

nos. EPI_ISL_632934 and EPI_ISL_632935. Sequence alignment analyses (4) revealed that the 2 SARS-CoV-2 sequences from Ruili shared 13 mutations: C241T, C3037T, G11083T, C14408T, G18756T, C18877T, C22444T, A23403G, G25494T, G25563T, C26735T, C28854T, and G29737C (Appendix Figure 2) (5,6). According to the Pangolin COVID-19 Lineage Assigner (7), 9 of these mutations (i.e., C241T, C3037T, C14408T, C18877T, C22444T, A23403G, G25563T, C26735T, and C28854T) indicate membership in the B.1.36 clade of SARS-CoV-2. Further phylogenetic analyses supported this conclusion (Appendix Table 2, Figure 3). Compared with sequences from earlier COVID-19 outbreaks in Beijing Xinfadi Market (1,8), Dalian (9), and Qingdao, the Ruili sequences had 7 previously unreported mutations (Appendix Figure 2, panel B) (5). The Ruili cases were not associated with the mentioned outbreaks and were probably imported.

Although the SARS-CoV-2-infected migrants did not cause a COVID-19 outbreak, the event illustrates a transmission pathway distinct from air travel and cold-chain food transmission (1). The International Health Regulations and World Health Organization encourage open borders and suggest that COVID-19 control measures be applied only in limited circumstances (10). In 2020, official land ports in Yunnan Province did not close for the COVID-19 pandemic. Because of the long international border, epidemic control remains challenging in this province. Governments should control illegal immigration to avoid future reintroductions of COVID-19. Regional guidelines for COVID-19 control and prevention should strengthen surveillance of undocumented movement across borders, especially from neighboring countries with high rates of infection.

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The order of the authors was incorrect for Drug-Resistant Tuberculosis in Pet Ring-Tailed Lemur, Madagascar (M. LaFleur et al.). The article has been corrected online (https://wwwnc.cdc.gov/eid/article/27/3/20-2924_article).