



Risk of Viral Emergence from Bats

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▼ Abstract

Emerging zoonoses are a significant threat to global public health and our economies. The majority are caused by pathogens that emerge with increasing frequency from wildlife hosts (e.g. HIV-1 from chimpanzees, SARS CoV from bats and civets, Nipah virus from fruit bats). This group of diseases alone causes tens of thousands of deaths each year, and some outbreaks (e.g. SARS) have cost the global economy tens of billions of dollars. However, despite the huge social, demographic and economic impact of EIDs, there has been little advance in our understanding of the underlying process of how these wildlife zoonoses emerge, and in developing predictive approaches to prevent future emergence. Developing predictive and proactive approaches to zoonotic emergence is a key challenge to medical science. New zoonoses emerge regularly from wildlife in a seemingly random way, from disparate regions of the globe, and from a wide diversity of wildlife species. Our ability to understand what drives this process is hampered by a lack of rigorous analyses of the processes that cause emergence;our lack of knowledge of the diversity of microbes in wildlife (the 'zoonotic pool') from which new zoonoses regularly emerge;and our poor understanding of pathogenic factors that explain why some viruses are able to cross the species barrier while others are not. In this application, we bring together a multidisciplinary team of emerging disease ecologists and modelers, viral bioinformaticists, and molecular virologists who are leaders in their fields, and who have already collaborated together to study zoonotic disease emergence. Building on preliminary data that demonstrates bats are a key wildlife reservoir, and that emergence is due to a range of anthropogenic drivers, this team will 1) develop predictive models of global 'hotspots'for the future emergence of bat viruses;2) use a large repository of bat biological samples to conduct targeted surveillance in these 'hotspots'for known and undiscovered bat pathogens, elucidating the unknown diversity of the bat 'virome'and;3) using a range of in vitro techniques (including infection in bat cell culture), examine the pathogenesis of these new viruses, and a pool of available bat viruses which have not yet emerged in humans. This multidisciplinary approach represents the first, concerted effort to understand the depth and breadth of the process of emergence within a key group of wildlife hosts associated with the recent emergence of SARS, Nipah, Hendra, Ebola and Marburg viruses.

Public Health Relevance

Emerging zoonoses (e.g. HIV/AIDS, Influenza) are a major threat to health globally, causing tens of thousands of deaths each year in the USA and abroad and a number of these have emerged from bats recently (SARS, Ebola, Nipah). This research provides a way to predict the regions where the next new emerging zoonoses from bats is most likely to emerge, and proposes targeted surveillance of these animals using state-of-the-art molecular techniques in those regions. It will characterize new viruses, and study the pathogenesis of these, and a bank of known bat viruses that have not yet emerged in the human population: It is therefore a predictive, proactive approach to combating the most high profile group of emerging pathogens.

▼ Funding Agency

Agency	National Institute of Health (NIH)
Institute	National Institute of Allergy and Infectious Diseases (NIAID)
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Project #	5R01AI079231-02
Application #	7688507
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Program Officer	Park, Eun-Chung
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Support Year	2
Fiscal Year	2009
Total Cost	\$535,156
Indirect Cost	

▼ Institution

Name	Ecohealth Alliance, Inc.
Department	
Type	
DUNS #	077090066
City	New York
State	NY
Country	United States

Zip Code 10001

▼ Related projects

NIH 2012 R01 AI	Risk of Viral Emergence from Bats Daszak, Peter / Ecohealth Alliance, Inc.	\$518,980
NIH 2011 R01 AI	Risk of Viral Emergence from Bats Daszak, Peter / Ecohealth Alliance, Inc.	\$510,005
NIH 2010 R01 AI	Risk of Viral Emergence from Bats Daszak, Peter / Ecohealth Alliance, Inc.	\$480,423
NIH 2009 R01 AI	Risk of Viral Emergence from Bats Daszak, Peter / Ecohealth Alliance, Inc.	\$535,156
NIH 2008 R01 AI	Risk of Viral Emergence from Bats Daszak, Peter / Ecohealth Alliance, Inc.	\$534,989

▼ Publications

Olival, Kevin J; Hosseini, Parvies R; Zambrana-Torrelío, Carlos et al. (2017) Host and viral traits predict zoonotic spillover from mammals. *Nature* 546:646-650

Young, Cristin C W; Olival, Kevin J (2016) Optimizing Viral Discovery in Bats. *PLoS One* 11:e0149237

Brierley, Liam; Vonhof, Maarten J; Olival, Kevin J et al. (2016) Quantifying Global Drivers of Zoonotic Bat Viruses: A Process-Based Perspective. *Am Nat* 187:E53-64

Wray, Amy K; Olival, Kevin J; Morán, David et al. (2016) Viral Diversity, Prey Preference, and Bartonella Prevalence in *Desmodus rotundus* in Guatemala. *Ecohealth* 13:761-774

Schaer, Juliane; Reeder, DeeAnn M; Vodzak, Megan E et al. (2015) Nycteria parasites of Afrotropical insectivorous bats. *Int J Parasitol* 45:375-84

Loh, Elizabeth H; Zambrana-Torrelío, Carlos; Olival, Kevin J et al. (2015) Targeting Transmission Pathways for Emerging Zoonotic Disease Surveillance and Control. *Vector Borne Zoonotic Dis* 15:432-7

Jayme, Sarah I; Field, Hume E; de Jong, Carol et al. (2015) Molecular evidence of Ebola Reston virus infection in Philippine bats. *Virol J* 12:107

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Lei, Bonnie R; Olival, Kevin J (2014) Contrasting patterns in mammal-bacteria coevolution: bartonella and leptospira in bats and rodents. PLoS Negl Trop Dis 8:e2738

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