**Streptimonospora salina gen. nov., sp. nov., a new member of the family Nocardiopsaceae**

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Actinomycete strain YIM 90002T (= CCTCC 99003T = CCRC 16284T) was isolated from a soil sample collected from a salt lake in the west of China. The aerial mycelium of this organism is well developed but not fragmented and, at maturity, forms short chains of spores. Spores in short chains are oval- to rod-shaped and have wrinkled surfaces. Substrate mycelium is branched with non-fragmenting hyphae and forms single oval to round spores borne on sporophores or dichotomously branching sporophores. Single spores have wrinkled surfaces. Single spores and spores in short chains are non-motile.

Strain YIM 90002T contains meso-diaminopimelic acid, do-diaminopimelic acid, glycine, lysine and aspartic acid in its cell wall and has glucose, galactose, ribose, xylose, arabinose and mannose as whole-cell sugars (no diagnostic sugars). The phospholipids are phosphatidylglycerol, phosphatidylinositol and phosphatidylethanolamine. The major menaquinones are MK-9(H6), MK-10(H2) and MK-10(H4). Phylogenetic data indicate that this strain belongs to the family Nocardiopsaceae. The morphological and physiological characteristics and chemotaxonomic and phylogenetic data for this strain differ from those of previously described actinomycetes. Therefore, a new genus, *Streptimonospora*, is proposed for this organism; the type species of the genus is *Streptimonospora salina* gen. nov., sp. nov., and the type strain of *S. salina* is strain YIM 90002T.

**Keywords:** Nocardiopsaceae, Streptimonospora salina sp. nov., 16S rDNA

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**INTRODUCTION**

The family Nocardiopsaceae (Rainey et al., 1996) contains two genera, namely *Nocardiopsis* (Meyer, 1976) and *Thermobifida* (Zhang et al., 1998). Although 16S rRNA sequence-based phylogenetic analysis shows that they form a distinct clade in the suborder Streptosporangiineae (Stackebrandt et al., 1997), *Nocardiopsis* and *Thermobifida* are morphologically and chemotaxonomically different. Currently, the genus *Nocardiopsis* contains the following validly described species and subspecies: *Nocardiopsis dassonvillei*, *Nocardiopsis alborubida*, *Nocardiopsis antarctica*, *Nocardiopsis listeri*, *Nocardiopsis lucentensis*, *Nocardiopsis halophila*, *Nocardiopsis alba* subsp. alba, *Nocardiopsis alba* subsp. prasina and *Nocardiopsis symnemataformans* (Meyer, 1976; Grund & Kroppenstedt, 1990; Abyzov et al., 1983; Yassin et al., 1993, 1997; Al-Tai & Ruan, 1994; Miyashita et al., 1984). The subspecies *N. alba* subsp. *prasina* has been elevated to species rank as *Nocardiopsis prasina* (type strain DSM 43845T) on the basis of levels of DNA–DNA hybridization (24-25%) between *N. alba* subsp. *alba* and *N. alba* subsp. *prasina* (Yassin et al., 1997). Three species, *N. antarctica*, *N. alborubida* and *N. dassonvillei*, were designated as synonyms of *N. dassonvillei* on the basis of both 16S rDNA sequence similarity and DNA–DNA hybridization data (Yassin et al., 1997). The genus Thermobifida includes *Thermobifida fusca* and *Thermobifida alba* and both of them were transferred from the genus *Thermomonospora* (Zhang et al.,

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**Abbreviations:** DAP, diaminopimelic acid, GL, phospholipids of unknown structure containing glucosamine; ISP, International Streptomyces Project; PC, phosphatidylcholine; PE, phosphatidylethanolamine; PG, phosphatidylglycerol; PI, phosphatidylinositol; PME, phosphatidymethylethanolamine.

The GenBank accession number for the 16S rDNA sequence of *Streptimonospora salina* strain YIM 90002T (= CCTCC 99003T = CCRC 16284T) is AF178988.
The species *Thermomonospora mesouiformis* was proposed to be a synonym of *Thermomonospora alba* (Zhang et al., 1998; McCarthy & Cross, 1984).

During our taxonomic studies on extremophilic actinomycetes, we isolated a strain, YIM 90002\(^T\), from soil samples collected from a salt lake in Xinjiang, the western province of China. After a primary analysis of the 16S rDNA sequence of the strain, together with the 16S rDNA sequence of the strain, we found high levels of sequence similarity between *Nocardiopsis* species and *Thermobifida* species. Strain YIM 90002\(^T\), however, formed a distinct branch in the phylogenetic tree. This strain was morphologically different from any other species of actinomycete in databases, we found high levels of sequence similarity between *Nocardiopsis* species and *Thermobifida* species. Strain YIM 90002\(^T\), however, formed a distinct branch in the phylogenetic tree. This strain was morphologically different from any other species of actinomycete.

In this work, we have analysed and classified strain YIM 90002\(^T\) by reconciling the genotypic and phenotypic features (Embley & Stackebrandt, 1994). We propose that the micro-organism should be included in a new genus, *Streptimonospora* gen. nov., as *Streptimonospora salina* sp. nov.

### Methods

#### Organism and culture conditions

Strain YIM 90002\(^T\) (as type species of the genus) was isolated from soil samples collected from a salt lake in Xinjiang, China, and deposited in the Chinese Centre for Type Cultures Collection as strain CCTCC 90003\(^T\) and the Culture Collection of the Food Industry Research & Development Institute, Taiwan, as strain CCRC 16284\(^T\). *International Streptomyces Project* (ISP) medium 5 (salt concentration, 15%, w/v; pH 7.0) (Shirling & Gottlieb, 1966) was used for the isolation and pure-culture incubation of strain YIM 90002\(^T\). Cell material for DNA extraction was grown on ISP medium 5 for YIM 90004\(^T\) at 28 °C for 28 d. The wet biomass used for whole-cell analysis of amino acids and sugars was obtained from cultures grown in ISP 5 broth (salt concentration, 15%, w/v) for 28 d at 28 °C. All strains investigated in this study are listed in Table 1.

#### Preparation of genomic DNA and amplification of the 16S rRNA gene

Genomic DNA was isolated from the test strain by using a procedure (Hopwood et al., 1985) that was modified slightly by us. 16S rDNA was amplified by PCR using TaKaRa Ex Taq (TaKaRa Biotechnology) and primers A 8–27f (5'-CCGTAGACCTAGAGTATTGATCCGCGTTCG-3') and B 1523–1504r (5'-CCCGGTGACCGTTGAGTGTCCGCGCCGCA-3'). The conditions used for thermal cycling were as follows: denaturation at 95 °C for 5 min, followed by 35 cycles of denaturation at 95 °C for 1 min, annealing at 56 °C for 1 min and extension at 72 °C for 3 min. At the end of the cycles, the reaction mixture was kept at 72 °C for 5 min and then cooled to 4 °C. The 1.5 kb amplified 16S rDNA fragment was separated by agarose gel electrophoresis and purified by using a Watson gel extraction kit. The purified fragment was sequenced directly by using the Big Dye terminator cycle sequencing ready reaction kit (Perkin-Elmer) and was analysed with an ABI PRISM 377 DNA sequencer. The sequencing primers were KMS098PBr (5'-TAAGGAGGTATCCGCAGCC-3'), KMS098PDr (5'-GGTTGCCGCTCGTTG-3') and KMS098Pcr (5'-TCTGC-GCATTTACCGCTAC-3').

#### Sequence alignment and phylogenetic analysis

Reference strains were chosen from BLAST (Altschul et al., 1997) search results. Multiple alignments of sequences determined in this study together with reference sequences obtained from databases and calculations of levels of sequence similarity were carried out using CLUSTAL W 1.74 (Higgins et al., 1992). A phylogenetic tree was reconstructed using the neighbour-joining method of Saitou & Nei (1987) from \(K_{\text{ace}}\) values (Kimura, 1980, 1983). Maximum-likelihood and parsimony trees (not shown) were generated using the treeing algorithms contained in the PHYLIP package (Felsenstein, 1995). The topology of the neighbour-joining phylogenetic tree was evaluated by using the bootstrap resampling method of Felsenstein (1985) with 1000 replicates.

#### Nucleotide sequence accession numbers

The accession numbers of the reference strains, which are closely related to strain YIM 90002\(^T\), are listed in Table 1.

#### Morphological and physiological characteristics

Morphological features were observed on glycerol/asparagine agar (ISP medium 5) (15% salt, w/v) and the incubation time was 28–30 d at 28 °C. Physiological features were observed on media commonly used for the characterization of *Streptomyces* species (Shirling & Gottlieb, 1966). Cultural characteristics were determined after 28–30 d at 28 °C by using ISP methods (Shirling & Gottlieb, 1966). Morphological observations of spores and mycelia were obtained by scanning electron microscopy, as described previously (O'Donnell et al., 1993), with a JÉOL model JSM35CF scanning electron microscope. The media and procedures used to examine the physiological features and carbon-source utilization of strain

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### Table 1 Strains investigated in this study

<table>
<thead>
<tr>
<th>Taxon</th>
<th>Strain</th>
<th>16S rDNA accession no.</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>Nocardiopsis halophila</em></td>
<td>was not included in this study.</td>
<td></td>
</tr>
<tr>
<td><em>Streptimonospora salina</em></td>
<td>YIM 90002(^T)</td>
<td>AF178988</td>
</tr>
<tr>
<td><em>Thermobifida alba</em></td>
<td>JCM 3077(^T)</td>
<td>AF002260</td>
</tr>
<tr>
<td><em>Thermobifida fusca</em></td>
<td>JCM 3262(^T)</td>
<td>AF002264</td>
</tr>
<tr>
<td><em>Thermobifida mesouiformis</em></td>
<td>JCM 3169(^T)</td>
<td>AF002265</td>
</tr>
<tr>
<td><em>Nocardiopsis prasina</em></td>
<td>DSM 43845(^T)</td>
<td>X97884</td>
</tr>
<tr>
<td><em>Nocardiopsis listeri</em></td>
<td>DSM 43297(^T)</td>
<td>X97887</td>
</tr>
<tr>
<td><em>Nocardiopsis alba</em></td>
<td>DSM 43377(^T)</td>
<td>X97883</td>
</tr>
<tr>
<td><em>Nocardiopsis lauentensis</em></td>
<td>DSM 44048(^T)</td>
<td>X97888</td>
</tr>
<tr>
<td><em>Nocardiopsis</em></td>
<td>DSM 44143(^T)</td>
<td>Y13593</td>
</tr>
<tr>
<td><em>syngenetaformans</em></td>
<td></td>
<td></td>
</tr>
<tr>
<td><em>Nocardiopsis dassonvillei</em></td>
<td>DSM 43111(^T)</td>
<td>X97886</td>
</tr>
<tr>
<td><em>Thermomonospora curvata</em></td>
<td>IFO 15933(^T)</td>
<td>D86945</td>
</tr>
<tr>
<td><em>Streptosporangium album</em></td>
<td>DSM 43023(^T)</td>
<td>X89934</td>
</tr>
<tr>
<td><em>Actinomadura madurae</em></td>
<td>DSM 43067(^T)</td>
<td>X97889</td>
</tr>
<tr>
<td><em>Microtetraspora glauca</em></td>
<td>DSM 43311(^T)</td>
<td>X93190</td>
</tr>
<tr>
<td><em>Saccharothrix australiensis</em></td>
<td>NRR L1123(^T)</td>
<td>AF114803</td>
</tr>
<tr>
<td><em>Streptomyces megasporus</em></td>
<td>DSM 41476(^T)</td>
<td>Z68100</td>
</tr>
</tbody>
</table>

* Synonym of *Thermobifida alba* (Zhang et al., 1998).
YIM 90002<sup>T</sup> were those described by Shirling & Gottlieb (1966) and Locci (1989). Colour determinations were made by comparing pure cultures with colour chips from the ISCC–NBS colour charts (standard samples, no. 2106) (Kelly, 1964).

**Analysis of chemotaxonomic characteristics.** Cell wall was purified and analysed using the TLC protocol of Lechevalier & Lechevalier (1980). The procedures of Becker et al. (1964) and Lechevalier & Lechevalier (1980) were used for the analysis of whole-cell composition. GC/MS was used for the quantitative determination of sugar content (Saddler et al., 1991). The phospholipid analysis was carried out by the method of Lechevalier et al. (1981). Menaquinones were determined using the procedures of Collins (1985).

**RESULTS**

**Morphological observations**

Morphological observation of a 28-d-old culture of strain YIM 90002<sup>T</sup> grown on glycerol/ascoragine agar (ISP medium 5) containing 15% (w/v) salt revealed that the vegetative hyphae with irregular branches were well developed but not fragmented (Fig. 1).

Fig. 1. Scanning electron micrographs of *Streptimonospora salina* (YIM 90002<sup>T</sup>) grown on ISP medium 5 for 28 d at 28 °C, showing single spores (a) and a short chain of spores (b). Bars, 2 µm.

The aerial mycelium, at maturity, formed short chains of spores; spores in short chains were oval- to rod-shaped (1.5–2 × 1 µm) with wrinkled surfaces (Fig. 1b). Substrate mycelium was extensively branched with non-fragmenting hyphae. Single spores, oval to round and 1.4–1.6 µm in diameter, were borne on sporophores of substrate mycelium (Fig. 1a) or dichotomously branched sporophores, and the surfaces of single spores were wrinkled. Therefore, the spores consist of two types, both of which are non-motile.

**Cultural characteristics**

As shown in Table 2, strain YIM 90002<sup>T</sup> produced well-developed white to pale-yellow colonies on most media tested. It showed good growth on most media except oatmeal agar (ISP medium 3). No diffusible pigments were produced. It developed aerial hyphae on most media tested, especially Czapek’s agar and glycerol/ascoragine agar (ISP medium 5).

**Physiological characteristics**

Strain YIM 90002<sup>T</sup> utilized glucose, sucrose, maltose, arabinose, raffinose, starch, glycerol, mannitol and histidine. It was positive for starch hydrolysis and melanin production, but negative for milk coagulation, milk peptonization, growth in cellulose, H<sub>2</sub>S production and gelatin liquefaction.

**Chemotaxonomic characteristics**

The cell-wall amino acid composition and whole-cell sugar pattern of strain YIM 90002<sup>T</sup> are shown in Table 3. The cell walls contained meso-diaminopimelic acid (DAP), glycine, aspartic acid and lysine and trace amounts of d-DAP. Whole cells of strain YIM 90002<sup>T</sup> contained large amounts of glucose and galactose and smaller amounts of ribose, arabinose, xylose and mannose. Rhamnose and madurose were not detected, indicating that the strain contains no characteristic wall sugars (according to the scheme of Lechevalier & Lechevalier, 1980). The phospholipids are phosphatidylglycerol (PG), phosphatidylinositol (PI) and phosphatidylethanolamine (PE). The major menaquinones are MK-9(H<sub>8</sub>), MK-10(H<sub>2</sub>) and MK-10(H<sub>4</sub>).

**Phylogenetic position**

An almost complete 16S rDNA sequence was determined for strain YIM 90002<sup>T</sup> (> 95% of the *Escherichia coli* sequence) from position 8 to position 1523 (*E. coli* numbering system; Brosius et al., 1978). BLAST search results for strain YIM 90002<sup>T</sup> came from non-redundant GenBank + EMBL + DDBJ + PDB; when reference sequences were chosen, unidentified and unpublished sequences were excluded (Table 1). The number of nucleotides compared was 1436 after elimination of sites for which the nucleotides were not
Table 2: Cultural characteristics of strain YIM 90002<sup>T</sup>

Diffusible pigments were not produced on any of the media listed.

<table>
<thead>
<tr>
<th>Medium&lt;sup&gt;*&lt;/sup&gt;</th>
<th>Growth</th>
<th>Sporulation</th>
<th>Colour of colonies†</th>
</tr>
</thead>
<tbody>
<tr>
<td>Yeast extract/malt extract (ISP medium 2)</td>
<td>Good</td>
<td>Moderate</td>
<td>Pale white</td>
</tr>
<tr>
<td>Oatmeal agar (ISP medium 3)</td>
<td>Poor</td>
<td>Poor</td>
<td>White</td>
</tr>
<tr>
<td>Inorganic salt/starch agar (ISP medium 4)</td>
<td>Moderate</td>
<td>Moderate</td>
<td>White/white</td>
</tr>
<tr>
<td>Glycerol/asparagine agar (ISP medium 5)</td>
<td>Good</td>
<td>Good</td>
<td>White</td>
</tr>
<tr>
<td>Czapek’s agar</td>
<td>Good</td>
<td>Good</td>
<td>White</td>
</tr>
<tr>
<td>Potato agar</td>
<td>Good</td>
<td>Moderate</td>
<td>White</td>
</tr>
<tr>
<td>Nutrient agar</td>
<td>Good</td>
<td>Moderate</td>
<td>Deep orange/yellow</td>
</tr>
</tbody>
</table>

* Containing 15% (w/v) salt; pH 7.0.
† Colours taken from ISCC–NBS colour charts (standard samples, no. 2106) (Kelly, 1964).

Table 3: Chemotaxonomic characteristics of strain YIM 90002<sup>T</sup> and the genera of the Nocardiopsaceae

The genera Nocardiopsis and Thermobifida follow the classification of Zhang et al. (1998). None of the taxa exhibited any diagnostic sugars. Abbreviations: DAP, diaminopimelic acid; GL, phospholipids of unknown structure containing glucosamine; PC, phosphatidylcholine; PE, phosphatidylethanolamine; PG, phosphatidylglycerol; PI, phosphatidylinositol; PME, phosphatidylmethylethanolamine.

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>Strain YIM 90002&lt;sup&gt;T&lt;/sup&gt;</th>
<th>Nocardiopsis</th>
<th>Thermobifida</th>
</tr>
</thead>
<tbody>
<tr>
<td>Sugar content</td>
<td>15% Ribose, 6% xylose, 5% arabinose, 2% mannose, 34% galactose, 38% glucose*</td>
<td>Type C</td>
<td>Type C</td>
</tr>
<tr>
<td>Wall peptidoglycan</td>
<td>meso-DAP [glycine, lysine and aspartic acid (detected), DD-DAP (trace)]</td>
<td>Cell wall type III (meso-DAP)</td>
<td>Cell wall type III [meso-DAP, L-L-DAP (trace)]</td>
</tr>
<tr>
<td>Phospholipids</td>
<td>PI, PE, PG</td>
<td>Type III (PC, PME, GL)</td>
<td>Type III (PE, PME, GL)</td>
</tr>
<tr>
<td>Menaquinones</td>
<td>MK-9(H&lt;sub&gt;2&lt;/sub&gt;), MK-10(H&lt;sub&gt;2&lt;/sub&gt;), MK-10(H&lt;sub&gt;4&lt;/sub&gt;)</td>
<td>Type 4c [MK-10(H&lt;sub&gt;2&lt;/sub&gt;), MK-10(H&lt;sub&gt;2&lt;/sub&gt;), MK-10(H&lt;sub&gt;4&lt;/sub&gt;)]</td>
<td>Type 4d [MK-10(H&lt;sub&gt;2&lt;/sub&gt;), MK-10(H&lt;sub&gt;2&lt;/sub&gt;), MK-11(H&lt;sub&gt;4&lt;/sub&gt;)]</td>
</tr>
</tbody>
</table>

* Relative content. Rhamnose and madurose were not detected.

determined in all sequences. The BLAST search results and the phylogenetic tree (Fig. 2) generated from representative strains of the related genera showed that strain YIM 90002<sup>T</sup> had high levels of sequence similarity to species of Thermobifida (Zhang et al., 1998) and members of the genus Nocardiopsis. The phylogenetic tree obtained by applying the neighbour-joining method to K<sub>nuc</sub> values is shown in Fig. 2. 16S rDNA analysis revealed that strain YIM 90002<sup>T</sup> is phylogenetically closely related to members of the genera Nocardiopsis and Thermobifida (the sequence similarity levels were 94%–95% to Thermobifida and 93%–94% to Nocardiopsis). All strains of the genera Nocardiopsis and Thermobifida, together with strain YIM 90002<sup>T</sup>, formed a distinct clade that was strongly supported by a high bootstrap value (100%). Phylogenetically, strain YIM 90002<sup>T</sup> forms a branch that is distinct from the groups containing the genera Nocardiopsis and Thermobifida and which lies between the two groups.

**DISCUSSION**

The results of 16S rDNA sequence comparisons clearly demonstrated that strain YIM 90002<sup>T</sup> is a member of the family Nocardiopsaceae, and the 16S rDNA sequence of strain YIM 90002<sup>T</sup> contains all the signature nucleotides defined for the family Nocardiopsaceae, as described by Stackebrandt et al. (1997). The high levels of 16S rDNA sequence similarity to species of the genera Nocardiopsis (93.7%–94.7%) and Thermobifida (94.9%–95.1%) place strain YIM 90002<sup>T</sup> in the Nocardiopsaceae as a distinct member between Nocardiopsis and Thermobifida (Fig. 2).

Strain YIM 90002<sup>T</sup> is morphologically different from members of the genera Thermobifida and Nocardiopsis. On aerial mycelium, strain YIM 90002<sup>T</sup> forms short chains of spores that are somewhat like the spores formed on aerial mycelium by members of Nocardiopsis. Strain YIM 90002<sup>T</sup> also forms single spores, borne on sporophores or dichotomously branched.
**Streptomonospora salina** gen. nov., sp. nov.

Nocardiopsis prasina DSM 43845<sup>T</sup>

Nocardiopsis listeri DSM 40297<sup>T</sup>

Nocardiopsis alba DSM 43377<sup>T</sup>

Nocardiopsis lucentensis DSM 44048<sup>T</sup>

Nocardiopsis synnemataformans DSM 44143<sup>T</sup>

Nocardiopsis dassonvillei DSM 43111<sup>T</sup>

**Thermobifida alba** JCM 3077<sup>T</sup>

**Thermobifida mesouviformis** JCM 3169<sup>T</sup>

**Thermobifida fusca** JCM 3262<sup>T</sup>

**Actinomadura madurae** DSM 43067<sup>T</sup>

**Thermomonospora curvata** IFO 15933<sup>T</sup>

**Microtetraspora glauca** DSM 43311<sup>T</sup>

**Streptosporangium album** DSM 43023<sup>T</sup>

**Saccharothrix australiensis** NRRL 11239<sup>T</sup>

**Streptomyces megasporus** DSM 41476<sup>T</sup>

**Fig. 2.** Neighbour-joining tree showing the phylogenetic relationships among Streptomonospora salina and representative members of the families Nocardiopsaceae, Streptosporangiaceae and Thermomonosporaceae in the suborder Streptosporangineae. Streptomycetes was used as the outgroup. The ‘m’ and ‘p’ labels indicate branches that were also found with the maximum-likelihood (Felsenstein, 1981) and parsimony (Kluge & Farris, 1969) algorithms, respectively: asterisks indicate branches that were recovered with all three methods. The analysis included 1436 unambiguous nucleotide positions. Bootstrap values (> 50%) from 1000 analyses are shown at the nodes of the tree. The strain shown in bold is the type species of the new genus Streptomonospora. Bar, 1 nucleotide substitution per 100 nucleotides of 16S rDNA sequence.

sporophores of substrate hyphae, that are morphologically similar to the spores found on dichotomously branched sporophores (resulting in spore clusters on aerial hyphae) of members of the genus Thermobifida.

Strain YIM 90002<sup>T</sup> is chemotaxonomically different from members of the genera Nocardiopsis and Thermobifida. The cell wall of strain YIM 90002<sup>T</sup> contains meso-DAP, ddm-DAP, glycine and aspartic acid; whole-cell hydrolysates contain no diagnostic sugars; the phospholipids are PG, PI and PE and the major menaquinones are MK-9(H<sub>4</sub>), MK-10(H<sub>4</sub>) and MK-10(H<sub>5</sub>). For members of the genus Thermobifida, cell walls contain meso-DAP (cell wall type III), a trace amount of LL-DAP may be detected in whole-cell hydrolysates, the sugar pattern is type C (no diagnostic sugars), the predominant menaquinones are MK-10(H<sub>6</sub>), MK-10(H<sub>6</sub>) and MK-11(H<sub>6</sub>) and the phospholipid pattern is type II [PE, PME (phosphatidylmethylethanolamine), GL (phospholipids of unknown structure, containing glucosamine)] (Zhang et al., 1998). For members of the genus Nocardiopsis, the peptidoglycan contains meso-DAP, no diagnostic sugars are present (cell wall chemotype III/C) (Lechevalier & Lechevalier, 1970), the phospholipid pattern is type III (phosphatidylcholine, PME, GL).
and the menaquinone pattern is type 4c [MK-10(H₂), MK-10(H₄) and MK-10(H₈)] (Zhang et al., 1998).

Therefore, we propose that strain YIM 90002T should be classified as a member of a new genus, Streptimonospora. The type species is Streptimonospora salina gen. nov., sp. nov.

Description of Streptimonospora gen. nov.

Streptimonospora (Strep.ti.mo.no.spo’ra. Gr. adj. streptos pliant, bent; Gr. adj. monos single, solitary; Gr. fem. n. spora a seed, spore; M.L. fem. n. Streptimonospora indicating that this organism forms two types of spore, with wrinkled surfaces, on aerial mycelium and substrate mycelium).

Gram-positive, aerobic organisms with branching hyphae. Non-fragmenting substrate mycelia are present. The aerial mycelium, at maturity, forms short chains of spores; the spores in short chains are oval-to rod-shaped (1.5 – 2 x 1 μm) with wrinkled surfaces. Substrate mycelium is extensively branched with non-fragmenting hyphae. Single spores, which are oval to round (1.4 – 1.6 μm), are borne on sporophores or dichotomously branched sporophores of substrate hyphae; the surfaces of the spores are wrinkled. Both types of spore are non-motile. The cell wall contains meso-DAP, dD-DAP, glycine and aspartic acid. Whole-cell hydrolysates contain large amounts of glucose and galactose and smaller amounts of ribose, arabinose, xylose and mannose. The phospholipids are phosphatidylglycerol, phosphatidylinositol and phosphatidylethanolamine. The major menaquinones are MK-9(H₄), MK-10(H₄) and MK-10(H₈). The type species is Streptimonospora salina.

Description of Streptimonospora salina sp. nov.

Streptimonospora salina (sa.li’na. L. adj. salina salted, saline).

Aerial mycelium is well developed but not fragmented. Colonies are white on most media. Two types of spore with wrinkled surfaces are borne on aerial mycelium and substrate mycelium. No diffusible pigment is produced, but melanin is produced. Utilizes glucose, sucrose, maltose, arabinose, raffinose, starch, glycerol, mannitol and histidine. Positive for starch hydrolysis and melanin production, but negative for milk coagulation, milk peptonization, growth in cellulose, H₂S production and gelatin liquefaction. Optimum growth occurs in media supplemented with salt at a concentration of 15% (w/v) at 28 °C and pH 7.0.

Isolated from hypersaline habitats (a salt lake in China). The type strain is strain YIM 90002T (= CCTCC 99003T = CCRC 16284T).

ACKNOWLEDGEMENTS

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REFERENCES


Streptimonospora salina gen. nov., sp. nov.


