Open Archive Toulouse Archive Ouverte (OATAO)

OATAO is an open access repository that collects the work of some Toulouse researchers and makes it freely available over the web where possible.

This is an author’s version published in: http://oatao.univ-toulouse.fr/20529

Official URL: https://doi.org/10.1099/ijsem.0.001114

To cite this version:
Lahoum, Abdelhadi and Bouras, Noureddine and Verheecke, Carol and Mathieu, Florence and Schumann, Peter and Spröer, Cathrin and Klenk, Hans-Peter and Sabaou, Nasserdine Actinomadura adrarensis sp. nov., an actinobacterium isolated from Saharan soil. (2016) International Journal of Systematic and Evolutionary Microbiology, 66 (7). 2724-2729. ISSN 1466-5026

Any correspondance concerning this service should be sent to the repository administrator: tech-oatao@listes-diff.inp-toulouse.fr
Actinomadura adraensis sp. nov., an actinobacterium isolated from Saharan soil

Abdelhadi Lahoum,1 Noureddine Bouras,1,2 Carol Verheecke,3 Florence Mathieu,3 Peter Schumann,4 Cathrin Spröer,4 Hans-Peter Klenk5 and Nasserdine Sabaou1

A novel actinobacterial strain, designated ACD12T, was isolated from a Saharan soil sample collected from Adrar province, southern Algeria. A polyphasic study was carried out to establish the taxonomic position of this strain. Strain ACD12T was observed to form extensively branched substrate mycelia. Aerial mycelium was absent or was weakly produced on all media tested, while spore chains were short with a hooked and irregular spiral form (2–3 turns). The dominant diaminopimelic acid isomer in the cell wall was meso-diaminopimelic acid. Glucose, ribose, galactose, mannose and madurose occurred in whole-cell hydrolysates. The major phospholipid was diphosphatidylglycerol and phosphatidylinositol. The predominant menaquinone was MK-9(H6). The fatty acid profile was characterized by the presence of C16 : 0, C17 : 0, C16 : 0, C18 : 0, C18 : 1 cis9 and iso-C16 : 0. Results of 16S rRNA gene sequence comparisons revealed that strain ACD12T shared the highest degree of 16S rRNA gene sequence similarity with Actinomadura sputi DSM 45233T (98.3 %) and Actinomadura hallensis DSM 45043T (97.8 %). All tree-making algorithms used also supported strain ACD12T forming a distinct clade with its most closely related species. In addition, DNA–DNA hybridization indicated only 39.8 % relatedness with A. sputi DSM 45233T and 18.7 % relatedness with A. hallensis DSM 45043T. The combined phenotypic and genotypic data show that the novel isolate represents a novel species of the genus Actinomadura, for which the name Actinomadura adraensis sp. nov., is proposed, with the type strain ACD12T (=DSM 46745T =CECT 8842T).

The genus Actinomadura, a member of the family Thermomonosporaceae, was proposed by Lechevalier & Lechevalier (1968). The strains of species of the genus Actinomadura have been principally isolated from soil (Lu et al., 2003; Quintana et al., 2003; Ara et al., 2008). However, some species have been isolated from patients, such as Actinomadura sputi (Yassin et al., 2010). This genus is of great importance in several domains, including the production of new bioactive metabolites active against pathogenic microorganisms (Euanoraset et al., 2015). Species of the genus Actinomadura produce an extensively branched non-fragmenting substrate mycelium and, generally, aerial mycelium is moderately developed or absent. Spore chains are short and differentiate into straight, spiral or hooked forms. The strains of species of the genus Actinomadura are characterized by the presence of type III cell walls (meso-diaminopimelic acid without glycine). Whole-cell hydrolysates contain madurose as the diagnostic sugar. Cell membranes contain diphosphatidylglycerol and phosphatidylinositol as the diagnostic phospholipids, and MK-9(H4) and MK-9(H6) as the major menaquinones.

The GenBank/EMBL/DDBJ accession number for the 16S rRNA gene sequence of strain ACD12T is KU356942.
Actinomadura species of actinobacteria belonging to the genus Strain ACD12 Meklat et al. Aouiche et al. During our study on the actinobacterial diversity of Saharan published names (http://www.bacterio.net). Time of writing, the genus comprises 53 species with validly published names. Several physiological tests were used to characterize the actinobacterial strain. The utilization of carbohydrates and decarboxylation of organic acids were studied using the method of Goodfellow (1971) and Marchal et al. (1987). DNA hybridization was carried out according to the methods of Goodfellow (1971) and Marchal et al. (1987). Growth at different temperatures (15, 20, 25, 30, 37, 40 and 45 °C) and at different pH values (5, 6, 7, 8, 9, 10 and 11) was determined on ISP 2 medium.

Biomass for chemotaxonomic studies was obtained by growing strain ACD12T on ISP 2 broth in flasks on a rotary shaker at 250 r.p.m at 30 °C for one week. Cells were harvested by centrifugation and washed several times with distilled water, than dried at 37 °C. Isomers of diaminopimelic acid and cell sugars were detected following the standard procedures described by Becker et al. (1964) and Lechevalier & Lechevalier (1970). Menaquinones were extracted and purified by using the methods of Minnikin et al. (1984) and were analysed by HPLC (Kroppenstedt, 1982, 1985).

Genomic DNA was extracted with a DNA extraction kit (MasterPure Gram-Positive DNA Purification Kit, Epicentre Biotechnologies). PCR amplification of the 16S rRNA gene sequence of strain ACD12T was carried out according to the procedures described by Rainey et al. (1996). The EzTaxon-e server (Kim et al., 2012) was employed to identify phylogenetic neighbours and to calculate pairwise 16S rRNA gene similarities. The 16S rRNA gene sequence of strain ACD12T was aligned against corresponding nucleotide sequences using the CLUSTAL W program (Larkin et al., 2007) of representatives of the genus Actinomadura retrieved from the EzTaxon-e server. Phylogenetic trees were reconstructed with the neighbour-joining algorithm (Saitou & Nei, 1987) with the model of Jukes & Cantor (1969), the maximum-likelihood algorithm (Felsenstein, 1981) with the Kimura 2-parameter model (Kimura, 1980) and maximum-parsimony algorithm (Fitch, 1977) using molecular evolutionary genetics analysis, (MEGA version 5) (Tamura et al., 2011). The topology of the phylogenetic trees was evaluated by bootstrap analysis (Felsenstein, 1985), based on 1000 resamplings of the neighbour-joining dataset.

For DNA–DNA relatedness studies, DNA was isolated by using a French pressure cell (Thermo Spectronic) and was purified by chromatography on hydroxyapatite, as described by Cashion et al. (1977). DNA–DNA hybridization was carried out in duplicate, as described by De Ley et al. (1970) with the modifications described by Huss et al. (1983).

Strain ACD12T exhibited moderate growth on ISP 2, ISP 3, ISP 4 and Bennett’s media. The isolate formed extensively branched substrate mycelium, which were light beige. No aerial mycelium was observed on the media tested, while a polar lipid profile was determined by using two-dimensional TLC (Minnikin et al., 1984). The fatty acid profile was determined by the method of Sasser (1990), using the Microbial Identification System (MIDI) Sherlock software version 6.1 (method TSBA40, TSBA6 database).

Polar lipids were extracted and identified by using two-dimensional TLC (Minnikin et al., 1984). The fatty acid profile was determined by the method of Sasser (1990), using the Microbial Identification System (MIDI) Sherlock software version 6.1 (method TSBA40, TSBA6 database).

Genomic DNA was extracted with a DNA extraction kit (MasterPure Gram-Positive DNA Purification Kit, Epicentre Biotechnologies). PCR amplification of the 16S rRNA gene sequence of strain ACD12T was carried out according to the procedures described by Rainey et al. (1996). The EzTaxon-e server (Kim et al., 2012) was employed to identify phylogenetic neighbours and to calculate pairwise 16S rRNA gene similarities. The 16S rRNA gene sequence of strain ACD12T was aligned against corresponding nucleotide sequences using the CLUSTAL W program (Larkin et al., 2007) of representatives of the genus Actinomadura retrieved from the EzTaxon-e server. Phylogenetic trees were reconstructed with the neighbour-joining algorithm (Saitou & Nei, 1987) with the model of Jukes & Cantor (1969), the maximum-likelihood algorithm (Felsenstein, 1981) with the Kimura 2-parameter model (Kimura, 1980) and maximum-parsimony algorithm (Fitch, 1977) using molecular evolutionary genetics analysis, (MEGA version 5) (Tamura et al., 2011). The topology of the phylogenetic trees was evaluated by bootstrap analysis (Felsenstein, 1985), based on 1000 resamplings of the neighbour-joining dataset.

For DNA–DNA relatedness studies, DNA was isolated by using a French pressure cell (Thermo Spectronic) and was purified by chromatography on hydroxyapatite, as described by Cashion et al. (1977). DNA–DNA hybridization was carried out in duplicate, as described by De Ley et al. (1970) with the modifications described by Huss et al. (1983).

Strain ACD12T exhibited moderate growth on ISP 2, ISP 3, ISP 4 and Bennett’s media. The isolate formed extensively branched substrate mycelium, which were light beige. No aerial mycelium was observed on the media tested, while a polar lipid profile was determined by using two-dimensional TLC (Minnikin et al., 1984). The fatty acid profile was determined by the method of Sasser (1990), using the Microbial Identification System (MIDI) Sherlock software version 6.1 (method TSBA40, TSBA6 database).

Polar lipids were extracted and identified by using two-dimensional TLC (Minnikin et al., 1984). The fatty acid profile was determined by the method of Sasser (1990), using the Microbial Identification System (MIDI) Sherlock software version 6.1 (method TSBA40, TSBA6 database).

Genomic DNA was extracted with a DNA extraction kit (MasterPure Gram-Positive DNA Purification Kit, Epicentre Biotechnologies). PCR amplification of the 16S rRNA gene sequence of strain ACD12T was carried out according to the procedures described by Rainey et al. (1996). The EzTaxon-e server (Kim et al., 2012) was employed to identify phylogenetic neighbours and to calculate pairwise 16S rRNA gene similarities. The 16S rRNA gene sequence of strain ACD12T was aligned against corresponding nucleotide sequences using the CLUSTAL W program (Larkin et al., 2007) of representatives of the genus Actinomadura retrieved from the EzTaxon-e server. Phylogenetic trees were reconstructed with the neighbour-joining algorithm (Saitou & Nei, 1987) with the model of Jukes & Cantor (1969), the maximum-likelihood algorithm (Felsenstein, 1981) with the Kimura 2-parameter model (Kimura, 1980) and maximum-parsimony algorithm (Fitch, 1977) using molecular evolutionary genetics analysis, (MEGA version 5) (Tamura et al., 2011). The topology of the phylogenetic trees was evaluated by bootstrap analysis (Felsenstein, 1985), based on 1000 resamplings of the neighbour-joining dataset.

For DNA–DNA relatedness studies, DNA was isolated by using a French pressure cell (Thermo Spectronic) and was purified by chromatography on hydroxyapatite, as described by Cashion et al. (1977). DNA–DNA hybridization was carried out in duplicate, as described by De Ley et al. (1970) with the modifications described by Huss et al. (1983).

Strain ACD12T exhibited moderate growth on ISP 2, ISP 3, ISP 4 and Bennett’s media. The isolate formed extensively branched substrate mycelium, which were light beige. No aerial mycelium was observed on the media tested, while a polar lipid profile was determined by using two-dimensional TLC (Minnikin et al., 1984). The fatty acid profile was determined by the method of Sasser (1990), using the Microbial Identification System (MIDI) Sherlock software version 6.1 (method TSBA40, TSBA6 database).

Polar lipids were extracted and identified by using two-dimensional TLC (Minnikin et al., 1984). The fatty acid profile was determined by the method of Sasser (1990), using the Microbial Identification System (MIDI) Sherlock software version 6.1 (method TSBA40, TSBA6 database).

Genomic DNA was extracted with a DNA extraction kit (MasterPure Gram-Positive DNA Purification Kit, Epicentre Biotechnologies). PCR amplification of the 16S rRNA gene sequence of strain ACD12T was carried out according to the procedures described by Rainey et al. (1996). The EzTaxon-e server (Kim et al., 2012) was employed to identify phylogenetic neighbours and to calculate pairwise 16S rRNA gene similarities. The 16S rRNA gene sequence of strain ACD12T was aligned against corresponding nucleotide sequences using the CLUSTAL W program (Larkin et al., 2007) of representatives of the genus Actinomadura retrieved from the EzTaxon-e server. Phylogenetic trees were reconstructed with the neighbour-joining algorithm (Saitou & Nei, 1987) with the model of Jukes & Cantor (1969), the maximum-likelihood algorithm (Felsenstein, 1981) with the Kimura 2-parameter model (Kimura, 1980) and maximum-parsimony algorithm (Fitch, 1977) using molecular evolutionary genetics analysis, (MEGA version 5) (Tamura et al., 2011). The topology of the phylogenetic trees was evaluated by bootstrap analysis (Felsenstein, 1985), based on 1000 resamplings of the neighbour-joining dataset.
very scanty white aerial mycelium was observed only on humic acid-vitamin agar medium. Spore chains (2–12 spores) were observed to be short with hooked and irregular spiral forms and with a smooth surface (Fig. 1). No diffusible pigments were detected on any of the media tested. No sporangia, sclerotia or synnemata were observed.

Strain ACD12\(^T\) was found to grow at 25–37 °C, at pH 7–10 and at 0–2 % (w/v) NaCl. Strain ACD12\(^T\) and its two most closely related reference type strains (Actinomadura spuri DSM 45233\(^T\) and Actinomadura hallensis DSM 45043\(^T\)) were positive for the utilization of adenine and cellobiose, and negative for the utilization of adonitol, glycero, galactose and mannose. These results indicate that this strain has type IIIB (Lechevalier & Lechevalier, 1970). The predominant menaquinone was determined to be MK-9(H\(_8\)) (64.5 %) with small amounts of MK-9(H\(_4\)) (12.5 %), MK-9(H\(_6\)) (12 %) and MK-9(H\(_2\)) (2.3 %) also detected. The diagnostic phospholipids detected were diphosphatidylglycerol and phosphatidylglycerol, which corresponds to phospholipid type PI (Lechevalier et al., 1977); phosphatidylglycerol mannosides and phosphatidylglycerol were also present (Fig. S1, available in the online Supplementary Material). The cellular fatty acids higher than 5 % were identified as C\(_{16:0}\) (22.2 %), 10-methyl C\(_{17:0}\) (15.2 %), C\(_{17:1}\)-9c (11.5 %), C\(_{15:0}\) (11.1 %), 10-methyl C\(_{18:0}\) (9.3 %) and C\(_{18:1}\)-9c (5 %). Details are given in Table S1.

Phylogenetic analysis of the 16S rRNA gene sequence (1484 bp, GenBank accession KU356942) confirmed the placement of strain ACD12\(^T\) within the genus *Actinomadura*. High degrees of 16S rRNA gene sequence similarity were found between strain ACD12\(^T\) and its nearest neighbours, *A. spuri* DSM 45233\(^T\) (98.3 %) and *A. hallensis* DSM 45043\(^T\) (97.8 %).

The similarity of the 16S rRNA gene sequence of strain ACD12\(^T\) to those of other members of the genus *Actinomadura* were found to be lower than 97.7 %. The phylogenetic relationships between strain ACD12\(^T\) and members of the genus *Actinomadura* are demonstrated in the neighbour-joining (Fig. 2), maximum-parsimony and maximum-likehood dendrograms (Fig. S2). The levels of DNA–DNA relatedness of strain ACD12\(^T\) with *A. spuri* DSM 45233\(^T\) and *A. hallensis* DSM 45043\(^T\) were 39.8 % and 18.7 %, respectively (standards deviations were 5.6 and 0.7 %, respectively). These values are well below the 70 % threshold proposed by Wayne et al. (1987) for the delineation of separate species.

Based on these phenotypic and genotypic data, strain ACD12\(^T\) is a member of the genus *Actinomadura* and represents a novel species, for which the name *Actinomadura adrarensis* sp. nov. is proposed.

### Description of *Actinomadura adrarensis* sp. nov.

*Actinomadura adrarensis* (ad.rar.e.n’sis. N.L. fem. adj. *adraren-*is pertaining to Adrar, the source of the soil from which the type strain was isolated).

Aerobic, Gram-stain-positive, non-motive actinobacterium that forms an extensively branched, light beige substrate.

---

**Table 1. Phenotypic characteristics that differentiate strain ACD12\(^T\) from its most closely related species of the genus *Actinomadura*.

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>1</th>
<th>2</th>
<th>3</th>
</tr>
</thead>
<tbody>
<tr>
<td>Aerial mycelium on ISP2 medium</td>
<td>–</td>
<td>+</td>
<td>–</td>
</tr>
<tr>
<td>Spore-chains arrangement</td>
<td>Hooks, spirals</td>
<td>Straight, spirals</td>
<td>Hooks, spirals</td>
</tr>
<tr>
<td>Spore-surface ornamentation</td>
<td>Smooth</td>
<td>Smooth</td>
<td>Warty</td>
</tr>
<tr>
<td>Utilization of:</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Adonitol</td>
<td>+</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>L-arabinose</td>
<td>–</td>
<td>–</td>
<td>+</td>
</tr>
<tr>
<td>D-fructose</td>
<td>–</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>D-glucose</td>
<td>–</td>
<td>–</td>
<td>+</td>
</tr>
<tr>
<td>D-lactose</td>
<td>–</td>
<td>–</td>
<td>+</td>
</tr>
<tr>
<td>D-maltose</td>
<td>+</td>
<td>–</td>
<td>+</td>
</tr>
<tr>
<td>D-mannitol</td>
<td>–</td>
<td>–</td>
<td>+</td>
</tr>
<tr>
<td>D-Rhamnose</td>
<td>–</td>
<td>+</td>
<td>–</td>
</tr>
<tr>
<td>D-sorbitol</td>
<td>–</td>
<td>–</td>
<td>+</td>
</tr>
<tr>
<td>D-trehalose</td>
<td>+</td>
<td>–</td>
<td>+</td>
</tr>
<tr>
<td>D-xylose</td>
<td>–</td>
<td>–</td>
<td>+</td>
</tr>
<tr>
<td>Decomposition of:</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Casein</td>
<td>+</td>
<td>–</td>
<td>+</td>
</tr>
<tr>
<td>Gelatin</td>
<td>+</td>
<td>–</td>
<td>+</td>
</tr>
<tr>
<td>Hypoxanthine</td>
<td>+</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Tween 80</td>
<td>+</td>
<td>+</td>
<td>–</td>
</tr>
<tr>
<td>L-tyrosine</td>
<td>–</td>
<td>+</td>
<td>–</td>
</tr>
<tr>
<td>Starch</td>
<td>–</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Growth at:</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>45 °C</td>
<td>–</td>
<td>–</td>
<td>+</td>
</tr>
<tr>
<td>Growth in 3 % (w/v) NaCl</td>
<td>–</td>
<td>+</td>
<td>+</td>
</tr>
</tbody>
</table>
mycelium. No aerial mycelium is observed on ISP 2, ISP 3, ISP 4 and Bennett’s media, while a very scanty white aerial mycelium is observed on humic acid–vitamin agar medium. Aerial mycelium bear chains of spores (2–12 spores) with hooked and irregular spiral forms. No diffusible pigments are detected on any of the media tested. The optimum growth temperature, pH and NaCl concentration are 30°C, 8 and 0% (w/v), respectively. Acetate, aesculin, casein, gelatin, hypoxanthine, pyruvate and Tween 80 are degraded, but adenine, arbutin, tyrosine and xanthine are not. Negative for nitrate reduction. Milk peptonisation is positive, while milk coagulation is negative. Adonitol, D-cellulbiose, D-maltose, D-mannose, D-ribose and D-trehalose are utilized, but L-arabinose, D-fructose, D-galactose, D-glucose, D-lactose, D-mannitol, D-melibiose, D-raffinose, L-rhamnose, D-sorbitol and D-xyllose are not decomposed. The diaminoc acid in the cell wall is meso-diaminopimelic acid. Madurose is the diagnostic sugar in whole-cell hydrolysates. The major phospholipids are diphostatidyglycerol and phosphatidylinositol. The predominant menaquinone is MK-9(H8). The major fatty acids are C16:0, 10-methyl C17:0, C17:0 10-methyl C17:0, C15:0 and 10-methyl C18:0.

The type strain is ACD12T (=DSM 46745T =CECT 8842T) isolated from a Saharan soil sample collected from Bouda region, Adrar province (South Algeria).

Acknowledgements

We would like to gratefully acknowledge the help of Gabriele Pötter (DSMZ) for growing Actinomadura adraensis cultures and for assistance with chemotaxonomical analyses and Bettina Sträubler (DSMZ) for assistance with DNA–DNA hybridizations.

Reference


Tamura, K., Peterson, D., Peterson, N., Stecher, G., Nei, M. & Kumar, S. (2011). MEGAS: molecular evolutionary genetics analysis using


