However, treating pregnant women with XDR TB is more challenging. Our patient was given a regimen that included bedaquiline and linezolid, neither of which has data available on its safety during pregnancy. Even though the newborn was in good health at birth, no general conclusion could be drawn about the potential teratogenicity of these drugs because the treatment had been introduced only 3 weeks before delivery. In this single case, no specific maternal or fetal side effects were noticed, indicating the potential for using this drug combination. However, more data are needed to ensure the safety of these drugs during pregnancy.

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Mycobacterium riyadhense in Saudi Arabia

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Infections caused by nontuberculous mycobacteria (NTM) appear to be emerging globally, but the definitive reasons for this are unclear. Advances in diagnostic technologies have led to the identification of >160 species of Mycobacterium, including several human pathogens. M. riyadhense is a slow-growing NTM identified as a cause of pulmonary and extrapulmonary illnesses in humans from Riyadh, Saudi Arabia (1,2). At least 8 clinical cases have been reported from France, Bahrain, Saudi Arabia, and South Korea, with 5 of the 8 cases in Saudi Arabia (1–6) (Table). M. riyadhense can be misidentified by commercially available line probe assays as M. tuberculosis complex, mostly because of confusing banding patterns (7). A recent nationwide study of NTM prevalence in Saudi Arabia showed no suspected cases of M. riyadhense, which could be due to limiting the screening to line probe assays (7).

To explore the presence of M. riyadhense in clinical settings in Saudi Arabia, we conducted a prospective study on a nationwide collection of isolates. Suspected NTM isolates reported as M. tuberculosis complex or Mycobacterium species with nonspecific banding pattern by line probe assays were subjected to different conservative gene sequencing to identify M. riyadhense.

During April 2014–September 2015, we collected 458 NTM isolates, with clinical and epidemiological data, from all 9 national referral laboratories in different provinces of Saudi Arabia. We formulated the isolate enrollment strategy to suspect M. riyadhense on the basis of previous studies (1,2). In brief, we conducted primary identification of the
isolates using line probe assay—Genotype MTBC (Hain Life-
science, Nehren, Germany). We further tested isolates that
showed a nonspecific banding pattern (1,2,3) by using Geno-
type Mycobacteria CM and AS assays (Hain Lifescience).
The Genotype Mycobacteria CM assay showed a specific
banding pattern of 1,2,3,10,15,16 (1,2,3,10,16 in previous
study) for a group of isolates; AS assay identified these iso-
lates as Mycobacterium species. We subjected all isolates to
partial sequencing of 16S rRNA, rpoB and hsp65 genes using
BigDye Terminator chemistry (Applied Biosystems, Foster
City, CA, USA) (8–10). We then subjected the assembled
sequences of all 3 genes to analysis via BLAST (https://blast.
cbi.nlm.nih.gov) and the EzTaxon database. We followed
stringent identification criteria, requiring similarity ≥99% be-
tween isolate and reference strain for species confirmation.

We identified 14 isolates that fit the inclusion criteria;
most were reported from the Central province, Riyadh, in
Saudi Arabia, but the reason is unclear. Microbiological anal-
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database strains (GenBank accession nos. JF896094, JF896095, and NR044449). On the other hand, \textit{rpoB} and \textit{hsp65} sequences also showed 99%–100% similarity with other sequences (accession nos. EU921671, EU27644.1, JF896095 and NR 044449.1). The other closest species observed during the analysis were \textit{M. alseone}, \textit{M. szulgai}, and \textit{M. angelicum} (98% similarity with 16S rRNA gene sequences); \textit{M. genavens} and \textit{M. simulans} (96% similarity with \textit{hsp65} gene sequences); and \textit{M. lacus}, \textit{M. intracellulare}, and \textit{M. malmoense} (94% similarity with \textit{rpoB} gene sequences). Two isolates that matched inclusion criteria could not be identified as \textit{M. riyadhense}; BLAST analysis showed the closest matching species as \textit{M. lacus} DSM 44577(T), with 89% similarity. Two 16S rRNA gene sequences from this study were deposited in GenBank (accession nos. KX898970 and KX898971).

We identified 12 clinical cases of \textit{M. riyadhense} infection, including pulmonary and extrapulmonary invasive infections, over a period of 18 months. Demographically, Saudi citizens dominated; 11 of 12 case-patients were male, and mean age was 50 years. Geographic distribution of cases showed 10 cases from Riyadh (Central province) and 2 from Dammam (Eastern province). Clinical data revealed 9 cases with pulmonary involvement and 3, including a pediatric case, with lymphadenitis. Of note, 75% of the respiratory cases were clinically relevant according to American Thoracic Society criteria for NTM pulmonary disease. Most patients recovered with isoniazid, rifampin, and ethambutol therapy (Table).

The lack of advanced molecular diagnostic tools in clinical laboratories in Saudi Arabia impedes the accurate identification of \textit{M. riyadhense}. Without an accurate diagnosis, treatment is delayed. In this study, most of the patients were treated with standard TB regimens; some of them received clarithromycin, which did not appear to be highly effective (2). To date, no standard treatment regimen for \textit{M. riyadhense} disease has been developed, likely due to its status as a rare species. In the cases reported here, patients generally responded well to the initial therapies, but drug resistance may challenge the empirical treatment used. A strain resistant to isoniazid is already reported from South Korea (3). We recommend that clinicians in Saudi Arabia be vigilant to the possible emergence of \textit{M. riyadhense} as a more common pathogen.

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