Yuhushiella deserti gen. nov., sp. nov., a new member of the suborder Pseudonocardineae

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A thermotolerant, Gram-stain-positive, aerobic, sporangium-forming actinomycete, strain RA45T, was isolated from a desert region in Xinjiang Uigur Autonomous Region, north-western China. Comparative analysis of the 16S rRNA gene sequence and phenotypic characterization revealed that strain RA45T belonged phylogenetically to the family Pseudonocardiaceae of the suborder Pseudonocardineae. Strain RA45T showed more than 5% 16S rRNA gene sequence divergence from recognized species of genera in the family Pseudonocardiaceae, forming a distinct lineage within the evolutionary radiation occupied by the genera Amycolatopsis, Prauserella, Thermocrispum, Saccharomonospora, Saccharopolyspora and Sciscionella, but distinct from each of them. The affiliation to the family was supported by the presence of suborder- and family-specific 16S rRNA signature nucleotides, a DNA G+C content of 69.9 mol%, the presence of meso-diaminopimelic acid, ribose, arabinose, glucose and galactose, which are characteristic components of cell-wall chemotype IV of actinomycetes, the presence of menaquinone MK-9(H4) as the major respiratory lipoquinone, a lack of mycolic acids and the presence of an N-acetylated type of muramic acid. However, strain RA45T differed from known genera of the family in its polar lipid composition: the major phospholipids were phosphatidylethanolamine, phosphatidylinositol mannosides, phosphatidylethanolamine, diphosphatidylglycerol, phospholipids of unknown structure and phospholipids of unknown structure containing glucosamine (phospholipid type IV). Based on its morphological, chemotaxonomic and phylogenetic characteristics, strain RA45T is considered to represent a novel species of a new genus in the family Pseudonocardiaceae, for which the name Yuhushiella deserti gen. nov., sp. nov. is proposed. The type strain of Yuhushiella deserti is RA45T (=CGMCC 4.5579T =JCM 16584T).

INTRODUCTION

The family Pseudonocardiaceae was described by Embley et al. (1988), and the description was emended by Stackebrandt et al. (1997) on the basis of 16S rRNA gene sequence analysis. As recognized by Stackebrandt et al. (1997), the genera Actinosynnema, Saccharothrix and Streptoalloteichus were included in the family. Later studies by Labeda (1998) and Labeda & Kroppenstedt (2000) suggested that the genera Actinokineospora, Actinosynema, Lentzea and Saccharothrix should be assigned to a putative new taxon, the family Actinosynemataceae. The genera Kutzneria and Streptoalloteichus might also belong to this group, according to the 16S rRNA gene sequence data given by Kim & Goodfellow (1999). At the beginning of 2009, the family Pseudonocardiaceae included 15 genera with validly published names: Actinoalloteichus (Tamura et al., 2000), Actinonycetospora (Jiang et al., 2008), Allokutzneria (Labeda & Kroppenstedt, 2008), Amycolatopsis (Lechevalier et al., 1986), Crossiella (Labeda, 2001), Goodfellowiella

†These authors contributed equally to this work.

Abbreviations: ML, maximum-likelihood; MP, maximum-parsimony; NJ, neighbour-joining.

The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain RA45T is FJ526746.
Morphology. Cultural characteristics of the strain were determined after growth at 28, 37 and 45 °C for 2 weeks by methods used in the International Streptomyces Project (ISP) (Shirling & Gottlieb, 1966) as well as by using Gause’s asparagine agar (Gause et al., 1983) and Bennett’s agar (Jones, 1949). Colour determination was performed with colour chips from the ISCC-NBS Color Charts Standard Samples no. 2106 (Kelly, 1964). Morphological observations of spore chains and mycelium were made by light microscopy (Olympus BH-2) and scanning electron microscopy (Quanta 200 FEG) after 7 days of incubation at 45 °C. Gram staining (Hucker, 1921) and Ziehl–Neelsen preparations (Gordon, 1967) were evaluated by light microscopy.

PCR amplification using genus-specific primers. 16S rRNA gene primers AMY2 (Tan et al., 2006) and ATOP (McVeigh et al., 1994) specific for the genus Amycolatopsis were employed in this study to screen soil samples and to test the genus-specificity of these primers. Genomic DNA extraction, PCR amplification and electrophoresis were performed as described by Tan et al. (2006).

PCR amplification of the 16S rRNA gene and sequence analysis. Genomic DNA extraction, PCR amplification and sequencing of the 16S rRNA gene of strain RA45T were carried out according to the procedures described by Xu et al. (2003).

Phylogenetic analysis. The 16S rRNA gene sequence of strain RA45T (1493 nt) was determined and compared with sequences downloaded from the DDBJ, EMBL and GenBank databases. For initial taxonomic classification, a combination of BLAST search (Altschul et al., 1997; http://www.ncbi.nlm.nih.gov/blast) and the classifier program of the Ribosomal Database Project II (http://rdp.cme.msu.edu/index.jsp) was used. For phylogenetic analysis, sequences of the type strain of the type species of the type genus of each recognized suborder belonging to the phylum Actinobacteria (and some other sequences commonly used by taxonomists) were selected as the outgroup and, in a second step, sequences from the type species of all recognized genera (including Actinopolyspora and Thermobispora) in the family Pseudonocardiacaeae and representatives of all six recognized genera in the sister family Actinosynmmataeae were used. Sequences shorter than 1300 bp or which contained ambiguous nucleotides were excluded. A similarity matrix of all 16S rRNA gene sequences was generated after multiple alignments of the data by CLUSTAL_X (Thompson et al., 1997). Representative sequences were chosen to make a small and robust phylogenetic dendrogram with high bootstrap values at each node. Three tree construction methods were employed in this study. Neighbour-joining (NJ) trees (Saitou & Nei, 1987) were calculated by using distances corrected according to Kimura’s two-parameter model (Kimura, 1980, 1983), with the software package TREECON version 1.3b (Van de Peer & De Wachter, 1994, 1997). For construction of the maximum-parsimony (MP) tree, the software package MEGA version 4.0 (Tamura et al., 2007) was used. For construction of the maximum-likelihood (ML) tree, the online version of PhyML (Guindon et al., 2005) was used. The topologies of the trees were evaluated by performing a bootstrap analysis (Felsenstein, 1985) of 1000 resamplings for the NJ and MP trees and 500 resamplings for the ML tree. The root position of the tree based on the NJ method was estimated by using 28 outgroup organisms, Escherichia coli (unknown strain; GenBank accession no. J01695), Bacillus subtilis W168 (K00637), Acidimicrobium ferrooxidans ICT (AFU75647), Coriobacterium glomerans PW2 (X79048), Rubrobacter radiotolerans DSM 5868 (X98372), Bifidobacterium bifidum KCTC 3202 (BBU25951), Actinomyces bovis NCTC 11355 (X81061), Actinopolyspora halophila ATCC 27976 (X54287), Catenulispora aphidiphila DSM 44928 (AJ685857), Corynebacterium diptheriae NCTC 11397 (X84248), Frankia abii ACN14a (NC_008278), Glycycmesis harbinesis IFO 14487 (D85483), Kine- spora aurantiaca NRRL B-16913 (AF095336), Micrococcus luteus DSM 20030 (AJ536198), Propionibacterium freudenreichii DSM 20271 (X53217), Streptosporangium roseum DSM 43021 (X89947), Micromonospora chalcea DSM 43026 (X92594), Streptomyces albus DSM 4013 (AJ621602), Streptomyces antibioticus ATCC 23877 (M27245), Streptomyces griseus NRBC 15744 (AB184699), Atopobium minutum NCFB 2751 (X67148), Archaeobacter globiformis DSM 20124 (M23441), Microbacterium lactuum IFO 14135.
RESULTS AND DISCUSSION

A database search based on the 16S rRNA gene sequence demonstrated that strain RA45T belongs to the family Pseudonocardiaeae (Stackebrandt et al., 1997; Zhi et al., 2009). A phylogenetic study was performed with 16S rRNA gene sequences of type strains of the type species of all genera with validly published names in the family Pseudonocardiaeae and the sister family Actinosynnemataeae (Labeđa & Kropenstedt, 2000). According to the similarity matrix based on the alignment of all cited representative 16S rRNA gene sequences, the closest relatives of strain RA45T were Prauserella rugosa DSM 43194T, with 94.67 % sequence identity, Prauserella halophila YIM 90001T (94.45 %), Amycolatopsis palatopharyngis 1BDZT (94.38 %), Amycolatopsis sacchari K24T (94.35 %), Saccharomonospora saliphila YIM 90502T (94.34 %) and Thermocrispum municipale DSM 44069T (94.32 %). The sequence identity to type strains belonging to other genera of the suborder Pseudonocardiaeae was below 94.30 %. The 16S rRNA gene sequence similarity between members of the genus Actinopolyspora and representatives of the emended suborder Pseudonocardiaeae (Zhi et al., 2009) ranged from 85.89 to 90.52 % and the similarity between members of the genus Thermobispora and representatives of the emended suborder Pseudonocardiaeae (Zhi et al., 2009) ranged from 85.91 to 88.43 %, supporting the decision of Zhi et al. (2009) to exclude these two genera from the suborder Pseudonocardiaeae.

Although the use of genus-specific primers designed for Amycolatopsis (AMY2 and ATOP) (Tan et al., 2006; McVeigh et al., 1994) showed that strain RA45T yielded the same ~440 bp 16S rRNA gene fragment as members of the genus Amycolatopsis, as shown by the consensus phylogenetic tree (Fig. 1), strain RA45T always formed a subclade distinct from the phylogenetic radiation formed by the genera Prauserella, Amycolatopsis, Thermocrispum, Saccharomonospora and Saccharopolyspora, adjacent to the Thermocrispum clade. However, the separate branching of strain RA45T was supported by bootstrap values below 50 %. Furthermore, the whole-suborder phylogenetic tree was consistently divided into two large, approximately symmetrical clusters with high bootstrap values (>70 %), and the family Actinosynnemataeae formed a subclade that fell into one of the large clusters, while RA45T fell into the other, as discussed above. Interestingly, the Siscionella, Pseudonocardia and Actinomycetospora sequences formed three long, deep branches into the two large radiations.

Analysis of the patterns of signature nucleotides also supported our conclusions given above. Signature nucleotides of the 16S rRNA gene sequence of strain RA45T were shared in all positions (according to the Escherichia coli numbering scheme) with the pattern of signature nucleotides reported for the suborder Pseudonocardiaeae described by Zhi et al. (2009) (Table 1). However, for the 16S rRNA signatures of the families Pseudonocardiaeae and Actinosynnemataeae at positions 211, 480 and 142:221, our observations differed from those of Zhi et al. (2009). There were no differences between the two families at these positions, with members of the two families sharing A at position 211, U at position 480 and C–C at positions 142:221, with only two exceptions, Siscionella marina SCsIO 00231T and our isolate RA45T, which both carried U at position 221.

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Strain RA45T could also be distinguished from all other representatives of the suborder Pseudonocardiaeae (Zhi et al., 2009) by a combination of morphological and chemical characteristics (Table 2). Growth of strain RA45T was good on most media tested, especially on yeast extract-malt extract (ISP 2) agar, and the optimal growth temperature was 37–45 °C. Soluble brown pigments were produced at 37
and 45 °C on Bennett’s agar, but were absent at other temperatures. No aerial mycelium was observed under any of the culture conditions used in this study. The hyphae (0.2 μm in diameter) which covered the surfaces of colonies were straight to flexuous, smooth and branched (Fig. 2) and were pale yellow to light yellow. The vegetative hyphae frequently formed aggregates and globose or irregular-formed sporangium-like structures (5–10 μm) with irregular surfaces (Fig. 2), which differed from those formed by *Kibdelosporangium* strains and the ‘pseudosporangia’ of *Thermocrispum* and *Crossiella* strains. Sessile global swellings (0.2–0.3 μm) were found consistently, especially at the ends of the aerial mycelium. Fragmentation seldom occurred in the substrate mycelium. Motile spores were not detected despite extensive observation.

Strain RA45T lacked mycolic acids and contained muramic acid in the N-acetylated form, which is consistent with the properties of other genera of the family *Pseudonocardiaecae*. The cell wall of strain RA45T contained meso-diaminopimelic acid as the diagnostic peptidoglycan diamino acid. Whole-cell hydrolysates contained ribose, arabinose, glucose and galactose as diagnostic sugars (cell-wall chemotype IV; Lechevalier & Lechevalier, 1970). Analysis of phospholipids revealed that phosphatidylethanolamine, phosphatidylinositol mannosides, phosphatidyl-methylethanolamine, diphosphatidylglycerol, phospholipids of unknown structure and glucosamine-containing phospholipids of unknown structure were the major phospholipids, indicating phospholipid type IV (Lechevalier et al., 1977). The predominant menaquinone was MK-9(H4) (66.12 %), and minor amounts of MK-9 (12.69 %), MK-9(H2) (9.08 %), MK-10(H2) (3.52 %), MK-8(H2) (2.10 %) and MK-8 (0.59 %) were detected. The fatty acid profile consisted of the predominant component iso-branched hexadecanoic acid (iso-C16 : 0; 24.41 %) and smaller amounts of C14 : 0 (2.04 %), iso-C15 : 1 (1.61 %), iso-C16 : 1 (2.66 %), C16 : 1ω7c/iso-C15 : 0 2-OH (9.96 %), and 45 °C on Bennett’s agar, but were absent at other temperatures. No aerial mycelium was observed under any of the culture conditions used in this study. The hyphae (0.2 μm in diameter) which covered the surfaces of colonies were straight to flexuous, smooth and branched (Fig. 2) and were pale yellow to light yellow. The vegetative hyphae frequently formed aggregates and globose or irregular-formed sporangium-like structures (5–10 μm) with irregular surfaces (Fig. 2), which differed from those formed by *Kibdelosporangium* strains and the ‘pseudosporangia’ of *Thermocrispum* and *Crossiella* strains. Sessile global swellings (0.2–0.3 μm) were found consistently, especially at the ends of the aerial mycelium. Fragmentation seldom occurred in the substrate mycelium. Motile spores were not detected despite extensive observation.

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Table 1. Signature nucleotides of the 16S rRNA sequences of members of the family Pseudonocardiaceae

Data were analysed in this study unless indicated, from the type strain of the type species of each genus. For the family Pseudonocardiaceae, ‘other genera’ represents Amycolatopsis, Prauserella, Saccharomonospora, Saccharopolyspora, Actinomycetospora, Pseudonocardia, Crossiella, Actinoalloteichus, Goodfellowiella, Allokatzensia, Katzensia, Kibélosporangium and Streptoalloteichus. For the family Actinosynnemataceae, the genera included were Actinokineospora, Umezawaiaceae, Saccharothrix, Lentzea, Lechevalieria and Actinosynema. Positions are given relative to the Escherichia coli numbering scheme. Y. Pyrimidine. Signatures specific for the suborder Actinosynnemataceae and differences in morphological and chemotaxonomic features of the genomic DNA of the strain was 69.9 mol%. 

On the basis of a combination of phylogenetic distinctness and differences in morphological and chemotaxonomic features, we consider that strain RA45T represents a novel genus and species, for which the name Yuhushiella deserti gen. nov., sp. nov. is proposed.

![Table 1](http://ijs.sgmjournals.org/625)

<table>
<thead>
<tr>
<th>Position(s)</th>
<th>Pseudonocardiaceae</th>
<th>Actinosynnemataceae</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Strain RA45T</td>
<td>Thermocrispum</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Other genera</td>
</tr>
<tr>
<td></td>
<td>Zhi et al. (2009)</td>
<td>Our study</td>
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<td></td>
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<tr>
<td>Suborder</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Pseudonocardiae</td>
<td></td>
<td></td>
</tr>
<tr>
<td>127:234</td>
<td>G–C</td>
<td>A–U/G–C</td>
</tr>
<tr>
<td>564</td>
<td>U</td>
<td>U</td>
</tr>
<tr>
<td>672:734</td>
<td>U–G</td>
<td>U–G</td>
</tr>
<tr>
<td>831:855</td>
<td>U–G</td>
<td>U–G</td>
</tr>
<tr>
<td>952:1229</td>
<td>U–A</td>
<td>U–A</td>
</tr>
<tr>
<td>986:1219</td>
<td>U–A</td>
<td>U–A</td>
</tr>
<tr>
<td>Suborder</td>
<td></td>
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<tr>
<td>Pseudonocardiae</td>
<td></td>
<td></td>
</tr>
<tr>
<td>211</td>
<td>G</td>
<td>A</td>
</tr>
<tr>
<td>480</td>
<td>U</td>
<td>U</td>
</tr>
<tr>
<td>142:221</td>
<td>C–G</td>
<td>C–U</td>
</tr>
</tbody>
</table>

![Molecular structures](http://ijs.sgmjournals.org/625)

C16:0 (7.55 %), 10-methyl C16:0 (2.12 %), iso-C17:0 (3.54 %), anteiso-C17:0 (6.04 %), C17:0ω8c (3.50 %), C17:1ω6c (11.37 %), C17:0 (1.25 %), 10-methyl C17:0 (1.53 %), iso-C18:0 (2.60 %), C18:1ω9c (4.24 %), C18:1ω7c (1.06 %) and C18:0 (8.48 %). The G+C content of the genomic DNA of the strain was 69.9 mol%.

On the basis of a combination of phylogenetic distinctness and differences in morphological and chemotaxonomic features, we consider that strain RA45T represents a novel genus and species, for which the name Yuhushiella deserti gen. nov., sp. nov. is proposed.

Description of Yuhushiella gen. nov.

Yuhushiella (Yu.hu.shi.el’la. N.L. dim. ending -ella; N.L. fem. n. Yuhushiella named after Professor Yuhu Shi, a Chinese microbiologist, in recognition of his leadership and contributions to the exploration of the microbial resources of Xinjiang Uigur Autonomous Region, China). Aerobic, Gram-stain-positive, non-acid-fast, non-motile actinomycetes. Vegetative mycelium is straight to flexuous, smooth and branched. Swelling and aggregation of the hyphae occur, but fragmentation is seldom observed. The cell wall contains meso-diaminopimelic acid. Whole-cell hydrolysates contain ribose, arabinose, glucose and galactose (cell-wall chemotype IV). Diphosphatidylglycerol, phosphatidylethanolamine, phosphatidylmethyllethanolamine, phosphatidyllysinothiol mannosides, phospholipids of unknown structure and glucosamine-containing phospholipids of unknown structure are the diagnostic phospholipids. Mycolic acids are absent and N-acetylated-type muramic acid is present. The predominant menaquinone is MK-9(H4). The genus is a member of the family Pseudonocardiaceae in the suborder Pseudonocardiaceae. The type species is Yuhushiella deserti.

Description of Yuhushiella deserti sp. nov.

Yuhushiella deserti (de.ser’ti. L. gen. n. deserti of a desert). In addition to the characteristics given in the genus description, the species has the following properties. Vegetative mycelium is pale yellow to light yellow. Two types of sporangia are observed: swellings (0.5–2 μm) are formed at the ends or branch joints of the mycelium and ‘post-pseudosporangia’ (5–10 μm) are formed from mycelial aggregation and merging (Fig. 2). The ‘post-pseudosporangia’, similar to the pseudosporangia of Thermocrispum and Crossiella strains, are not surrounded by a well-defined wall and contain hyphae that fragment into rod-like structures, but the hyphae are not totally septate. A brown...
Table 2. Diagnostic characteristics of strain RA45<sup>T</sup> and phylogenetically closely related genera in the suborder *Pseudonocardineae*


<table>
<thead>
<tr>
<th>Characteristic</th>
<th>Strain RA45&lt;sup&gt;T&lt;/sup&gt;</th>
<th><em>Thermocrispum</em></th>
<th><em>Amycolatopsis</em></th>
<th><em>Prauserella</em></th>
<th><em>Saccharomonospora</em></th>
<th><em>Saccharopolyspora</em></th>
<th><em>Sciscionella</em></th>
</tr>
</thead>
<tbody>
<tr>
<td>Aerial hyphae (hyphal differentiation)</td>
<td>−</td>
<td>+</td>
<td>+&lt;sup&gt;*&lt;/sup&gt;</td>
<td>+ (except <em>P. rugosa</em>)</td>
<td>+</td>
<td>+</td>
<td>Sparse</td>
</tr>
<tr>
<td><strong>Substrate hyphae</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Spores†</td>
<td>−</td>
<td>−</td>
<td>+ Primordial spore chains from hyphal fragmentation*</td>
<td>−</td>
<td>− Petiolate spores singly or in longitudinal pairs</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Sporangium-like structures</td>
<td>+</td>
<td>Pseudosporangia (hyphal aggregates)</td>
<td></td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
</tr>
<tr>
<td><strong>Aerial hyphae</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Spores†</td>
<td>NA</td>
<td>+ (into rod-like structures)</td>
<td></td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
</tr>
<tr>
<td>Sporangium-like structures</td>
<td>NA</td>
<td>ND</td>
<td></td>
<td>−</td>
<td>− Petiolate spores singly or in longitudinal pairs</td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>Chemical properties</strong></td>
<td></td>
<td></td>
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<td></td>
<td></td>
</tr>
<tr>
<td>Phospholipid type§</td>
<td>IV</td>
<td>II</td>
<td>II</td>
<td>II</td>
<td>III</td>
<td>III</td>
<td>II</td>
</tr>
<tr>
<td>Predominant menaquinone(s)&lt;sup&gt;§†&lt;/sup&gt;</td>
<td>9(H&lt;sub&gt;4&lt;/sub&gt;)</td>
<td>9(H&lt;sub&gt;4&lt;/sub&gt;)</td>
<td>9(H&lt;sub&gt;2&lt;/sub&gt;, H&lt;sub&gt;4&lt;/sub&gt;, H&lt;sub&gt;6&lt;/sub&gt;)</td>
<td>9(H&lt;sub&gt;2&lt;/sub&gt;, H&lt;sub&gt;4&lt;/sub&gt;)</td>
<td>8(H&lt;sub&gt;4&lt;/sub&gt;)</td>
<td>9(H&lt;sub&gt;2&lt;/sub&gt;, 9(H&lt;sub&gt;4&lt;/sub&gt;)</td>
<td>9(H&lt;sub&gt;4&lt;/sub&gt;)</td>
</tr>
<tr>
<td>DNA G + C content (mol%)</td>
<td>69.9</td>
<td>69–73</td>
<td>66–73</td>
<td>65.8–69.9</td>
<td>66–74</td>
<td>70–77</td>
<td>69</td>
</tr>
</tbody>
</table>

*Except *Amycolatopsis taiwanensis*.
†Refers to the presence of sporal differentiation, motile spores, conidiospores, etc.
§A. taiwanensis forms bud-like structures separated from the substrate hyphae.
§II, Phosphatidylethanolamine; III, phosphatidylcholine (with phosphatidylethanolamine, phosphatidymethyl ether and phosphatidylglycerol variable; no phospholipids containing glucosamine); IV, phospholipids containing glucosamine, phosphatidylethanolamine variable, phosphatidymethyl ether variable, no phosphatidylglycerol, no phosphatidylcholine (Lechevalier *et al.*, 1977).
IIAra, Arabinose; Gal, galactose; Glc, glucose; Man, mannose; Rib, ribose. Compounds in parentheses are present in trace amounts.
§Abbreviations are exemplified by 9(H<sub>4</sub>), menaquinones with four of the nine isoprene units hydrogenated.

Soluble pigment is produced during cultivation at 37–45 °C. Grows well on all tested media; optimal culture conditions are 37–45 °C, pH 9.0 and 3.5% (w/v) NaCl. Casein, starch, L-tyrosine, uric acid and urea are hydrolysed or decomposed. Adenine, allantoin, xylan, hypoxanthine and xanthine are not hydrolysed or decomposed. The major cellular fatty acids are iso-C<sub>16:0</sub>, C<sub>16:1ω7c</sub>/iso-C<sub>15:0</sub> 2-OH, C<sub>16:0</sub> anteiso-C<sub>17:0</sub>, C<sub>17:1ω6c</sub> and C<sub>18:0</sub>. The DNA G + C content of the type strain is 69.9 mol%. The type strain, RA45<sup>T</sup> (=CGMCC 4.5579<sup>T</sup> = JCM 16584<sup>T</sup>), was isolated from soil collected from a desert region in Xinjiang Uigur Autonomous Region, northwestern China.
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