

Characterizing Pathogen Diversity in the Common Vampire Bat (*Desmodus rotundus*)

AMY K. WRAY¹, Kevin J. Olival^{1,2,3}, Simon J. Anthony^{2,4}, and Nancy B. Simmons³

¹ Department of Ecology, Evolution, and Environmental Biology, Columbia University, New York, New York, USA; ² EcoHealth Alliance, New York, New York, USA; ³ American Museum of Natural History, New York, New York, USA; ⁴ Center for Infection and Immunity, Mailman School of Public Health, Columbia University, New York, New York, USA

ABSTRACT: Bats represent approximately 20% of all mammals with over 1,200 different species distributed worldwide. Certain bat species serve as the reservoirs for viral diseases including Henipa-, Lyssa-, Corona-, and Filoviruses, which can pose serious threats to human health^[1,2]. However, for many bat species, ecological patterns of viral diversity remain uncharacterized. The common vampire bat, *Desmodus rotundus*, has historically been a species of interest due to its sanguivorous feeding habit and unique social behaviors. Although these bats more frequently feed on the blood of non-human animals such as cows and other livestock, the potential for interspecies disease transmission via human bites makes them a species of particular concern^[3]. Rabies and other lyssaviruses have been well studied in these bats, and other viruses such as coronaviruses and adenoviruses have also been detected^[4,5]. However, the total viral diversity hosted by *D. rotundus*, and the ecology which may contribute to disease spread, remains largely unknown. *This study will seek to characterize pathogen diversity in common vampire bat (D. rotundus) populations and nearby livestock in Belize, and will analyze the ecology of these bats and potential microbe sharing with their prey.* This research project has already completed viral and bacterial screening tests on blood, urine, saliva, and fecal samples taken from 103 individual *D. rotundus*, which were previously collected from the Suchitepequez and Cobán regions of Guatemala. Additional samples from at least 100 individuals from *D. rotundus* populations in the Orange Walk District of Belize will also be collected and screened for viral and bacterial diversity. Both of these sites are located in regions of high biodiversity where interactions between wildlife, livestock, and human populations are also known to occur.

Feeding behavior



photo by N.B. Simmons

feeding preference: domestic animals

prey CytB sequences detected in bat fecal samples

Previous studies have shown preference for domestic animals including:



Bos taurus



Equus sp.

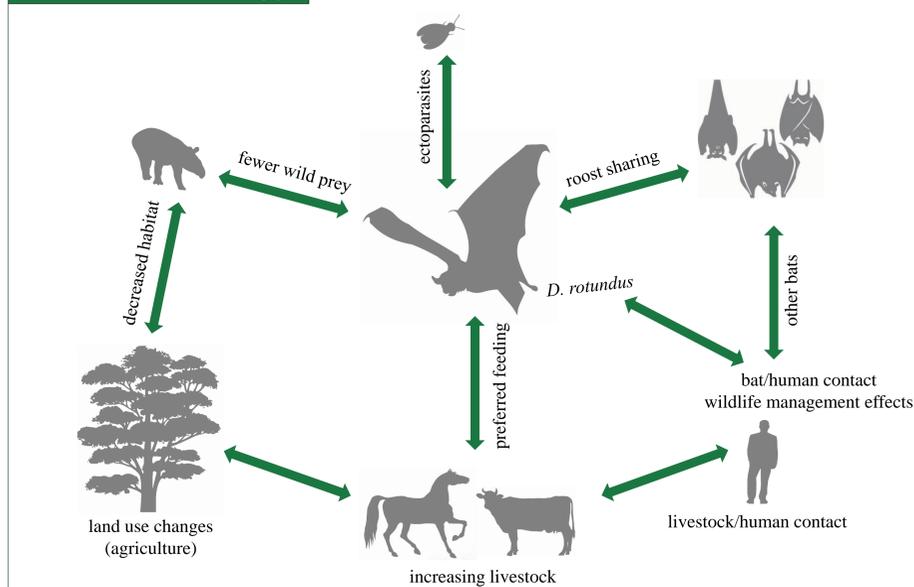


Bos indicus

Hypothesis

Viral and bacterial screening of *D. rotundus* and their prey will indicate evidence of microbe sharing between species.

Desmodus ecology



Why is *D. rotundus* a species of interest for pathogen surveillance?

- Natural history:** *D. rotundus* live in large colonies, are highly social, and can disperse over long distances
- Preferential feeding on livestock:** *D. rotundus* come in direct contact with domestic animals, which are often also near humans
- Potential direct spillover:** Human encroachment into *D. rotundus* habitat is associated with increase in bites & rabies cases^[6]
- Roost sharing:** *D. rotundus* have been known to share roosting habitat with other bat species^[7]
- Bioindicator potential:** *D. rotundus* abundance may be useful as an indicator of habitat disturbance^[8]

This species occurs at an important interface between wildlife, livestock, and humans AND where land use changes may create opportunities for pathogen spillover events.

What kinds of wildlife management strategies can help reduce spillover risk?

Culling practices have not demonstrated effectiveness at reducing disease, and can actually increase levels of disease seroprevalence by disproportionately targeting adult bats^[9]. Alternative management strategies that incorporate a One Health approach include prevention of exposure, continuation of pathogen surveillance, targeted vaccination, and reduction of habitat disturbance.

Study sites: Belize



Methods

Bats will be captured in mist nets and oral swabs, fecal, urine, and blood samples will be collected from bats using non-lethal, minimally invasive methods with IACUC approval. Blood samples from nearby cattle will also be collected, inactivated in TRIzol, and frozen immediately in liquid nitrogen. DNA and RNA will be extracted from and synthesis of cDNA will be performed to reverse transcribe viral RNA into DNA for amplification purposes. PCR assays will be performed with degenerate viral and bacterial family-level primers targeting highly conserved regions, and positive PCR products will be purified and cloned. Sequencing will be performed to determine the presence of viral co-occurrence, and phylogenetic trees will be constructed for viral and bacterial sequences using maximum likelihood and Bayesian algorithms. Recently ingested prey of *D. rotundus* will also be identified via detection of cytochrome B sequences in bat fecal samples using a generalized mammalian CytB assay and prey identity matches will be determined using NCBI BLAST. These results will demonstrate feeding preferences of *D. rotundus* in this area. This technique also yields CytB sequences for *D. rotundus*, which will be combined with *D. rotundus* CytB sequences from GenBank to infer population genetic connectivity using a haplotype network analysis.



photo by E.H. Loh

References: (1) Wibbelt, G. *et al.* 2010. *Biology letters*, 6(4), 438-440; (2) Olival, K. J. *et al.* 2012. *New Directions in Conservation Medicine: Applied Cases of Ecological Health*, 195-212; (3) Wong, S. *et al.* (2007). *Reviews in medical virology*, 17(2), 67-91. (4) Brandão, P. E. *et al.* 2008. *Brazilian Journal of Infectious Diseases*, 12(6), 466-468; (5) Lima, F. E. *et al.* 2013. *Virus Genes*, 47(2), 378-381; (6) Johnson, N. *et al.* 2014. *Viruses*, (6)5, 1911-1928; (7) Wohlgenant, T.J. 1994. *Biotropica*, 344-348; (8) Fenton, M.B. *et al.* 1992. *Biotropica*, 24(3), 440-446; (9) Streicker, D.G. *et al.* 2012. *Proceedings of the Royal Society B: Biological Sciences*, 279, 3384-92.

This study has received support from the Earth Institute and Columbia University. The previous study in Guatemala was supported by the PREDICT project of the United States Agency for International Development (USAID) Emerging Pandemic Threats Program and in part by a NIAID Non-Biodefense Emerging Infectious Disease Research Opportunities award R01 AI079231.