

**BIOGRAPHICAL SKETCH**  
**DO NOT EXCEED FIVE PAGES.**

NAME: Peter Daszak

eRA COMMONS USER NAME (credential, e.g., agency login): (b) (6)

POSITION TITLE: President &amp; Chief Scientist

EDUCATION/TRAINING (*Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.*)

INSTITUTION AND LOCATION	DEGREE (if applicable)	Completion Date MM/YYYY	FIELD OF STUDY
Bangor University, UK	B.S (hons)	07/1986	Zoology
University of East London, UK	Ph.D.	03/1993	Infectious Diseases

**A. Personal Statement**

I have the broad expertise in emerging viral zoonoses, and scientific management experience to support this proposed work that involves an international interdisciplinary team working on field collection of wildlife and human samples, human behavioral risk surveys, modeling and analytics, and viral characterization *in vitro* and *in vivo*. I am President and Chief Scientist of EcoHealth Alliance, a US-based 501 (c) 3 institution that conducts research on emerging zoonoses and global health capacity building. My 20+ years of NIH-funded research focuses on understanding the links among disease emergence in wildlife, livestock and people, particularly viral zoonoses. This includes identifying the bat origin of SARS-CoV and SADS-CoV, analyzing the ecology of West Nile, Nipah and Hendra virus emergence, publishing the first unbiased analysis of global emerging disease hotspots, and developing the scientific rationale for the Global Virome Project (GVP). Over the past 18 years I have been the PI on 4 multidisciplinary R01s that use modeling, epidemiology, laboratory and field science to test hypotheses on the emergence of wildlife-origin viral zoonoses, including SARS-CoV, Nipah and Hendra virus, Avian influenza and novel viruses from bats. I have successfully managed teams of virologists, field biologists, mathematical modelers, veterinarians, epidemiologists, laboratorians and anthropologists. Much of the groundwork for the current proposal has developed from my previous collaborative research with each member of the team assembled in the current R01 renewal proposal.

1. Li W, Shi Z, Yu M, Ren W, Smith C, Epstein JH, Wang H, Crameri G, Hu Z, Zhang H, Zhang J, McEachern J, Field H, **Daszak P**, Eaton BT, Zhang S & Wang L-F (2005). Bats are natural reservoirs of SARS-like coronaviruses. **Science** 310: 676-679.
2. Jones KE, Patel NG, Levy MA, Storeygard A, Balk D, Gittleman JL, and **Daszak P\*** (2008). Global trends in emerging infectious diseases. **Nature** 451:990-993
3. Olival KJ\*, Hosseini PR, Zambrana-Torrel C, Ross N, Bogich TL, **Daszak P\*** (2017). Host and viral traits predict zoonotic spillover from mammals. **Nature** 546, 646–650.
4. Carroll D, **Daszak P\***, Wolfe ND, Gao GF, Morel C, Morzaria S, Pablos-Méndez A, Tomori O, Mazet JAK (2018). The global virome project. **Science** 359: 872-874.

Program Director/Principal Investigator (Last, First, Middle): Daszak, P.

**B. Positions and Honors****Positions and Employment**

- 1993 -98 Senior Faculty Research Scientist, Kingston University UK
- 1998 Guest Researcher, Centers for Disease Control and Prevention (CDC)
- 1999 -01 Faculty Research Scientist, University of Georgia
- 2001 - Sr. Adjunct Faculty, Columbia University
- 2001 - 09 Executive Director, Consortium for Conservation Medicine, EcoHealth Alliance, New York
- 2009 - President & Chief Scientist, EcoHealth Alliance New York

**Other Experience and Professional Membership**

- 2003 - 7 NIH: ad hoc member, ZRG1 IDM-G 90 (2003-5) ZRG1 IRAP-Q (2005-7)
- 2004 - Editorial Board, *Conserv. Biol.*
- 2005 NIAID: Steering Committee, workshop on virus-host shifts & emergence of new pathogens
- 2010 - Editor-in-Chief, *EcoHealth*; Member of IOM Forum on Microbial Threats; External Advisory Board, DHS and Kansas State Univ. Ctr. of Excellence for Emerg. & Zoonotic Animal Diseases (CEEZAD)
- 2011 Steering Committee, NIAID Workshop on Arboviruses
- 2014 - Member NRC Advisory Committee to advise the US Global Change Research Program (USGCRP)
- 2015 - Member of Supervisory Board, One Health Platform; Editorial Board *One Health*
- 2016 - Member, WHO Expert group on Public Health Emergency Disease Prioritization
- 2016 - Member, Core Steering Committee & Co-Chair, Science & Technol WG, Global Virome Project
- 2017 External Review Committee, CSIRO Health & Biosecurity Business Unit
- 2017 - Chair, Forum on Microbial Threats, National Academies of Science, Engineering & Medicine

**Honors**

- 1999 Meritorious service award, CDC
- 2000 CSIRO silver medal for collaborative research
- 2002 Honored by the naming of a new species of centipede, *Cryptops daszaki* (*J Nat Hist* 36: 76-106)
- 2003 6<sup>th</sup> Annual Lecturer, Medicine & Humanities, Texas A&M
- 2007 Finalist, Director's Pioneer Award
- 2008 Presidential Lecturer, University of Montana
- 2012 Elected member of the Cosmos Club, Washington DC
- 2013 Honored by the naming of a new parasite species, *Isospora daszaki* (*Parasit. Res.* 111:1463-1466)
- 2013 Hsu-Li Distinguished Lectureship in International Epidemiology, Univ. Iowa
- 2015 Robert Leader Endowed Lecture in Food Safety, Michigan State Univ.
- 2018 - Member, National Institute of Medicine (NAM), USA.

**C. Contribution to Science**

**1. Research on the bat origins of emerging viruses.** A range high impact emerging viruses appear to have bat reservoirs (e.g. SARS-CoV, EBOV, NiV, HeV, MERS-CoV, SADS-CoV). As PI on four prior R01s, my work has helped demonstrate the bat-origin for some of these (SARS-CoV, SADS-CoV), analyze the drivers of emergence and risk factors for spillover. Collaborating with virologists in China, we have isolated and characterized SARS-like CoVs from bats that use the same human host cell receptor (ACE-2) as SARS-CoV. This work provides critical reagents and resources that have helped advance understanding of virus-host binding and may contribute to vaccine development. My other work identified factors underlying the emergence of NiV from *Pteropus* bats in Malaysia and Bangladesh; that MERS-CoV likely originated in bats; that SADS-CoV originates in bats; and that bats harbor a significantly higher proportion of zoonoses than all other mammalian groups after correcting for reporting biases.

Program Director/Principal Investigator (Last, First, Middle): **Daszak, P.**

- a. Pulliam JRC, Epstein JH, Dushoff J, Rahman SA, Bunning M, HERG, Jamaluddin AA, Hyatt AD, Field HE, Dobson AP & **Daszak P\*** and the Henipavirus Ecology Research Group (HERG). (2012). Agricultural intensification, priming for persistence, and the emergence of Nipah virus: a lethal bat-borne zoonosis. **J Roy Soc Interface** 9:89-101
- b. Ge X-Y, Li J-L, Yang X-L, Chmura AA, Zhu G, Epstein JH, Mazet JK, Hu B, Zhang W, Peng C, Zhang Y-J, Luo C-M, Tan B, Wang N, Zhu Y, Crameri G, Zhang S-Y, Wang L-F, **Daszak P\***, Shi Z-L\* (2013). Isolation and characterization of a bat SARS-like Coronavirus that uses the ACE2 receptor. **Nature** 503: 535-538.
- c. Memish ZA, Mishra N, Olival KJ, Fagbo SF, Kapoor V, Epstein JH, Al Hakeem R, Durosinloun A, Al Asmari M, Islam A, Kapoor A, Briese T, **Daszak P**, Al Rabeeah A, Lipkin WI. (2013). Middle East respiratory syndrome coronavirus in bats, Saudi Arabia. **EID** 19(11): 1819-1823.
- d. Zhou P, Fan H, Lan T, Yang X-L, Shi W-F, Zhang W, Zhu Y, Zhang Y-W, Xie Q-M, Mani S, Zheng X-S, Li B, Li J-M, Guo H, Pei G-Q, An X-P, Chen J-W, Zhou L, Mai K-J, Wu Z-X, Li D, Anderson DE, Zhang L-B, Li S-Y, Mi Z-Q, He T-T, Cong F, Fuo P-J, Huang R, Luo Y, Liu X-L, Chen J, Huang Y, Sun Q, Zhang X-L-L, Wang Y-Y, Xing S-Z, Chen Y-S, Sun Y, Li J, **Daszak P\***, Wang L-F\*, Shi Z-L\*, Tong Y-G\*, Ma J-Y\* (2018). Fatal Swine Acute Diarrhea Syndrome caused by an HKU2-related Coronavirus of Bat Origin. **Nature** 556: 255-258.

**2. Analyzing the process of disease emergence.** Emerging infectious diseases are a significant threat to global health. However, their emergence is sporadic, complex, and seemingly unpredictable. In the early 2000s I started to use analytical approaches to see if there are patterns in disease emergence, and if these are predictable. By collating a database of all known prior EID events, identifying their point origins, and correcting for reporting biases, I published the first ever predictive 'hotspots' maps of where disease emergence is most likely. Under various grants that I have led, or been a co-investigator on, I have published spatial analyses of the drivers of disease spread, and strategies to predict pandemic emergence.

- a. Kilpatrick AM, Chmura AA, Gibbons DW, Fleischer RC, Marra PP & **Daszak P** (2006). Predicting the global spread of H5N1 avian influenza. **PNAS** 103: 19368-19373.
- b. Morse SS, Mazet JAK, Woolhouse M, Parrish CR, Carroll D, Karesh WB, Zambrana-Torrel C, Lipkin WI, **Daszak P\*** (2012). Prediction and prevention of the next pandemic zoonosis. **Lancet** 380:1956-1965.
- c. **Daszak P\***, Zambrana-Torrel C, Bogich TL, Fernandez M, Epstein JH, Murray KA, Hamilton H (2013). Interdisciplinary approaches to understanding disease emergence: The past, present and future drivers of Nipah virus emergence. **PNAS** 110: 3681-3688
- d. Allen T, Murray KA, Zambrana-Torrel C, Morse SS, Rondinini C, Di Marco M, Breit N, Olival KJ, **Daszak P\*** (2017). Global hotspots and correlates of emerging zoonotic diseases. **Nature Comm** 8: 1124

**3. Studies of wildlife disease ecology to understand emerging zoonoses.** The majority of EIDs are zoonotic, with the majority of these originating in wildlife. In the 1990s, new collaborations among ecologists and medical researchers began to show that understanding disease dynamics in wildlife can allow better forecasting of disease risk in people. I reviewed this field in a paper in *Science* in 2000 and in a more recent paper in *Nature* on the links among biodiversity and health. During the last two decades, I have led collaborative research programs on how the ecology of specific wildlife-origin zoonoses can help explain patterns of risk to people. This includes my work in 4 R01s and as EHA institutional lead for USAID-EPT-PREDICT, and Chief of Party for USAID-IDEEAL. This work has led to strategies to estimate the diversity of yet-to-be discovered viruses, and a program to identify them (the Global Virome Project).

Program Director/Principal Investigator (Last, First, Middle): **Daszak, P.**

- a. **Daszak P\***, Cunningham AA, Hyatt AD (2000). Emerging infectious diseases of wildlife - threats to biodiversity and human health. **Science** 287: 443-449
- b. Keesing F, Belden LK, **Daszak P**, Dobson A, Harvell CD, Holt RD, Hudson P, Jolles A, Jones KE, Mitchell CE, Myers SS, Bogich T & Ostfeld RS. (2010). Impacts of biodiversity on the emergence and transmission of infectious diseases. **Nature** 468:647-652.
- c. Anthony SJ, Epstein JH, Murray KA, Navarrete-Macias I, Zambrana-Torrel CM, Solovyov A, Ojeda-Flores R, Arrigo NC, Islam A, Ali Khan S, Hosseini P, Bogich TL, Olival KJ, Sanchez-Leon MD, Karesh W, Goldstein T, Luby SP, Morse SS, Mazet JAK, **Daszak P**, Lipkin WI. (2013). A strategy to estimate unknown viral diversity in mammals. **MBio** 4(5): e00598-13.

#### **D. Additional Information: Research Support and/or Scholastic Performance**

##### **Ongoing Research Support**

USAID Emerging Pandemic Threats      Mazet (PI)      10/01/14 – 09/30/19  
 PREDICT-2

The goal of this work is to conduct surveillance for novel pathogens in wildlife, livestock and people; characterize human risk behavior; analyze EID risk; and design interventions in >20 countries  
 Role: PI on Subcontract

1R01 AI110964      Daszak (PI)      06/01/14 – 05/31/19  
 Understanding the Risk of Bat Coronavirus Emergence

The goal of this work is to conduct ecological and virological studies on bats in China that harbor SARS-like coronaviruses, and conduct behavioral risk surveys and testing in people, with a goal of identifying risk factors for further spillover of SARS-like CoVs, and help identify the likely drivers of the SARS-CoV outbreak in 2003.  
 Role: PI

USAID 1414374 (RDMA, Thailand)      Daszak (CoP)      10/01/13 - 03/30/19  
 Infectious Disease Emergence and Economics of Altered Landscapes (IDEEAL)

The goal of this cooperative agreement is to analyze how land use change affects disease risk in SE Asia, and how economic costs of disease can be used to develop novel intervention policies.  
 Role: Chief of Party

##### **Completed Research Support**

NSF DEB 1414374      Perrings (PI)      10/15/14 - 04/14/18  
 US-UK Collab: Risks of Animal and Plant Infectious Diseases through Trade (RAPID Trade)

The goal of this NSF-NIH-USDA EEID award, joint with a UK BBSRC grant is to analyze and model how policy changes to trade affect emerging disease risk globally  
 Role: Co-Investigator

HDTRA1      Allen (PI)      04/15/15 - 04/14/17  
 Global Rapid Identification of undiagnosed EID Events

The goal of this project was to design software that can be used in the DoD biosurveillance ecosystem (BSVE) to rapidly diagnose novel EID events.  
 Role: Co-Investigator

1R01GM100471 (NIGMS)      Perrings (PI)      09/15/11-06/30/15  
 MASpread: Modeling Anthropogenic Effects in the Spread of Infectious Disease

The goal of this project was to develop novel approaches to modeling and analyzing disease spread and the social decisions involved in control  
 Role: Co-Investigator

NSF      Daszak (PI)      07/01/10-06/30/15

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## EcoHealthNet - a Research Coordination Network

Funding for student exchange and workshops to fuse veterinary science, ecology and human medical sciences

Role: PI

USAID Emerging Pandemic Threats Mazet (PI) 10/01/09 – 09/30/14  
 PREDICT-1

The goal of this work was to conduct surveillance for novel pathogens in wildlife, livestock and people in developing countries

Role: PI on Subcontract

2 R01TW005869 Daszak (PI) 09/01/08 – 08/31/13

The Ecology, Emergence and Pandemic Potential of Nipah virus in Bangladesh

This project involved mathematical modeling and fieldwork on the dynamics of Nipah virus in Bangladesh

Role: PI

NSF DEB-1257513 Daszak (PI) 08/15/12-07/31/13

US-China Ecology and Evolution of Infectious Diseases Collaborative Workshop; Kunming, China

The goal of this work was to organize a workshop among NIH, NSF, leading US and Chinese scientists to discuss potential for a jointly funded NIH-NSF-China funding mechanism

Role: PI

1 R01AI079231 (NIAID) Daszak (PI) 09/18/08 – 08/31/13

Risk of viral emergence from bats.

The goal was to model hotspots for bat viral diversity, identify & characterize new bat viruses & understand their pathology

Role: PI

NSF BCS 0826779 Daszak (PI) 10/01/08 – 03/31/12

AOC - HSD – Collaborative Research: Human-related factors affecting emerging infectious diseases

The goal of this work was to analyze how socio-economic and environmental drivers predict risk of EIDs

Role: PI on lead proposal

R01TW005869 - supplemental Daszak (PI) 09/01/08 – 08/31/11

Supplemental funding: Predicting the risk of global H5N1 spread

This project involved mathematical modeling and fieldwork in Bangladesh and China to understand risk of H5N1 spread.

Role: PI

NSF EF-062239 Kilpatrick (PI) 09/01/06 - 08/30/11

Predicting spatial variation in West Nile virus transmission

The goal was to study interaction among WNV vector, reservoir host populations across an urban-to-rural gradient.

Role: Co-PI

R01 TW05869 (Fogarty Intl. Ctr.) Daszak (PI) 08/01/02 - 05/31/07

Anthropogenic change &amp; emerging zoonotic paramyxoviruses

The goal was to identify the cause of emergence of Nipah and Hendra viruses in Malaysia and Australia.

Role: PI

NSF HSD 0525216 Daszak (PI) 10/15/05 - 10/14/06

Collaborative Research: Socio-Economic and Environmental Drivers of Emerging Diseases

The goal of this work was to analyze patterns of disease emergence globally leading to development of a global hotspots map of disease emergence.

Role: PI