# Targeting surveillance in apparently healthy versus diseased wild bats and rodents for zoonotic virus discovery

## Authors

* [Bogich, Tiffany (L)](https://sci.pe/user/tiffany) “[Dr. Tiffany L Bogich, PhD](http://orcid.org/0000-0002-8143-5289)” (EHA; EEB; NIH)[[1]](#footnote-1)
* Olival, Kevin (J) “Kevin J Olival, PhD” (EHA)1
* [Epstein, Jonathan (H)](https://sci.pe/user/epstein) “Jonathan H Epstein, DVM, MPH” (EHA)[[2]](#footnote-2)

## Affiliations

* [EcoHealth Alliance (EHA)](http://www.ecohealthalliance.org/) - New York, NY, USA
* [Fogarty International](http://www.fic.nih.gov/) < [National Institutes of Health (NIH)](http://www.nih.gov/) - Bethesda, Maryland, USA
* Department of Ecology and Evolutionary Biology (EEB) < [Princeton University](http://www.princeton.edu/main/) - Princeton, NJ, USA

## Abbreviations

* EID: Emerging Infectious Diseases

## License

[CC-BY-4.0](https://creativecommons.org/licenses/by/4.0/legalcode).

## Impact statement

Bats and rodents can harbor viruses that are potentially harmful to humans. In order to find new viruses that may pose a threat to humans, it is better to survey healthy bats and rodents for viruses than apparently diseased bats and rodents.

## Introduction

Nearly two-thirds of emerging infectious diseases (EID) (Eidson, et al. 2001) that affect humans are zoonotic, and three-quarters of these originate in wildlife, making surveillance of wildlife for novel pathogens part of a logical strategy to prevent future zoonotic EIDs (Morse 1993).

## Methods

We focused our analysis on mammalian hosts and viruses as they are more likely to be associated with human EIDs than any other host-pathogen type. See Database for additional information on datasources.

<file:///Users/tiffany/app-suite/test/fixtures/data-xlsx.xlsx>

Dataset 1 Database of all human emerging viruses previously identified as originating in wildlife. Data from: (Morse 1993, 12-25).

## Results

Figure 1. Authors: Dr. Tiffany L Bogich, PhD (NIH)[[3]](#footnote-3); Kevin J Olival, PhD[[4]](#footnote-4). License: [CC0-1.0](http://creativecommons.org/publicdomain/zero/1.0/legalcode). Keywords: [diseases](https://science.ai/subjects/diseases), symptomatic disease. (A) Percentage of reports of host-virus pairs in which observable disease was described, ‘Symptomatic’, no observable disease was described, ‘Asymptomatic’, or no description of disease was included, ‘No data’. (B) The proportion of hosts symptomatic by mammal order are given with standard error bars, calculated assuming binomial error structure. The total number of each host order or virus family included in the database is given above each bar. Note, all host orders and virus families in the database are included here, but analyses are limited to those host orders or virus families with at least three entries in the database. Figure from: Jones et al. (2008, Fig. 1). (C) The proportion of virus families for which hosts are reported symptomatic are given with standard error bars, calculated assuming binomial error structure. The total number of each host order or virus family included in the database is given above each bar. Note, all host orders and virus families in the database are included here, but analyses are limited to those host orders or virus families with at least three entries in the database. Figure courtesy of: Jones, Kate “Kate Jones” (University College London (UCL) – London, UK).

Our search of 605 mammal-virus associations investigated yielded explicit information on host health in 52% of the 312 mammal-virus pairs. Of these, approximately 28% of infected wildlife hosts were reported to present with visible disease (n = 88) and 72% (n = 224) were reported without evidence of visible disease (Figure 1A). The proportion of hosts that were symptomatic differed across host order (Figure 1B) and virus family (Figure 1C).

Hosts infected with filoviruses were marginally more likely to be visibly diseased (Table 1).

Table 1 Logistic regression analysis with bias reduction of whether a host presents with disease for 234 mammal–virus pairs from 5 taxonomic orders of mammals and 10 taxonomic families of viruses. The subset of data used was selected by using a cutoff of at least 3 records in the database to avoid making inference about host orders or virus families, for which we had very little information.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Predictor[[5]](#footnote-5) | Coefficient | SE | Test statistic (Z) | p-value | OR | 95% CI |
| Constant | -0.33 | 0.58 | -0.56 | 0.58 | 0.72 | (0.23, 2.26) |
| Virus Family (Reference category: Flaviviridae) | | | | | | |
| Bunyaviridae | -1.74 | 0.64 | -2.71 | 0.01 | 0.18 | (0.05, 0.62) |
| Filoviridae | 3.26 | 1.83 | 1.78 | 0.08 | 26.07 | (0.72, 944.49) |
| Herpesviridae | 0.10 | 0.65 | 0.16 | 0.87 | 1.11 | (0.31, 3.94) |
| Paramyxoviridae | 3.43 | 1.42 | 2.41 | 0.02 | 30.95 | (1.90, 503.52) |
| Picornaviridae | 1.12 | 0.76 | 1.48 | 0.14 | 3.08 | (0.69, 13.68) |
| Poxviridae | 2.29 | 0.81 | 2.82 | <0.001 | 9.90 | (2.01, 48.72) |
| Reoviridae | 2.13 | 1.05 | 2.02 | 0.04 | 8.39 | (1.07, 66.12) |
| Rhabdoviridae | 9.20 | 2.39 | 3.85 | <0.001 | NA | NA |
| Togaviridae | -0.36 | 0.63 | -0.58 | 0.56 | 0.70 | (0.20, 2.38) |

Species in the order Chiroptera have a lower probability of visible disease than in other orders (Figure 2), though **all Chiroptera infected with non-rabies rhabdoviruses have a high probability of visible disease**.

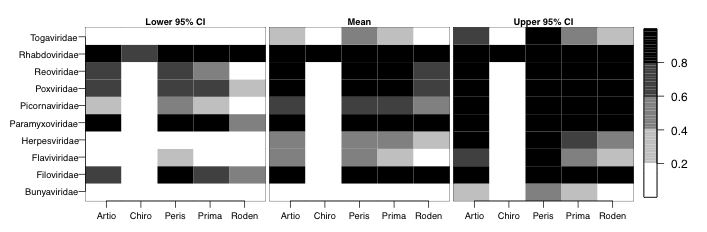
****

Figure 2 The probability of being symptomatic based on a logistic regression analysis with bias reduction of whether or not a host presents with disease for 234 mammal-virus pairs from 5 orders of mammals and 10 families of viruses, including the lower 95% confidence interval (left), mean (center), and upper 95% confidence interval (right). Probabilities are based on the predicted values of the logistic regression and are given on a five-point gray scale from white (0.0 – 0.2) to black (0.8 - 1.0). Confidence values were calculated as the coefficient plus 1.96 times the standard error.

## Conclusions

Our data suggest that Chiroptera and Rodentia, two of the three main mammalian orders often targeted for zoonotic disease surveillance (the third being non-human primates (Wolfe, Daszak, et al. 2005, Wolfe, Escalante, et al. 1998) are less likely to present with visible disease than other orders (Figure 1).

## Supporting Information

Previous analyses show that zoonotic disease emergence events and human pathogen species richness are spatially correlated with mammal and bird diversity (Jones, et al. 2008). We used generalized additive models (GAMs) to identify and rank host-specific predictors (ecological, life history, taxonomic, and phylogenetic traits, and a control for research effort) of the number of total and zoonotic viruses in mammals.

## Database

To construct the mammal–virus association database we initially extracted all viruses listed as occurring in any mammal from the International Committee on Taxonomy of Viruses database (ICTVdb), and further individually went through each virus listed in the ICTV 8th edition master list and searched the literature for mammalian hosts.

<video.mp4>

Video 1 Cross-sectional view of a virus.

# References

Eidson, Millicent, et al. "Crow deaths as a sentinel surveillance system for West Nile virus in the northeastern United States, 1999." *Emerging Infectious Diseases* 7, no. 4 (August 2001): 615-620.

Jones, Kate E., et al. "Global Trends in Emerging Infectious Diseases." *Nature* 451, no. 7181 (2008): 990-993.

McQuarrie, C. *The Usual Suspects.* Screenplay. Directed by Bryan Singer. Produced by Bryan Singer, & M. McDonnell. Performed by K. Spacey, G. Byrne, C. Palminteri, S. Baldwin, & B. del Toro. Gramercy Pictures (I), 1995.

Morse, Stephen S. *Emerging Viruses.* illustrated edition. Edited by Stephen S. Morse. New York, NY: Oxford University Press, 1993.

Wolfe, Nathan D., Ananias A. Escalante, William B. Karesh, Annelisa Kilbourn, Andrew Spielman, and Altaf A. Lal. "Wild Primate Populations in Emerging Infectious Disease Research: The Missing Link?" *Emerging infectious diseases* 4, no. 2 (1998): 149-158.

Wolfe, Nathan D., Peter Daszak, A. Marm Kilpatrick, and Donald S. Burke. "Bushmeat hunting, deforestation and prediction of zoonotic emergence." *Emerging Infectious Diseases* 11, no. 12 (2005): 1822-1827.

1. Authors contributed equally. [↑](#footnote-ref-1)
2. Email: [epstein@ecohealthalliance.org](mailto:epstein@ecohealthalliance.org). Address: EcoHealth Alliance, 460 West 34th Street, 17th Floor, New York, NY 10001. [↑](#footnote-ref-2)
3. Email: [bogich@ecohealthalliance.org](mailto:bogich@ecohealthalliance.org). [↑](#footnote-ref-3)
4. Prepared the figure. [↑](#footnote-ref-4)
5. Virus and host reference groups were selected as those for which sample size was sufficiently large and symptomatic infection was moderate (see Figure 1). [↑](#footnote-ref-5)