Surveillance for Ebola Virus in Wildlife, Thailand


Author affiliations: King Chulalongkorn Memorial Hospital and Faculty of Medicine, Chulalongkorn University, Bangkok, Thailand (S. Wacharapluesadee, N. Sittidetboripat, T. Kaewpom, S. Petcharat, S. Yingsakmongkon, T. Hemachudha); EcoHealth Alliance, New York, New York, USA (K.J. Olival); Department of National Parks, Bangkok (B. Kanchanasaka, S. Kaewchot, P. Srongmongkol, G. Ieamsaard, P. Maneenorn); Kasetsart University Faculty of Forestry, Bangkok (P. Duengkae); Centers for Disease Control and Prevention, Atlanta, Georgia, USA (P.E. Rollin, J.S. Towner)

DOI: http://dx.doi.org/10.3201/eid2112.150860

To the Editor: Active surveillance for zoonotic pathogens in wildlife is particularly critical when the pathogen has the potential to cause a large-scale outbreak. The recent outbreak of Ebola virus (EBOV) disease in West Africa in 2014 was initiated by a single spillover event, followed by human-to-human transmission (1). Projection of filovirus ecologic niches suggests possible areas of distribution in Southeast Asia (2). Reston virus was discovered in macaques exported from the Philippines to the United States in 1989 and in sick domestic pigs in the Philippines in 2008 (with asymptomatic infection in humans) (3). Dead insectivorous bats in Europe were found to be infected by a filovirus, similar to other members of the genus Ebola virus (4).

Although EBOV has historically been viewed as a virus from Africa, recent studies found that bat populations in Bangladesh and China contain antibodies against EBOV and Reston virus recombinant proteins, which suggests that EBOV is widely distributed throughout Asia (5,6). Thus, an outbreak in Asian countries free of EBOV diseases may not only be caused by importation of infected humans and/or wildlife from Africa but may arise from in-country filovirus–infected wildlife. Serologic and molecular evidence for filoviruses suggests that members of the order Chiroptera (bats) may be their natural reservoir (7).

As part of a proactive biosurveillance program, we conducted a cross-sectional study for EBOV infection in bats and macaques in Thailand. We screened 500 Pteropus lylei bats collected from 10 roosting sites during March–June 2014 (online Technical Appendix, http://wwwnc.cdc.gov/EID/article/20/12/15-0860-Techapp1.pdf) for antibodies against EBOV antigen by using an ELISA validated by the Centers for Disease Control and Prevention (Atlanta, GA, USA) (8).

Bats and macaques were captured with permission from the Department of National Parks, Wildlife and Plant Conservation. The Institutional Animal Care and Use Committee at the University of California, Davis (protocol #16048) approved the capture and sample collection protocols.

To further screen a wide range of wildlife species in Thailand for active EBOV infection, we sampled and tested 699 healthy bats, representing 26 species, and 50 long-tailed macaques (Macaca fascicularis). Additional bat species were randomly captured (≥50/site) in 6 provinces in Thailand during 2011–2013 and identified by morphologic traits. Macaques were captured and sampled in March 2013 from 1 site at Khao Chakan, Sa Kaeo Province, and released at the same site. Blood, saliva, urine, and feces were collected from anesthetized macaques or nonanesthetized bats. All animals were released after sample collection. Details on species screened, sample sizes, and trapping localities are provided in the Table.

All nonblood specimens were collected in nucleic acid extraction buffer (lysis buffer) and transported on ice to the World Health Organization Collaborating Centre for Research and Training on Viral Zoonoses laboratory (Bangkok, Thailand) for storage and testing. Three types of specimen (saliva, urine, and serum) were collected from individual animals and pooled.

Nucleic acid was then extracted with NuCliSENS easyMAG (bioMérieux, Boxtel, the Netherlands) and analyzed by reverse transcription PCR (RT-PCR). A consensus RT-PCR was used to screen for all known species of Ebola virus and Marburg virus, including EBOV (9). In total, 5 RT-PCRs were performed on each specimen, a regimen that included 4 sets of primers specific to known filoviruses and 1 degenerate primer set to detect novel viruses in this family. The sensitivity of RT-PCR on synthetic standard was 50–500 copies/reaction (9). We ran 3,745 PCRs, covering a range of assays, to increase detection sensitivity. All specimens examined were negative for filoviruses by EBOV ELISA and PCR (Table). For P lylei ELISA screening, optical density values for all 500 bats ranged from 0.000 to 0.095, well below the potential positive cutoff value of 0.2.

Assuming a population size of ≥5,000 bats/roost and a sample size of 50 bats/site, we have 95% confidence that...
if >6% of the population had antibodies against EBOV antigen, we would have detected it. If we assume that all 500 animals are part of 1 large panmictic population, and we have 95% confidence that if EBOV were circulating in >0.5% of the population, we would have detected it. There we have 95% confidence that if EBOV were circulating in >6% of the population had antibodies against EBOV antigen, we would have detected it. Therefore, although we cannot rule out infection of this species with 100% confidence, P. lylei bats, the most abundant species of large pteropid bats in Thailand, are highly unlikely to be reservoirs for EBOV.

Our sample sizes for PCR screening of other bat species in this study were much smaller, and we had no supported serologic data, but these negative results could add to the knowledge of filovirus infection in nontissue specimens from healthy bats. Previous studies have detected Ebola virus--like filovirus RNA in lung tissue of healthy Rousettus leschenaultia bats in China (10) and from organs and throat and rectal swab specimens from a die-off of Miniopterus schreibersii bats in Spain (4). In our study, which included 22 M. schreibersii and 132 M. magnate bats, none of the bats tested positive for filoviruses. One limitation of the cross-sectional sampling strategy used here, however, is that PCR-negative findings do not necessarily mean that the bats were not infected in the past. Although we found no evidence of filovirus infection in wildlife species tested in Thailand, we believe that continuing targeted surveillance in wildlife should enable early detection and preparedness to preempt emerging zoonoses.

This study was supported by a research grant from Department of National Parks, Wildlife and Plant Conservation, the Thailand Research Fund (RDG420089), the Ratchadaphiseksomphot Endowment Fund of Chulalongkorn University (RES560530148-HR), Health and Biomedical Science Research Program by National Research Council of Thailand and Health System Research Institute, the Research Chair Grant, the National Science and Technology Development Agency, Thailand, and the Naval Health Research Center (BAA-10-93) under the Cooperative Agreement no. W911NF-11-2-0041, and the United States Agency for International Development Emerging Pandemic Threats PREDICT project.

References

Address for correspondence: Supaporn Wacharapluesadee, World Health Organization Collaborating Centre for Research and Training on Viral Zoonoses, King Chulalongkorn Memorial Hospital, Faculty of Medicine, Chulalongkorn University, Bangkok 10330, Thailand; email: spwa@hotmail.com

Probability of Spirochete Borrelia miyamotoi Transmission from Ticks to Humans

Denis S. Sarksyan, Alexander E. Platonov, Lyudmila S. Karan, German A. Shipulin, Hein Spong, Joppe W.R. Hovius

Author affiliations: Izhevsk State Medical Academy, Izhevsk, Russia (D.S. Sarksyan); Central Research Institute of Epidemiology, Moscow, Russia (A.E. Platonov, L.S. Karan, G.A. Shipulin); National Institute of Public Health and the Environment, Bilthoven, the Netherlands (H. Spong); Academic Medical Center, Amsterdam, the Netherlands (J.W.R. Hovius)

DOI: http://dx.doi.org/10.3201/eid2112.151097

To the Editor: Borreliosis caused by Borrelia miyamotoi is an emerging disease transmitted by Ixodes ticks (1). Each year in the Netherlands during 2007–2009, ≈70,000 bites by hard ticks occurred per 1 million inhabitants (2). In the Republic of Udmurtia, Russia, ≈10,000 hard tick bites per 1 million inhabitants are reported annually among persons seeking medical help. Recent studies indicate that almost 3% of I. ricinus ticks in the Netherlands and 2%–6% of I. persulcatus ticks in Russia are infected with B. miyamotoi (1,3,4). Human exposure is substantial, and comparable exposure to B. miyamotoi is expected in many Eurasian countries and in North America (4,5). The probability of B. miyamotoi transmission from ticks to humans requires examination to estimate the true risk for human disease.

In Izhevsk (population 650,000), a city in European Russia (Republic of Udmurtia), we identified 95 human cases of B. miyamotoi infection during 2010–2014 (6). In this city, primarily because of concern about tickborne encephalitis (TBE), all patients with suspected tickborne infection are hospitalized in the Republican Hospital of Infectious Diseases (RHID). A service also enables tick-bitten persons to bring the removed tick for PCR for TBE virus (TBEV) and B. burgdorferi sensu lato. We supplemented that with PCR testing for B. miyamotoi (3).

In June 2014, twenty-four persons (~5% of those bitten by ticks subjected to PCR-based investigation for TBEV, B. burgdorferi sensu lato, and B. miyamotoi) were bitten by adult I. persulcatus ticks infected with B. miyamotoi only. We informed these persons of their results and about the clinical features of B. miyamotoi infection and recommended self-observation during 2 months (twice the maximum incubation period for B. miyamotoi infection [3,6]). These persons were advised to contact their medical supervisor at RHID (D.S. Sarksyan) if fever, fatigue, erythema migrans, or any other possible symptom of a tickborne infection developed. In 2 patients, such symptoms developed: one 12 days (patient 1), the other 16 days (patient 2), after the tick bite. B. miyamotoi DNA was detected by PCR in their blood on admission to RHID. Neither IgM nor IgG were found by a nonspecific ELISA (Omnix, St. Petersburg, Russia [7]) that reacts with serum from B. burgdorferi infected persons to bring the removed tick for PCR for TBE virus (TBEV) and B. burgdorferi sensu lato. We supplemented that with PCR testing for B. miyamotoi (3).
Surveillance for Ebola Virus in Wildlife, Thailand

Technical Appendix

Technical Appendix Figure. Map showing 20 Pteropus lylei bat roosting sites (gray circles, update 2015) in Thailand from 10 years of population surveys by the Department of National Parks, Wildlife and Plant Conservation and Kasetsart University, Thailand. These bats form large, colonial aggregations of individual animals, which often roost near human dwellings and primarily in the central region of the country. The map
shows that populations of this species are concentrated in Central Thailand. Ten sampling sites (black star) included in the current study, March–June 2014, were selected on the basis of the size of the bat population, >2,000 bats/colony (50 individual bats sampled/locality). Abbreviations indicate provinces where *P. lylei* bats were found: AT, Ang Thong; AY, Phra Nakhon Si Ayutthaya; BK, Bangkok; CH, Chonburi; CHS, Chachoengsao; NY, Nakhon Nayok; PBR, Prachinburi; SAK, Srakaeo; SB, Saraburi; SH, Singburi; SMR, Samut Sakhon; SP, Suphan Buri.