# 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” (EHA; EEB; NIH)[[1]](#footnote-1)
* Olival, Kevin (J) “Kevin J Olival, PhD” (EHA)
* Epstein, Jonathan (H) “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

## 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) 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.

## 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 Supporting Information for more[[3]](#endnote-1).

<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: Jones, Kate “Kate Jones” (University College London (UCL) – London, UK).

## Results

Figure 1 Summary of findings. Authors: Dr. Tiffany L Bogich, PhD. (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. (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.

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[[4]](#footnote-3) | 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**.

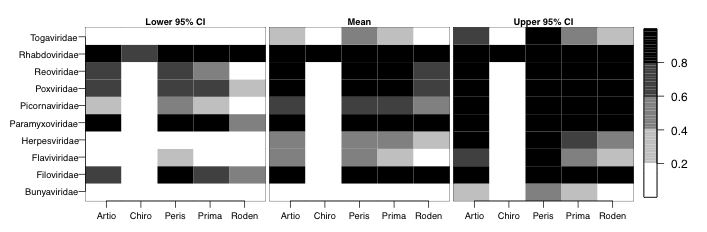
****

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 are less likely to present with visible disease than other orders (Figure 1).

## Supporting Information

We hypothesize that the number of viruses a given mammal species shares with humans decreases with phylogenetic distance from humans and increases with opportunity for human contact.

### Methods

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.

<video.mp4>

Video 1 Cross-sectional view of a virus.

1. Wrote the manuscript. [↑](#footnote-ref-1)
2. Email: [epstein@ecohealthalliance.org](mailto:epstein@ecohealthalliance.org). [↑](#footnote-ref-2)
3. See also Jones et al 2008 Nature. [↑](#endnote-ref-1)
4. 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-3)