Prauserella isguenensis sp. nov., a halophilic actinomycete isolated from desert soil

Rafika Saker,1 Noureddine Bouras,1,2 Atika Meklat,1,3 Abdelghani Zitouni,1 Peter Schumann,4 Cathrin Spröer,4 Nasserdine Sabaou1 and Hans-Peter Klenk 4

1Laboratoire de Biologie des Systèmes Microbiens (LBSM), Ecole Normale Supérieure, Kouba, Alger, Algeria
2Département de Biologie, Faculté des Sciences de la Nature et de la Vie et Sciences de la Terre, Université de Ghardaïa, BP 455, Ghardaïa 47000, Algeria
3Faculté des Sciences de la Nature et de la Vie, Département de Biologie, Université Saâd Dahleb, Bliida, Algeria
4DSMZ – German Collection of Microorganisms and Cell Cultures, Inhoffenstraße 7B, 38124 Braunschweig, Germany

Two actinomycete strains, designated H225T and H137, were isolated from two soil samples collected from the arid region of Ahbas at Béni-Isguen (Mzab), located in the Algerian Sahara. Phylogenetic analyses based on 16S rRNA gene sequences indicated that the novel strains should be assigned to the genus Prauserella of the family Pseudonocardiaceae, and they were therefore subjected to a polyphasic taxonomic study. These two strains contained meso-diaminopimelic acid as the diagnostic diamino acid and arabinose and galactose as major whole-cell sugars. The diagnostic phospholipid was phosphatidylethanolamine. The predominant menaquinone was MK-9(H4), and the major fatty acid was iso-C16 : 0. DNA–DNA hybridization values between strain H225T and its closest phylogenetic neighbours, namely Prauserella flava DSM 45265T, Prauserella alba DSM 44590T, Prauserella aidingensis DSM 45266T, Prauserella salsuginis DSM 45264T and Prauserella sediminis DSM 45267T, were clearly below the 70 % threshold used for species delineation. The genomic DNA G+C content of strains H225T and H137 was 70.4 mol%. On the basis of phenotypic and genotypic data, strains H225T and H137T are considered to represent a novel species of the genus Prauserella, for which the name Prauserella isguenensis sp. nov. is proposed. The type strain is H225T (=DSM 46664T = CECT 8577T).

The genus Prauserella, a member of the family Pseudonocardiaceae, was first described by Kim & Goodfellow (1999) with the transfer of a species previously included in the genera Nocardia (Di Marco & Spalla, 1957) and Amycolatopsis (Lechevalier et al., 1986). Members of the genus Prauserella are characterized by the presence of meso-diaminopimelic acid, arabinose and galactose in whole-cell hydrolysates (wall chemotype IV sensu Lechevalier & Lechevalier, 1970), the predominance of menaquinone MK-9(H4) and the absence of mycolic acids. Members of the genus Prauserella are aerobic, non-acid-fast, halophilic or halotolerant actinobacteria that form branched substrate mycelium that undergoes fragmentation into irregular rod-shaped elements. If present, the aerial mycelium forms spores in chains. At the time of writing, the genus comprised 11 recognized species, namely Prauserella rugosa (Kim & Goodfellow, 1999), P. halophila and P. alba (Li et al., 2003), P. salsuginis, P. flava, P. aidingensis and P. sediminis (Li et al., 2009), P. marina (Wang et al., 2010), P. muralis (Schäfer et al., 2010), P. shujinwangii (Liu et al., 2014) and P. coralliicola (Wu et al., 2014). The present polyphasic study was designed to determine the taxonomic position of two Prauserella-like strains. The resultant data show that the strains represent a novel species of the genus Prauserella.

During our investigation of halophilic actinobacteria from the arid region of Ahbas (32° 27’ N 3° 41’ E) at Béni-Isguen (Ghardaïa), an arid area in the Mzab region, located in the Algerian Sahara, two novel strains designated H225T...
and H137 were isolated by the serial dilution method using chitin-vitamin agar medium (Hsu & Lockwood, 1975) supplemented with 15% (w/v) NaCl and cycloheximide (50 mg l\(^{-1}\)). The strains were purified and maintained at 4 °C on complex medium agar described by Chun et al. (2000) [Casamino acids, 7 g; yeast extract, 10 g; sodium citrate, 3 g; magnesium sulfate, 10 g; potassium chloride, 2 g; iron sulfate, 1 ml of a solution of 4.98% (w/v); agar, 20 g; distilled water, 1 litre; pH 7.2] supplemented with 15% (w/v) NaCl.

Morphological features were observed by light microscopy (B1 series; Motic) on International Streptomyces Project (ISP) media (Shirling & Gottlieb, 1966), nutrient agar and complex medium agar (Chun et al., 2000), prepared with 15% (w/v) NaCl, and following incubation for 2 weeks at 30 °C. The colour of the substrate and aerial mycelia and any diffusible pigments produced were determined by comparison with ISCC-NBS colour charts (Kelly, 1964).

Several physiological tests were used to characterize the actinobacterial strains. Growth with and production of acid from carbohydrates, and decarboxylation of organic acids were studied using the method of Gordon et al. (1974). Degradation of other organic compounds was evaluated as described by Goodfellow (1971). Lysozyme sensitivity and reduction of nitrate were examined according to the methods of Gordon & Barnett (1977) and Marchal et al. (1987), respectively. Growth in the presence of erythromycin (15 \(\mu\)g ml\(^{-1}\)), tetracycline (30 \(\mu\)g ml\(^{-1}\)) and nalidixic acid (30 \(\mu\)g ml\(^{-1}\)), at different temperatures (10, 20, 30, 37, 45 and 50 °C) and at different pH values (4, 5, 7, 9 and 10) was determined on nutrient agar. All media used for physiological tests contained 15% (w/v) NaCl (except for the NaCl concentration test).

Biomass for chemotaxonomic analysis was grown in complex medium broth containing 15% (w/v) NaCl, on a rotary shaker (250 r.p.m.) at 30 °C for 1 week, harvested by centrifugation and washed twice with distilled water. Amino acid and sugar analysis of whole-cell hydrolysates was performed according to the procedures described by Becker et al. (1964) and Lechevalier & Lechevalier (1970). Phospholipids and mycolic acids were analysed using the procedure of Minnikin et al. (1977, 1980). Menaquinones were extracted following the procedure of Minnikin et al. (1984) and separated by HPLC (Kroppenstedt, 1982). Cellular fatty acids were analysed as described by Sasser (1990) using the Microbial Identification System (MIDI Sherlock version 6.1 (TSBA40 database).

Genomic DNA was extracted with a DNA extraction kit (MasterPure Gram Positive DNA Purification Kit; Epicentre Biotechnologies). PCR-mediated amplification of the 16S rRNA gene was performed as described by Rainey et al. (1996). The sequences obtained were compared with sequences in public databases as well as in the EzTaxon-e server (http://eztaxon-e.ezbiocloud.net; Kim et al., 2012). Phylogenetic analyses were conducted using MEGA version 5 (Tamura et al., 2011). The 16S rRNA gene sequences of strains H225\(^{T}\) and H137 were aligned against neighbouring nucleotide sequences using CLUSTAL W (with default parameters) (Thompson et al., 1994). Phylogenetic trees were reconstructed by using the neighbour-joining method (Saitou & Nei, 1987) with the model of Jukes & Cantor (1969), the maximum-likelihood method (Felsenstein, 1981) with Kimura's two-parameter model (Kimura, 1980) and the maximum-parsimony method (Fitch, 1977). The topology of the phylogenetic tree was evaluated by using the bootstrap resampling method of Felsenstein (1985) with 1000 replicates.

The G+C content of the chromosomal DNA of strains H225\(^{T}\) and H137 was determined by HPLC as described by Mesbah et al. (1989).

DNA–DNA hybridization was carried out as described by De Ley et al. (1970) under consideration of the modifications described by Huss et al. (1983), using a model Cary 100 Bio UV/VIS spectrophotometer equipped with a Peltier-thermostatted 6 × 6 multichannel changer and a temperature controller with in-situ temperature probe (Varian). DNA–DNA hybridization experiments were performed in duplicate in 2 × SSC in the presence of 10% formamide at 71 °C.

Strains H225\(^{T}\) and H137 exhibited very good growth on ISP 2, complex medium agar and nutrient agar media, and moderate growth on ISP 4, with well-developed whitish aerial mycelium on all these media except on complex medium agar. The colour of substrate mycelium was light brownish yellow on ISP 2, very pale yellow on nutrient agar, beige on complex medium agar and white on ISP 4. The substrate mycelium fragmented into irregular rod-shaped elements. The aerial mycelium formed short to long spore chains at maturity, which were straight to flexuous, and spores were non-motile. Diffusible pigments and melanoid pigments were not produced. No sporangia, sclerotia or synnemata were observed.

Strains H225\(^{T}\) and H137 differed physiologically from their closest neighbours in the genus Prauserella, as can be seen from the differential characters given in Table 1. They differed from P. flava DSM 45265\(^{T}\), the phylogenetically closest relative (see below), by the presence of aerial mycelium, spor production and eight physiological tests (NaCl range, L-arabinose, D-galactose, myo-inositol, maltose, D-mannitol, raffinose, rhamnose and starch). Strains H225\(^{T}\) and H137 differed from P. alba DSM 44590\(^{T}\) based on six physiological tests (NaCl range, cellobiose, myo-inositol, raffinose, L-serine and starch), from P. aidingensis DSM 45266\(^{T}\) based on seven tests (NaCl range, L-arabinose, maltose, D-mannitol, raffinose, trehalose and starch), from P. salsuginis DSM 45264\(^{T}\) based on eight tests (NaCl range, cellobiose, myo-inositol, maltose, D-mannose, raffinose, trehalose and starch) and from P. sediminis DSM 45267\(^{T}\) based on ten tests (NaCl range, L-arabinose, D-fructose, D-galactose, maltose, D-mannitol, raffinose, D-ribose, D-xylene and starch). More complete physiological characteristics of strain H225\(^{T}\) are given in the species description.
Strains H225\textsuperscript{T} and H137 contained *meso*-diaminopimelic acid as the diagnostic peptidoglycan diamino acid, but not glycine. Whole-cell hydrolysates contained arabinose, galactose, ribose and glucose (H225\textsuperscript{T}) or mannose (H137) (wall chemotype IV sensu; Lechevalier & Lechevalier, 1970), typical of members of the genus *Prauserella*. The phospholipids comprised phosphatidylethanolamine, phosphatidylglycerol, phosphatidyldimethylethanolamine, phosphatidylhydroxyethyl ethanolamine, diphosphatidylglycerol and phosphatidylinositol, with trace amounts of phosphadicholine, phosphatidylglycerol and phosphatidylglycerol mannosides as well as two unknown glycolipids (Fig. S1, available in the online Supplementary Material). Mycolic acids were absent. The predominant menaquinone of strains H225\textsuperscript{T} and H137 was MK-9(H\textsubscript{4}), which is different from *P. rugosa* DSM 43194\textsuperscript{T} which has MK-9(H\textsubscript{2}) and MK-9(H\textsubscript{4}) as the predominant menaquinones, but the same as *P. flava* DSM 45265\textsuperscript{T}, *P. alba* DSM 44590\textsuperscript{T}, *P. aidingensis* DSM 45266\textsuperscript{T}, *P. salsuginis* DSM 45264\textsuperscript{T}, and *P. sediminis* DSM 45267\textsuperscript{T}. The DNA–DNA relatedness values of 94.1 % with strain H137, indicating that they belonged to the same species. Mean DNA–DNA relatedness values between strain H225\textsuperscript{T} and *P. flava* DSM 45265\textsuperscript{T} and *P. alba* DSM 44590\textsuperscript{T}, *P. aidingensis* DSM 45266\textsuperscript{T}, *P. salsuginis* DSM 45264\textsuperscript{T}, and *P. sediminis* DSM 45267\textsuperscript{T} were 43.6 % (40.7 and 46.5 %), 65.5 % (68.4 and 62.6 %), 40.6 % (37.6 and 43.6 %), 27.9 % (32.8 and 23.0 %) and 45.0 % (49.0 and 41.0 %), respectively, which are clearly below the 70 % threshold proposed by Wayne et al. (1987) for the delineation of separate species.

The G+C content of the genomic DNA of strains H225\textsuperscript{T} and H137 was 70.4 mol%.

The phenotypic, chemotaxonomic and molecular data presented here show that the two novel strains can be

### Table 1. Phenotypic characteristics that differentiate strains H225\textsuperscript{T} and H137 from their closest recognized species of the genus *Prauserella*

<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>
</tr>
</thead>
<tbody>
<tr>
<td>Aerial mycelium</td>
<td>+</td>
<td>+</td>
<td>−</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Spore formation</td>
<td>+</td>
<td>+</td>
<td>−</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Optimum NaCl concentration (%) w/v</td>
<td>7–15</td>
<td>7–15</td>
<td>7–10</td>
<td>10–15</td>
<td>7–10</td>
<td>7–10</td>
<td>7–10</td>
</tr>
<tr>
<td>Growth with and production of acid from:</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>L-Arabinose</td>
<td>+</td>
<td>+</td>
<td>−</td>
<td>+</td>
<td>−</td>
<td>−</td>
<td>−</td>
</tr>
<tr>
<td>Cellobose</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>+</td>
<td>−</td>
<td>−</td>
<td>−</td>
</tr>
<tr>
<td>D-Fructose</td>
<td>+</td>
<td>+</td>
<td>−</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>D-Galactose</td>
<td>+</td>
<td>+</td>
<td>−</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>myo-Inositol</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>+</td>
<td>+</td>
<td>−</td>
<td>−</td>
</tr>
<tr>
<td>Maltose</td>
<td>+</td>
<td>+</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
</tr>
<tr>
<td>D-Mannitol</td>
<td>+</td>
<td>+</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
</tr>
<tr>
<td>D-Mannose</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
</tr>
<tr>
<td>Raffinose</td>
<td>+</td>
<td>+</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
</tr>
<tr>
<td>L-Rhamnose</td>
<td>+</td>
<td>+</td>
<td>−</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>D-Ribose</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Trehalose</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
</tr>
<tr>
<td>D-Xylose</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>L-Serine</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
</tr>
<tr>
<td>Degradation of starch</td>
<td>+</td>
<td>+</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
</tr>
</tbody>
</table>

Strains H225\textsuperscript{T} and H137 contained *meso*-diaminopimelic acid as the diagnostic peptidoglycan diamino acid, but not glycine. Whole-cell hydrolysates contained arabinose, galactose, ribose and glucose (H225\textsuperscript{T}) or mannose (H137) (wall chemotype IV sensu; Lechevalier & Lechevalier, 1970), typical of members of the genus *Prauserella*. The phospholipids comprised phosphatidylethanolamine, phosphatidylglycerol, phosphatidyldimethylethanolamine, phosphatidylhydroxyethyl ethanolamine, diphosphatidylglycerol and phosphatidylinositol, with trace amounts of phosphadicholine, phosphatidylglycerol and phosphatidylglycerol mannosides as well as two unknown glycolipids (Fig. S1, available in the online Supplementary Material). Mycolic acids were absent. The predominant menaquinone of strains H225\textsuperscript{T} and H137 was MK-9(H\textsubscript{4}), which is different from *P. rugosa* DSM 43194\textsuperscript{T} which has MK-9(H\textsubscript{2}) and MK-9(H\textsubscript{4}) as the predominant menaquinones, but the same as *P. flava* DSM 45265\textsuperscript{T}, *P. alba* DSM 44590\textsuperscript{T}, *P. aidingensis* DSM 45266\textsuperscript{T}, *P. salsuginis* DSM 45264\textsuperscript{T}, and *P. sediminis* DSM 45267\textsuperscript{T}. The DNA–DNA relatedness values of 94.1 % with strain H137, indicating that they belonged to the same species. Mean DNA–DNA relatedness values between strain H225\textsuperscript{T} and *P. flava* DSM 45265\textsuperscript{T} and *P. alba* DSM 44590\textsuperscript{T}, *P. aidingensis* DSM 45266\textsuperscript{T}, *P. salsuginis* DSM 45264\textsuperscript{T}, and *P. sediminis* DSM 45267\textsuperscript{T} were 43.6 % (40.7 and 46.5 %), 65.5 % (68.4 and 62.6 %), 40.6 % (37.6 and 43.6 %), 27.9 % (32.8 and 23.0 %) and 45.0 % (49.0 and 41.0 %), respectively, which are clearly below the 70 % threshold proposed by Wayne et al. (1987) for the delineation of separate species.

The G+C content of the genomic DNA of strains H225\textsuperscript{T} and H137 was 70.4 mol%.

The phenotypic, chemotaxonomic and molecular data presented here show that the two novel strains can be
Table 2. Cellular fatty acid composition of strains H225T and H137 and their most closely related neighbours in the genus Prauserella

<table>
<thead>
<tr>
<th>Fatty acid</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
<th>5</th>
<th>6</th>
<th>7</th>
</tr>
</thead>
<tbody>
<tr>
<td>iso-C14:0</td>
<td>1.45</td>
<td>2.62</td>
<td>0.58</td>
<td></td>
<td>1.67</td>
<td>0.46</td>
<td>0.49</td>
</tr>
<tr>
<td>C15:0</td>
<td>3.10</td>
<td>3.76</td>
<td>2.15</td>
<td>1.36</td>
<td>2.99</td>
<td>2.36</td>
<td>1.66</td>
</tr>
<tr>
<td>iso-C15:0</td>
<td>1.55</td>
<td>3.45</td>
<td>0.82</td>
<td>1.50</td>
<td>0.78</td>
<td>1.08</td>
<td>1.26</td>
</tr>
<tr>
<td>anteiso-C15:0</td>
<td>0.92</td>
<td>2.32</td>
<td>0.26</td>
<td></td>
<td></td>
<td>0.32</td>
<td>0.28</td>
</tr>
<tr>
<td>C15:1 B</td>
<td>2.81</td>
<td>3.92</td>
<td>1.54</td>
<td>1.01</td>
<td>2.35</td>
<td>0.72</td>
<td>1.03</td>
</tr>
<tr>
<td>C16:0</td>
<td>5.67</td>
<td>3.38</td>
<td>12.13</td>
<td>9.09</td>
<td>1.04</td>
<td>17.99</td>
<td>13.61</td>
</tr>
<tr>
<td>iso-C16:0</td>
<td>38.40</td>
<td>33.03</td>
<td>37.23</td>
<td>25.98</td>
<td>56.86</td>
<td>42.83</td>
<td>37.33</td>
</tr>
<tr>
<td>iso-C16:0 2-0H</td>
<td>11.02</td>
<td>5.54</td>
<td>13.77</td>
<td>10.56</td>
<td>10.86</td>
<td>5.46</td>
<td>11.64</td>
</tr>
<tr>
<td>10-methyl C16:0</td>
<td></td>
<td>1.12</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>iso-C16:1 H</td>
<td>8.06</td>
<td>6.35</td>
<td>2.52</td>
<td>7.00</td>
<td>11.95</td>
<td>1.40</td>
<td>2.45</td>
</tr>
<tr>
<td>C16:0 cis 9</td>
<td>9.59</td>
<td>6.05</td>
<td>11.44</td>
<td>8.22</td>
<td>1.59</td>
<td>4.31</td>
<td>10.91</td>
</tr>
<tr>
<td>C17:0</td>
<td>3.17</td>
<td>3.74</td>
<td>3.37</td>
<td>2.83</td>
<td>2.20</td>
<td>6.87</td>
<td>3.69</td>
</tr>
<tr>
<td>iso-C17:0</td>
<td>0.83</td>
<td>1.64</td>
<td>1.00</td>
<td>1.50</td>
<td>0.51</td>
<td>1.91</td>
<td>1.93</td>
</tr>
<tr>
<td>anteiso-C17:0</td>
<td>4.93</td>
<td>11.47</td>
<td>3.60</td>
<td>8.63</td>
<td>0.48</td>
<td>6.21</td>
<td>4.92</td>
</tr>
<tr>
<td>anteiso-C17:0 2-0H</td>
<td></td>
<td>1.40</td>
<td></td>
<td>3.70</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>C17:1 cis 9</td>
<td>7.74</td>
<td>7.91</td>
<td>5.86</td>
<td>6.61</td>
<td>5.01</td>
<td>3.57</td>
<td>5.37</td>
</tr>
<tr>
<td>C18:0</td>
<td></td>
<td></td>
<td>2.02</td>
<td></td>
<td>2.21</td>
<td>1.03</td>
<td></td>
</tr>
<tr>
<td>iso-C18:0</td>
<td></td>
<td>0.56</td>
<td></td>
<td>0.29</td>
<td>0.82</td>
<td>0.55</td>
<td></td>
</tr>
<tr>
<td>C18:1 cis 9</td>
<td>0.76</td>
<td>0.34</td>
<td>0.92</td>
<td>3.97</td>
<td>0.24</td>
<td>0.45</td>
<td>0.92</td>
</tr>
</tbody>
</table>

Prauserella isguenensis sp. nov.

Prauserella isguenensis (is.guen.en’sis. N.L. fem. adj. isguenensis pertaining to Béni-Isguen, the source of the soil from which the type strain was isolated).

Gram-stain-positive, aerobic, non-motile actinobacterium. The colour of the substrate mycelium is light brownish yellow on ISP 2, very pale yellow on nutrient agar, beige on complex medium agar and white on ISP 4. The substrate mycelium fragments into irregular rod-shaped elements. The aerial mycelium is white on all media tested and forms short to long spore chains at maturity, which are straight to flexuous, and spores are non-motile. Diffusible pigments are not produced. Temperature and pH ranges for growth are 20–45 °C (optimal at 30–37 °C) and pH 5.0–9.0 (optimal at pH 7.0). The NaCl concentration range for growth is 5–25 % (w/v), with optimal growth occurring at 7–15 % (w/v). Grows with and produces acid from adonitol, L-arabinose, D-fructose, D-galactose, D-glucose, glycerol, lactose, maltose, mannitol, raffinose, L-rhamnose, D-ribose, sucrose and D-xylene, but not cellobiose, erithritol, myo-inositol, D-mannose, melizitose, melibiose, salicin, D-sorbitol or trehalose. Hydrolyses starch, tyrosine, Tween 80 and xanthine, but not adenine, ascinulin, arbutin, D-ribose, sucrose and D-xylose, but not cellobiose, erithritol, myo-inositol, D-mannose, melizitose, melibiose, salicin, D-sorbitol or trehalose. Hydrolyses starch, tyrosine, Tween 80 and xanthine, but not adenine, ascinulin, arbutin.
casein, gelatin, guanine, hypoxanthine or testosterone. Acetate, butyrate, citrate, pyruvate and succinate are decarboxylated, but not benzoate, oxalate, propionate or tartrate. Utilizes l-alanine and l-proline as source of nitrogen, but not l-serine. Resistant to lysozyme but not to erythromycin, tetracycline or nalidixic acid. Whole-cell hydrolysates contain meso-diaminopimelic acid, and arabinose and galactose as major whole-cell sugars. The major menaquinone is MK-9(H4). The major fatty acid is iso-C16:0. Mycolic acids are absent.

The type strain is H225T (=DSM 46664T = CECT 8577T), which was isolated from a Saharan soil sample collected from the arid region of Ahbas at Béni-Isguen (Ghardaïa, Algeria). The DNA G+C content of the type strain is 70.4 mol%.

Acknowledgements

We gratefully acknowledge the technical assistance of Gabriele Pötter and Bettina Straubler (both at DSMZ).

References


