

## Voucher Specimens for SARS-Linked Bats

WE READ WITH INTEREST THE REPORT "BATS are natural reservoirs of SARS-like coronaviruses" by W. Li *et al.* (28 Oct. 2005, p. 676). These authors and others (1) have identified bats in three genera as reservoirs of SARS-like coronaviruses (SL-CoVs), raising the possibility that SARS-CoVs arose among these or other bats. An omission in these papers is that no systematic attempt was made to preserve voucher specimens (2).

Properly vouchered specimens of reservoir hosts are a *sine qua non* in a research program whose goals are the accurate understanding of disease emergence and the ability to forecast disease risk (3, 4). In the present instance, this basic standard was not followed and, thus, there is little that can be done to verify species identifications; this is especially troublesome when new data indicate that in SARS and other diseases, some individuals transmit more infection than predicted by homogeneous null models (5, 6). Bat systematics is a dynamic area of research, and classifications change accordingly. This is especially the case in *Rhinolophus*, a group where species identification cannot be based solely on external morphological characters (7). Voucher specimens and associated data could be used for genetic validation of species identification and comparison to other forms



SARS has been found in horseshoe bats.

from Africa, Europe, and the Southwest Pacific. This would provide the potential for global prediction of SARS-like viruses.

We submit that work in epidemiology of infectious zoonotic disease is strengthened by following four steps: (i) depositing voucher specimens of all collected species in a local or international museum of natural history; (ii) preserving skin snips from all individuals, in alcohol or other preservative; (iii) identifying these samples by numbers so they can be cross-referenced to individual vouchers; and (iv) reporting these numbers in print.

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#### References and Notes

1. S. K. P. Lau *et al.*, *Proc. Natl. Acad. Sci. U.S.A.* **102**, 14040 (2005).
2. In the Supporting Online Material accompanying the report by Li *et al.*, the authors suggest they dissected only those animals that did not survive the sampling process and that "most" were released into the wild again.
3. J. Salazar-Bravo, L. A. Ruedas, T. L. Yates, *Curr. Top. Microbiol. Immunol.* **262**, 25 (2002).
4. L. A. Ruedas, J. Salazar-Bravo, J. W. Drago, T. L. Yates, *Mol. Phylogenet. Evol.* **17**, 129 (2000).
5. A. P. Galvani, R. M. May, *Nature* **438**, 293 (2005).
6. J. O. Lloyd-Smith, S. J. Schreiber, P. E. Kopp, W. M. Getz, *Nature* **438**, 355 (2005).
7. G. Csorba, P. Ujhelyi, N. Thomas, *Horseshoe Bats of the World* (Alana Books, Shropshire, UK, 2003).

#### Response

WE THANK SALAZAR-BRAVO *ET AL.* FOR RAISING the important issue of accurate species identification in studying wildlife reservoirs for emerging infectious diseases. We agree that the collection and deposit of voucher specimens is extremely important in biological studies, including those of wildlife epidemiology. Our group has done the following to ensure that specimens were archived and that the bats captured were correctly identified: (i) We deposited specimens of each species (morphological type) cap-

tured during this study in the Institute of Zoology, Chinese Academy of Sciences, Beijing. (ii) In addition to morphological characterization, the identification of *Rhinolophus* species was supported by DNA sequence phylogeny. (iii) In a paper currently submitted to a peer-reviewed journal, we describe the DNA sequence phylogeny of this group of bats in China. The molecular data support our morphological identification. (iv) We have undertaken a long-term study of the diversity of bats in China as part of a Darwin Initiative-funded project. (v) We did not submit each individual bat that tested positive because of conservation and biosecurity issues; however, samples of blood from each bat are

deposited at the Institute of Virology, Wuhan, China, as well as at the Australian Animal Health Laboratory, CSIRO, Australia. These institutions are able to safely store samples that potentially contain lethal infectious agents.

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