Low Prevalence of Mycobacterium bovis in Tuberculosis Patients, Ethiopia

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An estimated 17% of all tuberculosis cases in Ethiopia are caused by Mycobacterium bovis. We used M. tuberculosis complex isolates to identify the prevalence of M. bovis as the cause of pulmonary tuberculosis. Our findings indicate that the proportion of pulmonary tuberculosis due to M. bovis is small (0.12%).

In 2016, the World Health Organization (WHO) estimated that there were 147,000 cases and 12,500 deaths worldwide from tuberculosis, which is predominantly caused by Mycobacterium bovis. However, because of the lack of comprehensive surveillance data, particularly from developing countries, actual illness and death could exceed this estimate (1,2). To enhance efforts at addressing zoonotic TB, multiple international organizations collaboratively developed and recently released the Roadmap for Zoonotic Tuberculosis (1). The roadmap states 3 objectives, the first of which is to collect more accurate scientific evidence on zoonotic TB through improved surveillance efforts.

In Ethiopia, ≈80% of persons live in rural areas, where most of the population harvests crops or raises livestock (3). Because of the pastoral lifestyle, the burden of zoonotic TB is thought to be high in such rural communities because of a perceived higher risk of acquiring M. bovis infection (2). In 2013, Müller et al. estimated the proportion of all forms of TB cases caused by M. bovis in Ethiopia to be 17% (4). For this study, we evaluated the contribution of M. bovis toward causing pulmonary TB in Ethiopia.

We obtained a total of 1,785 stored M. tuberculosis complex isolates collected from patients testing followed by prolonged treatment with clarithromycin, which was finally curative.

In conclusion, the case reported here is a reminder that unusual pathogens, such as M. senegalense, should be considered as an etiology of infected breast prosthesis. Molecular techniques confirmed the accuracy of MALDI-TOF mass spectrometry to identify this emerging mycobacterial species. Patients should undergo prolonged treatment for ≥3 months, ideally with combined therapy, even with adequate surgical treatment.

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positive in smear tests. These tests were performed in 32 health facilities across Ethiopia during November 2011–June 2013 as part of a drug resistance survey. Among the 32 sites enrolled in the drug resistance survey, 30 sites had participated in an earlier survey in 2003–2005; two additional sites were selected from the Gambella and Benishangul Gumuz regions to ensure that ≥1 health facility from each region was included (Table). We included data from all patients with positive results for TB on consecutive sputum smear tests.

To identify species, region of difference (RD) 9- and RD4-based PCR procedures were performed using HVD primers and QIAGEN HotStarTaq Master Mix reagents (QIAGEN, https://www.qiagen.com), which were described in earlier studies (5–8). The Capilia TB-Neo test (Goffin Molecular Technologies, http://www.goffinmoleculartechnologies.com) was used to distinguish *M. tuberculosis*-complex species from other nontuberculous mycobacterial (NTM) species. The same standard operating procedures were used to interpret the results.

Of the 1,785 isolates collected, 1,735 were available for typing. Among those typed, 1,599 (99.8%) yielded visible bands of *M. tuberculosis* complex. RD9 typing identified 1,597 (99.87%) of 1,599 isolates as *M. tuberculosis*, and RD4 typing identified only 2 (0.13%) of 1,599 of the isolates as *M. bovis*. These findings indicate that pulmonary TB due to *M. bovis* is rare in Ethiopia.

This study has certain limitations. We used *M. tuberculosis* complex isolates collected from a sentinel drug resistance survey. Data from smears testing negative for pulmonary TB cases, which account for some proportion of PTB and extrapulmonary TB cases, were not included.

One possible alternative explanation for finding few cases of *M. bovis* as a pathogen in pulmonary TB is that *M. bovis* may have been acquired through ingestion of food from livestock infected with extrapulmonary TB (7). In that case, sputum might not have been the ideal technique for isolating *M. bovis* samples. Previous studies in Ethiopia reported variable (0%–16%) prevalence of *M. bovis* in extrapulmonary TB patients (8,9). A second possible reason could be the low prevalence of bovine TB in zebu cattle, which comprise >95% of the cattle population of Ethiopia (10) and have been reported to have lower infection rates with *M. bovis* than other types of cattle. In addition, most cattle husbandry in Ethiopia is on extensively managed small farms in open fields, which poses a low risk for the spread of bovine TB (7). Thus, a low prevalence of bovine TB in the Ethiopia cattle population could result in a limited rate of transmission to humans.

This study included samples from all regions of Ethiopia to identify the prevalence of bovine TB among patients with pulmonary TB. We found that *M. bovis* was an etiologic agent of human pulmonary TB in only a small fraction of cases, a lower proportion than previously estimated. This finding indicates that aerosol transmission of *M. bovis* from livestock to humans is rare. A useful focus for future efforts might be to implement or strengthen pasteurization programs in *M. bovis*-prevalent areas to limit possible transmission of bovine TB through the consumption of dairy products.

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This study received ethics approval from the IRBs of the Ethiopian Public Health Institute and Addis Ababa University.

RD9 and RD4 typing were performed at the Ethiopian Public Health Institute (EPHI).

*Table.* Number of cases by region and results of *Mycobacterium tuberculosis* testing for isolates in study of contribution of *M. bovis* to pulmonary tuberculosis, Ethiopia*.

| Region             | Total no. cases | *M. tuberculosis* positive | *M. tuberculosis* negative |
|--------------------|-----------------|---------------------------|---------------------------|
|                    |                 | Culture positive          | Culture negative/         | Culture positive | Culture negative/ |
|                    |                 |                           | contaminated              |                | contaminated     |
| Addis Ababa        | 181             | 166                       | 10                        | 1              | 4               |
| Afar               | 68              | 58                        | 4                         | 3              | 3               |
| Amhara             | 138             | 121                       | 6                         | 5              | 6               |
| Benishangul Gumuz  | 21              | 19                        | 1                         | 0              | 1               |
| Dire Dawa          | 103             | 86                        | 1                         | 6              | 10              |
| Gambella           | 121             | 105                       | 4                         | 7              | 5               |
| Harar              | 52              | 50                        | 2                         | 0              | 0               |
| Oromia             | 518             | 469                       | 22                        | 12             | 15              |
| SNNPR              | 352             | 315                       | 19                        | 10             | 8               |
| Somali             | 104             | 101                       | 2                         | 1              | 0               |
| Tigray             | 77              | 62                        | 10                        | 2              | 3               |
| Total              | 1,735           | 1,552                     | 81                        | 47             | 55              |

*Of the 1,735 isolates available for typing, 1,599 yielded positive results for *M. tuberculosis* complex; of those, 1,597 (99.87%) were *M. tuberculosis* positive by RD9 testing and 2 (0.13%) were *M. bovis* positive by RD4 testing. Of the 2 RD4 positive results, 1 was from culture-positive and the other from smear-positive (culture negative) sediment. RD, region of difference.
About the Author
Dr. Getahun works at the national reference laboratory for Ethiopia. Her main areas of work include conducting research on priority public health problems, providing technical assistance on TB research, and providing supportive supervision for surveillance and program evaluation.

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9. Neelsen staining; we observed a florid histiocytic reaction or other nontuberculosis mycobacterial infection. Metagenomics sequencing can be used to identify multidrug-resistant M. leprae.

Leprosy is a chronic dermatologic and neurologic disease caused by the infectious agent Mycobacterium leprae and can lead to severe disabilities; >200,000 new cases are reported annually worldwide, according to the World Health Organization. A total of 242 leprosy cases were reported in Saudi Arabia during 2003–2012; however, little is known about the subtypes and prevalence of drug resistance among these M. leprae cases.

In May 2017, a 30-year-old woman from the Philippines sought treatment at the dermatology clinic of King Fahad Medical City (KFMC) Hospital in Riyadh, Saudi Arabia, for painful systemic skin nodules and joint pain without joint swelling. She had no medical history of leprosy. The initial clinical diagnosis of this patient was inconclusive, but her initial symptoms were suggestive of a connective tissue disease such as systemic lupus erythematosus, and initial clinical improvement was recorded after a short course of empiric steroids and hydroxychloroquine treatment. Other suspected diagnoses included lepromatous leprosy with type 2 erythema nodosum leprosum reaction or other nontuberculosis mycobacterial infection.

We performed a punch skin biopsy of the extensor surface of the forearm and performed Ziehl-Neelsen staining; we observed a florid histiocytic reaction to an imported case of multidrug-resistant M. leprae.