**Mycobacterium immunogenum** sp. nov., a novel species related to *Mycobacterium abscessus* and associated with clinical disease, pseudo-outbreaks and contaminated metalworking fluids: an international cooperative study on mycobacterial taxonomy

Rebecca W. Wilson,1,2 Vincent A. Steingrube,2 Erik C. Böttger,3 Burkhard Springer,3 Barbara A. Brown-Elliott,2 Véronique Vincent,4 Kenneth C. Jost,5 Yansheng Zhang,2 Maria J. García,6 Sher H. Chiu,5 Grace O. Onyi,5 Harold Rossmoor,7 Donald R. Nash1 and Richard J. Wallace, Jr1,2

Author for correspondence: Rebecca W. Wilson. Tel: +1 903 877 7680. Fax: +1 903 877 7652. e-mail: becky.wilson@uthct.edu

**PCR–restriction enzyme pattern analysis of a 439 bp hsp65 gene segment identified 113 unique isolates among non-pigmented rapidly growing mycobacteria (RGM) from clinical and environmental sources that failed to match currently recognized species patterns.** This group represented 40% of isolates recovered from bronchoscope contamination pseudo-outbreaks, 0% of disease-associated nosocomial outbreaks and 4% of routine clinical isolates of the *Mycobacterium abscessus/Mycobacterium chelonae* group submitted to the Mycobacteria/Nocardia laboratory for identification. It is grouped within the *Mycobacterium fortuitum* complex, with growth in less than 7 d, absence of pigmentation, positive 3-d arylsulfatase reaction and growth on MacConkey agar without crystal violet. It exhibited overlapping biochemical, antimicrobial susceptibility and HPLC characteristics of *M. abscessus* and *M. chelonae*. By 16S rRNA gene sequencing, these isolates comprised a homogeneous group with a unique hypervariable region A sequence and differed by 8 and 10 bp, respectively, from *M. abscessus* and *M. chelonae*. Surprisingly, this taxon contained two copies of the ribosomal operon, compared with single copies in the two related species. By DNA–DNA hybridization, this new group exhibited <30% homology with recognized RGM species. The name *Mycobacterium immunogenum* sp. nov. is proposed for this new taxon.

**Keywords:** *Mycobacterium immunogenum*, rapidly growing mycobacterium, mycobacterium taxonomy, metalworking fluids

**INTRODUCTION**

*Mycobacterium abscessus*, *Mycobacterium chelonae* and *Mycobacterium mucogenicum* have been the most commonly recovered mycobacteria involved in waterborne nosocomial outbreaks and pseudo-outbreaks (Band et al., 1982; Fraser et al., 1992; Maloney et al., 1994; Petersen et al., 1994; Wallace et al., 1993a, b) and metalworking fluid (MWF)-associated hypersensitivity pneumonitis (HP) (Kreiss & Cox-Ganser, 1997; Muilenberg et al., 1993). These rapidly growing mycobacterial (RGM) species are more resistant to free chlorine than are coliform bacteria (Carson et al., 1988a; Collins et al., 1984). They are found, along

---

**Abbreviations:** BAL, bronchoalveolar lavage; HP, hypersensitivity pneumonitis; MWF, metalworking fluid; PRA, PCR–restriction enzyme pattern analysis; RGM, rapidly growing mycobacteria.

The EMBL accession number for the 16S rDNA sequence of strain ATCC 700506 is AJ011771.
with other environmental species of mycobacteria (Picardeau et al., 1997), in 83–90% of samples from domestic water-purification systems (Carson et al., 1988a; Schulze-Röbbecke et al., 1992). They are prevalent in biofilms (Schulze-Röbbecke et al., 1992), are relatively resistant to disinfecting agents such as 2% alkaline glutaraldehyde and up to 8% formaldehyde (Carson et al., 1978) and are able to grow in distilled-water supplies (Carson et al., 1978). These characteristics enhance the capacity of these organisms to survive and proliferate in hospital water systems, which are the source of most nosocomial non-tuberculous mycobacterial outbreaks (Band et al., 1982; Bernstein et al., 1995; Hoffman et al., 1981; Kuritsky et al., 1993; Szabo & Sarkozy, 1980; Villaneuva et al., 1997).

HP has been characterized as a granulomatous lung disease similar to sarcoidosis and beryllium disease (Kreiss & Cox-Ganser, 1997). Since the first reported case in 1991, a total of 98 cases of HP have been associated with exposure of industrial workers to aerosolized water-based synthetic, semi-synthetic or soluble oil MWF (Kreiss & Cox-Ganser, 1997). While the HP generally resolved upon removal of patients from the MWF environment, a small number of cases were reported to have chronic interstitial lung disease and some had biopsy evidence of fibrosis. The complex microbial flora of used MWFs, acid-fast bacteria in particular, have been implicated as the aetiological agent of HP (Kreiss & Cox-Ganser, 1997).

The taxonomy and epidemiology of RGM and their involvement in nosocomial outbreaks and pseudo-outbreaks have been a major focus of the Mycobacteria/Nocardia Laboratory at the University of Texas Health Center at Tyler (UTHCT). Biochemical, antimicrobial susceptibility and PCR restriction enzyme analysis (PRA) testing of mycobacterial isolates recovered from several outbreaks, some involving MWFs, have resulted in the identification of a group of isolates that produced a hybrid pattern of phenotypic and genotypic characteristics that were common to both M. abscessus and M. chelonae. The potential of these environmental and nosocomial pseudo-outbreak isolates to cause human disease (Kreiss & Cox-Ganser, 1997) prompted further examination, in order to determine their relationship to the established mycobacterial pathogens M. abscessus and M. chelonae.

METHODS

Organisms. The first of these unusual isolates were recognized during a study of the use of PRA for taxonomic identification of clinical mycobacteria (Wilson et al., 1998). These isolates exhibited PRA band patterns from a 439 bp segment of the hsp65 gene (Telenti et al., 1993) that appeared to be a hybrid between those of M. chelonae and M. abscessus. The PRA pattern obtained with BstEII was characteristic for M. chelonae, while the HaeIII pattern was characteristic for M. abscessus. Environmental isolates with the same hybrid PRA pattern were subsequently identified as part of an environmental study of contaminated MWF, a portion of which has been published (Moore et al., 2000) (Table 1). Most isolates had high minimum inhibitory concentrations (MICs) for tobramycin and cefoxitin, so isolates within our culture collection with the same susceptibility pattern were screened by PRA. Based on DNA fingerprinting results of 10 previous nosocomial outbreaks of disease and 10 pseudo-breaks involving M. abscessus and/or M. chelonae (Wallace et al., 1993a; Zhang et al., 1997), one isolate representative of each outbreak pattern was selected and screened by PRA.

In 10 selected previous mycobacterial nosocomial outbreaks associated with disease (Szabo & Sarkozy, 1980; Hoffman et al., 1981; Lowry et al., 1988; Kuritsky et al., 1993; Wallace et al., 1993a; Bernstein et al., 1995; Villanueva et al., 1997), based on PRA species identification, M. abscessus was the predominant species, accounting for 9 of 10 (90%) outbreaks previously identified by biochemical testing as being due to M. abscessus or M. chelonae. M. chelonae was responsible for 1 of 10 (10%) of the outbreaks. The new taxon was not identified in any of these nosocomial outbreaks. Conversely, among the 10 pseudo-outbreaks studied, based on PRA species identification, strains of the new taxon were found in 5 of 10 (50%) water-related pseudo-outbreaks (Moore et al., 2000; Fraser et al., 1992; Wallace et al., 1993a), compared with 2 of 10 (20%) that involved M. abscessus (Kuritsky et al., 1993; Wallace et al., 1998). One additional PRA pattern was identified in 3 of 10 (30%) water-related pseudo-outbreaks (referred to as new taxon II in Fig. 3) (Maloney et al., 1994; Petersen et al., 1994) and was not studied further. M. chelonae was not identified in any of the pseudo-outbreaks.

Clinical isolates belonging to the M. chelonae/M. abscessus group submitted for identification were also screened for the new taxon pattern by PRA. Among 165 clinical isolates identified as members of the M. abscessus/M. chelonae group, 67% were M. abscessus, 30% were M. chelonae and 4% belonged to the new taxon.

A total of 112 isolates were identified that exhibited the M. chelonae/M. abscessus hybrid PRA pattern. This included 98 environmental isolates from MWF, two isolates from five separate nosocomial pseudo-outbreaks involving contaminated bronchoscopes in Missouri (MC 779) (Maloney et al., 1994) and Maryland (MC 926) (Wallace et al., 1993a), one environmental isolate from the Midwest and 11 clinical isolates isolated from skin, cornea, urine, joint fluid, bronchoalveolar lavage (BAL) fluid, Groshong exit site, pacemaker pocket, Broviac site and blood (catheter site) submitted to the UTHCT Mycobacteria/Nocardia laboratory for susceptibility testing (Table 1).

Control isolates included randomly chosen clinical isolates submitted to the UTHCT laboratory for identification by PRA (Wilson et al., 1997) and susceptibility testing, as well as reference isolates from the ATCC (Manassas, VA, USA). These comprised 11 M. abscessus isolates, including the type strain ATCC 19977T, and 13 M. chelonae isolates, including ATCC 35749, ATCC 35751 and the type strain, ATCC 35752T.

Phenotypic characteristics. Isolates were tested for their ability to utilize citrate, α-glucitol (α-sorbitol), L-myoinositol and D-mannitol as sole carbon sources according to the methods of Tsukamura (1981, 1984). Tests for 3-d arylsulfatase activity, iron uptake, nitrate reductase activity and growth on MacConkey agar without crystal violet were performed according to standard methods (Kent & Kubica,
Novel species related to *M. abscessus* and *M. chelonae*

Table 1. Clinical characteristics of isolates of the new taxon of RGM

<table>
<thead>
<tr>
<th>Isolate</th>
<th>Source</th>
<th>Disease</th>
<th>Location</th>
<th>Comments</th>
</tr>
</thead>
<tbody>
<tr>
<td>MC 779 (=) ATCC 700505</td>
<td>BAL fluid</td>
<td>None</td>
<td>Missouri</td>
<td>Pseudo-outbreak. Isolates highly resistant to cefoxitin</td>
</tr>
<tr>
<td>MC 926</td>
<td>BAL fluid</td>
<td>None</td>
<td>Maryland</td>
<td>Pseudo-outbreak</td>
</tr>
<tr>
<td>MC 1903</td>
<td>Hospital environment</td>
<td>Unknown</td>
<td>Midwest USA</td>
<td></td>
</tr>
<tr>
<td>MC 1991 (=) ATCC 700506</td>
<td>MWF</td>
<td></td>
<td>Wisconsin</td>
<td></td>
</tr>
<tr>
<td>MC 1993</td>
<td>MWF</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>MC 1995</td>
<td>MWF</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>MC 1996</td>
<td>MWF</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>MC 2233</td>
<td>MWF</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>MC 2234</td>
<td>Environment</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>MC 2236</td>
<td>MWF</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>MC 2244</td>
<td>MWF</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>MC 2241</td>
<td>Environment</td>
<td></td>
<td></td>
<td>Formaldehyde resistant</td>
</tr>
<tr>
<td>MC 2268</td>
<td>Environment</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

**Isolates**

**MC 779** \(=\) ATCC 700505 were reported previously, by Fraser et al. (1992), Wallace et al. (1993a) and Moore et al. (2000), respectively.

<table>
<thead>
<tr>
<th>Isolate</th>
<th>Source</th>
<th>Disease</th>
<th>Location</th>
<th>Comments</th>
</tr>
</thead>
<tbody>
<tr>
<td>MC 835</td>
<td>Skin</td>
<td>Disseminated cutaneous infection</td>
<td>Texas</td>
<td>SCID</td>
</tr>
<tr>
<td>MC 1878</td>
<td>Cornea</td>
<td>Suspected keratitis</td>
<td>Texas</td>
<td>No clinical data available</td>
</tr>
<tr>
<td>MC 1911</td>
<td>Urine</td>
<td>Unknown</td>
<td>Florida</td>
<td>No clinical data available</td>
</tr>
<tr>
<td>MC 1988</td>
<td>Intravenous catheter site (Groshong)</td>
<td>Catheter-related infection</td>
<td>Texas</td>
<td>Host immune status unknown</td>
</tr>
<tr>
<td>MC 2110</td>
<td>Hand-aspirated joint fluid</td>
<td>Septic joint</td>
<td>Texas</td>
<td>Normal host</td>
</tr>
<tr>
<td>MC 2230</td>
<td>BAL fluid</td>
<td>Chronic pneumonia</td>
<td>Texas</td>
<td>SCID</td>
</tr>
<tr>
<td>MC 2231</td>
<td>Intravenous catheter site, blood</td>
<td>Catheter-related sepsis</td>
<td>Iowa</td>
<td>Bone-marrow transplant</td>
</tr>
<tr>
<td>MC 2462</td>
<td>Pacemaker pocket, blood</td>
<td>Pacemaker-related sepsis</td>
<td>Michigan</td>
<td>Normal host</td>
</tr>
<tr>
<td>MC 2540</td>
<td>Broviac site</td>
<td>Catheter-related infection</td>
<td>Massachusetts</td>
<td>Acute leukaemia</td>
</tr>
<tr>
<td>MC 2570</td>
<td>Skin</td>
<td>Disseminated cutaneous infection</td>
<td>Louisiana</td>
<td>Liver transplant</td>
</tr>
<tr>
<td>MC 2605</td>
<td>Blood</td>
<td>Unknown</td>
<td>N. Carolina</td>
<td>No clinical data available</td>
</tr>
</tbody>
</table>

SCID, Severe combined immunodeficiency syndrome.

1985). Growth on Löwenstein–Jensen medium containing 5% NaCl (Kent & Kubica, 1985) was tested at both 30 and 35°C.

MIC values were determined for amikacin, cefoxitin, cefmetazole, ciprofloxacin, clarithromycin, doxycycline, imipenem, sulfamethoxazole and tobramycin by a broth microdilution method in cation-supplemented Müller–Hinton broth (Swenson et al., 1985; Wallace et al., 1993b).

Disc-diffusion zone sizes for polymyxin b (10 µg), amikacin (30 µg) and kanamycin (30 µg) were determined using Müller–Hinton agar swabbed with oleic acid, albumin and dextrose and incubation for 3 d at 30°C.

Genomic restriction endonuclease digestion and pulsed field gel electrophoresis (PFGE) analysis. All isolates of the new taxon were examined for genetic strain relatedness of their large restriction fragment (LRF) patterns by PFGE (Tenover et al., 1995). Genomic DNA was prepared and LRF patterns were obtained by restriction endonuclease digests with *Dra*I and *Xba*I, with separation by PFGE according to methods described previously (Wallace et al., 1993a). Strain relatedness was defined according to the methods of Tenover et al. (1995).

Fluorescence detection (FL)-HPLC. Ten strains of the new taxon, strains 2649, 2642 \(=\) ATCC 700505, 2648, 2645, 2623, 2647, 2646 \(=\) ATCC 700506, 2652, 2644 and 2651, were analysed by FL-HPLC. Ten reference strains of *M. abscessus*, strains 2612, 2603, 0203 \(=\) ATCC 19977, 2605, 2600, 2611, 2608, 2607, 2606 and 2602, and 10 reference strains of *M. chelonae*, strains 0187 \(=\) ATCC 35752, 0189 \(=\) ATCC 19236, 0188, 0183 \(=\) ATCC 35749, 0195, 0186, 0194, 0185, 0191 and 0190, were used as comparative strains. For HPLC analysis, isolates were obtained from the ATCC or from the HPLC Users Group.
Steering Committee (Butler et al., 1996a, b). Mycobacterial isolates were analysed by FL-HPLC according to the method of Jost & Dunbar (1992) and Jost et al. (1995) with the modifications described by Brown et al. (1999). The method of Butler & Kilburn (1990) was used to number chromatographic peaks and to calculate peak-height ratios.

PCR amplification for PRA. DNA from cells was prepared for PCR amplification as described previously (Steingrube et al., 1995a; Telenti et al., 1993; Wilson et al., 1998). A 439 bp segment of the hsp65 gene was amplified from mycobacterial ground-cell supernatants, together with the appropriate positive and negative controls, according to a modification of the method of Telenti et al. (1993) (Steingrube et al., 1995a; Wilson et al., 1998).

PRA. Six restriction endonucleases, BstEII, HaeIII, HhaI, MspI, HinI and BsaHI (New England Biolabs and Promega), were used to produce PRA band patterns using methods described previously (Steingrube et al., 1995a, b; Telenti et al., 1993; Wilson et al., 1998). Fragments of ≤ 60 bp were disregarded and restriction fragment sizes were rounded to the nearest 5 bp, as recommended by Telenti et al. (1993).

Sequence determination of 16S rRNA gene. The 16S rRNA gene regions chosen for analysis were based on published sequence data available in the EMBL/GenBank database (Kazda et al., 1992; Kirschner et al., 1992a, b, 1993a, b; Pitulle et al., 1992; Rogall et al., 1990; Stahl & Urbance, 1990). GenBank accession numbers for selected 16S rRNA gene sequences used for comparison were as follows: Mycobacterium fortuitum ATCC 6841T, X52933; M. abscessus ATCC 1977T, X82235; and M. chelonae ATCC 35752T, X82236.

The methods used for DNA extraction, amplification of 16S rRNA gene fragments and sequence determination have been described previously (Hultman et al., 1989; Kirschner et al., 1993a, b). The sequences obtained were aligned with selected 16S rRNA gene sequences as described previously (Rogall et al., 1990).

For phylogenetic analyses, only 16S rRNA gene regions that were available for the rapidly growing species were included (corresponding to Escherichia coli positions 126–554, 894–1084 and 1101–1332). Pairwise distances (Hamming distances) were calculated by weighting nucleotide differences and insertions/deletions equally. A phylogenetic tree was constructed using the neighbourliness method as described previously (Rogall et al., 1990).

Sequence determination of hsp65 gene. The hsp65 gene region selected for analysis was described by Telenti et al. (1993). The methods used for DNA extraction, amplification, sequence determination and construction of the phylogenetic tree were described previously (Ringuet et al., 1999).

DNA–DNA hybridization. DNA–DNA homology experiments were performed as described previously (Domenech et al., 1997). Genomic DNA (0–5 µg) was labelled in vitro using a nick-translation labelling kit (Boehringer Mannheim) and 30 µCi [α-32P]dCTP (Amersham).

Portions (1 µg) of each unlabelled DNA were bound to nylon membrane filters (Amersham) by alkaline denaturation and UV fixation. Hybridizations were carried out under stringent conditions for 40 h. Filters were washed and counted with a liquid scintillation counter (Beckman). The relative binding ratios for each strain were calculated from the counts of homologous DNA bound and were expressed as percentages.

RFLP analysis of the 16S rRNA gene. RFLP analysis of the 16S rRNA gene was performed using genomic DNA digested with BanHI and PstI. The digests were separated by electrophoresis on horizontal gels containing 0.75% (w/v) agarose and then transferred to nylon membrane filters (Amersham).

An 804 bp fragment of the 16S rRNA gene of the M. fortuitum type strain, ATCC 6841T, was obtained by PCR and used as a probe. For DNA amplification, the Rc1 and Rc2 oligonucleotide sequences from the Mycobacterium bovis BCG 16S rRNA gene sequence were used in 50 µl amplification mixtures as described previously (Domenech et al., 1997). The cycling profile consisted of 30 cycles of 1 min at 94°C, 30 s at 58°C and 1 min at 72°C, followed by a final 5 min extension at 72°C. The ribosomal probe was labelled using the prime-z-gene system (Promega) and 20 µCi [α-32P]dCTP (Amersham).

RESULTS

Phenotypic characteristics

Isolates of the new taxon had the growth and biochemical characteristics of the M. fortuitum complex (Silcox et al., 1981) (Table 2). This included typical morphology with acid-fast staining, the absence of pigmentation, growth on tryptic soy and Middlebrook 7H10 agar in less than 7 d incubation at 30 and 35°C, no growth at 45°C, growth on MacConkey agar without crystal violet and a positive 3-d arylsulfatase reaction (Silcox et al., 1981). Most isolates grew better at 30 than at 35°C.

These isolates appeared to be related to the M. abscessus/M. chelonae group, based on negative iron uptake and nitrate reductase reactions, properties common to the latter two species (Silcox et al., 1981). They exhibited some reactions typical of M. abscessus, including the inability to utilize citrate, d-glucitol (d-sorbitol), i-myo-inositol and d-mannitol as sole carbon sources (Silcox et al., 1981) (Table 2) and resistance to tobramycin (MIC ≥ 16 µg ml−1) (Swenson et al., 1985) (Table 3). However, they were unable to grow on Löwenstein–Jensen medium containing 5% NaCl at 35°C (Table 2) and most isolates exhibited high levels of resistance to cefoxitin (MIC 256 µg ml−1), phenotypic characteristics typical of M. chelonae (Silcox et al., 1981; Swenson et al., 1985; Wallace et al., 1991b) (Table 3). Interestingly, isolates of both the new taxon and M. chelonae exhibited 25–50% growth in the presence of 5% NaCl at 30°C compared with control growth on Löwenstein–Jensen medium.

In terms of drug susceptibilities, the new taxon differed from both M. chelonae and M. abscessus. The ratio of kanamycin to amikacin disc-zone sizes for the 10 control strains of M. abscessus ranged from 1:3 to 1:7, with a mean of 1:5, while for 16/18 isolates of the new taxon, the ratio was < 1:2 with a mean of 0:92. For the new taxon, 14/17 had cefoxitin MICs of ≥ 256 µg ml−1 and 16/18 had tobramycin MICs of ≥ 16 µg ml−1. All isolates of the new taxon had at least one of these features and 17/18 (95%) had two of the three. No isolate showed any (partial or complete) zone of
Table 2. Growth and biochemical properties of M. abscessus, M. immunogenum and M. chelonae

Data for clinical isolates were taken from Springer et al. (1995) and Wallace et al. (1993b). Characters are scored as: +, positive (≥90%); −, negative (≤10%).

<table>
<thead>
<tr>
<th>Character</th>
<th>M. abscessus</th>
<th>M. immunogenum</th>
<th>M. chelonae</th>
</tr>
</thead>
<tbody>
<tr>
<td>Utilization of carbon sources:</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Citrate</td>
<td>−</td>
<td>−</td>
<td>+</td>
</tr>
<tr>
<td>D-Glucitol (D-sorbitol)</td>
<td>−</td>
<td>−</td>
<td>−</td>
</tr>
<tr>
<td>i-Myo-Inositol</td>
<td>−</td>
<td>−</td>
<td>−</td>
</tr>
<tr>
<td>D-Mannitol</td>
<td>−</td>
<td>−</td>
<td>−</td>
</tr>
<tr>
<td>3-d Arylsulfatase activity</td>
<td>+</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Growth in presence of 5% NaCl (35 °C)</td>
<td>+</td>
<td>−</td>
<td>−</td>
</tr>
<tr>
<td>Iron uptake</td>
<td>−</td>
<td>−</td>
<td>−</td>
</tr>
<tr>
<td>Nitrate reduction</td>
<td>−</td>
<td>−</td>
<td>−</td>
</tr>
<tr>
<td>Growth in &lt; 7 d</td>
<td>+</td>
<td>+</td>
<td>+</td>
</tr>
<tr>
<td>Pigment production</td>
<td>−</td>
<td>−</td>
<td>−</td>
</tr>
<tr>
<td>Mycolic acids by HPLC</td>
<td>+</td>
<td>+</td>
<td>+</td>
</tr>
</tbody>
</table>

Table 3. Antimicrobial susceptibility results for M. abscessus, M. immunogenum and M. chelonae

Values are MICs (µg ml⁻¹), expressed as modal values for groups of isolates. NT, Not tested.

<table>
<thead>
<tr>
<th>Agent</th>
<th>M. abscessus</th>
<th>M. immunogenum</th>
<th>M. chelonae</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Ten clinical isolates</td>
<td>ATCC 19977T</td>
<td>Ten isolates</td>
</tr>
<tr>
<td>Amikacin</td>
<td>8</td>
<td>32</td>
<td></td>
</tr>
<tr>
<td>Cefoxitin</td>
<td>16</td>
<td>16</td>
<td>&gt; 256</td>
</tr>
<tr>
<td>Cefmetazole</td>
<td>16</td>
<td>128</td>
<td>&gt; 128</td>
</tr>
<tr>
<td>Ciprofloxacin</td>
<td>16</td>
<td>&gt; 16</td>
<td>&gt; 16</td>
</tr>
<tr>
<td>Clarithromycin</td>
<td>0-5</td>
<td>0-4</td>
<td>0-25</td>
</tr>
<tr>
<td>Doxycycline</td>
<td>&gt; 128</td>
<td>&gt; 128</td>
<td>&gt; 128</td>
</tr>
<tr>
<td>Imipenem</td>
<td>8</td>
<td>8</td>
<td>16</td>
</tr>
<tr>
<td>Sulfamethoxazole</td>
<td>&gt; 64</td>
<td>&gt; 64</td>
<td>&gt; 64</td>
</tr>
<tr>
<td>Tobramycin</td>
<td>16</td>
<td>16</td>
<td>&gt; 16</td>
</tr>
</tbody>
</table>

* By PRA, this isolate is a strain of M. abscessus.

inhibition by polymyxin b. Susceptibility results for the isolates of the new taxon are compared with isolates of M. chelonae and M. abscessus in Table 3.

PFGE analysis

Fourteen different LRF patterns (genotypes) of the new taxon were identified by PFGE analysis. Details of some of the MWF results have already been presented (Moore et al., 2000). The two isolates of the new taxon representative of the two nosocomial pseudo-outbreaks from contaminated bronchoscopes (MC 779 and MC 926, Table 1) were different genotypes. Nine of the 11 clinical isolates were unique genotypes, with the remaining two displaying the predominant LRF pattern seen with the environmental isolates. As observed previously (Wallace et al., 1993a), undigested genomic DNA satisfactory for PFGE analysis could be obtained from only 50% of the M. abscessus isolates, including those from nosocomial outbreaks, while 100% of the isolates of the new taxon in the current study produced satisfactory genomic DNA.

FL-HPLC analysis

Analysis of strains of the new taxon by FL-HPLC-generated mycolic acid patterns identified all strains as belonging to the M. abscessus/M. chelonae group. These strains exhibited mycolic acid elution patterns
Fig. 1. Incubation-temperature-mediated variation of HPLC-generated mycolic acid 6,7-dimethoxy-4-coumarinylmethyl ester elution patterns for *M. abscessus*, *M. chelonae* and *M. immunogenum* strains grown on Löwenstein–Jensen medium at 30 (a) and 35 (b) °C. HMMS, High molecular mass internal standard. Peaks were named using the method of Butler & Kilburn (1990).
that were characterized by two peak clusters, each cluster containing two to four peaks (Fig. 1a, b). Visually, most patterns from strains of the new taxon were indistinguishable from \textit{M. abscessus} strains, but distinct from \textit{M. chelonae} strains. \textit{M. abscessus} and \textit{M. chelonae} strains incubated at 35 °C produced peak 8/peak 9 height ratios that ranged from 0·34 to 0·54 and 1·06 to 2·66, respectively. The corresponding range for strains of the new taxon was 0·25–1·00. Butler & Kilburn (1990) observed peak 8/peak 9 height ratios of \( \leq 0·86 \) for \textit{M. abscessus} and \( \geq 1·00 \) for \textit{M. chelonae}.

Mean-centred hierarchical cluster analysis of aligned whole data obtained at 35 °C between the two internal standard markers revealed a single distinct cluster that contained all of the strains of \textit{M. chelonae} (Fig. 2). At a similarity index of 0·70, the \textit{M. abscessus} strains grouped into two clusters, one of six strains and a second of four strains. At a similarity index of 0·70, the strains of the new taxon were more polymorphic than either \textit{M. abscessus} or \textit{M. chelonae}. The strains of the new taxon grouped into two clusters, with one strain unclustered. The pattern of the unclustered strains resembled that produced by \textit{M. chelonae} at 30 °C and was distinct from all other patterns produced at 35 °C.

The incubation temperature exerted a pronounced effect on the HPLC patterns of \textit{M. abscessus}, \textit{M. chelonae} and the new taxon. Compared with patterns of strains incubated at 35 °C, patterns of the strains incubated at 30 °C exhibited a diminished front peak cluster height relative to rear peak cluster height. Within each peak cluster, a shift in peak height towards the earlier-eluting peaks was observed. Strains of \textit{M. abscessus} and the new taxon incubated at 30 °C yielded patterns similar to those of \textit{M. chelonae} strains incubated at 35 °C (Fig. 1).

Fig. 2. Dendrogram illustrating phylogenetic relationships between \textit{M. abscessus}, \textit{M. chelonae} and \textit{M. immunogenum} strains grown on Lowenstein–Jensen medium at 35 °C, based on mycolic acid composition analysis by HPLC. Suffixes AB, CH and IM respectively indicate strains of \textit{M. abscessus}, \textit{M. chelonae} and \textit{M. immunogenum}. The scale indicates the similarity index.

Fig. 3. Practical schematic illustrating the similarities and differences between \textit{M. immunogenum}, new taxon 2, \textit{M. abscessus} and \textit{M. chelonae} by PRA of a 439 bp segment of the hsp65 gene. PRA band sizes are expressed as the number of nucleotide base pairsbp rounded to the nearest 5 bp, as recommended by Telenti \textit{et al.} (1993).

Fig. 4. Comparison of PRA patterns for \textit{M. chelonae}, \textit{M. abscessus} and the proposed new species, \textit{M. immunogenum}. (a) Lanes 1–6 and 9–14: BsaHI- (lanes 1–6) and HaeIII- (lanes 9–14) derived patterns for \textit{M. chelonae} ATCC 35749 (lanes 1 and 9), \textit{M. chelonae} ATCC 35752 (2, 10), \textit{M. immunogenum} ATCC 700506 (3, 11), \textit{M. immunogenum} MC 1995 (4, 12), \textit{M. abscessus} ATCC 19977 (5, 13) and \textit{M. abscessus} MC 1148 (6, 14). Lanes 7 and 8 contain size standards (100 bp and pGEM base pair ladders). (b) BseII- (lanes 1–3), Hhal- (4–6), MspI- (9–11) and HaeIII- (12–14) derived patterns for \textit{M. chelonae} ATCC 35752 (lanes 1, 4, 9 and 12), strain ATCC 35751 (2, 5, 10 and 13) and \textit{M. abscessus} ATCC 19977 (3, 6, 11 and 14). Lanes 7 and 8 contain size standards (100 bp and pGEM base pair ladders).
Table 4. Signature nucleotides within hypervariable region A of the 16S rRNA gene for the pathogenic RGM

The first nucleotide corresponds to E. coli position 175. M. tuberculosis is used as the reference species. Dots indicate nucleotides identical to the M. tuberculosis sequence. Dashes indicate the absence of insertions. Proposed or accepted type strains are indicated.

<table>
<thead>
<tr>
<th>Taxon/species</th>
<th>Signature sequence</th>
</tr>
</thead>
<tbody>
<tr>
<td>M. tuberculosis–M. bovis</td>
<td>CGGATAGG-ACCACGGGATGCATGTC-TTGTGGTG</td>
</tr>
</tbody>
</table>
| M. fortuitum group | ..A..T.-..C.C.T.-..GT-G.......
| M. fortuitum ATCC 6841T | ..A..T.-..G..CAC.T.C.-..GT-G.....
| Mycobacterium peregrinum ATCC 14467T | ..A..T.-..C.C.T.-..GT-G.......
| M. fortuitum third biovariant complex (sorbitol-positive) ATCC 49403T; M. senegalense | ..A..T.-..G..CTC.T.-..GG-G.....
| M. fortuitum third biovariant complex (sorbitol-negative) ATCC 49404T | ..A..T.-..C.C.T.-..GT-G.......
| M. chelonae/M. abscessus group | ..A..T.-..C.C.T.-..GT-G.......
| M. abscessus ATCC 19977T | ..A..T.-..C.C.T.-..GT-G.......
| M. chelonae ATCC 35752T | ..A..T.-..C.C.T.-..GT-G.......
| M. immunogenenum ATCC 700506 | ..A..T.-..C.C.T.-..GT-G.......
| M. macrogenicum ATCC 49650T | ..A..T.-..C.C.T.-..GT-G.......
| M. smegmatis group | ..A..T.-..C.C.T.-..GT-G.......
| M. smegmatis sensu stricto ATCC 14468 | ..A..T.-..C.C.T.-..GT-G.......
| M. goodii ATCC 700504T | ..A..T.-..C.C.T.-..GT-G.......
| M. wolinskyi ATCC 700010T | ..A..T.-..C.C.T.-..GT-G.......
| M. mageritense ATCC 700351T | ..A..T.-..C.C.T.-..GT-G.......

PRA

Amplicons were obtained from all the isolates tested. Patterns identical to those seen with M. chelonae were exhibited by 98% (110/112) of the isolates of the new taxon after BstEII PRA and 100% of isolates after MspI and HhaI PRA. Two isolates contained no BstEII restriction site (Fig. 3). Isolates of the new taxon exhibited HinfI and HaeIII patterns that were identical to those seen with M. abscessus (Figs 3 and 4a, lanes 11–14) and differentiated them clearly from M. chelonae isolates (Figs 3 and 4a, lanes 9 and 10). The BsaHI pattern of the new taxon lacked a 100 bp band (Figs 3 and 4a, lanes 3 and 4) that was present in the common BsaHI pattern seen with M. chelonae and M. abscessus isolates (Figs 3 and 4a, lanes 1, 2, 5 and 6).

The three RGM isolates representing the three pseudo-outbreaks from contaminated bronchoscopes, which have been recognized but not characterized at this time, exhibited a unique PRA pattern, not seen previously, consisting of a 200 bp upper band with HhaI and a 160 bp upper band with HaeIII, compared with 235 and 145 bp bands seen with the new taxon (Fig. 3).

Misidentification of ATCC 35751

In this laboratory, M. chelonae reference isolate ATCC 35751 was found to be negative for utilization of citrate, d-glucitol (d-sorbitol), i-myos-inositol and d-mannitol as sole carbon sources and found to grow in the presence of 5% NaCl (Silcox et al., 1981) (Table 2). Results of susceptibility testing indicated that this strain was moderately susceptible to cefoxitin and resistant to tobramycin (MIC 16 μg ml⁻¹), similar to values for isolates of M. abscessus (Swenson et al., 1985; Wallace et al., 1991b) (Table 3). In addition to phenotypic characteristics typical of M. abscessus, PRA of isolate ATCC 35751 with all six restriction endonucleases produced band patterns that matched those of M. abscessus isolates, including the M. abscessus type strain, ATCC 19977T (Fig. 3). This strain appears to be misidentified and is a strain of M. abscessus rather than M. chelonae. A comparison of restriction fragment patterns for the M. chelonae type strain, ATCC 35752T, ATCC isolate 35751 and the M. abscessus type strain, ATCC 19977T, with BstEII, HhaI, MspI and HaeIII is shown in Fig. 4(b).

Sequence determination of 16S rRNA gene

Five isolates of the new taxon were sequenced in hypervariable regions A and B, with identical results. The isolates of the new taxon had a hypervariable region B that matched M. chelonae and M. abscessus, but a hypervariable region A that differed from these two species as well as all other species of RGM (Table 4). Over the sequence of the entire 16S rRNA gene, the new taxon differed by 8 and 10 bp from M. abscessus and M. chelonae, respectively, while the latter two species are known to differ from one other by 4 bp (Kirschner et al., 1993b; Springer et al., 1995). The new taxon differs by more than 35 bp from all other species. A phylogenetic tree showed M. chelonae,
Novel species related to *M. abscessus* and *M. chelonae*

*Fig. 5.* Dendrogram illustrating the phylogenetic relationships on the basis of 16S rRNA gene sequences among 30 species and taxa of RGM including *M. immunogenum* ATCC 700506, *M. abscessus* ATCC 19977T and *M. chelonae* ATCC 35752T.

*M. abscessus* and the new taxon to occupy a separate branch of the tree, quite distant from other recognized species (Fig. 5).

**Sequence determination of the hsp65 gene**

The 441 bp region described by Telenti et al. (1993), from nucleotide position 396 to 836 according to the published sequence from *Mycobacterium tuberculosis* (Shinnick, 1987), was investigated. The hsp65 sequences within this region differed by 21 and 33 bp, respectively, from *M. chelonae* and *M. abscessus*, while *M. chelonae* and *M. abscessus* differed from each other by 29 bp. As demonstrated previously, two hyper-variable regions of the hsp65 gene were identified, between positions 624 and 664 and positions 683 and 725. A comparison of *M. chelonae*, *M. abscessus*, *M. mucogenicum* and the new taxon in the first hyper-
Table 5. DNA–DNA genomic pairing between *M. immunogenum* and phylogenetically related RGM

<table>
<thead>
<tr>
<th>Test strain</th>
<th>Homology with ATCC 700505 (%)</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>M. immunogenum</em> ATCC 700505&lt;sup&gt;T&lt;/sup&gt;</td>
<td>100</td>
</tr>
<tr>
<td><em>M. abscessus</em> ATCC 19977&lt;sup&gt;T&lt;/sup&gt;</td>
<td>15</td>
</tr>
<tr>
<td><em>M. chelonae</em> ATCC 35752&lt;sup&gt;T&lt;/sup&gt;</td>
<td>18</td>
</tr>
<tr>
<td><em>M. fortuitum</em> ATCC 6841&lt;sup&gt;T&lt;/sup&gt;</td>
<td>9.3</td>
</tr>
<tr>
<td><em>M. mucogenicum</em> ATCC 49650&lt;sup&gt;T&lt;/sup&gt;</td>
<td>7</td>
</tr>
<tr>
<td><em>M. senegalense</em> ATCC 35796&lt;sup&gt;T&lt;/sup&gt;</td>
<td>5.3</td>
</tr>
</tbody>
</table>

variable region is shown in Fig. 6. A phylogenetic tree based on this 441 bp *hsp65* sequence obtained with 10 species of RGM and the new taxon is shown in Fig. 7 (data for the 10 recognized species were published by Ringuet et al., 1999).

DNA–DNA hybridization

DNA of the new taxon was hybridized with the following RGM reference isolates: *M. abscessus* ATCC 19977<sup>T</sup>, *M. chelonae* ATCC 35752<sup>T</sup>, *M. fortuitum* ATCC 6841<sup>T</sup>, *M. mucogenicum* ATCC 49650<sup>T</sup> and *Mycobacterium senegalense* ATCC 35796<sup>T</sup>. The new taxon displayed <25% homology with the five reference strains, with the highest degree of hybridization being shown with *M. chelonae* and *M. abscessus* (Table 5).

RFLP analysis of the 16S rRNA gene

*BamHI*– and *PstI*-generated chromosomal DNA restriction fragments from the new taxon and five other species of RGM were hybridized with an 804 bp, <sup>32</sup>P-labelled *M. fortuitum* 16S rRNA probe. Each of the six species of RGM produced a unique hybridization pattern with *BamHI*– and *PstI*-generated fragments. *M. abscessus* and *M. chelonae* had only a single copy of the ribosomal genes, while the new taxon and the other three species (*M. fortuitum*, *M. mucogenicum* and *M. senegalense*) had two copies.

**DISCUSSION**

This proposed newest member of the *M. fortuitum* complex resembled *M. abscessus* and *M. chelonae* so closely that molecular biological methods, including PRA and 16S rRNA gene sequencing, were required for its initial recognition. This almost certainly explains the failure until now to recognize this new taxon. Biochemically and by HPLC, it is related most closely to *M. abscessus*, and it was identified as such in previous recoveries from nosocomial pseudo-outbreaks (Fraser et al., 1992; Wallace et al., 1993a). An unusual feature that differentiated isolates recovered from some pseudo-outbreaks from those of *M. abscessus* was the high level of resistance to the cephamycins cefmetazole and cefoxitin (Fraser et al., 1992).

An unexpected finding was that, despite the similarity of new taxon to *M. chelonae* and *M. abscessus*, it has two copies of the rRNA operon, while the latter two species have only one. So far, *M. chelonae* and *M. abscessus* remain the only RGM species that contain just a single copy of the operon.

Isolates of the new taxon were recovered from 40% of nosocomial pseudo-outbreaks involving contaminated automated bronchoscope washers and were present in MWF used in the metal-grinding industry (Kreiss & Cox-Ganser, 1997). The new taxon was not identified among isolates that were recovered from 10 nosocomial outbreaks involving patient infections and were previously identified biochemically as *M. abscessus* and *M. chelonae*. The new taxon was responsible for a wide spectrum of clinical diseases (cutaneous infections, keratitis and catheter-related infections; Table 1), comparable to other species of RGM (Wallace et al., 1991a, 1993b). In addition to the 11 clinical isolates of the new taxon identified in this study, two other clinical isolates that appear to belong to the new taxon have been reported by other investigators. One isolate (M.3666/3667) was identified earlier by 16S rRNA gene sequencing by one of the authors (B. Springer, unpublished), but was not available for further examination. The other isolate was designated as presumptive *M. chelonae* (Taylor et al., 1997) and was referred to as *M. chelonae II* by Devalois et al. (1997). The latter isolate exhibited PRA patterns with *BstEII* and *HaeIII* that resembled very closely those of the new taxon in this study. These observations implicate this new mycobacterial taxon as a potential causative agent of human disease. Among clinical isolates of the *M. abscessus/M. chelonae* group submitted to the UTHCT laboratory for identification, 4% were identified by PRA as members of the new taxon. FL-HPLC did not resolve the new taxon from *M. abscessus*. However, *M. chelonae* could be distinguished from *M. abscessus* and the new taxon by either peak-height ratio or hierarchical cluster analysis of aligned whole chromatographic data.

By 16S rRNA gene sequencing, the new taxon isolates comprised a homogeneous group that exhibited a hypervariable region B sequence that was identical to
those of \textit{M. chelonae} and \textit{M. abscessus}. They exhibited a unique hypervariable region A sequence, however, and the entire sequence differed by 8 and 10 bp, respectively, from \textit{M. abscessus} and \textit{M. chelonae}.

Among non-ribosomal genes in the RGM, \textit{hsp65} has been shown to be of special interest for taxonomic purposes (Ringuet \textit{et al.}, 1993, 1999; Telenti \textit{et al.}, 1993; Steingrube \textit{et al.}, 1995a, b; Swanson \textit{et al.}, 1996). As established previously, the \textit{hsp65} gene displays more polymorphism than does the 16S rRNA gene. The \textit{M. chelonae} and \textit{M. abscessus} \textit{hsp65} sequences differed by 29 bp in the 441 bp hypervariable region, whereas their 16S rRNA genes differed by only four nucleotides. Despite this, the phylogenetic tree based on \textit{hsp65} sequences was consistent with the phylogeny based on 16S rRNA. Both trees showed that \textit{M. chelonae} and \textit{M. abscessus} are the more related species to the new taxon. However, due to the clear differentiation of \textit{M. chelonae} and \textit{M. abscessus} achieved by \textit{hsp65} sequencing, the \textit{hsp65} tree has an enlargement effect on the phylogenetic distances among the three groups and suggested that the new taxon is more related to \textit{M. chelonae} than to \textit{M. abscessus}. The use of phylogenetic trees of \textit{hsp65} alleles from various mycobacterial species, both slowly and rapidly growing, has been reported previously (Swanson \textit{et al.}, 1996; Kapur \textit{et al.}, 1995; Ringuet \textit{et al.}, 1999).

In a previous report on PRA identification of RGM (Steingrube \textit{et al.}, 1995a, b), the only isolate of \textit{M. chelonae} that failed to match the common PRA patterns for the species was the ATCC 35751 reference strain. More detailed examination of the original sample and a sample acquired recently from the ATCC revealed that it exhibited the biochemical, antimicrobial susceptibility and PRA pattern characteristics typical of \textit{M. abscessus}. These data support the identification of reference strain ATCC 35751 as a strain of \textit{M. abscessus} rather than \textit{M. chelonae}.

Reference has been made to the difficulties involved in achieving objective, reproducible results with the biochemical tests available for the identification of aerobic actinomycetes (Devallois \textit{et al.}, 1997; Silcox \textit{et al.}, 1981; Steingrube \textit{et al.}, 1995c, 1997), including the distinction between \textit{M. abscessus} and \textit{M. chelonae}. This difficulty was evident with evaluation of growth on Löwenstein–Jensen medium in the presence of 5% NaCl. Growth of \textit{M. chelonae} and isolates of the new taxon was inhibited by 5% NaCl when incubated at 30°C; however, 25–50% growth compared with positive controls was observed, and growth was not totally absent, as reported previously (Kent & Kubica, 1985; Springer \textit{et al.}, 1995; Wallace \textit{et al.}, 1993b). No growth was observed on Löwenstein–Jensen medium with 5% NaCl when \textit{M. chelonae} and isolates of the new taxon were incubated at 35°C. Growth of \textit{M. abscessus} and strain ATCC 35751 in the presence of 5% NaCl was unaffected by temperature (30 or 35°C), although the \textit{M. abscessus} type strain, ATCC 19977\textsuperscript{T}, showed some degree of inhibition at both temperatures.

Previous disc-diffusion susceptibility studies of \textit{M. abscessus} have shown that kanamycin disc zones of inhibition are larger than those for amikacin. A useful marker for the new taxon was that amikacin disc zones of \textit{M. chelonae} and isolates of the new taxon were generally equivalent to or larger than those for kanamycin and the isolates were resistant to cefoxitin and tobramycin. At least two of the three markers were present in 17/18 (95%) of isolates tested.

On the basis of the observed phenotypic (susceptibility) and genotypic characteristics that differentiate isolates of the new taxon from those of other species of \textit{Mycobacterium}, we propose the name \textit{Mycobacterium immunogenenum} sp. nov. for these isolates. The specific epithet refers to the association of these mycobacterial isolates with cases of HP (Bolan \textit{et al.}, 1985; Kreiss & Cox-Ganser, 1997; Muilenberg \textit{et al.}, 1993).
Differentiation of *M. immunogenum* from related species by PRA

The PRA patterns of a 439 bp fragment of the *hsp65* gene of *M. immunogenum* are distinguishable from those of *M. abscessus* and *M. chelonei* and include: 315 and 130 bp bands with BstEII; 140 and 70 bp bands with *Hae*III; 235, 120 and 65 bp bands with *Hha*I; 260 and 180 bp bands with *Msp*I; a 385 bp band with *Hin*I; and 260 and 80 bp bands with *Bsa*HI. Differentiation of *M. immunogenum* from *M. abscessus* and *M. chelonei* can be accomplished with as few as two enzymes, e.g. *Bst*EII and *Hae*III, *Bst*EII and *Bsa*HI or *Msp*I and *Hin*I.

**Description of Mycobacterium immunogenum** sp. nov.

*Mycobacterium immunogenum* (im.mu.no.gen’um. N. L. neut. adj. immunogenum eliciting an immune response).

A Gram-positive, acid- and alcohol-fast, curved bacillus that grows aerobically. It does not form spores or aerial hyphae. Visible growth appears in <7 d. Colonies on Middlebrook 7H10 agar and trypticase soy agar are off-white in colour and usually rough, although smooth forms are observed. No pigment is produced. Growth occurs at 30 and 35 °C, but not at 45 °C. Isolates are susceptible in vitro to amikacin and clarithromycin and resistant to cefoxitin (MIC ≥ 256 μg ml⁻¹), cefmetazole, ciprofloxacin, doxycycline, imipenem, sulfamethoxazole and tobramycin (MIC ≥ 16 μg ml⁻¹). They are positive for 3-d arylsulfatase activity, negative for iron uptake and nitrate reductase, do not grow on Löwenstein–Jensen medium containing 5% NaCl at 35 °C and do not utilize citrate, D-glucitol (D-sorbitol), i-myo-inositol or D-mannitol as sole sources of carbon. Mycolic acids are present and produce HPLC chromatograms typical of the *M. abscessus*/*M. chelonei* group. Intact genomic DNA for PFGE can be obtained from all strains.

Two strains, ATCC 700505T (formerly BH29T, MC 779T) and ATCC 700506 (formerly MN 3744, MC 1991), have been deposited with the ATCC (Manassas, VA, USA), with the type strain also deposited in the Mycobacterial Reference Collection of the Institute Pasteur as CIP 106684T. The type strain, ATCC 700505T, was recovered from a nosocomial pseudo-outbreak involving water-borne contamination of an automated bronchoscope washer in St Louis, MO, USA (Fraser et al., 1992), and strain ATCC 700506 was isolated from contaminated industrial MWF (Moore et al., 2000).

**ACKNOWLEDGEMENTS**

A portion of this work was presented as an abstract to the 98th General Meeting of the American Society for Microbiology, Atlanta, GA, USA, in May 1998. Contributions of authors: R.W.W., PRA technology and biochemical testing; V.A.S., computerized measurements, data evaluation and preparation of manuscript text and graphics; E.C.B. and B.S., 16S rRNA sequencing; B.A.B., biochemical and susceptibility testing; V.V., *hsp65* gene sequencing and phylogenetic tree; S.H.C. and K.C.J., HPLC analyses; Y.Z., PFGE analyses; G.O., susceptibility testing; H.R., procurement of MWF isolates; M.J.G., DNA–DNA pairing and RFLP experiments; D.R.N., project coordinator; R.J.W., project director, traditional identification of isolates and editing manuscript text and graphics.

This work was supported by the Department of Microbiology and the Center for Pulmonary and Infectious Disease Control at UTHCT. We express our appreciation to Phyllis Pienta, former Collection Manager of Bacteriology, American Type Culture Collection, Manassas, VA, who kindly provided the reference strains used in this study; to Steven J. Moore, Department of Occupational and Environmental Medicine, UTHCT, for facilitating the acquisition of isolates from metalworking fluids; and to Professor Hans G. Trüper, Institute for Microbiology and Biotechnology University of Bonn, Bonn, Germany, for providing the correct Latin nomenclature. We would also like to thank Joanne Woodring for preparation of this manuscript.

This work is in memory of our co-author and friend Vincent Steingrube, a dedicated and meticulous researcher, who passed away prior to completion of this work.

**REFERENCES**


Novel species related to *M. abscessus* and *M. chelonae*


