

Despite temporary suspension of all flights to or from Brazil from or through the United Kingdom as of December 25, 2020 (<http://www.gov.uk/foreign-travel-advice/brazil>), it is likely that the number of SARS-CoV-2 lineage B.1.1.7 infections in Brazil is higher than that reported. Increasing genomic surveillance of B.1.1.7 and other variants of concern that carry mutations of potential biological significance (e.g., E484K in the spike protein; C.M. Voloch, unpub data, <https://www.medrxiv.org/content/10.1101/2020.12.23.20248598v1>) is imperative for monitoring vaccination effectiveness and contextualizing the epidemiology and evolution of SARS-CoV-2 in Latin America.

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## ***Mycobacterium bovis* Pulmonary Tuberculosis, Algeria**

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We analyzed 98 *Mycobacterium tuberculosis* complex isolates collected in 2 regions of Algeria in 2015–2018 from 93 cases of pulmonary tuberculosis. We identified 93/98 isolates as *M. tuberculosis* lineage 4 and 1 isolate as *M. tuberculosis* lineage 2 (Beijing). We confirmed 4 isolates as *M. bovis* by whole-genome sequencing.

**I**n Algeria, interpreting tuberculosis (TB) incidence, estimated at 53–88 cases/100,000 population in 2017 (1), is limited by the fact that the diagnosis relies on microscopic examination of clinical samples. Iso-

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lates are presumptively identified as *Mycobacterium tuberculosis* complex based on colony phenotype.

We analyzed 98 sputum isolates identified as *M. tuberculosis* complex by 5 Tuberculosis and Respiratory Disease Control Service facilities in 2015–2018 (Appendix Table 1, Figure, <https://wwwnc.cdc.gov/EID/article/27/3/19-1823-App1.pdf>). Exact tandem repeat D analysis (2) confirmed these 98 isolates as *M. tuberculosis* complex. Large-sequence polymorphism analysis using PCR sequencing of genomic regions RD105, RD239, and RD750 and of the polyketide synthase gene *pks15/1* (3) yielded 88 (89.8%) *M. tuberculosis* sensu stricto Euro-American lineage 4 isolates and 1 East Asian lineage 2 (Beijing) isolate. Whole-genome sequencing (WGS) of 5 RD deletion-free unidentified isolates indicated that these 5 isolates, P9982(ERR3588223), P9983(ERR3588225), P9985(ERR3588243), P9984(ERR3588246), and P9986(ERR3588247), were *M. tuberculosis* sensu stricto Euro-American lineage 4. We conducted WGS analysis using TB-profiler for *M. tuberculosis* online tool (<https://tbd.r.lsh.mt.ac.uk/upload>) for lineage and sublineage determination. Altogether, *M. tuberculosis* lineage 4 was the predominant lineage in the 5 Algerian departments and the sole lineage documented in Bgayet, Tizi-Ouzou, and Medea (Appendix Table 2); it was found to be the cause of pulmonary TB in 79/93 (85%) cases, pleural TB in 11 (12%) cases, and lymph node TB in 3 (3%) cases. These observations updated those issued from a previous study conducted in 14 departments including 114 (88%) cases of pulmonary localization and 15 cases (12%) of extrapulmonary localization (4). In a later study, spoligotyping revealed that most isolates be-

longed to *M. tuberculosis* Euro-American lineage 4; the Haarlem clade accounted for 29.5% of studied isolates; the Latin American-Mediterranean clade, 25.6%; and the T clade, 24.8% (4). In our study, 1 *M. tuberculosis* Beijing strain was isolated from a bronchial fluid sample collected in Blida from the location at which 15 *M. tuberculosis* Beijing isolates had been identified  $\approx$ 10 years earlier from 14 workers from Algeria and 1 from China (5). Our observation suggests that 10-year circulation of *M. tuberculosis* Beijing strain in the community in Blida area most probably followed immigration of workers from China employed in the construction sector.

WGS analysis of 4 additional isolates exhibiting a 6-bp deletion in the *pks15/1* gene identified them as *M. bovis*. Using a Roary pangenome pipeline (<https://sanger-pathogens.github.io/Roary>), we found that *M. bovis* CSURP9981 grouped with *M. bovis* CSURP9979 and that *M. bovis* CSURP9980 grouped with *M. bovis* CSURP9978 (Figure). Further analysis based on the 3,732,808-bp core genome detected 3,761-bp (0.1%) of single-nucleotide polymorphisms (SNPs) between the 4 isolate genomes. Whole-genome sequences of *M. bovis* strains in the study have been deposited in GenBank (sequence P9978, accession no. ERR3587501; P9979, no. ERR3587591; P9980, no. ERR3587597; and P9981, no. ERR3588222).

All 4 patients had pulmonary TB and had no detectable lymph node swelling and no scrofula (6). Two case-patients in Blida were a 27-year-old unemployed man and a 60-year-old taxi driver who both declared that they did not consume raw milk and had no contacts with cattle; a neighbor of the 60-year-old patient was a butcher with whom he



**Figure.** Pangenome-based tree of 4 human *Mycobacterium bovis* isolates, Algeria. The tree was generated by Roary (<https://sanger-pathogens.github.io/Roary>) from binary gene presence or absence in the accessory genome. Scale bar indicates 10% sequence divergence.

spent a lot of time. Two case-patients in Ain Defla were 18-year-old and 43-year-old housewives living in 2 different rural areas. The interviews of these patients did not reveal contacts with cattle. Identification of human cases of *M. bovis* was unexpected because in 50 years, only 7 cases of *M. bovis* human infection have been reported in Algeria: 3 cases of pulmonary TB and 2 cases of cervical lymphatic TB detected in a total of 1,183 (0.4%) phenotypically identified *M. bovis* isolates (7), and 2 additional cases reported in 2009 (8).

*M. bovis* TB is clinically, pathologically, and radiologically indistinguishable from *M. tuberculosis*; diagnosis requires accurate identification of the causative mycobacterium, most efficiently by using WGS. Our report illustrates pitfalls in precisely tracing the natural history of *M. bovis* TB in patients, including sources, routes of transmission, and primary route of entry, which may determine the pathology of the infection. Zoonotic *M. bovis* TB was most often transmitted to humans by the consumption of *M. bovis*-contaminated dairy products that caused lymphatic TB, eventually becoming pulmonary TB (9). We previously reported a hidden circumstance for contacts with *M. bovis*-infected animals, tracing 1 *M. bovis* pulmonary TB case in a patient in Tunisia to contacts with an infected sheep during religious festivities in 2018 (10). In the case we report here, foodborne transmission cannot be ruled out, but it is possible that this may be a rare case of aerosol transmission.

Algeria is a bovine TB–enzootic country. We recommend comparing the genome sequences from the 4 patients reported here with those of future bovine isolates in the same departments to trace zoonotic *M. bovis* TB in Algeria and contribute to the understanding of its natural history.

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