4 showed susceptibility to amikacin, ciprofloxacin, clarithromycin, and doxycycline but resistance to cefoxitin, sulfamethoxazole, rifampin (MIC >16 μg/mL) and intermediate-resistance to imipenem (MIC 8–16 μg/mL).

According to the American Thoracic Society diagnostic criteria for NTM lung disease (9), patient 1 fulfilled all criteria and patient 3 fulfilled the radiographic and microbiological criteria. These findings suggest that M. conceptionense can cause lung disease. For the other patients, colonization with M. conceptionense is a more plausible explanation (Table).

These 4 recent cases of M. conceptionense infection are in accordance with the increasing prevalence of NTM (10). Increasing prevalence might be the result of technical advances in NTM identification, including use of liquid media and sequencing, or the result of a local outbreak or contamination event. We consider contamination to be an unlikely cause because specimens were completely separated from each other during collection and testing. Isolates from different patients yielded distinct randomly amplified polymorphic DNA patterns. In conclusion, M. conceptionense is not a rare NTM species in South Korea and can cause pulmonary disease.

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References


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Mycobacterium riadhense Pulmonary Infection, France and Bahrain

To the Editor: Mycobacterium riadhense is a newly described mycobacterial species that is potentially pathogenic for humans. Extrapulmonary infection with this nontuberculous mycobacterium (NTM) has been reported (1). We report 2 cases of pulmonary infection with this NTM.

The first case of infection was in a 39-year-old woman who was admitted to Toulon Military Hospital, Toulon, France, in December 2005 with suspected pulmonary tuberculosis. For 1 month, the patient had a persistent cough, fever, asthenia, and weight loss. Findings on chest radiographs were suggestive of tuberculosis, with cavitation in the right upper lobe, and the tuberculosis skin test reaction was positive. Sputum specimens collected on 3 consecutive days were negative for acid-fast bacilli (AFB), but broth cultures (BacT/ALERT 3D system; bioMérieux, Marcy l’Etoile, France) yielded mycobacterial growth.

We used 4 multiplex line-probe assays to identify the mycobacteria: GenoType MTBC (Hain Lifescience, Nehren, Germany) identified the organisms as members of the M. tuberculosis complex (MTBC; with a nonspecific reaction, banding pattern 1, 2, 3); GenoType Mycobacterium
The second case of infection was in a 43-year-old man who was admitted to Awali Hospital, Awali, Bahrain, in November 2006. The patient reported malaise, insomnia, cough, weight loss, and anorexia. Radiographs showed features suggestive of tuberculosis (left upper lobe consolidation with focal cavitation). Sputum specimens collected on 3 consecutive days were positive for AFB and mycobacterial growth. To identify the pathogen(s), we used the same 4 multiplex line-probe assays as used for case-patient 1, and results were similar. The identified strain was considered to be the pathogen responsible for the respiratory disease (2).

The patient was treated with a combination of clarithromycin (CLR) and ciprofloxacin (CIP) for 12 months; however, he had a clinical and microbiological (i.e., positive for AFB and culture results with the same type strain identical to that identified by the assays). The patient was treated with antituberculous drugs (INH, RIF, EMB, PZA, plus CLR and CIP) for 6 months, and then INH, RIF, CLR, CIP were continued for 2 additional months (Table), after which the patient showed clinical improvement.

In the 2 cases, molecular identification of the isolates as M. riyadhense was achieved by using partial hsp65 and rpoB gene sequencing, which was based on the high level of sequence identities with the type strain of M. riyadhense and a distance score of 3.5 and 4.6, respectively, to the next species, “M. simulans” (Table). Broth microdilution panels (SLOMYCO Sensititer; Trek Diagnosis Systems, Cleveland, OH, USA) were used to perform drug susceptibility testing using broth microdilution (SLOMYCO Sensititer; Trek Diagnosis Systems, Cleveland, OH, USA), and interpreted according to standards of the National Committee for Clinical Laboratory Standards (3).

<table>
<thead>
<tr>
<th>Patient age, y/sex</th>
<th>Clinical situation</th>
<th>Molecular-based identification of M. riyadhense</th>
<th>Drug susceptibility pattern, drug (MIC, μg/mL)</th>
<th>Antimicrobial drug therapy</th>
<th>Treatment duration, outcome</th>
</tr>
</thead>
<tbody>
<tr>
<td>19/M†</td>
<td>Bone infection in left maxillary sinus</td>
<td>16S rRNA, rpoB, hsp65 Type strain</td>
<td>AMK (10.0) R; CYP (20.0) S; CIP (2.0) S; CLF (&lt;0.5) S; CLR (2.0) S; EMB (5.0) S; INH (1.0) I; PAS (1.0) R; PRO (0.2) S; RIF (0.2) S; STR (5.0) S†</td>
<td>INH, RFP, EMB; then INH, RFP</td>
<td>9 mo, cured</td>
</tr>
<tr>
<td>39/F§</td>
<td>Pulmonary infection</td>
<td>16S rRNA, rpoB, hsp65</td>
<td>AMK (&lt;1.0) S; CIP (1.0) S; CLR (0.12) S; DOX (16.0) R; EMB (0.5) S; ETH (0.3) S; INH (0.5) S; LDD (1.0) S; MOX (0.12) S; RFC (0.25) S; RIF (0.12) S; STR (1.0) S; TMP/SMX (&lt;2.0/2.38) NA$$</td>
<td>INH, RFP, EMB; then INH, RFP</td>
<td>1 y, cured</td>
</tr>
<tr>
<td>43/M**</td>
<td>Pulmonary infection</td>
<td>16S rRNA, rpoB, hsp65</td>
<td>AMK (&lt;1.0) S; CIP (0.12) S; CLR (0.12) S; DOX (4.0) R; EMB (0.25) S; ETH (0.3) S; INH (0.5) S; LDD (1.0) S; LMOX (0.12) S; RFC (0.25) S; RIF (&lt;0.12) S; STR (0.5) S; TMP/SMX (&lt;2.0/38.0) NA$$</td>
<td>CLR, CIP; then INH, RFP, EMB; then INH, RFP, EMB, CLR, CIP</td>
<td>1 y, relapse; 8 mo, cured</td>
</tr>
</tbody>
</table>

*AMK, amikacin; R, resistant; CYP, cycloserine; S, susceptible; CIP, ciprofloxacin; CLF, clofazimine; CLR, clarithromycin; EMB, ethambutol; INH, isoniazid; I, intermediate; PAS, para-aminosalicylate sodium; PRO, prothionamide; RFC, rifabutin; RIF, rifampin; STR, streptomycin; R, resistant; DOX, doxycycline; ETH, ethionamide; LDD, linezolid; MOX, moxifloxacin; TMP/SMX, trimethoprim/sulfamethoxazole; NA, not available; PZA, pyrazinamide.
†Patient in Saudi Arabia; reported by van Ingen et al. (1).
‡Drug susceptibility testing was performed by using the agar dilution method.
§Patient in France.
¶Low 16S rRNA gene polymorphism between several mycobacterial species.
#Drug susceptibility testing was performed by using broth microdilution panels (SLOMYCO Sensititer; Trek Diagnosis Systems, Cleveland, OH, USA) and interpreted according to standards of the National Committee for Clinical Laboratory Standards (3).
**Patient in Bahrain.
USA) were used to determine drug susceptibility (Table) (3).

Commercial probes are frequently used for rapid identification of mycobacterial species (4); however, M. riyadhense and other recently proposed NTMs (e.g., M. kumamotonense and “M. simulans”) cross-react with MTBC DNA probes and may be missed by line-probe assays (5, 6). With the emergence of new NTM species, commercial probes could fail to discriminate between species, leaving clinical isolates either unidentified or misidentified. Because of its ease of use, accuracy, and discriminatory power, multilocus sequence analysis may soon become the standard for routine NTM species identification.

We have shown evidence for the pathogenic role of M. riyadhense in pulmonary diseases, a pathogen that has previously been reported to have extrapolummary pathogenicity (1). Clinical and radiologic signs and symptoms of pulmonary infection caused by M. riyadhense, including cough, weight loss, fever, and cavitating lung lesions, were similar to those in typical cases caused by MTBC strains. van Ingen et al. (7) suggested that the region of difference 1 (RD1) virulence locus identified in MTBC members may also play a crucial role in virulence of some NTM species. These authors found RD1 genes in NTMs that were causing human disease, including M. kansasii, M. szulgai, M. marinum, and the type strain of M. riyadhense (7).

We confirmed the presence of RD1 esat-6 and efp-10 genes in the M. riyadhense isolates reported here (GenBank accession nos. JF896090–JF896093). Because M. riyadhense is an emerging pathogen with, to our knowledge, only 1 previously reported extrapulmonary case of infection (1), the optimal treatment for infected patients is unknown. Our results and drug susceptibility testing indicate that antituberculous drugs, including INH, RMP, and EMB, are effective against M. riyadhense infection (Table), but the combination of CLR plus CIP was not effective in 1 case-patient reported here, despite in vitro susceptibility to both drugs.

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