Description of *Streptomonospora sediminis* sp. nov. and *Streptomonospora nanhaiensis* sp. nov., and reclassification of *Nocardiosis arabia* Hozzein & Goodfellow 2008 as *Streptomonospora arabica* comb. nov. and emended description of the genus *Streptomonospora*

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Two actinomycete strains isolated from marine sediment samples, designated YIM M11335T (from the Indian Ocean) and 12A09T (from the South China Sea), were obtained and examined by a polyphasic approach. The two Gram-staining-positive, aerobic strains produced branched substrate mycelia and aerial hyphae that were not fragmented, and no diffusible pigment was produced on the media tested. At maturity, spore chains and single spores were formed on aerial hyphae and substrate mycelium, respectively. Whole-organism hydrolysates of both strains contained meso-diaminopimelic acid and the diagnostic sugars glucose and galactose. Their predominant menaquinones were MK-10(H₄), MK-10(H₆), MK-11(H₄), MK-11(H₆) and MK-11(H₈) for strain YIM 11335T and MK-10(H₄), MK-10(H₆), MK-11(H₄), MK-11(H₆) and MK-11(H₈) for strain 12A09T. The polar lipids detected in the two strains were diphosphatidylglycerol, phosphatidylglycerol, phosphatidylinositol mannoside, phosphatidylinositol, phosphatidylcholine, an unknown phosphoglycolipid and several unknown glycolipids, phospholipids and polar lipids. The major fatty acids (>10%) were iso-C₁₆:0 and C₁₆:0 for strain YIM 11335T and iso-C₁₆:0 for strain 12A09T. The G+C contents of the genomic DNA of strains YIM 11335T and 12A09T were 70.7% and 74.4%, respectively. DNA–DNA hybridization relatedness values of these two isolates with the type strains *Nocardiosis arabia* DSM 45083T and *Streptomonospora halophila* YIM 91355T supported the hypothesis they are representatives of two different species. Based on phylogenetic analysis, phenotypic and genotypic data, it is concluded that the two isolates belong to the genus *Streptomonospora* of the family *Nocardiospaceae* and that the type strain of *N. arabia* should be reclassified as a representative of *Streptomonospora arabica* comb. nov. The names proposed for the two novel species are *Streptomonospora sediminis* sp. nov. (type strain YIM M11335T=DSM 45723T=CCTCC AB 2012051T) and *Streptomonospora nanhaiensis* sp. nov. (type strain 12A09T=KCTC 29145T=CCTCC AB 2013140T), respectively. An emended description of the genus *Streptomonospora* is also proposed in the light of the new data.

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Abbreviation: DAP, diaminopimelic acid.

The GenBank/EMBL/DBJ accession numbers for the 16S rRNA gene sequences of strains YIM M11335T and 12A09T are KC768773 and KC768774, respectively.

Three supplementary figures and two supplementary tables are available with the online version of this paper.
The genus *Streptomonospora* belongs to the family *Nocardio- diopsacae* of the suborder *Streptosporangineae* (Stackebrandt et al., 1997) and was first proposed by Cui et al. (2001) with the description of a single species *Streptomonospora salina*. Subsequently, Li et al. (2003) described another species, *Streptomonospora alba*, and further emended the description of the genus *Streptomonospora*. Currently, the genus contains five recognized species and the other three species are *Streptomonospora halophila* (Cai et al., 2008), *Streptomonospora amylyolitica* and *Streptomonospora flavula* (Cai et al., 2009). For rapid identification of species of the genus *Streptomonospora* among novel halophilic actinomycetes derived from a saline lake in western China, Zhi et al. (2006) introduced a genus-specific PCR amplification method.

In the year of the description of *Streptomonospora halophila* (Cai et al., 2008) being published, another novel species *Nocardiosis arabia* was concurrently described by Hozzein & Goodfellow (2008). The type strain of the species showed high 16S rRNA gene sequence similarity values (99.9 %) with *Streptomonospora halophila* and formed a separate lineage together with members of the genus *Streptomonospora*, not locating in any clade of the genus *Nocardiosis* in the phylogenetic tree. However, no conclusive evidence regarding its taxonomic relationships with genera *Nocardiosis* and *Streptomonospora* based on polyphasic taxonomic studies have been provided thus far.

To investigate actinobacterial diversity from marine sediments, strain YIM M11335<sup>T</sup> was isolated from a sample collected in Naval area, Little Andaman, India (92°34.150′ E 10°34.783′ N), and strain 12A09<sup>T</sup> was isolated from a sample collected from the South China Sea (119°19.896′ E 19°41.569′ N) at a depth of 2918 m. They were subjected to a polyphasic taxonomic study along with two of their closest phylogenetic neighbours: *Streptomonospora halophila* YIM 91355<sup>T</sup> and *N. arabia* DSM 45083<sup>T</sup>. Strains YIM M11335<sup>T</sup> and 12A09<sup>T</sup> showed high 16S rRNA gene sequence similarities to *Streptomonospora halophila* YIM 91355<sup>T</sup> (97.45 % and 96.9 %, respectively) and *N. arabia* DSM 45083<sup>T</sup> (97.16 % and 96.7 %, respectively), and the similarity between them is 97.0 %, but the two novel isolates displayed obvious different morphological and physiological characteristics from each other and from the two type strains of the related species. In order to determine the phylogenetic and taxonomic relationships between strains YIM M11335<sup>T</sup>, 12A09<sup>T</sup>, *Streptomonospora halophila* YIM 91355<sup>T</sup>, *N. arabia* DSM 45083<sup>T</sup> and other related species in the family *Nocardio- diopsacae*, morphological, physiological and chemotaxonomic characteristics of type strains belonging to these species were determined. DNA–DNA hybridization reactions were also performed between YIM M11335<sup>T</sup> and its two closest relatives and also between *Streptomonospora halophila* YIM 91355<sup>T</sup> and *N. arabia* DSM 45083<sup>T</sup>. Results from this study indicated that strains YIM M11335<sup>T</sup> and 12A09<sup>T</sup> represent two novel species of the genus *Streptomonospora*. It is also proposed that *N. arabia* should be reclassified as a member of the genus *Streptomonospora* as *Streptomonospora arabica* comb. nov. and an emended description of the genus *Streptomonospora* is proposed in the light of the new data.

Strains YIM M11335<sup>T</sup> and 12A09<sup>T</sup> were isolated by using the serial dilution technique. Sediment samples (1 g) was added to 9 ml sterile distilled water and mixed by vortexing. A 10-fold dilution of each of these suspensions was prepared in sterilized distilled water and 0.1 ml was spread on the media. Then, the plates were incubated at 28 °C for 25 days with an agar medium (glycerine 10.0 g; l-arginine 5.0 g; (NH₄)₂SO₄ 2.64 g; KH₂PO₄ 2.38 g; K₂HPO₄ 5.65 g; MgSO₄.7H₂O 1.0 g; CuSO₄.5H₂O 0.0064 g; FeSO₄.7H₂O 0.0011 g; MnCl₂.4H₂O 0.0079 g; ZnSO₄.7H₂O 0.0015 g; agar 15.0 g; distilled water 1.0 l; pH 7.0) for YIM M11335<sup>T</sup> and Gauze's synthetic medium No.1 (soluble starch 20.0 g; KNO₃ 1.0 g; NaCl 0.5 g; MgSO₄.7H₂O 0.5 g; K₂HPO₄ 0.5 g; FeSO₄.7H₂O 10.0 mg; agar 15.0 g; distilled water 1.0 l; pH 7.0) for 12A09<sup>T</sup>. The strains were cultivated and maintained on modified ISP2 medium containing (1<sup>−</sup>): yeast extract 4.0 g; malt extract 10.0 g; glucose 4.0 g; NaCl 25.0 g; agar 20.0 g (pH 7.0). The two isolates were routinely cultivated on ISP2 medium at 28 °C and stored as aqueous glycerol suspensions (20 %, v/v) at −80 °C.

Strains YIM M11335<sup>T</sup> and 12A09<sup>T</sup> were cultured for 14 days at 28 °C on modified ISP 2, modified ISP 5 (K₂HPO₄ 1 g, l-asparagine 1 g, glycerol 10 g, FeSO₄.7H₂O 0.001 g, MnCl₂.4H₂O 0.001 g, ZnSO₄.7H₂O 0.001 g, NaCl 100 g, agar 20 g, pH 7.0) and modified Bennett’s agar (Jones, 1949) using the coverslip technique of Kawato & Shinobu (1959), and morphological properties were observed by using a light microscope (BH-2; Olympus) and a scanning electron microscope (Quanta 200; FEI).

Culture characteristics were observed on various agar media at 15 and 30 days at 28 °C, according to the methods described by Shirling & Gottlieb (1966). Colours of the aerial and substrate mycelia were determined by using colour chips from the Inter-Society Color Council–National Bureau of Standards (ISCC–NBS) colour charts (standard sample no. 2106; Kelly, 1964). Carbon-source utilization tests were performed according to the methods described by Shirling & Gottlieb (1966) and Athalye et al. (1985) using the basal medium recommended by Pridham & Gottlieb (1948). Growth at various NaCl concentrations (0, 3, 5, 7, 10, 15, 20, 25 and 30 %, w/v) and temperatures (5, 10, 15, 18, 20, 28, 37, 40, 45, 50, 55 and 60 °C) was examined by growing the strains on ISP2 medium as the basal medium. Growth at different pH values (4.0–10.0, at intervals of 1.0 pH unit) was examined on ISP2 medium using the buffer system described by Xu et al. (2005). Oxidase activity was determined by the oxidation of tetramethyl-p-phenylenediamine. Catalase activity was determined using 3 % H₂O₂, and gas production was identified as a positive reaction. Nitrate reduction and degradation of cellulose, gelatin and urea were determined by using standard procedures (Goodfellow, 1971; Athalye et al., 1985).
The biomass used for analyses of cellular fatty acids, was obtained from cultures grown in tryptic soy broth (Difco) for 7 days, while that for the other studies of chemotaxonomic characteristics was grown in ISP2 medium for 14 days. They were all cultured in shaken flasks at 170 r.p.m. at 28 °C, harvested by centrifugation at 2219 g (for 10 min) and washed twice with distilled water. Cellular fatty acids were extracted, methylated and analysed by using the Sherlock Microbial Identification System (MIDI) according to the method of Sasser (1990) and the manufacturer’s instructions. Fatty acid methyl esters were then analysed by GC (7890A GC System; Agilent Technologies) by using the Microbial Identification software package (Sherlock Version 6.1; MIDI database TSBA6). The diaminopimelic acid (DAP) isomer was identified by using TLC as described by Stanec & Roberts (1974). The whole-cell sugars were separated by HPLC after precolumn derivatization with 1-phenyl-3-methyl-5-pyrazolone (Tang et al., 2009). Menaquinones were extracted (Collins et al., 1977) and detected by HPLC (Tamaoka et al., 1983). Polar lipids were determined according to published procedures (Minnikin et al., 1979; Collins & Jones, 1980).

Genomic DNAs were extracted from the isolates as described previously by Li et al. (2007). The 16S rRNA gene was amplified using the following primers: PA (5'-CAGAGT-TTGATCCTGGCT-3') as the forward primer and PB (5'-AGGAGTTGATCCAGCCGCA-3') as the reverse primer. PCR amplification was performed under the following conditions: 4 min at 95 °C; 30 cycles of 1 min at 94 °C, 1 min at 56 °C and 1.5 min at 72 °C, plus an additional 10 min cycle at 72 °C. The PCR product was ligated into the pEASY-T1 vector and transformed into Escherichia coli DH15a using a pEASY-T1 cloning kit (Transgen Biotechnology). Then, the 16S rRNA gene sequence was determined by Sangon Biotech (Shanghai, China). The 16S rRNA gene sequences obtained in this study were compared with sequences from EzBioCloud using BLAST (http://eztaxon-e.ezbiocloud.net/) (Kim et al., 2012). The 16S rRNA gene sequences were aligned with corresponding sequences (retrieved from the GenBank/EMBL/DDJB database) using CLUSTAL X1.83 (Thompson et al., 1997). Phylogenetic trees were reconstructed by the neighbour-joining (Saitou & Nei 1987), maximum-parsimony (Fitch, 1971) and maximum-likelihood (Felsenstein, 1981) tree-making algorithms by using the software packages MEGA version 5.0 (Tamura et al., 2011). The topologies of the resultant trees were evaluated by using the bootstrap resampling method of Felsenstein (1985) with 1000 replicates.

The G+C contents of chromosomal DNAs prepared by the method of Marmur (1961) were determined as described by Mesbah et al. (1989). The quantitative microplate DNA–DNA hybridizations were carried out under optimal conditions as described by Ezaki et al. (1988, 1989). One of the two DNAs for hybridization was labelled while the other was immobilized, and the reciprocal experiments were performed. The concentration of the two DNAs was strictly controlled. Six replications for hybridization were performed for each sample and the highest and lowest values in each sample were excluded. The relatedness values are expressed as the means of the remaining four values and the results of DNA–DNA hybridizations were taken from the two means of relatedness values.

Investigations of 14 day-old cultures of strains YIM M11335T, 12A09T, N. arabia DSM 45083T and Streptomonospora halophila YIM 91355T revealed that they all formed spore chains and single spores on the aerial mycelia or the substrate mycelium which were not fragmented. Strain 12A09T just formed single spores (smooth surface) (Fig. 1d) and spore-chain-like structures on aerial mycelia on modified Bennett’s agar though growth was very vigorous, but spore chains (wrinkled surface) (Fig. 1c) were formed on modified ISP 2 medium very well. And on modified ISP 5 medium, strain YIM M11335T formed spore chains (wrinkled surface) on the aerial mycelia and single spores (wrinkled surface) on the substrate mycelium (Fig. 1a, b), strain N. arabia DSM 45083T formed both spore chains (wrinkled surface) and single spores (wrinkled surface) on the aerial mycelia (Fig. 1e, f), and Streptomonospora halophila YIM 91355T formed both spore chains (wrinkled surface) and single spores (smooth surface) on the aerial mycelia (Fig. 1g, h), while strain 12A09T could not form very abundant aerial mycelia. Strains YIM M11335T and 12A09T could grow on all the media tested and no pigment was produced on any media. The aerial mycelia of the isolates were not very abundant and were white in colour on most media tested. However, strain 12A09T formed very abundant aerial mycelia on parts of some colonies spontaneously, while strain YIM M11335T could not. The substrate mycelia of strain YIM M11335T were yellow–white, while those of strain 12A09T displayed several colours on these media (Table 1).

Strains YIM M11335T and 12A09T grew at pH 6–9 and in up to 20 % (w/v) NaCl. Growth temperature for strain YIM M11335T was 15–45 °C (optimum 28) and for strain 12A09T it was 10–50 °C (optimum 37). The optimum growth for both strains occurred at 0–7 % (w/v) NaCl and pH 7.0–8.0. The results of other physiological and biochemical analyses are summarized in the species descriptions below. The range of carbon sources utilized could not be determined in this study because of negative reactions caused by extremely poor growth in basal media and the same result has been reported by Li et al. (2003) for Streptomonospora alba YIM 90003T.

Strains YIM M11335T and 12A09T exhibited chemical markers that are typical of the genus Streptomonospora, i.e. they had: meso-DAP as the cell wall diaminodic acid; galactose and glucose as whole cell sugars; diphosphatidylglycerol, phosphatidylglycerol, phosphatidylglycerol, phosphatidylcholine and phosphatidylinositol mannosides as major polar lipids (Fig. S1, available in IJSEM online); MK-10(H6) and MK-10(H8) among the predominant menaquinones; and iso-C16:0 as the major fatty acid. However, there were many differences from the other members of the genus Streptomonospora: both strains contain large amounts...
(>10%) of MK-11(H₆) and MK-11(H₄) and phosphoglycerolipids and several glycolipids (Table 2, Table S1).

Two almost complete 16S rRNA gene sequences (1540 bp; 1535 bp) were generated for isolates YIM M11335ᵀ and 12A09ᵀ. Comparative 16S rRNA gene sequence analysis showed that the two strains were phylogenetically related to members of the genus *Streptomonospora* (Fig. 2). In the phylogenetic tree of the neighbour-joining algorithm, they clustered with the type strains of *Streptomonospora halophila* and *N. arabia* together with the other four members of the genus *Streptomonospora*. This relationship was supported by all tree-making methods used in this study (Fig. S2 and S3). The results of the 16S rRNA gene sequence comparisons demonstrated that strains YIM M11335ᵀ, 12A09ᵀ and *N. arabia* S186ᵀ may be members of the genus *Streptomonospora*.

The genomic DNA G+C contents of strains YIM M11335ᵀ and 12A09ᵀ were 70.7 mol% and 74.4 mol%, respectively. The levels of DNA–DNA relatedness of strain YIM M11335ᵀ with *Streptomonospora halophila* YIM 91355ᵀ.
and N. arabia DSM 45083T and that between the two type strains of the species with validly published names were 35.0%, 40.3% and 54.8% (srs were 3.2%, 2.3% and 2.8%, respectively) (Table S2). These values are well below the 70% cut-off point recommended for the delineation of genomic species (Wayne et al., 1987).

On the basis of phenotypic, chemotaxonomic and phylogenetic analysis, strains YIM 91355T and 12A09T could be distinguished from species of the genus Streptomonospora with validly published names and each other easily, for example: (1) good growth of Streptomonospora halophile YIM 91355T and N. arabia DSM 45083T needs more NaCl (7–12%, w/v) than strains YIM M11335T and 12A09T (0–7%, w/v); (2) YIM M11335T and 12A09T were different from each other with respect to whole-cell diagnostic sugars. Although Streptomonospora halophile YIM 91355T and N. arabia DSM 45083T showed an extremely high 16S rRNA gene sequence similarity, both organisms should be classified as separate species based on the results of DNA–DNA hybridization and the surface and shape of single spores. More characteristics that differentiate these four strains from each other are shown in Tables 1, 2 and S1. Thus, it is considered that strains YIM M11335T, 12A09T, Streptomonospora halophile YIM 91355T and N. arabia DSM 45083T are representatives of four different species. The formation of spore chains and single spores, chemotaxonomic properties and the phylogenetic analysis supported the suggestion that strains YIM M11335T, 12A09T and N. arabia DSM 45083T belongs to the genus Streptomonospora. So, two novel species Streptomonospora sediminis sp. nov. and Streptomonospora nanhaiensis sp. nov. are proposed for strains YIM M11335T and 12A09T, respectively, and N. arabia is reclassified as Streptomonospora arabica comb. nov.

Before this study, the presence of MK-12, MK-12(H2), MK-12(H3) and MK-12(H4) (Table S1) as minor menaquinones has not been reported for members of the genus Streptomonospora, while medium- and age-dependent shifts in menaquinone compositions had been reported for some members of the class Actinobacteria before (Saddler et al., 1986; Hiraishi & Komagata, 1989; Li et al., 2003). Catalase activity, no utilization of urea and the presence of galactose as a whole-cell sugar, were common to the entire genus. Additionally, characteristic components of fatty acids among the members of the genus Streptomonospora under different cultural condition were observed. Therefore an emended description of the genus Streptomonospora is proposed.

**Emended description of Streptomonospora Cui et al. 2001 emend. Li et al. 2003**

Gram-staining-positive, aerobic organisms with branching hyphae. Non-fragmented substrate mycelium present. At maturity, spore chains and non-motile single spores are formed on extensively branched aerial mycelium or substrate mycelium. Spores in chains are rod–oval to rod-shaped with wrinkled surfaces, and single spores with smooth or wrinkled surface are oval to round, borne on short or long sporophores. Catalase-positive and utilization of urea-negative. Peptidoglycan contains meso-diaminopimelic acid as a diagnostic diamino acid. Whole-cells contain galactose. The phospholipid pattern is complex, consisting of phosphatidylglycerol, phosphatidylcholine and phosphaticylinositol; phosphatidylethanolamine, diphosphatidylglycerol, and methylphosphatidylethanolamine, glycolipids and phosphatidylserine may occur. The menaquinone compositions may depend on the growth medium and consist mainly of menaquinones with nine or ten isoprenoid chains and a varying degree of hydrogenation; i.e. a combination of one or more representative(s) of the series [MK-9(H2), (H3), (H4)], [MK-10(H2), (H3), (H4)], [MK-11(H2), (H3), (H4)], plus [MK-12(H2), (H3), (H4)] fatty acids C16:0, C15:0, iso-C15:0, iso-C16:0 and anteiso-C17:0 usually appear as major or minor component. The G+C content of the genomic DNA is 70.7–74.4 mol%. The type species is Streptomonospora salina.

**Description of Streptomonospora sediminis sp. nov.**

Streptomonospora sediminis (se.di’mi.nis. L. n. sedimen -inis sediment; L. gen. n. sediminis of sediment).
Table 2. Differential phenotypic and chemotaxonomic characteristics of strains YIM 11335<sup>T</sup>, 12A09<sup>T</sup>, *Nocardiopsis arabia* DSM 45083<sup>T</sup> and species of the genus *Streptomonospora*

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<td>-</td>
</tr>
<tr>
<td>Phenylalanine</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>-</td>
<td>-</td>
<td>-</td>
</tr>
<tr>
<td>Threonine</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Tryptophan</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>-</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Tyrosine</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>-</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Valine</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>-</td>
<td>-</td>
<td>-</td>
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</tr>
<tr>
<td>Predominant menaquinones (&gt;10 %)</td>
<td>MK-10(H&lt;sub&gt;4&lt;/sub&gt;),</td>
<td>MK-10(H&lt;sub&gt;4&lt;/sub&gt;,&lt;sub&gt;6&lt;/sub&gt;)</td>
<td>MK-10(H&lt;sub&gt;6&lt;/sub&gt;,&lt;sub&gt;8&lt;/sub&gt;)</td>
<td>MK-9(H&lt;sub&gt;4&lt;/sub&gt;),</td>
<td>MK-10(H&lt;sub&gt;2&lt;/sub&gt;,&lt;sub&gt;4&lt;/sub&gt;)</td>
<td>MK-10(H&lt;sub&gt;6&lt;/sub&gt;,&lt;sub&gt;8&lt;/sub&gt;)</td>
<td>MK-9(H&lt;sub&gt;4&lt;/sub&gt;,&lt;sub&gt;6&lt;/sub&gt;,&lt;sub&gt;8&lt;/sub&gt;)</td>
<td>MK-10(H&lt;sub&gt;2&lt;/sub&gt;,&lt;sub&gt;4&lt;/sub&gt;)</td>
</tr>
<tr>
<td>Diagnostic phospholipids</td>
<td>DPG, PC, PG,</td>
<td>DPG, PC, PG,</td>
<td>DPG, PC, PG,</td>
<td>DPG, PC, PG,</td>
<td>DPG, PC, PG,</td>
<td>DPG, PC, PG,</td>
<td>DPG, PC, PG,</td>
<td>DPG, PC, PG,</td>
</tr>
<tr>
<td>Major fatty acids (&gt;10 %)</td>
<td>i-C&lt;sub&gt;16&lt;/sub&gt;:0, C&lt;sub&gt;16&lt;/sub&gt;:0</td>
<td>i-C&lt;sub&gt;16&lt;/sub&gt;:0</td>
<td>i-C&lt;sub&gt;16&lt;/sub&gt;:0, 10-m-C&lt;sub&gt;18&lt;/sub&gt;:0</td>
<td>i-C&lt;sub&gt;16&lt;/sub&gt;:0, ai-C&lt;sub&gt;17&lt;/sub&gt;:0, 10-m-C&lt;sub&gt;18&lt;/sub&gt;:0</td>
<td>i-C&lt;sub&gt;16&lt;/sub&gt;:0, ai-C&lt;sub&gt;17&lt;/sub&gt;:0, 10-m-C&lt;sub&gt;18&lt;/sub&gt;:0</td>
<td>i-C&lt;sub&gt;16&lt;/sub&gt;:0, ai-C&lt;sub&gt;17&lt;/sub&gt;:0, 10-m-C&lt;sub&gt;18&lt;/sub&gt;:0</td>
<td>i-C&lt;sub&gt;16&lt;/sub&gt;:0, ai-C&lt;sub&gt;17&lt;/sub&gt;:0, 10-m-C&lt;sub&gt;18&lt;/sub&gt;:0</td>
<td>i-C&lt;sub&gt;16&lt;/sub&gt;:0, ai-C&lt;sub&gt;17&lt;/sub&gt;:0, 10-m-C&lt;sub&gt;18&lt;/sub&gt;:0</td>
</tr>
<tr>
<td>DNA G+C content (mol%)</td>
<td>70.7</td>
<td>74.4</td>
<td>72.3</td>
<td>72.1</td>
<td>71.2</td>
<td>72.5</td>
<td>74.4</td>
<td>72.9</td>
</tr>
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</table>
General characteristics are as given above for the genus. Growth is good on ISP 2, ISP 3, agars, nutrient agar and trypticase soy agar media. The colour of the aerial mycelium is white and the substrate mycelium is yellow–white. No diffusible pigments are produced. At maturity, on modified ISP 5 medium, aerial mycelium forms spore chains (wrinkled surface) and single spores (wrinkled surface) are borne on long sporophores on the substrate mycelium. Growth occurs on ISP medium 2 with 0–20 % NaCl (w/v), pH 6.0–9.0, at 15–45°C; optimum at 0–7 % NaCl, pH 7.0–8.0, 28°C. Positive in tests for catalase, nitrate reductase, cellulase, milk coagulation and milk peptonization. Negative in tests for H2S, melanin, gelatin hydrolysis, urease, amylase and oxidase. Utilizes L-alanine, L-arginine, DL-aspartic amide, L-glutamate, L-lysine, L-phenylalanine, L-threonine, L-tryptophan, L-tyrosine and L-valine as sole nitrogen and energy sources, but L-glycine, L-histidine, L-methionine are not utilized. Galactose is the diagnostic whole-cell sugar. Predominant menaquinones (>5 %) include MK-10(H2), MK-10(H4), MK-10(H6), MK-10(H8), MK-11(H2), MK-11(H4), MK-11(H6), MK-11(H8). The polar lipids consist of diphosphatidylglycerol, phosphatidylglycerol, phosphatidyl ethanolamine, two phosphatidylinositol mannosides, an unknown phosphoglycolipid, four unknown glycolipids, phosphatidylcholine, three unknown phospholipids and one unknown polar lipid. The major components of fatty acids (>10 %) are C16:0 and iso-C16:0.

The type strain is YIM M11335T (=DSM 45723T = CCTCC AB 2012051T) isolated from a sample collected in Naval area, Little Andaman, India (92°34.150’E 10°34.783’N). The G+C content of the genomic DNA is 70.7 mol%.

Description of *Streptomonospora nanhaiensis* sp. nov.

*Streptomonospora nanhaiensis* [nan.hai.en’sis. N.L. fem. adj. nanhaiensis of or pertaining to Nanhai (South China Sea), where the type strain was isolated].

General characteristics are as given above for the genus. Growth is good on ISP 2, ISP 3, ISP 4, agars, Czapek’s solution agar, nutrient agar and trypticase soy agar media. The colour of the aerial mycelium is white and the substrate mycelium displays different colours on different media. No diffusible pigments are produced. At maturity, the aerial mycelium forms spore chains on modified ISP 2 medium, and single spores on modified Bennett’s agar. Growth occurs on ISP medium 2
with 0–20 % NaCl (w/v), pH 6.0–9.0, at 10–50 °C; optimum at 0–7 % NaCl, pH 7.0–8.0, 37 °C. Positive in tests for catalase, nitrate reductase, cellulase and milk coagulation. Negative in tests for H₂S, melanin, gelatin hydrolysis, milk peptization, urease, amylase and oxidase. Utilizes L-arginine, DL-aspartic amide, L-glutamate, L-histidine, L-lysine, L-methionine, L-phenylalanine, L-threonine, L-tryptophan, L-tyrosine and L-valine as sole nitrogen and energy sources but L-alanine and L-glycine are not utilized. Glucose and galactose are diagnostic whole-cell sugars. Predominant menaquinones (>5 %) include MK-10(H₂), MK-10(H₄), MK-10(H₆), MK-11(H₂), MK-11(H₄), MK-11(H₆). The polar lipids consist of diphosphatidylglycerol, phosphatidylglycerol, phosphatidylglycositol, two phosphatidylinositol mannosides, six glycolipids, an unknown phosphoglycolipid, phosphatidylycerine, three unknown phospholipids and two unknown polar lipids. The major component of cellular fatty acids (>10 %) is iso-C₁₆:0.

The type strain is 12A09T (=KCTC 29145T=CCCTCC AB 2013140T) isolated from a sample collected from the South China Sea (119° 19.896′ E 19° 41.569′ N) at a depth of 2918 m. The G+C content of the genomic DNA is 74.4 mol%.

Description of Streptomonospora arabica comb. nov.

Streptomonospora arabica (a.ra′bi.ca. L. fem. adj. arabica pertaining to Arabia, referring to the isolation of the type strain in Egypt).

The description is as given for Nocardiopsis arabia by Hozzein & Goodfellow (2008) with the following additions. Growth is good on ISP 2, ISP 3, ISP 4 and ISP 5 agar, Czapek’s solution agar, nutrient agar and trypticase soy agar. At maturity, on modified ISP 5 medium, aerial mycelium forms spor chains (wrinkled surface) and single spores (wrinkled surface) are borne on short sporophores on the substrate mycelium. Growth occurs on ISP medium 2 with 0–20 % NaCl (w/v), pH 6.0–9.0, at 10–40 °C; optimum at 7–12 % NaCl, pH 7.0–8.0, 28 °C. Positive in tests for catalase, cellulase, milk peptization and coagulation. Negative in tests for H₂S, melanin, nitrate reductase, gelatin hydrolysis, urease, amylase and oxidase. Whole-cell sugars contain galactose, glucose and ribose. Predominant menaquinones (>5 %) include MK-10(H₂), MK-10(H₄), MK-10(H₆), MK-11(H₂), MK-11(H₄), MK-11(H₆). The major components of fatty acids (>10 %) are iso-C₁₆:0 and 10-methyl C₁₈:0 TBSA.

The type strain is S186T (=CGMCC 4.2057T=DSM 45083T). The G+C content of the genomic DNA is 72.3 mol%.

Acknowledgements

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References


