatty acids (>10%) are iso-C_{15:0} and iso-C_{17:0}.

The type strain, SCOS 11154T (=DSM 45903T=NBRC 109626T), was isolated from a sediment sample collected from the Indian Ocean (1° 03.300’ N 80° 03.099’ E) at a depth of 4593 m. The DNA G+C content of the type strain is 51.8 mol%.

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References


