A halophilic actinomycete strain, designated YIM 90500T, was isolated from a saline lake in Xinjiang province, north-west China, and subjected to a polyphasic taxonomic study. Good growth of the novel isolate occurred at 28–37 °C, pH 7–8 and with 10–15% (w/v) NaCl; no growth occurred without any salts. Strain YIM 90500T contained meso-diaminopimelic acid with glucose, arabinose and ribose as the whole-cell sugars. The major phospholipids were phosphatidylcholine and diphosphatidylglycerol. MK-9(H4) was the predominant menaquinone. The major fatty acids were iso-C15:0, iso-C16:0 and anteiso-C17:0. The chemotaxonomic data together with the morphological properties of strain YIM 90500T consistently assigned the strain as belonging to the genus Saccharopolyspora. Phylogenetic analysis based on 16S rRNA gene sequences further revealed that strain YIM 90500T formed a distinct phyletic lineage in the genus Saccharopolyspora and showed low 16S rRNA gene similarities (<96.4%) with other species of the genus. On the basis of the evidence from the polyphasic study, a novel species, Saccharopolyspora halophila sp. nov., is proposed. The type strain is YIM 90500T (DSM 45007T=KCTC 19162T).
colour charts (Kelly, 1964). Media and procedures used to determine physiological features and carbon source utilization were those described by Williams et al. (1989). Acid production from carbohydrates was assessed using previously described procedures (Minnikin et al., 1984). Menaquinones were isolated according to Minnikin et al. (1984) and separated by HPLC (Kroppenstedt, 1982). Cellular fatty acids analysis was performed as described by Sasser (1990) using the Microbial Identification System (MIDI). Strain YIM 90500T contained *meso*-diaminopimelic acid as the cell wall diamino acid, with glucose, arabinose and ribose as the major whole-cell sugars. The major cellular fatty acids were iso-C15:0 (20.8 %), iso-C16:0 (19.1 %) and anteiso-C17:0 (21.0 %); minor fatty acids iso-C14:0 (1.2 %), anteiso-C15:0 (6.2 %), C16:1o7c/iso-C15:0 2-OH (3.4 %), C18:0 (3.5 %), 10-methyl C16:0 (6.3 %), iso-C17:0 (7.0 %), C17:1o8c (2.3 %), C17:0 (1.2 %), 10-methyl C17:0 (1.8 %) and C18:1o9c (1.3 %) were also detected. Detailed data for phospholipids and menaquinones are given in the species description.

Extraction of genomic DNA and PCR amplification of the 16S rRNA gene were done as described by Li et al. (2007). Multiple alignments with sequences of the most closely related *Saccharopolyspora* species and calculations of levels of sequence similarity were carried out using CLUSTAL_X (Thompson et al., 1997). Phylogenetic analyses were performed using three tree-making algorithms, neighbour-joining (Saitou & Nei, 1987), maximum-likelihood (Felsenstein, 1981) and maximum-parsimony (Fitch, 1971). A phylogenetic tree was constructed using the neighbour-joining method of Saitou & Nei (1987) from K$_{\text{muc}}$ values (Kimura, 1980) using MEGA version 2.1 (Kumar et al., 2001). The topology of the phylogenetic tree was evaluated by using the bootstrap resampling method of

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>1</th>
<th>2</th>
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<tbody>
<tr>
<td>Fragments of substrate mycelium</td>
<td>−</td>
<td>+</td>
<td>+</td>
<td>+</td>
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<tr>
<td>Colour of*</td>
<td>Y</td>
<td>W</td>
<td>W</td>
<td>YP</td>
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<td>Aerial mycelia</td>
<td>Y-OY</td>
<td>Y</td>
<td>C-Bf</td>
<td>Y-YBr</td>
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<tr>
<td>Soluble pigment</td>
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<td>−</td>
<td>−</td>
<td>+</td>
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<td>Degradation of: Adenine</td>
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<td>+</td>
<td>+</td>
<td>−</td>
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<tr>
<td>Casein</td>
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<tr>
<td>Reduction of nitrate</td>
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<td>+</td>
<td>−</td>
<td>+</td>
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<tr>
<td>NaCl range for growth (% w/v)</td>
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<td>0–7</td>
<td>0–7</td>
<td>0–11</td>
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<td>Temperature range for growth (°C)</td>
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<td>28–37</td>
<td>45–55</td>
<td>15–37</td>
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<td>Menaquinones</td>
<td>MK-9(H$_2$), MK-9(H$_4$), MK-9(H$_6$)</td>
<td>MK-9(H$_2$)</td>
<td>MK-9(H$_4$), MK-9(H$_6$)</td>
<td>MK-9(H$_2$), MK-9(H$_4$)</td>
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<td>Polar lipids†</td>
<td>DPG, PC, PI</td>
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<tr>
<td>DNA G+C content (mol%)</td>
<td>66.3</td>
<td>67</td>
<td>73.1</td>
<td>ND</td>
</tr>
</tbody>
</table>

*S* Bf, buff; Br, brown; C, colourless; O, orange; P, pink; W, white; Y, yellow.

†DPG, Diphosphatidylglycerol; PC, phosphatidylcholine; PI, phosphatidylinositol.
Felsenstein (1985) with 1000 replicates. For the determination of the G+C content, the genomic DNA of strain YIM 90500T was prepared according to the method of Marmur (1961). The G+C content of the DNA was determined by using reversed-phase HPLC of nucleosides, according to Mesbah et al. (1989).

The results of the 16S rRNA gene sequence comparison clearly demonstrated that strain YIM 90500T is a member of the genus Saccharopolyspora. In the phylogenetic tree based on the neighbour-joining algorithm, strain YIM 90500T formed a distinct subclade with S. flava, and both shared the same branch with a high bootstrap value of 97 % (Fig. 1). Topologies of phylogenetic trees constructed using the maximum-likelihood and maximum-parsimony algorithms were similar to those of the tree constructed by using neighbour-joining analysis (data not shown). The 16S rRNA gene sequence similarities between strain YIM 90500T and its closest neighbours, S. spinosa and S. flava, were 96.3 and 96.2 %, respectively. The G+C content of the DNA was 66.3 mol%.

On the basis of the differential phenotypic and chemotaxonomic characteristics (Table 1) and the phylogenetic data of strain YIM 90500T and its closest neighbours in the genus Saccharopolyspora, strain YIM 90500T merits recognition as representing a novel species within the genus, for which we propose the name Saccharopolyspora halophila sp. nov.

**Description of Saccharopolyspora halophila sp. nov.**

Saccharopolyspora halophila (ha.lo.phi.‘la. Gr. n. hals halos, salt; Gr. adj. philos, loving; N.L. fem. adj. halophila, salt-loving, referring to the ability to grow at high NaCl concentrations).

Aerobic, Gram-positive, moderately halophilic filamentous actinomycete. Substrate mycelia are well-developed and no fragments are observed. Aerial mycelia form long chains of spores; spores are non-motile, smooth-surfaced, oval or spherical and 0.6–0.7 × 0.6–1.1 μm in size. Good growth occurs on Czapek agar, yeast extract-malt extract, potato agar, glycerol/asparagine agar and inorganic salts-starch agar. Moderate growth occurs on nutrient agar and oatmeal agar. Aerial mycelia are white-yellow in colour and substrate mycelia are yellow to moderate orange-yellow. No diffusible pigments are produced. Casein and tyrosine are degraded, but adenine, cellulose and chitin are not. Tests for gelatin liquefaction, nitrate reduction and milk coagulation and coagulation are positive and tests for H2S and melain production and starch hydrolysis are negative. L-Arabinose, cellobiose, D-fructose, D-galactose, D-glucose, myo-inositol, D-lactose, maltose, D-mannitol, D-mannose, raffinose, L-rhamnose, sucrose, sodium acetate, D-xylitol and D-xylose are utilized as carbon sources, whereas D-sorbitol and trehalose are not acid. Production occurs on L-arabinose, D-glucose, myo-inositol, L-rhamnose and D-xylose. Growth occurs on alanine, asparagine, arginine, cystine, glycine, histidine, homocysteine, hypoxanthine, lysine, praline, threonine, tyrosine, valine and urea as nitrogen sources, but not on adenine, hydroxyproline or glutamate. Major phospholipids are phosphatidylcholine and diphosphatidylglycerol; minor amounts of phosphatidylinositol are also detected. Menaquinones are MK-9(H2), MK-9(H4) and MK-9(H6) (ratio of peak areas, 13.1:82.9:3.9). Major cellular fatty acids are iso-C15 : 0, iso-C16 : 0 and anteiso-C17 : 0; minor fatty acids include C14 : 0, anteiso-C15 : 0, C16 : 0, iso-C15 : 0, 2-OH, C16 : 0, 10-methyl C16 : 0, iso-C17 : 0, C17 : 1ω8c, C17 : 0, 10-methyl C17 : 0 and C18 : 1ω9c are also detected. Temperature, pH and NaCl tolerance ranges are 10–45 °C, pH 6–8.5 and 3–20 % (w/v), respectively. Good growth occurs at 28–37 °C and pH 7–8 and with 10–15 % (w/v) NaCl. The G+C content of the DNA of the type strain is 66.3 mol%.

The type strain, YIM 90500T (=DSM 45007T = KCTC 19162T), was isolated from a saline lake in Xinjiang, north-west China.

![Fig. 1. Phylogenetic dendrogram obtained by using distance matrix analysis of 16S rRNA gene sequences, showing the position of strain YIM 90500T and related phylogenetic neighbours. Numbers at branch nodes are bootstrap values (1000 resamplings; only values over 50 % are given). The sequence of Thermobifida alba DSM 43795T (AF002260) was used as the outgroup. Bar, 1 % sequence divergence.](http://ijs.sgmjournals.org)
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