

Acknowledgments

We thank Brad Biggerstaff and Becky Eisen for statistical analyses used in this study. S.E.K. was supported by The Oak Ridge Institute for Science and Education.

**Cherilyn Sackal,
Anne Laudisoit, Michael Kosoy,
Robert Massung,
Marina E. Ereemeeva,
Sandor E. Karpathy,
Kristen Van Wyk,
Elizabeth Gabitzsch,
and Nordin S. Zeidner**

Author affiliations: Centers for Disease Control and Prevention, Fort Collins, Colorado, USA (C. Sackal, M. Kosoy, K. Van Wyk, N. Zeidner); University of Antwerp, Antwerp, Belgium (A. Laudisoit); University of Liege, Liege, Belgium (A. Laudisoit); Centers for Disease Control and Prevention, Atlanta, Georgia, USA (R. Massung, M.E. Ereemeeva, S.E. Karpathy); and Etubics Corporation, Seattle, Washington, USA (E. Gabitzsch)

DOI: 10.3201/eid1412.080610

References

1. Parola P, Davoust B, Raoult D. Tick and flea-borne rickettsial emerging zoonoses. *Vet Res.* 2005;36:469–92. DOI: 10.1051/vetres:2005004
2. Perez-Osorio CE, Zavala-Velazquez JE, Leon JJ, Zavala-Castro J. *Rickettsia felis* as emergent global threat for humans. *Emerg Infect Dis.* 2008;14:1019–22. DOI: 10.3201/eid1407.071656
3. Schmidt A., editor. *Contributions to microbiology.* Basel (Switzerland): Karger; 1998.
4. Koehler JE. *Bartonella* infections. *Adv Pediatr Infect Dis.* 1996;11:1–27.
5. Schwartzman W. *Bartonella (Rochalimaea)* infections: beyond cat scratch. *Annu Rev Med.* 1996;47:355–64. DOI: 10.1146/annurev.med.47.1.355
6. Chanteau S, Rahalison L, Ralafiarisoa L, Foulon J, Ratsitorahina M, Ratsifasoamana L, et al. Development and testing of a rapid diagnostic test for bubonic and pneumonic plague. *Lancet.* 2003;361:211–6. DOI: 10.1016/S0140-6736(03)12270-2
7. Laudisoit A, Leirs H, Makundi RH, Van Dongen S, Davis S, Neerinckx S, et al. Plague and the human flea, Tanzania. *Emerg Infect Dis.* 2007;13:687–93.
8. Norman AF, Regnery PL, Jameson P, Greene C, Krause DC. Differentiation of *Bartonella*-like isolates at the species level by PCR-restriction fragment length polymorphism in the citrate synthase gene. *J Clin Microbiol.* 1995;33:1797–803.
9. Kettle DS, editor. *Medical and veterinary entomology.* 2nd ed. Wallingford (MA): CABI Publishing; 1995.
10. Bitam I, Parola P, De La Cruz K, Matsumoto K, Bazia B, Rolain JM, et al. First molecular detection of *Rickettsia felis* in fleas from Algeria. *Am J Trop Med Hyg.* 2006;74:532–5.

Address for correspondence: Nordin S. Zeidner, Centers for Disease Control and Prevention, Division of Vector-Borne Infectious Diseases, 3150 Rampart Rd, Foothills Campus, Fort Collins, CO 80521, USA; email: naz2@cdc.gov

Antibodies to Nipah or Nipah-like Viruses in Bats, China

To the Editor: *Hendra virus* (HeV) and *Nipah virus* (NiV), the only known members of the genus *Henipavirus*, are 2 emerging paramyxoviruses that are highly pathogenic in a variety of vertebrate animals, including humans (1). Since the initial discovery of the viruses in Australia and Malaysia (2,3), sporadic HeV outbreaks have been reported from 1995 to 2007 in Australia (4), and regular NiV outbreaks have occurred in Bangladesh (5) and India (6). Numerous frugivorous bat species (genus *Pteropus*), and some insectivorous bat species have been found to be reservoir hosts of henipaviruses in Australia and Asian countries (7–9).

In this study conducted during 2004–2007, bats were trapped within their natural habitat from 10 provinces in mainland People's Republic of Chi-

na. Serum, pharyngeal, and fecal swab samples were collected and stored as described previously (10). An ELISA was developed to detect antibodies to the NiV nucleocapsid (N) and attachment glycoprotein (G) proteins. For confirmation, ELISA-positive samples were tested by using Western blot against a recombinant NiV G fragment (aa 71–193) fused with the maltose-binding protein. Virus neutralization tests were conducted with live NiV and HeV under Biosafety Level 4 containment in Australia. In addition, a surrogate neutralization test was developed by using recombinant *env* HIV-1, pseudotyped with NiV G and F. RNA was extracted by using the QIA amp Viral RNA Mini Kit (QIAGEN, Hilden, Germany). Reverse transcription-PCR (RT-PCR) was performed by using primers against the NiV N gene as described previously (3).

In total, 692 bat serum specimens were screened for antibody to NiV N or G protein (or both) by ELISA, and 33 were positive (online Appendix Table, available from www.cdc.gov/EID/content/14/12/1974-appT.htm). These specimens were from 9 of the 23 bat species examined in this study. Of the 33 serum samples reactive in ELISA, 25 with sufficient quantity left were further tested by Western blot, and 17 of 25 serum samples were reactive with MBP-NiV G fusion fragment, but not with the control MBP. None of the samples inhibited entry of NiV F/G-pseudotyped virus or neutralized either HeV or NiV. No NiV-specific RNA was detected by RT-PCR among 479 fecal swab samples and 67 throat swab samples tested; therefore, virus isolation was not attempted.

This study systematically investigated NiV presence among bats in China. The detection of henipavirus antibody suggests that several bat species have been exposed to NiV or a closely related virus. The prevalence of antibody was especially prominent among *Myotis* species from Yunnan

Province. Antibody was detected in samples from 3 of 4 *Myotis* species captured in the same location in 2006 and 2007. A relatively high prevalence of henipavirus antibody was also found among *Rousettus leschenaultia* samples from Hainan Province in 2007. Notably, Yunnan and Hainan are both located in southern China. Although pteropid bats are not found in China, these data suggest henipaviruses could be introduced into China by other susceptible bat species that overlap their habitat with pteropid bats in neighboring countries.

Several possibilities may explain the failure to detect neutralizing antibodies. One might be the unique immune response among those nonpteropid bats, which results in a low level of neutralizing antibodies that are difficult to detect in the current assay systems. Alternatively, and perhaps more likely, ≥ 1 Nipah-like viruses could be circulating among the bat populations sampled in this study, producing antibodies that cross-react with, but do not neutralize, the prototype Malaysian NiV virus isolate. This phenomenon has been observed previously by our group for severe acute respiratory syndrome (SARS)-like viruses in horseshoe bats, whose sera cross-reacted with, but did not neutralize, the SARS virus in humans (10).

Obtaining serologic evidence of viruses in bat populations is typically more successful as a screening tool than either nucleic acid based assays or virus isolation; this is likely attributable to the often low-level of virus replication, the transient nature of the infection in bats, or both. The inability

to amplify NiV sequences may have been attributable to the viral RNA present among these samples being below the threshold of detection in our assay or to the absence of infection in the population at the time of sampling. In addition, the primers used in the PCR may target regions of the NiV N protein that exhibit substantial sequence divergence in a Nipah-like virus.

Bat species in the genera *Rousettus*, *Myotis*, *Miniopterus*, and *Hipposideros* naturally reside in trees, buildings, and caves that can be in close proximity to human residential areas, which increases the potential of transmission of zoonotic pathogens from bats to humans. The increased risk for these zoonotic infections to spread from bats to humans in areas of cohabitation is best illustrated by the repeated spillover events involving NiV in Bangladesh (5). Given the present initial evidence of exposure among bats in mainland China shown here, there is an urgent need to continue and expand surveillance studies for henipaviruses in China and elsewhere on the Asian continent.

This work was jointly funded by State Key Program for Basic Research grant 2005CB523004 from the Chinese Ministry of Science and Technology, the Knowledge Innovation Program Key Project administered by the Chinese Academy of Sciences (KSCX1-YW-R-07), the Australian Biosecurity Cooperative Research Centre for Emerging Infectious Diseases, Project 1.026RE (L.-F. W.), The Middle Atlantic Regional Center of Excellence for Biodefense and Emerging Infectious Disease Research, National Institutes of

Health grant AI057168 (C.C.B.), and the East Asia and Pacific Summer Institutes program administered by the United States National Science Foundation (A.C.H).

**Yan Li, Jianmin Wang,
Andrew C. Hickey,
Yunzhi Zhang, Yuchun Li,
Yi Wu, Huajun Zhang,
Junfa Yuan, Zhenggang Han,
Jennifer McEachern,
Christopher C. Broder,
Lin-Fa Wang, and Zhengli Shi**

Author affiliations: State Key Laboratory of Virology—Chinese Academy of Sciences, Wuhan, People's Republic of China (Y. Li, J. Wang, Y. Zhang, H. Zhang, J. Yuan, Z. Han, Z. Shi); Uniformed Services University, Bethesda, Maryland, USA (A.C. Hickey, C.C. Broder); Yunnan Institute of Endemic Diseases Control and Prevention, Dali, People's Republic of China (Y. Zhang); Shandong University at Weihai, Weihai, People's Republic of China (Y. Li); University of Guangzhou, Guangzhou, People's Republic of China (Y. Wu); and Commonwealth Scientific and Industrial Research Organisation Livestock Industries, Geelong, Victoria, Australia (J. McCachern, L.-F. Wang)

DOI: 10.3201/eid1412.080359

References

1. Eaton BT, Mackenzie JS, Wang LF. Henipaviruses. In: Knipe DM, Griffin DE, Lamb RA, Straus SE, Howley PM, Martin MA, et al., editors. *Fields virology*. 5th ed. Philadelphia: Lippincott Williams & Wilkins; 2007. p. 1587–1600.
2. Murray K, Selleck P, Hooper P, Hyatt A, Gould A, Gleeson L, et al. A morbillivirus that caused fatal disease in horses and humans. *Science*. 1995;268:94–7. DOI: 10.1126/science.7701348

Erratum—Vol. 14, No. 9

The article *Obligations to Report Outbreaks of Food-borne Disease under the International Health Regulations (2005)* (M.D. Kirk et al.) contained incorrect figures in the abstract and conclusion. The text stated that 7 (50%) of 14 outbreaks would have required notification to the World Health

Organization (WHO). The correct proportion is 6 (43%) of 14 outbreaks that would have required notification to the WHO. The article has been corrected online (www.cdc.gov/eid/content/14/9/1440.htm).

LETTERS

3. Chua KB, Bellini WJ, Rota PA, Harcourt BH, Tamin A, Lam SK, et al. Nipah virus: a recently emergent deadly paramyxovirus. *Science*. 2000;288:1432–5. DOI: 10.1126/science.288.5470.1432
4. Field HE, Breed AC, Shield J, Hedlefs RM, Pittard K, Pott B, et al. Epidemiological perspectives on Hendra virus infection in horses and flying foxes. *Aust Vet J*. 2007;85:268–70. DOI: 10.1111/j.1751-0813.2007.00170.x
5. Epstein JH, Field HE, Luby S, Pulliam JR, Daszak P. Nipah virus: impact, origins, and causes of emergence. *Curr Infect Dis Rep*. 2006;8:59–65. DOI: 10.1007/s11908-006-0036-2
6. Chadha MS, Comer JA, Lowe L, Rota PA, Rollin PE, Bellini WJ, et al. Nipah virus-associated encephalitis outbreak, Siliguri, India. *Emerg Infect Dis*. 2006;12:235–40.
7. Yob JM, Field H, Rashdi AM, Morrissy C, van der Heide B, Rota P, et al. Nipah virus infection in bats (order Chiroptera) in peninsular Malaysia. *Emerg Infect Dis*. 2001;7:439–41.
8. Reynes JM, Counor D, Ong S, Faure C, Seng V, Molia S, et al. Nipah virus in Lyle's flying foxes, Cambodia. *Emerg Infect Dis*. 2005;11:1042–7.
9. Wacharapluesadee S, Lumlertdacha B, Boongird K, Wanghongsa S, Chanhome L, Rollin P, et al. Bat Nipah virus, Thailand. *Emerg Infect Dis*. 2005;11:1949–51.
10. Li W, Shi Z, Yu M, Ren W, Smith C, Epstein JH, et al. Bats are natural reservoirs of SARS-like coronaviruses. *Science*. 2005;310:676–9. DOI: 10.1126/science.1118391

Address for correspondence. Zhengli Shi, State Key Laboratory of Virology, Wuhan Institute of Virology, Chinese Academy of Sciences, Wuhan, Hubei 430071, People's Republic of China; email: zshi@wh.iov.cn

**EMERGING
INFECTIOUS DISEASES**
A Peer-Reviewed Journal Tracking and Analyzing Disease Trends Vol.11, No.2, February 2005

**Search
past Issues**
**EID
Online**
www.cdc.gov/eid

Hazards of travel

Appendix Table. Detection of Nipah virus antibody among bat serum samples collected from 10 provinces in China, 2004–2007*

Bat species	No. positive/no. tested by ELISA, 2007†						No. positive/no. tested by ELISA, 2004–2006‡					
	Hainan	Guangdong	Yunnan	Hunan	Hubei	Tianjin	Yunnan, 2006	Shanxi, 2006	Guizhou, 2005	Henan, 2005	Guangxi, 2004	Hubei, 2004, 2006
<i>Cynopterus sphinx</i>		0/2										
<i>Rousettus leschenaulti</i>	5/16 (5)									0/36		
<i>Rhinolophus pusillus</i>	0/11	0/1								0/7		0/9
<i>Rhinolophus affinis</i>	0/48	1/26 (1)					0/2		0/17			
<i>Rhinolophus luctus</i>	0/1			0/9								0/1
<i>Rhinolophus sinicus</i>	0/5	1/15 (0)	0/1		0/9		0/3		0/17			0/1
<i>Rhinolophus pearsonii</i>			0/3							0/32		
<i>Rhinolophus rex</i>								0/1				
<i>Rhinolophus macrotis</i>												0/3
<i>Rhinolophus ferrumequinum</i>												0/3
<i>Hipposideros armiger</i>	0/11	2/10 (0)	0/20	0/1	0/12					0/4		0/5
<i>Hipposideros larvatus</i>	0/1	0/20										
<i>Hipposideros pomona</i>	0/20	1/39 (0)					0/1					
<i>Pipistrellus pipistrellus</i>										0/1		
<i>Scotophilus kuhlii</i>		0/20										
<i>Myotis daubentoni</i>	0/10		3/22 (1)				6/57 (ND)					
<i>Myotis ricketti</i>			6/38 (4)		2/11 (2)	0/35						
<i>Myotis altarium</i>												0/2
<i>Myotis</i> spp.			1/19 (1)									
<i>Nyctalus velutinus</i>												0/1
<i>Miniopterus</i> spp.			5/15 (3)		0/1		0/5	0/3	0/6			0/2
<i>la io</i>									0/7			
<i>Megaderma lyra</i>									0/1			

*ND, not done.

†Glycoprotein ELISA (no. positive by Western blot).

‡Nucleocapside protein ELISA (no. positive by Western blot).