rabies-endemic countries, physicians should emphasize the high likelihood of transmission of rabies virus after mucosal exposure and try to persuade persons at risk to receive postexposure prophylaxis.

About the Author
Dr. Zhao is a chief clinician specializing in the diagnosis and treatment of infectious diseases at the Department of Infectious Diseases, Second Hospital of Nanjing. Her research interests include viral hepatitis and other viral diseases.

References

Address for correspondence: Yi-Hua Zhou, Nanjing Drum Tower Hospital, Departments of Laboratory Medicine and Infectious Diseases, 321 Zhongshan Rd, Nanjing 210008, China; email: zgr03summer@126.com

Endemic Severe Fever with Thrombocytopenia Syndrome, Vietnam

Xuan Chuong Tran, Yeojun Yun, Le Van An, So-Hee Kim, Nguyen T. Phuong Thao, Phan Kim C. Man, Jeong Rae Yoo, Sang Taek Heo, Nam-Hyuk Cho, Keun Hwa Lee

Author affiliations: The Hue University Hospital and Hue University of Medicine and Pharmacy, Hue, Vietnam (X.C. Tran, L.V. An, N.T.P. Thao, P.K.C. Man); Ewha Womans University, Seoul, South Korea (Y. Yun); The Kyung Hee University, Seoul (S.-H. Kim); The Jeju National University College of Medicine, Jeju, South Korea (J.R. Yoo, S.T. Heo, K.H. Lee); Seoul National University College of Medicine, Seoul (N.-H. Cho)

DOI: https://doi.org/10.3201/eid2505.181463

Severe fever with thrombocytopenia syndrome (SFTS), a tickborne viral disease, has been identified in China, South Korea, and Japan since 2009. We found retrospective evidence of SFTS virus (SFTSV) infection in Vietnam, which suggests that SFTSV infections also occur in Vietnam, where the virus has not been known to be endemic.

Severe fever with thrombocytopenia syndrome virus (SFTSV) is a tickborne virus (genus Phlebovirus, family Phenuiviridae) that can cause a mild to severe febrile illness similar to hemorrhagic fever (1). Phleboviruses have been found in the Americas, Asia, Africa, and the Mediterranean region. For example, Heartland virus (HRTV), another tickborne phlebovirus, was identified in northwestern Missouri, USA, in 2009 (2). Malsoor virus, a new bat phlebovirus closely related to SFTSV and HRTV, was identified in western India, and a phlebovirus similar to SFTSV and HRTV was isolated from ticks in Australia (3,4).

Severe fever with thrombocytopenia syndrome (SFTS) illness was first confirmed in China in 2009. It was retrospectively identified in South Korea in 2010 and the western regions of Japan in 2013 (1,5,6). SFTS is characterized by acute high fever, thrombocytopenia, leukopenia, elevated serum hepatic enzymes, gastrointestinal symptoms, and multiorgan failure and has a death rate of 16.2%–30% (1,6,7). Atypical signs and symptoms and asymptomatic infections also have been identified (5,8). Most SFTSV infections occur through Haemaphysalis longicornis ticks, although SFTSV transmission can also occur through close contact with an infected patient (8).

To investigate evidence of SFTSV infections in Vietnam, we collected serum samples from 80 patients with acute febrile illnesses admitted to Hue University Hospital (Hue, Vietnam)
We confirmed 2 SFTSV infections in Hue in 2017 by amplifying the partial S segment of the viral RNA in stored serum from patients with thrombocytopenia; elevated levels of serum hepatic enzymes, including aspartate aminotransferase and alanine aminotransferase; and gastrointestinal symptoms, such as vomiting. The signs and symptoms were milder than the major signs and symptoms of SFTS, which has a high death rate.

H. longicornis, Amblyomma testudinarium, and Ixodes nipponensis ticks are vectors of SFTSV, and A. testudinarium has been found in Vietnam. Migratory birds are known to be long-distance carriers of virus-bearing ticks (10). Therefore, virus-bearing A. testudinarium ticks and migratory birds may play a role in dispersing SFTSV to Vietnam (10).

This study expands the understanding of the distribution of SFTSV in Southeast Asia and suggests that SFTSV may have a much wider global distribution than previously thought. The 2 patients reported here had relatively mild illness, and I did not have leukopenia. Therefore, further epidemiologic and clinical research is needed to clarify the epidemiology, geographic distribution, and transmission dynamics of SFTSV in Vietnam and other areas of Southeast Asia. This subject deserves further discussion and might warrant changes in the background description of the disease (5,8).

Acknowledgments
We thank L. Bøkkensen for providing comments on this paper.

This work was supported by the Bio & Medical Technology Development Program of the National Research Foundation (NRF), funded by the South Korean government (grant no. NRF-2016M3A9B6021161), and a grant from the Korean Health Technology R&D Project of the Ministry of Health and Welfare, South Korea (grant no. HI15C2891).

About the Author
Dr. Tran is a professor at the Department of Infectious Diseases, Hue University Hospital and Hue University of Medicine and Pharmacy, Hue, Vietnam. His research interest is infectious diseases.

References
Mixed Mycobacterium tuberculosis Lineage Infection in 2 Elephants, Nepal

Sarad Paudel, Chie Nakajima, Susan K. Mikota, Kamal P. Gairhe, Bhagwan Maharjan, Suraj Subedi, Ajay Poudel, Mariko Sashika, Michito ShIMOzuru, Yasuhiko Suzuki, Toshio Tsubota

Author affiliations: Hokkaido University, Sapporo, Japan (S. Paudel, C. Nakajima, M. Sashika, M. ShIMOzuru, Y. Suzuki, T. Tsubota); Elephant Care International, Hohenwald, Tennessee, USA (S.K. Mikota); Department of National Parks and Wildlife Conservation, Kathmandu, Nepal (K.P. Gairhe); German Nepal Tuberculosis Project, Kathmandu (B. Maharjan); National Trust for Nature Conservation, Lalitpur, Nepal (S. Subedi); Chitwan Medical College, Chitwan, Nepal (A. Poudel)

DOI: https://doi.org/10.3201/eid2505.181898

These first authors contributed equally to this article.

Tuberculosis in elephants is primarily caused by Mycobacterium tuberculosis. We identified mixed M. tuberculosis lineage infection in 2 captive elephants in Nepal by using spoligotyping and large sequence polymorphism. One elephant was infected with Indo-Oceanic and East African–Indian (CAS-Delhi) lineages; the other was infected with Indo-Oceanic and East Asian (Beijing) lineages.

M. tuberculosis is a primary cause of tuberculosis (TB) in elephants (1). Culture of trunk wash samples is regarded as the standard method for the diagnosis of TB in elephants; however, this method has many limitations (2). We previously reported TB in 3 elephants in Nepal that was caused by M. tuberculosis of Indo-Oceanic lineage (3). Here, we report on mixed M. tuberculosis lineage infection in 2 captive elephants from Chitwan National Park (CNP) in Nepal.

Elephant A was a female elephant ≈65–70 years old. She had been in retirement for 3 years before she died in February 2013. We observed TB-like lesions in the lungs postmortem (Appendix Figure 1, https://wwwnc.cdc.gov/EID/article/25/5/18-1898-App1.pdf). Elephant B was a 32-year-old male. His body condition had substantially deteriorated for several months before he died. We found extensive TB-like lesions in the lungs at postmortem.

We performed the DPP VetTB Assay (Chembio Inc., http://chembio.com), a serologic test, on the postmortem wash samples is regarded as the standard method for the diagnosis of TB in elephants; however, this method has many limitations (2). We previously reported TB in 3 elephants in Nepal that was caused by M. tuberculosis of Indo-Oceanic lineage (3). Here, we report on mixed M. tuberculosis lineage infection in 2 captive elephants from Chitwan National Park (CNP) in Nepal.

We performed genetic analyses on the 2 M. tuberculosis isolates by using spoligotyping and large-sequence polymorphism (LSP) as described previously (5). We amplified the direct-repeat region with a primer pair and hybridized the PCR products to a set of 43 oligonucleotide probes corresponding to each spacer covalently bound to the membrane. We identified the spoligo-international type by comparing spoligotypes with the international spoligotyping database (SpolDB4) (6). We performed LSP on the isolates by using specific primers for respective lineages, as described previously (7).

We identified the elephant isolates as a mixture of 2 strains based on uneven spoligotyping color development (suggesting mixture) and LSP detection PCR results (2 bands were observed). The spoligotyping results showed that the elephant A isolate had a new spoligotype that was not found in the international spoligotyping database. The elephant B isolate belonged to the Indo-Oceanic (East African–Indian 5 spoligo-international type 1365) lineage. The prevalence of the Indo-Oceanic lineage among human TB patients in Nepal is only 11.5% (8). The drug


Address for correspondence: Keun Hwa Lee, Jeju National University College of Medicine, Department of Microbiology and Immunology, 15, Aran 13-gil, Jeju 63241, South Korea; email: yomust7@jejunu.ac.kr