To the Editor: Virk et al. (1) reported a *Mycobacterium lepromatosis* infection in a US citizen with a history of multiple international travels and concluded that *M. lepromatosis* lepromatous leprosy is a travel-related hazard for travelers to endemic areas. The conclusions drawn, however, need extensive support of thoroughly conducted case studies before generalizing *M. lepromatosis* as a travel-related hazard.

In the case report, the exact source of *M. lepromatosis* infection was unclear. Moreover, experimental evidence used in this work are not enough to prove that *M. lepromatosis* is a travel-related hazard. Confirming a source of infection by DNA fingerprinting of *M. lepromatosis* can be ideal to rule out infection from unreported native patients or environmental reservoirs (2).

It is possible that the patient in this report may have contracted *M. lepromatosis* infection as a result of his host-susceptible genetic factors. Host genetic susceptibility to leprosy is complicated because of the genetics of *M. lepromatosis*, interaction between genetic and environmental factors, gene–gene interactions, and ethnicity (3). Host genetics plays a major role in determining a person’s risk of developing clinical leprosy. Thus, even a short trip to a leprosy-endemic country is sufficient for a host susceptible to *M. lepromatosis* to acquire an infection. The host