Mycobacterium elephantis sp. nov., a rapidly growing non-chromogenic Mycobacterium isolated from an elephant

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A strain isolated from a lung abscess in an elephant that died from chronic respiratory disease was found to have properties consistent with its classification in the genus Mycobacterium. An almost complete sequence of the 16S rDNA of the strain was determined following the cloning and sequencing of the amplified gene. The sequence was aligned with those available on mycobacteria and phylogenetic trees inferred by using three tree-making algorithms. The organism, which formed a distinct phyletic line within the evolutionary radiation occupied by rapidly growing mycobacteria, was readily distinguished from members of validly described species of rapidly growing mycobacteria on the basis of its mycolic acid pattern and by a number of other phenotypic features, notably its ability to grow at higher temperatures. The type strain is Mycobacterium elephantis DSM 44368T.

Keywords: Mycobacterium elephantis sp. nov., polyphasic taxonomy, lung abscess of adult elephant

INTRODUCTION

A rapidly growing, weakly acid–alcohol-fast organism isolated from a lung abscess of an elephant had properties consistent with its classification in the genus Mycobacterium (Lévy-Frébault & Portaels, 1992; Goodfellow & Magee, 1997). In the present investigation, the organism was examined for a selection of genotypic and phenotypic properties to clarify its taxonomic position. It is apparent from the results that the organism represents a new species, for which the name Mycobacterium elephantis is proposed.

METHODS

Organism and growth conditions. The organism (strain 484T) was isolated on Löwenstein–Jensen medium after 7 d incubation at 37 °C. It was then cultivated on the same medium at 25, 36, 42 and 45 °C and on Columbia blood, MacConkey, Middlebrook 7H10 and 5% (w/v) sodium chloride agars at 25 and 36 °C for between 3 and 10 d. The strain was maintained on Middlebrook 7H10 agar and grown at 36 °C for the remaining phenotypic tests.

Phenotypic characterization. Standard methods were used throughout. The Gram and Ziehl–Neelsen stains were carried out on cells grown for 5 d on Middlebrook 7H10 agar. Catalase activity, niacin activity and nitrate reduction were determined after 10 d, aryl sulphatase production after 3 and 14 d, tellurite reduction after 5 d, Tween hydrolysis after 10 d and urease production after 3 d. Antibiotic-susceptibility studies were carried out using the resistance ratio method.

Extraction and analysis of mycolic acids. Lyophilized biomass from 10-d-old Middlebrook 7H10 agar plates was degraded by alkaline methanolsysis (Saddler et al., 1987) and two-dimensional TLC of the methanolysates was carried out according to the method of Minnikin et al. (1980).

16S rDNA sequencing. The test strain was shaken in 100 ml Sauton’s broth (Mordarska et al., 1972) at 150 r.p.m. for 14 d at 36 °C. The biomass was harvested by centrifugation at 10000 r.p.m. for 10 min and washed twice in sterile TE buffer (Tris/HCl, pH 8, 10 mM; EDTA 1 mM); approximately 100 mg wet weight biomass was used for DNA extraction. The extraction and purification of DNA and the amplification, cloning and sequencing of the 16S rRNA gene were carried out as described previously (Chun & Goodfellow, 1995; Shojaei et al., 1997). The 16S rDNA sequence of strain 484T was aligned manually with all available sequences of rapidly growing mycobacteria by using the AL16s program (Chun, 1995). The additional sequence data were obtained from the GenBank and EMBL databases.

The EMBL accession number for the 16S rDNA sequence of strain 484T is AJ010747.
RESULTS AND DISCUSSION

An almost complete 16S rDNA sequence (1517 nucleotides) was obtained for strain 484T. Comparison of this nucleotide sequence with available sequences for representatives of the genus Mycobacterium showed that the organism fell within the evolutionary radiation occupied by rapidly growing mycobacteria (Fig. 1). The pairwise nucleotide similarity value found between strain 484T and the rapidly growing mycobacteria ranged from 95.6 to 97.7%, giving a mean of 96.7 ± 0.5%. The corresponding mean nucleotide similarity value found between strain 484T and the representative slowly growing mycobacteria was 96.2 ± 0.4%.

The nucleotide sequence of strain 484T shows substantial differences from the corresponding sequences of its nearest neighbours, namely Mycobacterium confluents (97.8%), Mycobacterium madagascariense (97.6%) and Mycobacterium phlei (97.7%); these values correspond to 29, 33 and 30 nucleotide differences, respectively. Comparable scales of difference exist between the nucleotide sequences of validly described species of rapidly growing mycobacteria (Shojaei et al., 1997). The positions of the test and marker strains in the phylogenetic tree were not markedly affected by either the tree-making algorithms or the outgroup strains (Fig. 1). It is also clear from Fig. 1 that the relationship between strain 484T and its nearest neighbour is not supported by high bootstrap values. However, the sequence of this strain, like those of other rapidly growing mycobacteria, has the charac-

![Fig. 1. Neighbour-joining tree (Saitou & Nei, 1987) based on nearly complete 16S rDNA sequences of rapidly growing mycobacteria (1446 nucleotides) showing the phylogenetic position of strain 484T. The sequence of the type strain of Mycobacterium haasiacum was not included in this analysis as the phylogenetic position of this rapidly growing organism is with the slowly growing mycobacteria (Schroder et al., 1997). The numbers at the nodes indicate the level of bootstrap support, based on a neighbour-joining analysis of 1000 resampled datasets; only values greater than 40% are given. Bar, 0.005 substitutions per nucleotide position.](image)

Evolutionary trees were inferred by using three algorithms, namely the Fitch–Margoliash (1967), maximum-parsimony (Kluge & Farris, 1969) and neighbour-joining (Saitou & Nei, 1987) methods. Evolutionary distance matrices for the Fitch–Margoliash and neighbour-joining methods were generated as described by Jukes & Cantor (1969). The PHYLIP package (Felsenstein, 1993) was used for all of the analyses. The resultant unrooted tree topologies were evaluated by performing bootstrap analyses (Felsenstein, 1985) of the neighbour-joining database on 1000 resamplings with the SEQBOOT and CONSENSE programs in the PHYLIP package. The root positions of the unrooted tree based on the neighbour-joining method was estimated by using three outgroup organisms, namely Gordona terrae DSM 43249T (sequence accession no. X79286), Nocardia asteroides ATCC 19247T (Z36934) and Rhodococcus equi DSM 20307T (X80614), as described by Swofford & Olsen (1990).

**Table 1. Characteristics that differentiate strain 484T from related mycobacteria**

<table>
<thead>
<tr>
<th>Strain/species</th>
<th>Growth at 45 °C</th>
<th>Nitrate reduction</th>
<th>Aryl sulphatase (14 d)</th>
<th>Growth on 5% (w/v) NaCl agar</th>
<th>Pigmentation</th>
</tr>
</thead>
<tbody>
<tr>
<td>Strain 484T</td>
<td>+</td>
<td>+</td>
<td>–</td>
<td>–</td>
<td>n</td>
</tr>
<tr>
<td><em>M. confluents</em></td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>n</td>
</tr>
<tr>
<td><em>M. madagascariense</em></td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>–</td>
<td>s</td>
</tr>
<tr>
<td><em>M. phlei</em></td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>+</td>
<td>s</td>
</tr>
</tbody>
</table>

n, Non-chromogenic; s, scotochromogenic.
teristic short helix at positions 451–482 (Escherichia coli numbering system; Brosius et al., 1978).

The phenotypic properties of strain 484T are also consistent with its classification in the genus Mycobacterium (Lévy-Frébault & Portaels, 1992). The organism is aerobic, non-motile, Gram-positive and weakly acid–alcohol-fast. It is catalase- and urease-positive, reduces nitrate and is positive for Tween hydrolysis. Older cultures may show weak chromogenicity. The detection of α- and keto-mycolates and wax esters in methanolysates of the strain distinguishes it from the rapidly growing mycobacteria Mycobacterium abscessus, Mycobacterium chelonae, M. confluentis and Mycobacterium fortuitum, but not from M. madagascariense or M. phlei. However, these species are scotochromogenic and can be distinguished from strain 484T by the phenotypic characteristics shown in Table 1.

It is evident from the chemical, 16S rDNA sequencing and microbiological data that strain 484 is the type strain of Mycobacterium elephantis. It is proposed, therefore, that this organism be classified in the genus Mycobacterium as Mycobacterium elephantis.

Description of Mycobacterium elephantis sp. nov.

Mycobacterium elephantis (e.le.phan’tis. L. n. elephas elephant; L. gen. n. elephantis of the elephant).

Aerobic, Gram-positive, weakly acid–alcohol-fast, asporogenous, non-motile organism which is non-chromogenic. Cells are cocco-bacillary and 1·2–1·4 μm long. The organism is positive for catalase (45 mm foam), nitrate reductase, Tween hydrolysis and urease. Negative for tellurite reduction (5 d) and aryl sulphatase activity (14 d). Good growth occurs at 25, 37, 42 and 45 °C. Growth is inhibited by isoniazid (1·4 mg l−1), rifampicin (16 mg l−1), pyrazinamide (66 mg l−1), thiacetazone (10 mg l−1) and thiophen-2-carboxylic acid hydrazide, but not by ciprofloxacin (2·5 mg l−1) or ethambutol (3·2 mg l−1). Isolated from a lung abscess of an adult elephant that had died from chronic respiratory disease. The type strain of M. elephantis is strain 484T (= DSM 44368T).

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REFERENCES


