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 (1). 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 assay and AS assays (Hain Life-
science, Nehren, Germany). 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.
cnbil.nlm.nih.gov) and the EzTaxon database. We followed stringent identification criteria, requiring similarity $\geq 99\%$
between 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-
ysis showed slow-growing mycobacteria producing rough
white colonies on LJ medium within 3–4 weeks of incubation
at 37°C. Primary sequencing of the 16S rRNA gene showed
12 cases of *M. riyadhense* had a 99%–100% match with 3
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