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.

About the Author

Dr. Carretero is on the faculty of the Department of Microbiology, Hospital Universitario 12 de Octubre, Madrid. His primary research interests include nontuberculosis mycobacteria and prosthesis infections.

References

1. Brown BA, Wallace RJ Jr, Onyi GO, De Rosas V, Wallace RJ III. Activities of four macrolides, including clarithromycin, against *Mycobacterium fortuitum*, *Mycobacterium chelonae*, and *M. chelonae*–like organisms. Antimicrob Agents Chemother. 1992;36:180–4. https://doi.org/10.1128/AAC.36.1.180
2. Oh WS, Ko KS, Song JH, Lee MY, Ryu SY, Taek S, et al. Catheter-associated bacteremia by *Mycobacterium senegalense* in Korea. BMC Infect Dis. 2005;5:107. https://doi.org/10.1186/1471-2334-5-107
3. Talavlikar R, Carson J, Meatherill B, Desai S, Sharma M, Shandro C, et al. *Mycobacterium senegalense* tissue infection in a child after fish tank exposure. Can J Infect Dis Med Microbiol. 2011;22:101–3. https://doi.org/10.1155/2011/206532
4. Wallace RJ Jr, Brown-Elliott BA, Brown J, Steigerwalt AG, Hall L, Woods G, et al. Polyphasic characterization reveals that the human pathogen *Mycobacterium peregrinum* type II belongs to the bovine pathogen species *Mycobacterium senegalense*. J Clin Microbiol. 2005;43:5925–35. https://doi.org/10.1128/JCM.43.12.5925-5935.2005
5. Adékambi T, Colson P, Drancourt M. *rpoB*-based identification of nonpigmented and late-pigmenting rapidly growing mycobacteria. J Clin Microbiol. 2003;41:5699–708. https://doi.org/10.1128/JCM.41.12.5699-5708.2003
6. Wallace RJ Jr, Steele LC, Labidi A, Silcox VA. Heterogeneity among isolates of rapidly growing mycobacteria responsible for infections following augmentation mammaplasty despite case clustering in Texas and other southern coastal states. J Infect Dis. 1989;160:281–8. https://doi.org/10.1093/infdis/160.2.281
7. Brown-Elliott BA, Wallace RJ Jr. Clinical and taxonomic status of pathogenic nonpigmented or late-pigmenting rapidly growing mycobacteria. Clin Microbiol Rev. 2002; 15:716–46. https://doi.org/10.1128/CMR.15.4.716-746.2002
8. Betal D, Macneill FA. Chronic breast abscess due to *Mycobacterium fortuitum*: a case report. J Med Case Reports. 2011;5:188. https://doi.org/10.1186/1752-1947-5-188

Address for correspondence: Paula López-Roa, Hospital Universitario 12 de Octubre, Department of Clinical Microbiology, Avenida de Córdoba, s/n, 28041 Madrid, Spain; email: plroa@salud.madrid.org

Low Prevalence of *Mycobacterium bovis* in Tuberculosis Patients, Ethiopia

Muluwork Getahun, H.M. Blumberg, Waganeh Sinshaw, Getu Diriba, Hilina Mollalign, Ephrem Tesfaye, Bazezew Yenew, Mengistu Taddess, Aboma Zewdie, Kifle Dagne, Dereje Beyene, Russell R. Kempker, Gobena Ameni

Author affiliations: Ethiopian Public Health Institute, Addis Ababa, Ethiopia (M. Getahun, W. Senshaw, G. Diriba, H. Mollalign, E. Tesfaye, B. Yenew, M. Taddess); Addis Ababa University, Addis Ababa (M. Getahun, A. Zewdie, K. Dagne, D. Beyene, G. Ameni); Emory University, Atlanta, Georgia, USA (H.M. Blumberg, R.R. Kempker)

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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

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 (92%) 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/ contaminated	Culture positive	Culture negative/ 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.

References

1. World Health Organization, Food and Agriculture Organization of the United Nations, and World Organisation for Animal Health. Roadmap for zoonotic tuberculosis. Geneva: WHO Press; 2017 [cited 2019 Feb 1]. http://www.fao.org/3/a-i7807e.pdf
2. Olea-Popelka F, Muwonge A, Perera A, Dean AS, Mumford E, Erlacher-Vindel E, et al. Zoonotic tuberculosis in human beings caused by *Mycobacterium bovis*—a call for action. Lancet Infect Dis. 2017;17:e21–5. https://doi.org/10.1016/S1473-3099(16)30139-6
3. Central Statistical Agency, World Bank. Ethiopia rural socioeconomic survey. 2013 [cited 2019 Feb 1]. http://siteresources.worldbank.org/INTLSMS/Resources/3358986-1233781970982/5800988-1367841456879/9170025-1367841502220/ERSS_Survey_Report.pdf
4. Müller B, Dürr S, Alonso S, Hattendorf J, Laisse CJ, Parsons SD, et al. Zoonotic *Mycobacterium bovis*–induced tuberculosis in humans. Emerg Infect Dis. 2013;19:899–908. https://doi.org/10.3201/eid1906.120543
5. Parsons LM, Brosch R, Cole ST, Somoskövi A, Loder A, Bretzel G, et al. Rapid and simple approach for identification of *Mycobacterium tuberculosis* complex isolates by PCR-based genomic deletion analysis. J Clin Microbiol. 2002;40:2339–45. https://doi.org/10.1128/JCM.40.7.2339-2345.2002
6. Mamo G, Bayleyegn G, Sisay Tessema T, Legesse M, Medhin G, Bjune G, et al. Pathology of camel tuberculosis and molecular characterization of its causative agents in pastoral regions of Ethiopia. PLoS One. 2011;6:e15862. https://doi.org/10.1371/journal.pone.0015862
7. Portillo-Gómez L, Sosa-Iglesias EG. Molecular identification of *Mycobacterium bovis* and the importance of zoonotic tuberculosis in Mexican patients. Int J Tuberc Lung Dis. 2011;15:1409–14. https://doi.org/10.5588/ijtld.10.0608
8. Firdessa R, Berg S, Hailu E, Schelling E, Gumi B, Erenso G, et al. Mycobacterial lineages causing pulmonary and extrapulmonary tuberculosis, Ethiopia. Emerg Infect Dis. 2013;19:460–3. https://doi.org/10.3201/eid1903.120256
9. Regassa A, Medhin G, Ameni G. Bovine tuberculosis is more prevalent in cattle owned by farmers with active tuberculosis in central Ethiopia. Vet J. 2008;178:119–25. https://doi.org/10.1016/j.tvjl.2007.06.019
10. Sibhat B, Asmare K, Demissie K, Ayelet G, Mamo G, Ameni G. Bovine tuberculosis in Ethiopia: a systematic review and meta-analysis. Prev Vet Med. 2017;147:149–57. https://doi.org/10.1016/j.prevetmed.2017.09.006

Address for correspondence: Muluwork Getahun, Ethiopian Public Health Institute, National TB Reference Laboratory, Addis Ababa, 1242, Ethiopia; email: mimishaget@yahoo.com

Metagenomics of Imported Multidrug-Resistant *Mycobacterium leprae*, Saudi Arabia, 2017

Qingtian Guan, Talal S. Almutairi, Tahani Alhalouli, Arnab Pain,[1] Faisal Alasmari[1]

Author affiliations: King Abdullah University of Science and Technology, Thuwal-Jeddah, Saudi Arabia (Q. Guan, A. Pain); King Saud University Medical City, Riyadh, Saudi Arabia (T.S. Almutairi); King Fahad Medical City, Riyadh (T.S. Almutairi, T. Alhalouli, F. Alasmari)

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Using shotgun metagenomics, we identified an imported case of multidrug-resistant *Mycobacterium leprae* in a Filipino resident of Saudi Arabia in 2017. We determined the phylogenomic lineage (3K1) and identified mutations in *rpoB* and *rrs* corresponding to the multidrug-resistance phenotype clinically observed. 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 (*1*).

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 signs and 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

[1]These senior authors contributed equally to this article.