SARS-CoV-2 Superspread in Fitness Center, Hong Kong, China, March 2021

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To the Editors: I read with interest the article by Chu et al. (*1*), which concluded that poor ventilation might have contributed to a severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) superspreading event at a fitness center in Hong Kong, China. As an example of SARS-CoV-2 not spreading in a converse environment, I report the absence of apparent transmission at a gym in Montgomery County, Virginia, USA, that emphasized ventilation as part of its coronavirus disease (COVID-19) precautions upon reopening in June 2020. The gym (Appendix Figure 1, https://wwwnc.cdc.gov/EID/article/27/9/21-1177-App1.pdf) increased ventilation by opening 10 exterior doors and keeping them open even during cold or inclement weather. The gym also limited class sizes, stressed hygiene, and required ≥10 feet of distancing. Masks were not worn.

With the doors closed, the air change rate was estimated to be 0.07 air changes/hour, corresponding to a ventilation rate of 7.6 L/second/person (L/s/p) on the basis of an occupancy of 10 persons, below the 10 L/s/p minimum recommended by ASHRAE (American Society of Heating and Air-Conditioning Engineers) for health clubs (*2*). With the doors open, these values were estimated to be 2.4 air changes/hour and 240 L/s/p (Appendix).

On September 24, 2020, an instructor at the gym developed upper respiratory symptoms and lost his sense of smell and taste. He was tested for SARS-CoV-2 infection and received a positive result on September 28, 2020. That day, the gym owner contacted 50 persons who had attended ≥1 of the instructor's classes during September 21–25, 2020 to notify them of potential exposure. During subsequent follow-up, none of these 50 persons reported any COVID-19 symptoms, and 5 people who got tested received negative results (Appendix Figure 2). It is likely that increasing ventilation greatly mitigated the risk of transmission (*3*). Subsequently, the gym acquired a CO_2 sensor and kept the CO_2 level, an indicator of respiratory emissions, well below 600 ppm (*4*) by adjusting the number of open doors.

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Fecal Excretion of *Mycobacterium leprae*, Burkina Faso

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To the Editor: Millogo et al. (*1*) documented presence of *Mycobacterium leprae* in a fecal sample from a patient in Burkina Faso, raising questions about the role of fecal excretion of *M. leprae* in the natural history and diagnosis of leprosy. They speculated that *M. leprae* were swallowed by the patient along with blood

or upper respiratory secretions during leprosy rhinitis and epistaxis (*1*) but failed to address other factors that could influence fecal excretion of *M. leprae* and utility of fecal specimens in diagnosing leprosy.

Previous studies have demonstrated the presence of *M. leprae* in water and soil samples from habitations of patients with leprosy (*2*,*3*). This finding means that patients, contacts, or healthy persons can ingest *M. leprae* from environmental sources through drinking contaminated water or eating *M. leprae*–containing food and may excrete leprosy bacilli in their feces without establishing an infection. The role of environmental sources and simple pass-through phenomena in fecal excretion of *M. leprae* has not been investigated by Millogo et al. (*1*) and other studies (*4*,*5*).

Koshy et al. (*4*) reported the presence of leprosy bacilli in gastric juice of 9 of 16 patients with lepromatous leprosy; 3 were found to excrete the bacilli in their feces. Manzullo et al. (*5*) demonstrated the presence of acid-fast bacilli in biliary secretions of 7 of 20 patients with leprosy and in 2 of 7 fecal samples. These observations indicate that clinical manifestation of leprosy varies widely. The exact mechanism of fecal excretion of *M. leprae* can be more complex, as presumed in previous studies (*1*,*4*,*5*), and may be associated with high bacillary burden (as in lepromatous leprosy), gastrointestinal symptoms (abdominal pain or diarrhea), disseminated disease, environmental factors, or combinations of these aspects. Verification of transmission routes of *M. leprae* to fecal samples using genotyping techniques (i.e., whole-genome sequencing) is crucial to establish the diagnostic utility of fecal specimens in leprosy.

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CORRECTION

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The rate of pregnancy-related invasive group B *Streptococcus* episodes was misstated in Invasive Group B *Streptococcus* Infections in Adults, England, 2015–2016 (S.M. Collins et al.). The correct rate is 4.09/10,000 live births. The article has been corrected online (https://wwwnc.cdc.gov/eid/article/26/6/19-1141_article).