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)

DOI: https://doi.org/10.3201/eid2603.190661

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.

proliferation containing numerous *Mycobacterium* bacilli without an obvious granuloma (Appendix Figure 1, https://wwwnc.cdc.gov/EID/article/26/3/19-0661-App1.pdf). We referred the patient to the infectious disease clinic, which performed QuantiFERON-TB Gold (QIAGEN, https://www.quantiferon.com) and took a biopsy for bacterial and fungal culture, and all test results were negative. Mycobacterial culture showed >9 acid-fast bacilli/high-power field on smears, and no growth was observed on Lowenstein-Jensen slants after 8 weeks of incubation.

Her treatment started with a daily regimen of clofazimine (50 mg), dapsone (100 mg), and rifampin (600 mg). Treatment with moxifloxacin (400 mg/d) and macrolides was briefly added (clarithromycin and azithromycin were both stopped because of gastrointestinal side effects) in case of possible nontuberculosis mycobacterial infection. The patient had multiple relapses during 12 months of follow-up and became steroid dependent (i.e., her skin lesions reappeared shortly after steroid treatment ended).

Because initial test reports were inconclusive and the etiologic agent was unconfirmed, we attempted to confirm the etiology by subjecting the patient's skin biopsy sample to metagenomic sequencing; a DNA sequencing protocol without target DNA–enrichment steps (*2*) was needed to unambiguously identify the etiologic agent. From the metagenomics datasets, we reconstructed the near-complete genome of the *M. leprae* species (which we named KFMC-1) at 99.2% completeness when compared with *M. leprae* TN, a strain commonly used for reference (*3*). We assembled the 3.24-Mb genome of *M. leprae* KFMC-1 in 19 DNA segments, and average coverage was 20.02× (Appendix Table 1, Figure 2, panel A). A single-nucleotide polymorphism comparison of *M. leprae* KFMC-1 with a globally representative set of *M. leprae* revealed KFMC-1 was most closely related to 3K1 Ryukyu-2 (Appendix Figure 2, panel B), which was originally isolated in Japan (*4*).

We identified 158 polymorphic sites in the genome (Appendix Table 2), which corresponded to 136 single-nucleotide polymorphisms and 22 insertion/deletions. In total, 53 of the 158 changes were new, and 63 appeared within gene-coding regions, a couple of which helped us predict the multidrug-resistance profile. We identified a G→T nucleotide change, which leads to a nonsynonymous change (Q438H) in the *rpoB* gene (Appendix Figure 2, panel C). This substitution results in rifampin resistance (*5*), matching our clinical records. The C1414A mutation in the *rrs* locus is predicted to confer capreomycin resistance, as observed previously in *M. tuberculosis* (*6*).

After we confirmed the clinical diagnosis as an *M. leprae* infection, we halted moxifloxacin treatment and kept the patient on 3 standard antimicrobial drugs (clofazimine, dapsone, and rifampin). Afterward, the patient left Saudi Arabia and continued her antimicrobial drug course in her country of origin.

The predominant genotypes of *M. leprae* strains in the Middle East are subtypes 2 and 3 (*7*). Most 3K cases are found in countries of East Asia, such as China (*8*), Japan (*9*), Korea (*2*), and the Philippines (*8*). In addition, >37% of the leprosy cases in Saudi Arabia occur in persons from other countries (*1*). Our results suggest that this case of leprosy was imported from the patient's country of origin. Saudi Arabia hosts a massive number of expatriates from all over the world, including persons from *M. leprae*–endemic countries, and also hosts one of the largest recurring religious gatherings in the world. Therefore, genomics-guided infection control efforts are needed to monitor the potential importation and prevent the spread of *M. leprae* infections in the region.

About the Author

Mr. Guan is a graduate student in the Pathogen Genomics Laboratory of King Abdullah University of Science and Technology. His research focuses on the applications of bioin-formatics tools in understanding of pathogens and infectious diseases.

References

1. Alotaibi MH, Bahammam SA, Ur Rahman S, Bahnassy AA, Hassan IS, Alothman AF, et al. The demographic and clinical characteristics of leprosy in Saudi Arabia. J Infect Public Health. 2016;9:611–7. https://doi.org/10.1016/j.jiph.2015.12.015
2. Schuenemann VJ, Avanzi C, Krause-Kyora B, Seitz A, Herbig A, Inskip S, et al. Ancient genomes reveal a high diversity of *Mycobacterium leprae* in medieval Europe. PLoS Pathog. 2018;14:e1006997. https://doi.org/10.1371/journal.ppat.1006997
3. Cole ST, Eiglmeier K, Parkhill J, James KD, Thomson NR, Wheeler PR, et al. Massive gene decay in the leprosy bacillus. Nature. 2001;409:1007–11. https://doi.org/10.1038/35059006
4. Hosokawa A. A clinical and bacteriological examination of *Mycobacterium leprae* in the epidermis and cutaneous appendages of patients with multibacillary leprosy. J Dermatol. 1999;26:479–88. https://doi.org/10.1111/j.1346-8138.1999.tb02032.x
5. Kai M, Nguyen Phuc NH, Nguyen HA, Pham THBD, Nguyen KH, Miyamoto Y, et al. Analysis of drug-resistant strains of *Mycobacterium leprae* in an endemic area of Vietnam. Clin Infect Dis. 2011;52:e127–32. https://doi.org/10.1093/cid/ciq217
6. Suzuki Y, Katsukawa C, Tamaru A, Abe C, Makino M, Mizuguchi Y, et al. Detection of kanamycin-resistant

Mycobacterium tuberculosis by identifying mutations in the 16S rRNA gene. J Clin Microbiol. 1998;36:1220–5.
7. Monot M, Honoré N, Garnier T, Zidane N, Sherafi D, Paniz-Mondolfi A, et al. Comparative genomic and phylogeographic analysis of *Mycobacterium leprae*. Nat Genet. 2009;41:1282–9. https://doi.org/10.1038/ng.477
8. Weng X, Xing Y, Liu J, Wang Y, Ning Y, Li M, et al. Molecular, ethno-spatial epidemiology of leprosy in China: novel insights for tracing leprosy in endemic and non endemic provinces. Infect Genet Evol. 2013;14:361–8. https://doi.org/10.1016/j.meegid.2012.12.009
9. Benjak A, Avanzi C, Singh P, Loiseau C, Girma S, Busso P, et al. Phylogenomics and antimicrobial resistance of the leprosy bacillus *Mycobacterium leprae*. Nat Commun. 2018; 9:352. https://doi.org/10.1038/s41467-017-02576-z

Address for correspondence: Arnab Pain, King Abdullah University of Science and Technology, BESE Division, Thuwal-Jeddah, 239556900, Saudi Arabia; email: arnab.pain@kaust.edu.sa

Three New Cases of Melioidosis, Guadeloupe, French West Indies

Bénédicte Melot, Sylvaine Bastian, Nathalie Dournon, Eric Valade, Olivier Gorgé, Anne Le Fleche, Charlotte Idier, Mireille Vernier, Elisabeth Fernandes, Bruno Hoen, Sébastien Breurec, Michel Carles

Author affiliations: University Hospital of Guadeloupe, Pointe-à-Pitre, France (B. Melot, S. Bastian, N. Dournon, C. Idier, B. Hoen, S. Breurec, M. Carles); Ecole du Val-de-Grâce, Paris, France (E. Valade); Aix Marseille University, Marseille, France (E. Valade, O. Gorgé); Institut Pasteur, Paris (A. Le Fleche); Hospital of Basse-Terre, Basse-Terre, France (M. Vernier, E. Fernandes); Pasteur Institute of Guadeloupe, Pointe-à-Pitre (S. Breurec); University of the French West Indies and French Guiana, Pointe-à-Pitre (B. Hoen, S. Breurec, M. Carles)

DOI: https://doi.org/10.3201/eid2603.190718

Melioidosis has been detected in the Caribbean, and an increasing number of cases has been reported in the past few decades, but only 2 cases were reported in Guadeloupe during the past 20 years. We describe 3 more cases that occurred during 2016–2017 and examine arguments for increasing endemicity.

Melioidosis, caused by the telluric gram-negative rod *Burkholderia pseudomallei*, is endemic in Southeast Asia and northern Australia (*1*) but may be underdiagnosed in other tropical regions (*2*). Increasing occurrences have been reported in the Caribbean during the past few decades among persons with no exposure to known endemic areas (*3*–*5*). Tropical environmental conditions and the presence of this bacterium in soil samples in the Caribbean support the plausibility of endemicity (*3*). We describe 3 new cases detected in Guadeloupe during 2016–2017.

Patient 1 was a 54-year-old man, receiving renal replacement therapy, with a history of hypertensive vascular nephropathy. He developed a pulmonary form of melioidosis in November 2016. Thoracoabdominal computed tomography (CT) scan showed bilateral nodular lesions. *B. pseudomallei* grew from bronchoalveolar lavage fluid obtained by fiberoptic bronchoscopy. Treatment with ceftazidime (6 g/d intravenously) was given for 2 weeks and switched to trimethoprim/sulfamethoxazole (TMP/SMX) (320/1,600 mg 2×/d orally) for 1 month, then changed to doxycycline because rash developed. The patient complied poorly with treatment; he died in March 2017 under unknown circumstances.

Patient 2 was a 66-year-old woman with a history of arterial hypertension and diabetes mellitus, a subcutaneous abscess in the prepubic area surgically treated without microbiological identification (June 2016), a lumbar hematoma (March 2017), and bacteremic obstructive pyelonephritis caused by *Escherichia coli* (April 2017). In April 2017, she developed a severe and disseminated form of melioidosis with pneumonia, bacteremia, and deep abscess. CT scan showed multiple pulmonary nodes consistent with hematogenous pneumonia, a deep abscess between kidney and psoas, and splenic emboli. *B. pseudomallei* was isolated from blood cultures performed at admission and from the abscess. The patient developed multiple complications: acute respiratory distress syndrome, systemic candidiasis, renal failure, hemodynamic failure, nonspecific encephalopathy, refractory septic shock related to catheter infection, and bacteremia caused by extended spectrum β-lactamase *Klebsiella pneumoniae*. In the intensive care unit, she was treated with ceftazidime (6 g/d for 24 d), then with meropenem (1 g 3×/d) plus TMP/SMX (320/1,600 mg 2×/d). Blood cultures grew *B. pseudomallei* until day 40. The patient died on day 60 from multiple organ failure.

Patient 3 was a 52-year-old man with a history of chronic alcoholism. He developed pneumonia in April 2017. Thoracic tomography showed an excavated condensation of the right middle lobe, right