A New Group (Type 3) of *Mycobacterium celatum* Isolated from AIDS Patients in the London Area

T. J. BULL,*, D. C. SHANSON, L. C. ARCHARD, M. D. YATES, M. E. HAMID, and D. E. MINNIKIN

Medical Microbiology Department, Charing Cross Hospital, London W6 8RF, Regional Centre for Tuberculosis Bacteriology, Public Health Laboratory, Dulwich Hospital, London SE22 8QF, and School of Organic Chemistry, University of Newcastle-upon-Tyne, Newcastle, NE1 7RU, England

We describe a new group (type 3) of the recently proposed species *Mycobacterium celatum* isolated from eight patients with AIDS in London, England. Sequences of genes coding for 16S rRNA (EMBL accession no. Z46664) showed a divergence of 17 bases from *M. celatum* type 2 reference isolates and a divergence of 7 bases from *M. celatum* type 1 reference isolates. A reference strain is available (NCTC 12882).

Recent developments in the genetic identification and classification of bacteria by sequencing of the genes coding for 16S rRNA (16S rDNA) (13) and other genes (5, 18) have yielded phylogenetically derived descriptions of a new group of isolates designated *Mycobacterium celatum*, within which type 1 and type 2 have been described (7). These organisms are similar, biochemically, to the *Mycobacterium avium* complex (MAC) (2), but they have unique species-specific 16S rDNA sequences and superoxide dismutase sequences (5) that indicate that they are more closely related to *Mycobacterium xenopi*. The differentiation of this group is important therefore because these unique sequences are not detected by commercial genomic identification systems for MAC (4) and have caused some confusion because of the similarity of the 16S rDNA sequence of *Mycobacterium tuberculosis* cross-reacting in some tests (3, 6, 17). *M. celatum* has been reported as causing mycobacterial opportunistic infection in a small number of AIDS patients in the United States and Italy (7, 19) but not in the United Kingdom.

Fourteen isolates were recovered over a 2-year period from eight patients with AIDS in London, England, by standard clinical isolation methods (15). One isolate was obtained from a lesion on the thumb, and one was obtained from stool; the remainder were from induced sputum, blood culture, or bronchial washing samples. Four patients had multiple isolates, and disseminated infection was indicated in six patients.

Isolates were originally distinguished by their inability to react with the AccuProbe MAC (GenProbe, Inc., San Diego, Calif.) identification kit, but they appeared biochemically indistinct from MAC. Cells were acid-fast (as determined by auramine-phenoix or Ziehl-Neelsen staining) coccobacilli and did not form spores, capsules, or aerial hyphae. Visible growth on Middlebrook 7H10 agar (9) from dilute inocula could be seen after 6 to 10 days. Colonies exhibited two forms designated rough and smooth, similar to those exhibited by *M. avium* (1). Colonies were initially transparent, but on prolonged culture they became creamy white and after 8 to 12 weeks they developed an intense yellow pigmentation independent of light. Growth occurred on Löwenstein-Jensen egg medium at 25, 37, 42, and 44°C. Further distinguishing characteristics included negative Tween hydrolysis, negative nitrate reductase reaction, and susceptibility to thiostrepton.
shown to be limited, when used in isolation, in differentiating closely related strains (16). The isolates described in this study most resemble closely related strains (16). The isolates described in this study
netic differences from the two previously described reference
strains. We suggest therefore that they should be classified as
Kingdom, as

Sequence has been submitted to EMBL under accession no.

\[
\text{Table 1. Diversity among 16S rDNA gene sequences obtained from } M. \text{ celatum type 1 (ATCC 51131*), } M. \text{ celatum type 2 (ATCC 51130), and } M. \text{ celatum type 3 (NCTC 12882) and EMBL sequences for } M. \text{ celatum type 1 (L08169) and } M. \text{ celatum type 2 (L08170).}
\]

<table>
<thead>
<tr>
<th>Sequence</th>
<th>Nucleotide at base position:</th>
</tr>
</thead>
<tbody>
<tr>
<td>L08169</td>
<td>T T T X G G C A T G T T G C G G T</td>
</tr>
<tr>
<td>L08170</td>
<td>T T T X G G T C C A G T T G T C G</td>
</tr>
<tr>
<td>Type 1</td>
<td>C C T T T C G A C A T G T T G C G G T</td>
</tr>
<tr>
<td>Type 2</td>
<td>C C T T T C G A T C C A A G T T T G T C G</td>
</tr>
<tr>
<td>Type 3</td>
<td>C G C T C T T C G T A C A T G T T C G C C G T G G</td>
</tr>
</tbody>
</table>

\* Base positions correspond to those in M. tuberculosis 16S rRNA (EMBL accession no. X32917).

\* Inserted after this base position.