



EcoHealth Alliance

Identifying predictable patterns in disease emergence

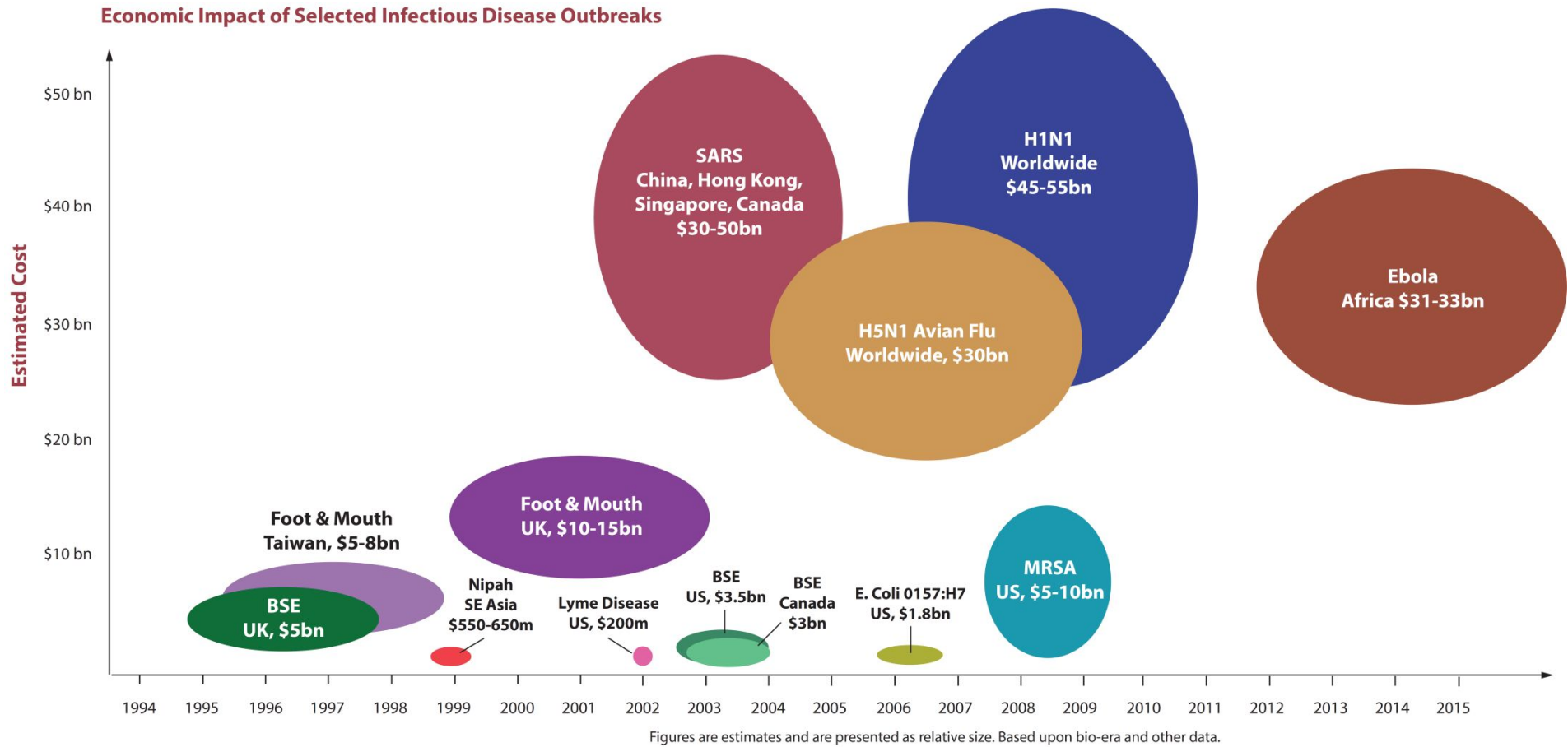
Peter Daszak

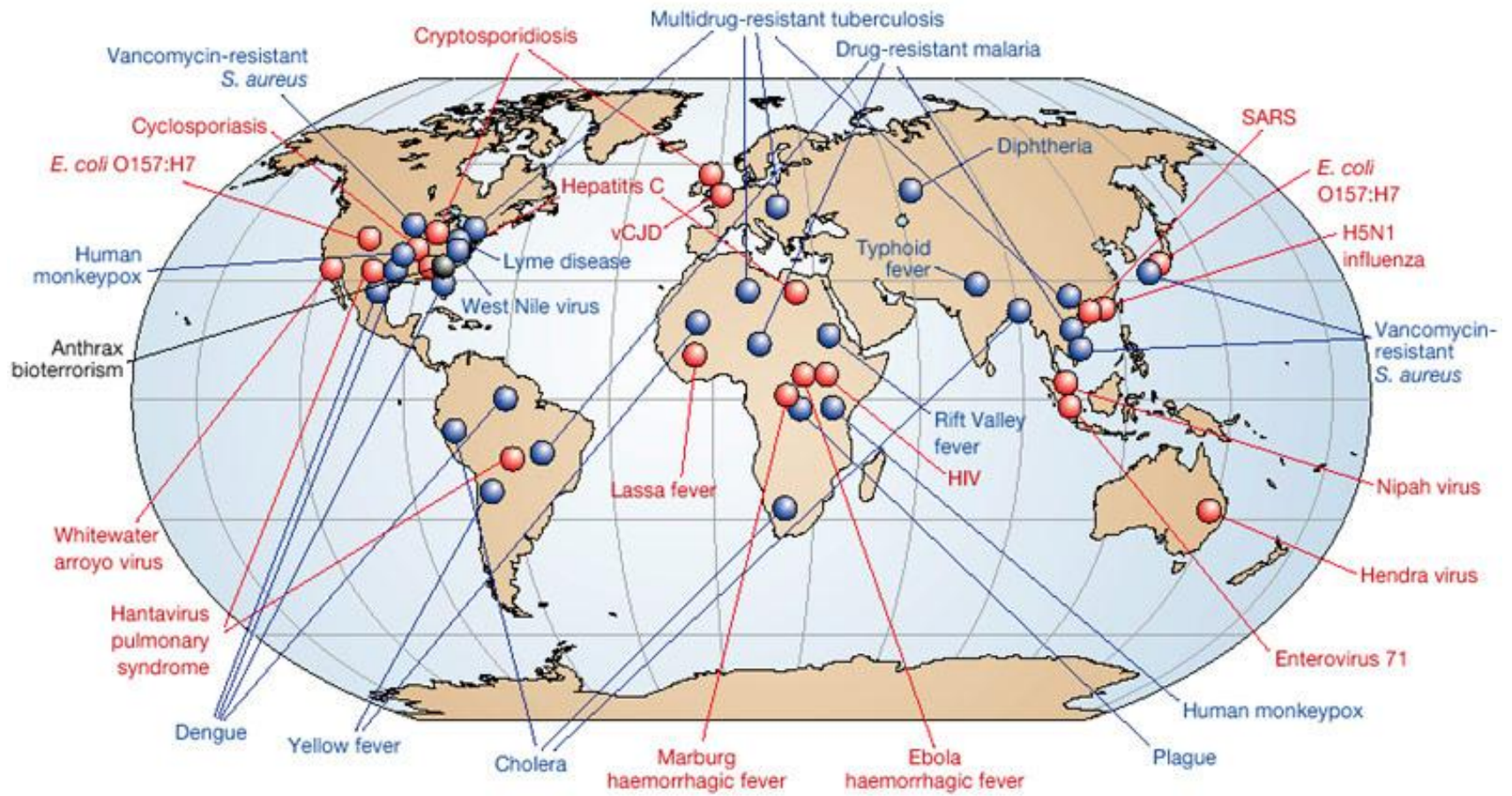
EcoHealth Alliance, New York, USA

www.ecohealthalliance.org

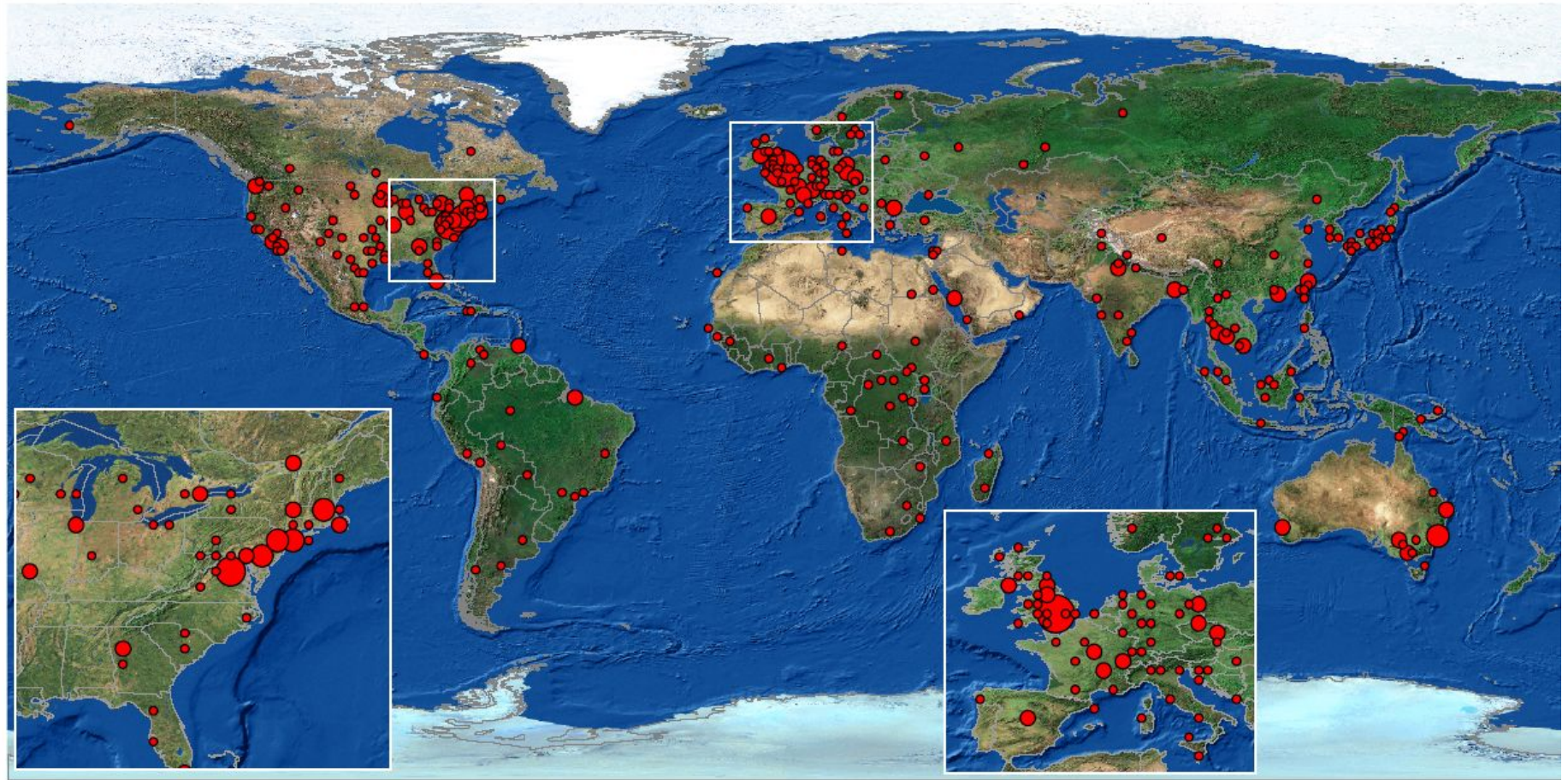


Economic Impact of Emerging Diseases

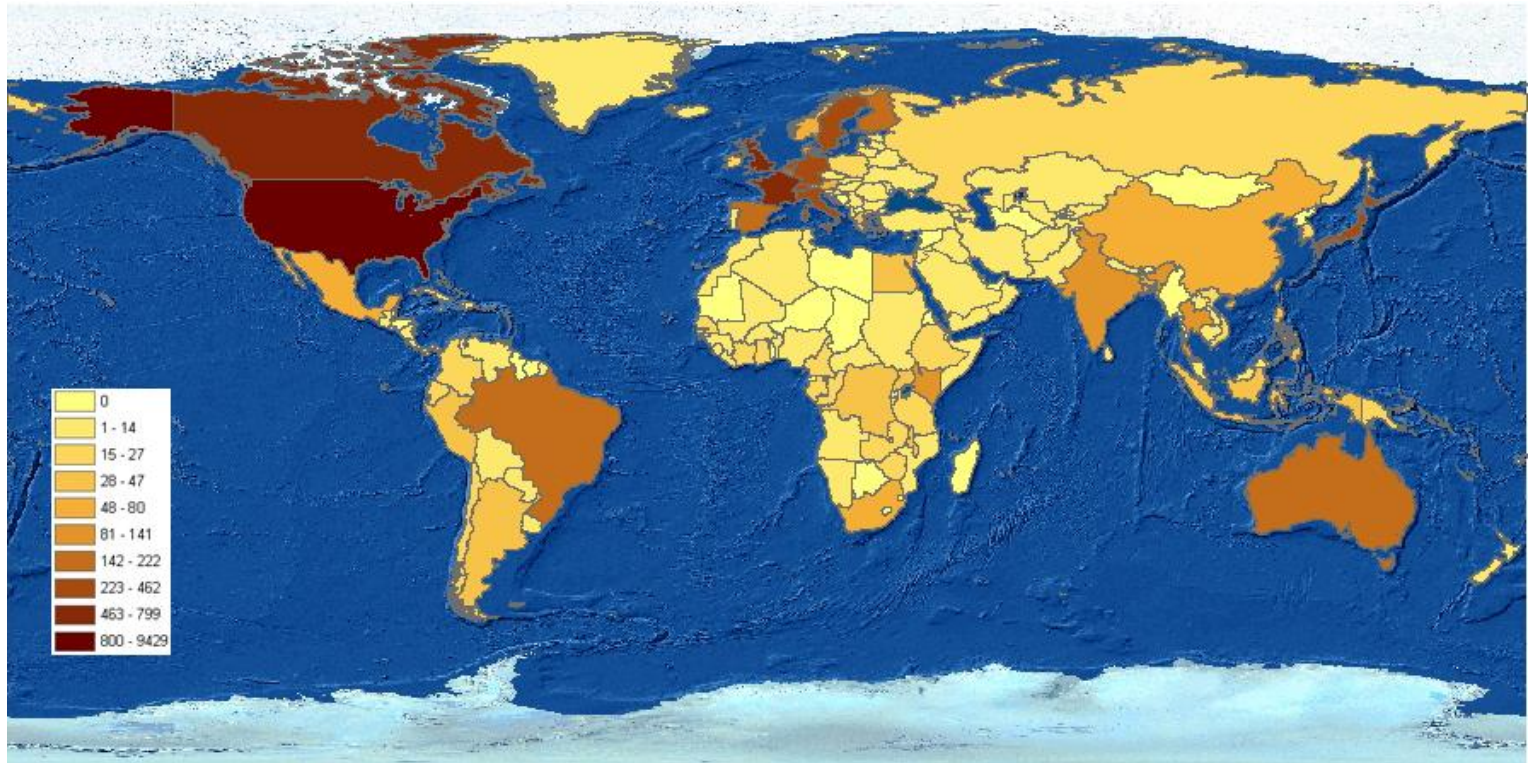




Total EID events ● 1 ● 2-3 ● 4-5 ● 6-7 ● 8-11

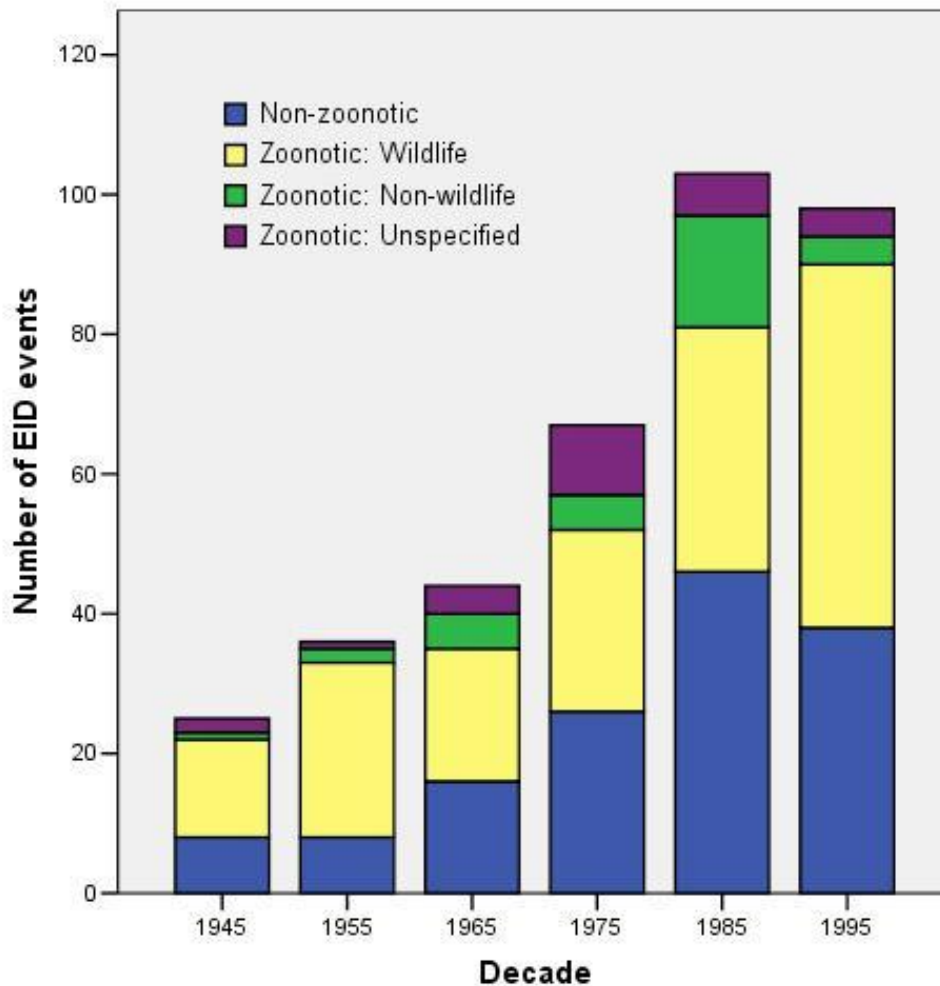


Spatial reporting bias by country

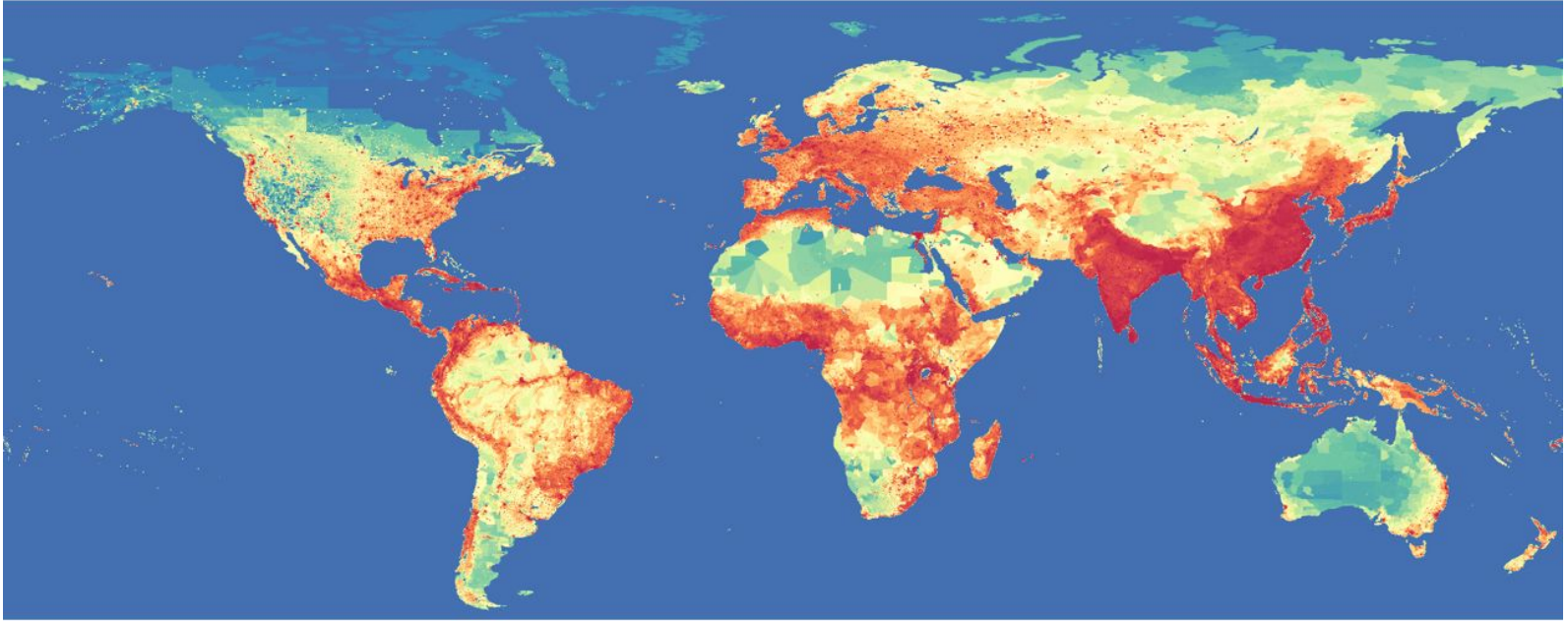


Each author's country from every *JID* paper 1973-2004

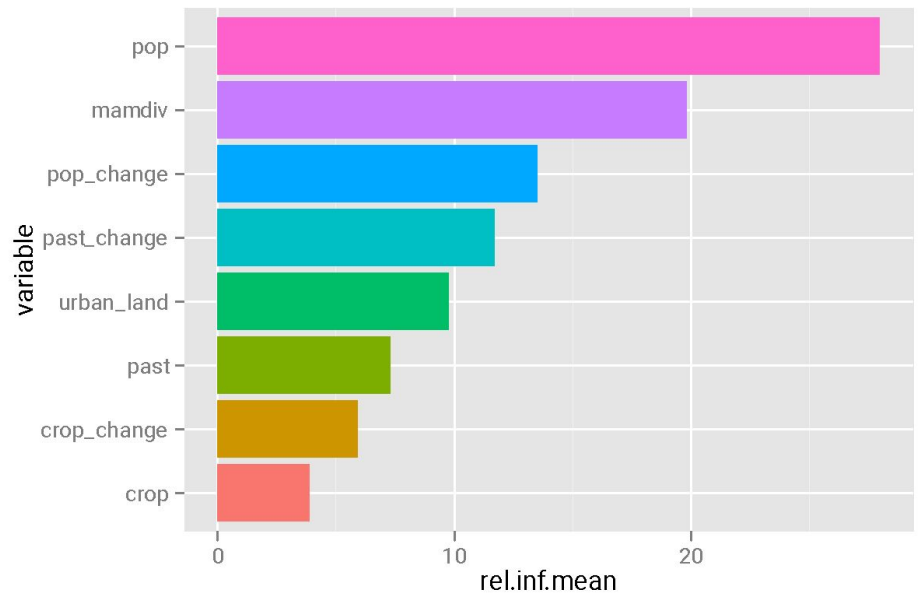
Temporal patterns in EID events



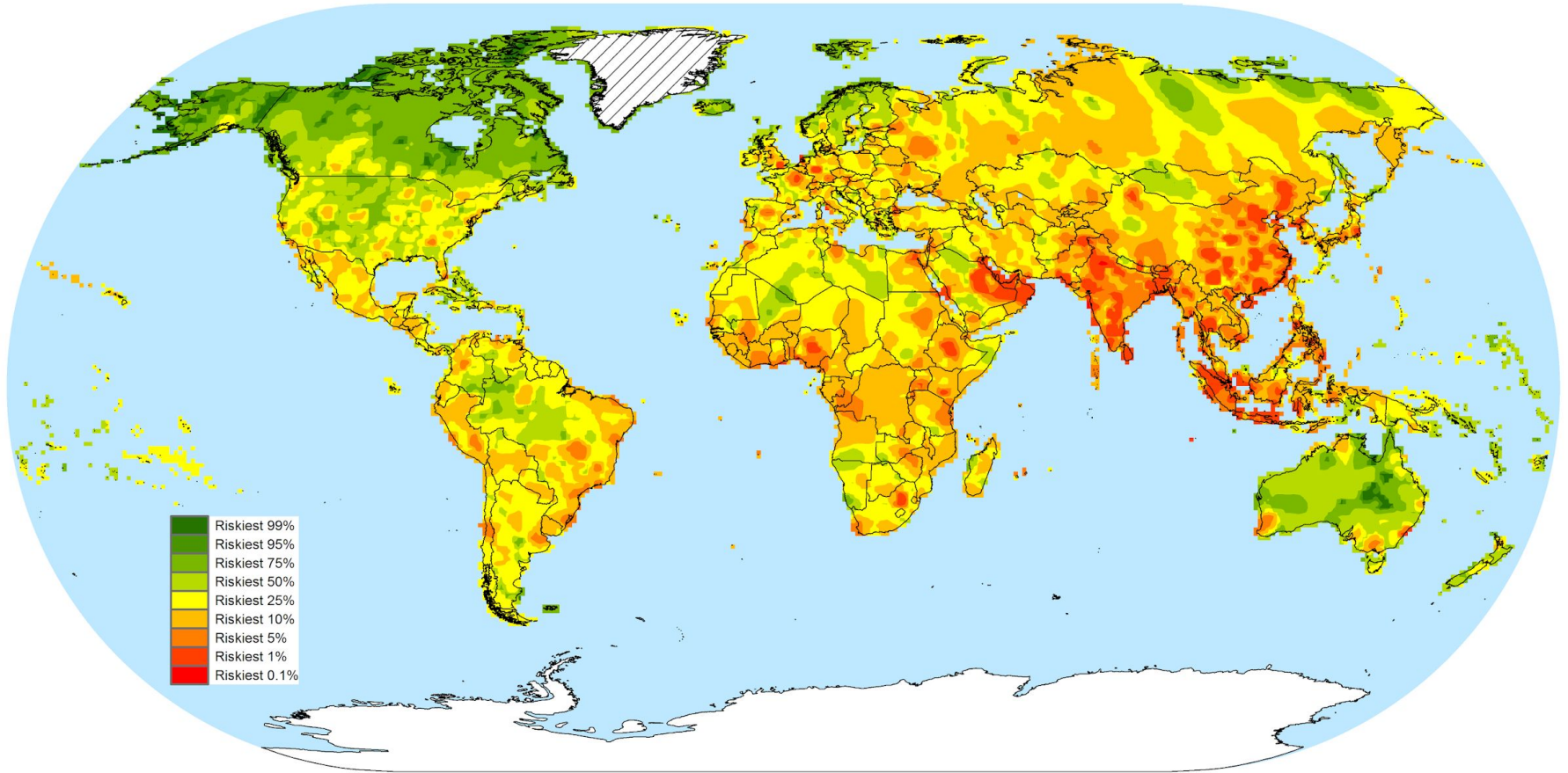
- EID events have increased over time, correcting for reporter bias ($\text{GLM}_{\text{P, JID}}$ $F = 86.4$, $p < 0.001$, $d.f. = 57$)
- ~5 new EIDs each year
- ~3 new Zoonoses each year
- **Zoonotic EIDs from wildlife** reach highest proportion in recent decade



	relative influence (%)	std. dev.
population	27.99	2.99
mammal diversity	19.84	3.30
change: pop	13.54	1.54
change: pasture	11.71	1.30
urban extent	9.77	1.62
...	...	...

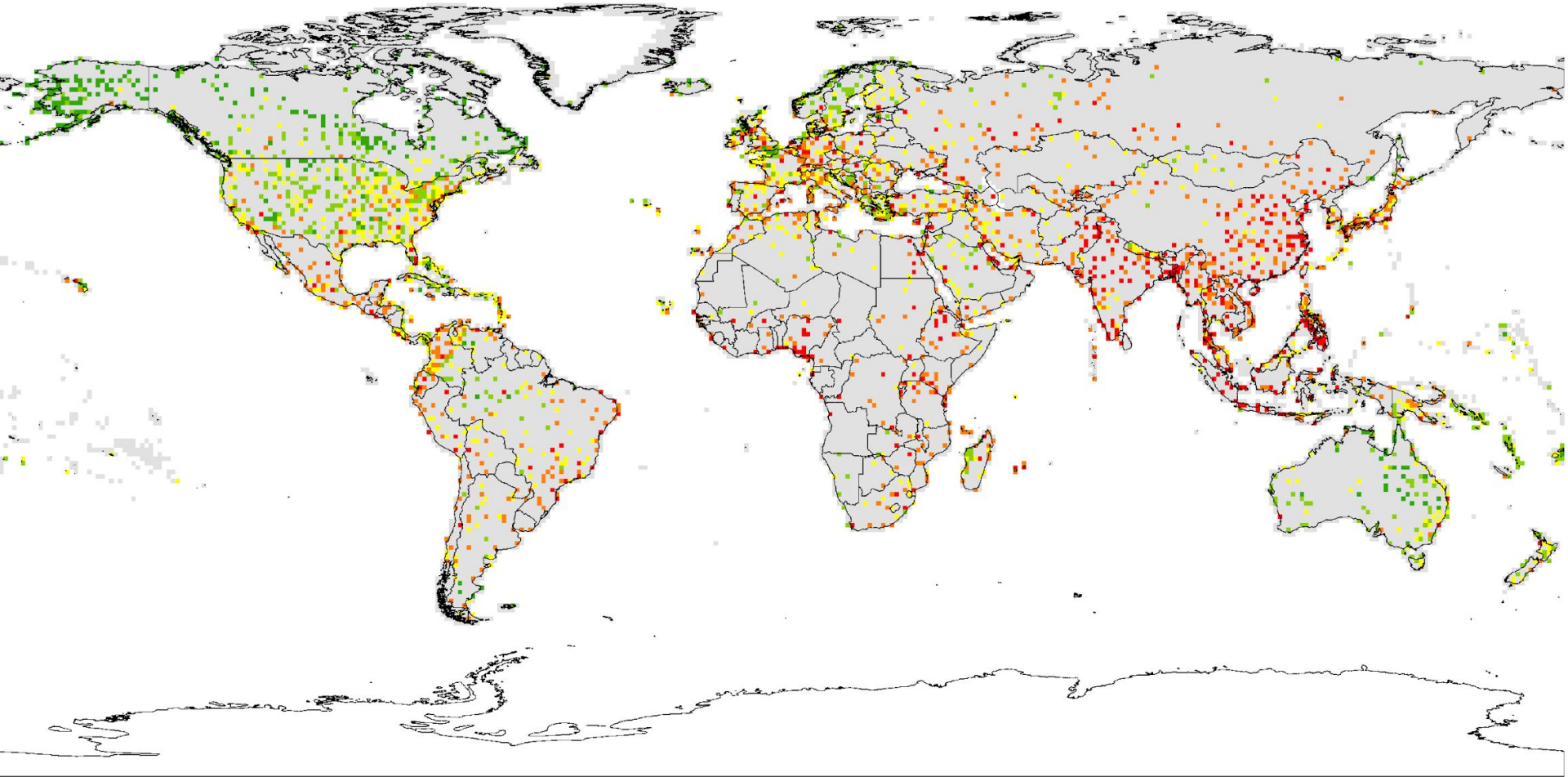


Global Vulnerability: Zoonotic EIDs

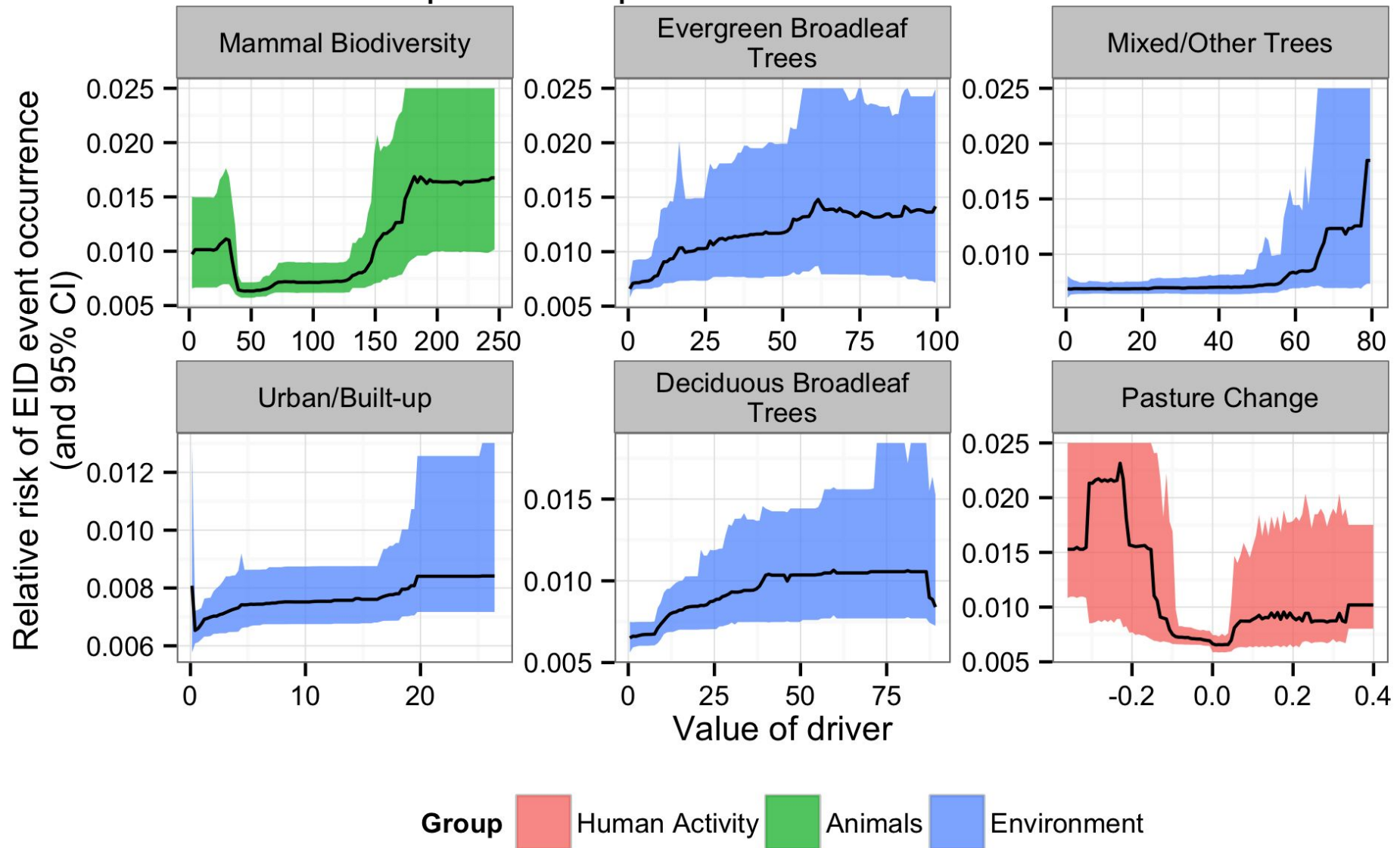


Hotspot risk + travel and trade out of a region

EID risk per airport



Partial dependence plot for zoonotic EID event occurrence



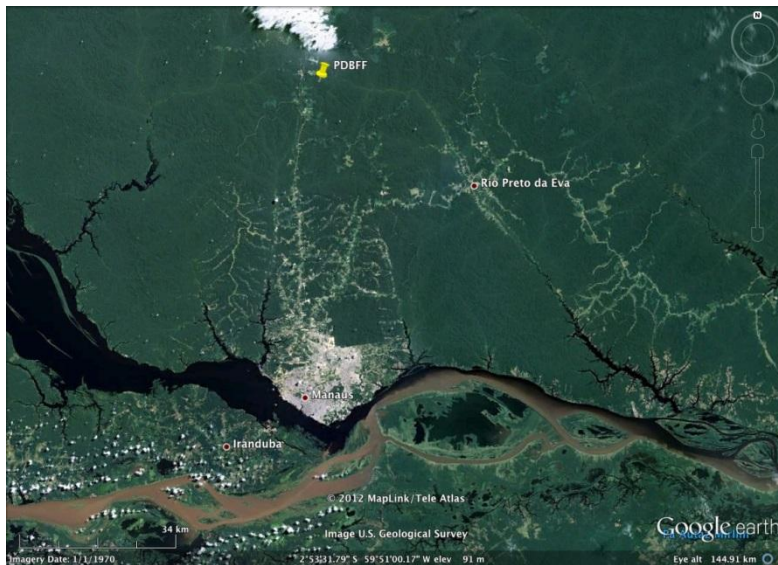
y-axis: relative probability of an EID event in a grid cell with this characteristic
x-axis: min. to max. values of each driver (except 'Pasture Change')
Plots show effect relative to human pop. Distribution, factoring out reporting bias.
Model: 2 levels of interaction between drivers,

Ground-truthing hypotheses: “DEEP FOREST” project

Borneo, Kinabatangan R.



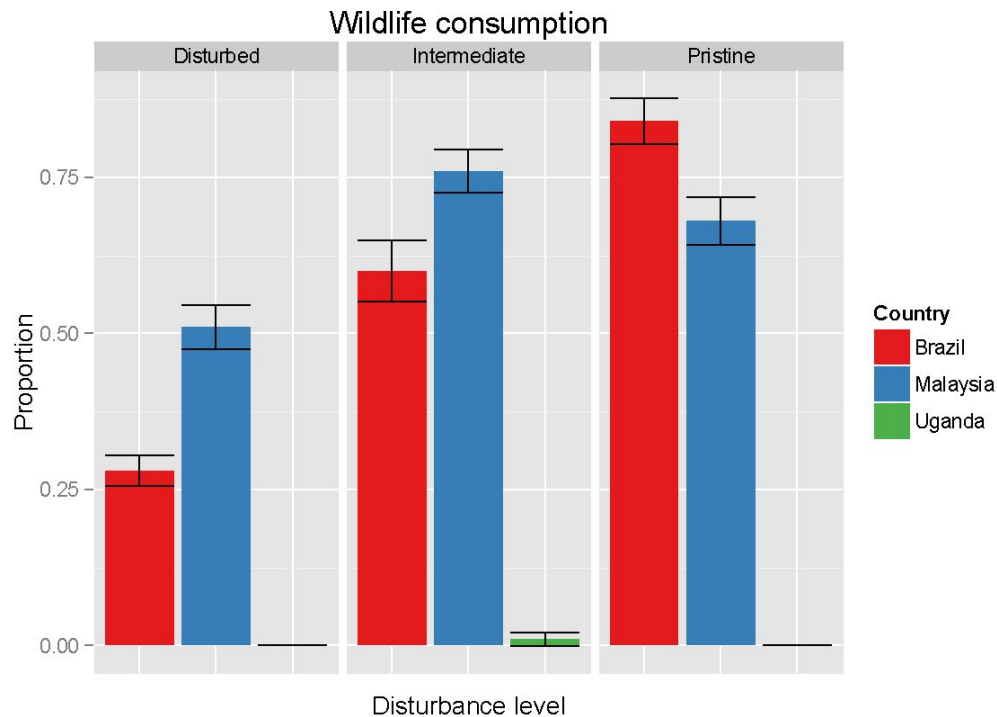
Brazil, Amazon basin



Uganda, Bwindi Impenetrable Forest



Q1. Have you eaten any wildlife during the past year?



Take homes:

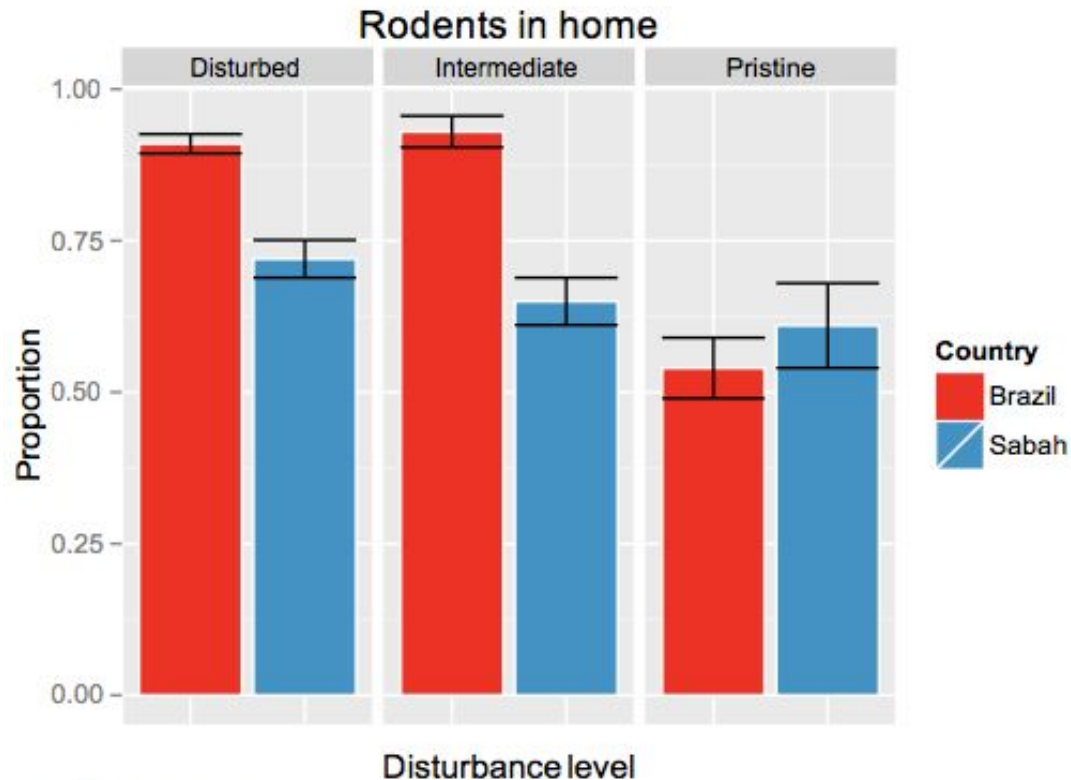
- Eating wildlife is more common in more pristine areas.
- Overall difference in the proportion of people reporting eating wildlife between countries
- Significant interaction effect which suggests that this trend was not consistent across the gradient levels.

Table 1, Table of Deviance

<u>Term</u>	<u>Df</u>	<u>Dev Resid</u>	<u>Df</u>	<u>Resid Dev</u>	<u>p</u>
NULL			840	1162.0	
Gradient	2	115.232	838	1046.8	***
Country	1	24.633	837	1022.1	***
Country*Gradient	2	12.896	835	1009.2	**

Note: The dependent variable is wildlife consumption coded so that 0 = Not in the last year and 1 = Sometime in the last year. Significance codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Q2. During the past year, have you seen rodents inside your home?



Take homes:

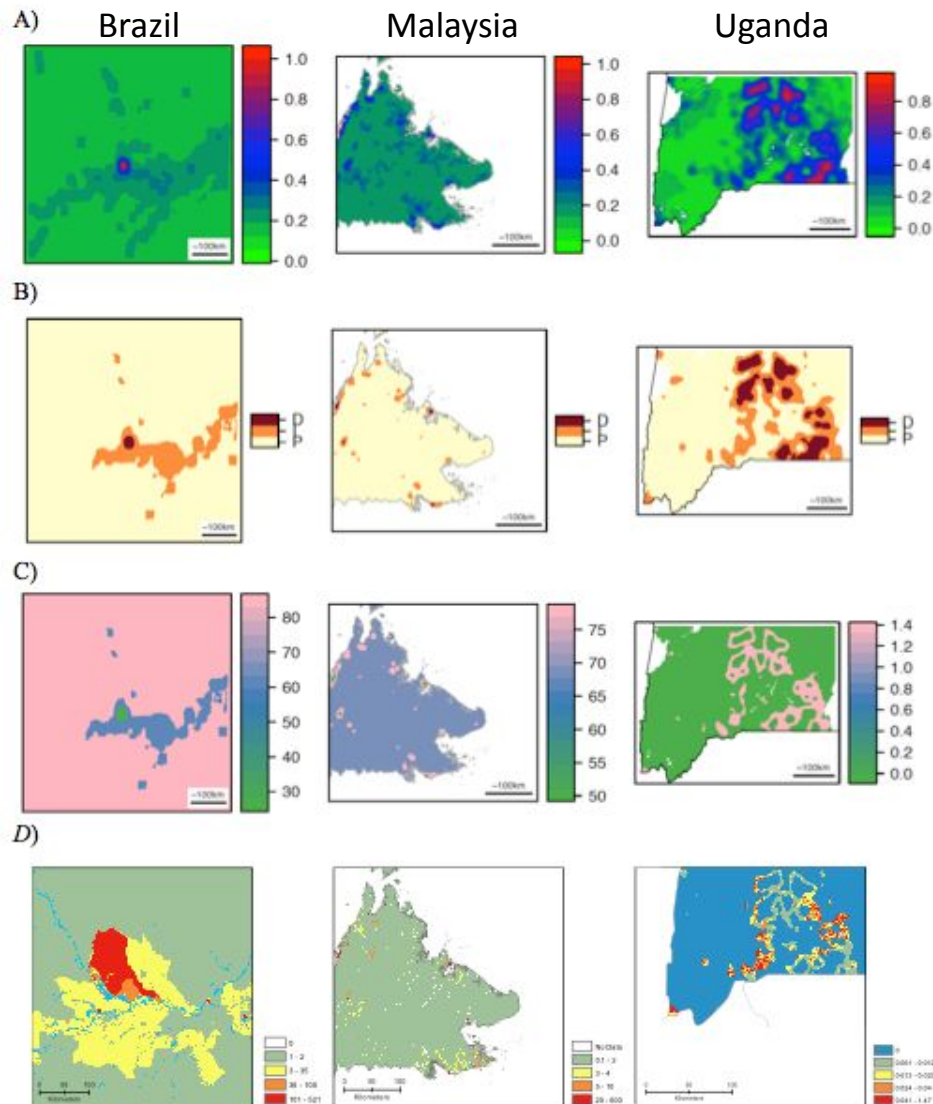
- Rodents entering into the home is more common in more disturbed areas
- People in the disturbed and intermediate areas are more likely to report rodents coming into their homes than people in the pristine areas

Table 3, Table of Deviance

<u>Term</u>	<u>Df</u>	<u>Dev Resid</u>	<u>Df</u>	<u>Resid Dev</u>	<u>p</u>
NULL			874	933.35	
Gradient	2	38.155	872	895.19	***
Country	1	43.348	871	851.84	***
Country*Gradient	2	14.952	869	836.89	***

Note: The dependent variable is whether a respondent reports wildlife coming into their home coded so that 0 = Never and 1 = Sometimes

DEEP FOREST: Mapping human-animal contact risk



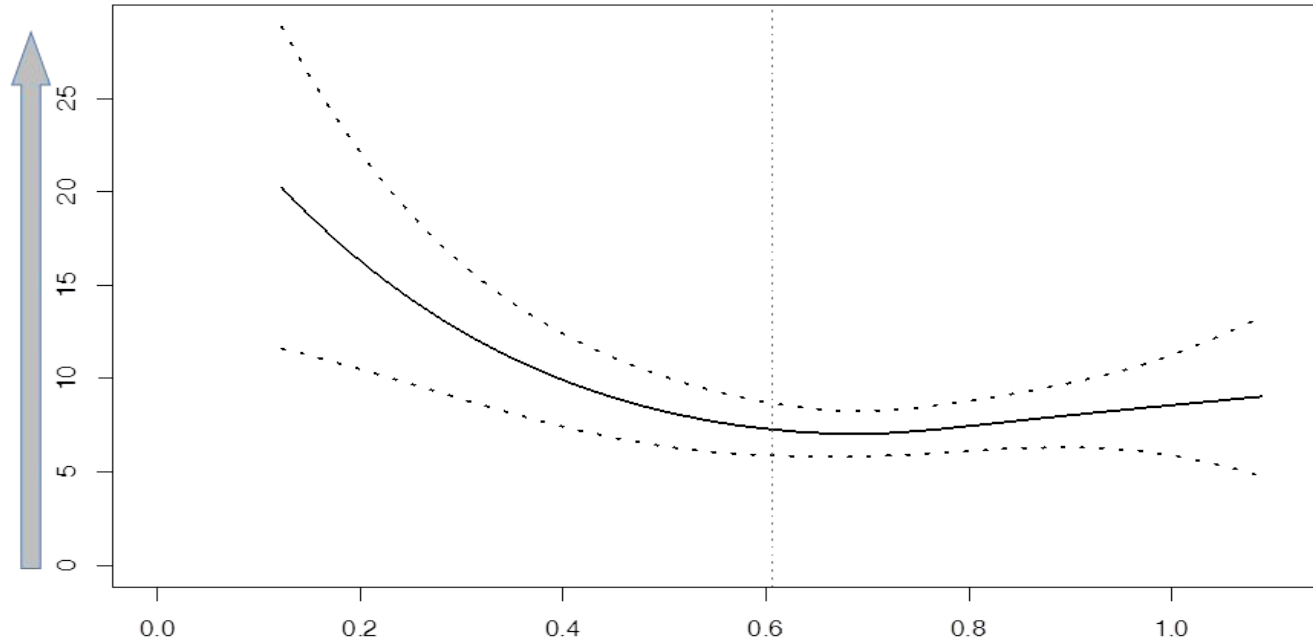
A) Land use change (raw LDI)

B) Reclassified LDI to match disturbance gradient levels

C) Wildlife consumption map from our DF surveys per gradient.

D) Map of relative human-animal contact risk (derived from proportion of people consuming wildlife x pop density)

Expected Number of Shared Viruses

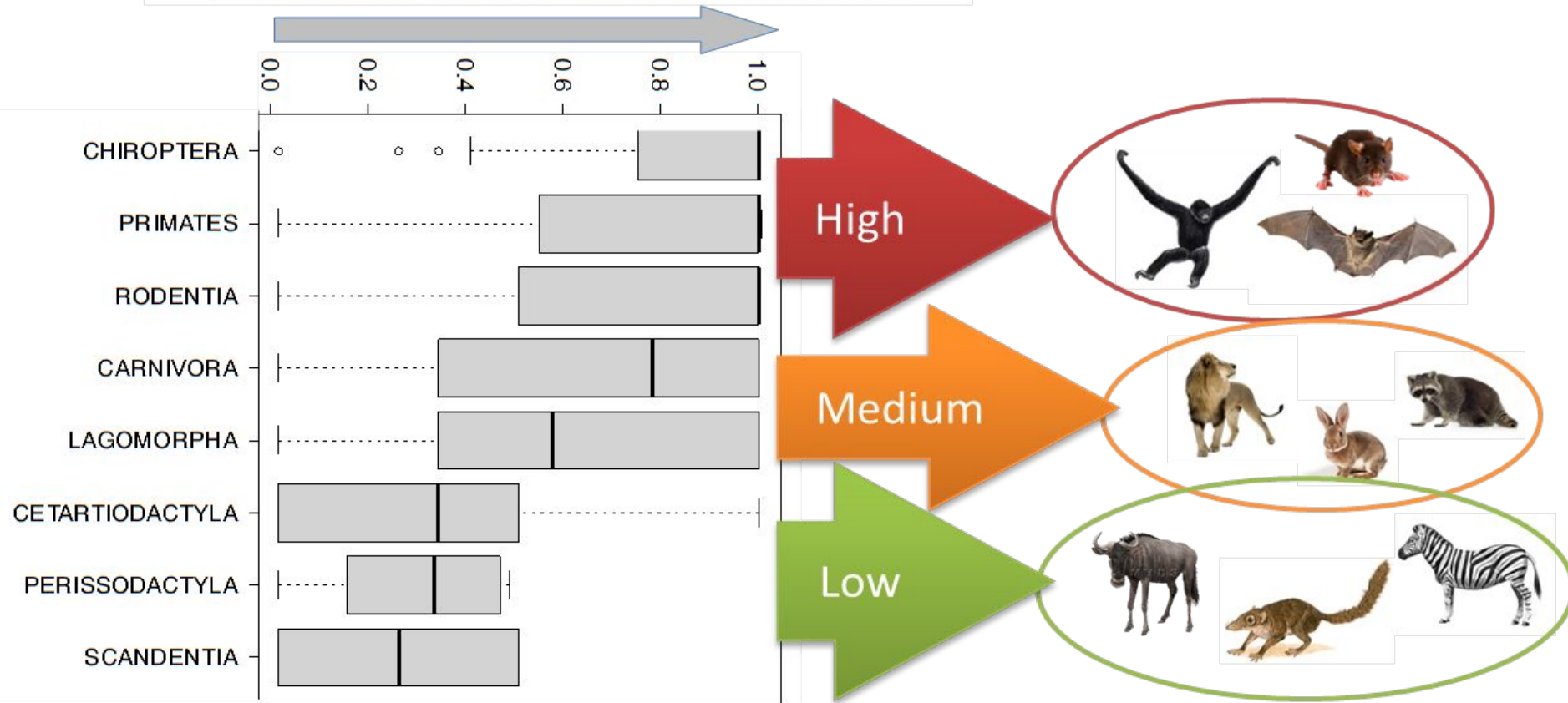


Phylogenetic Distance to Humans

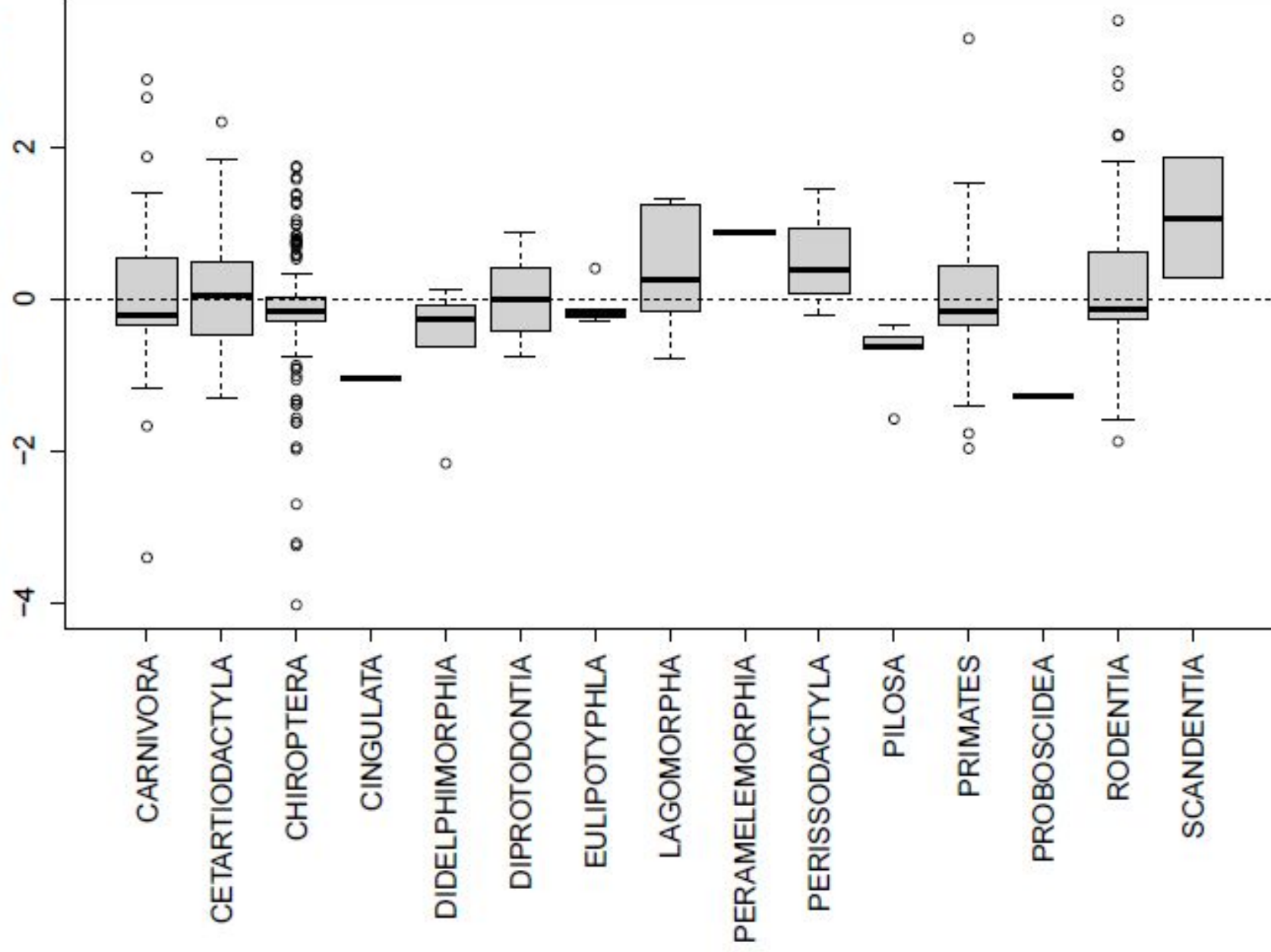


Which species will the next pandemic emerge from?

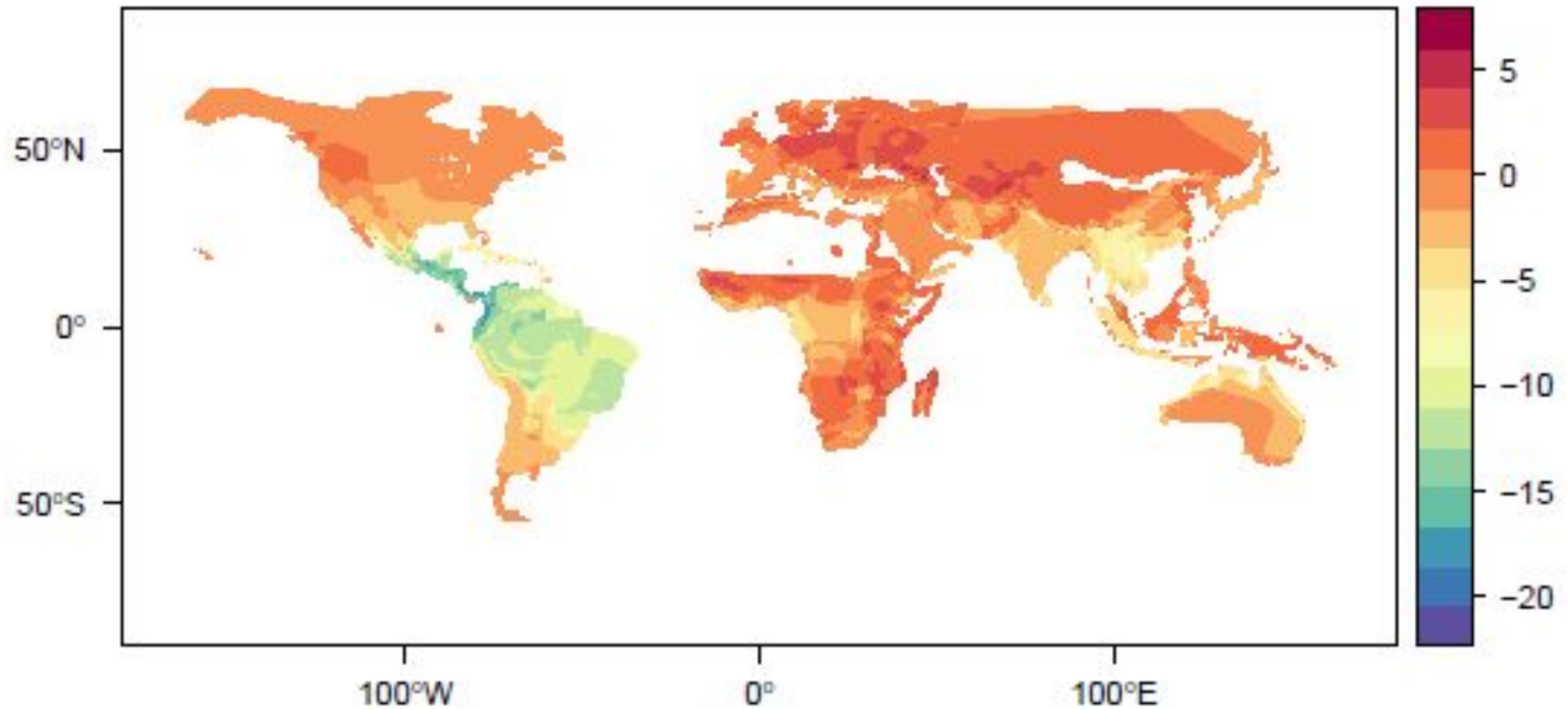
Proportion of viruses shared with humans



Model Residuals, Zoonotic Viruses per Species

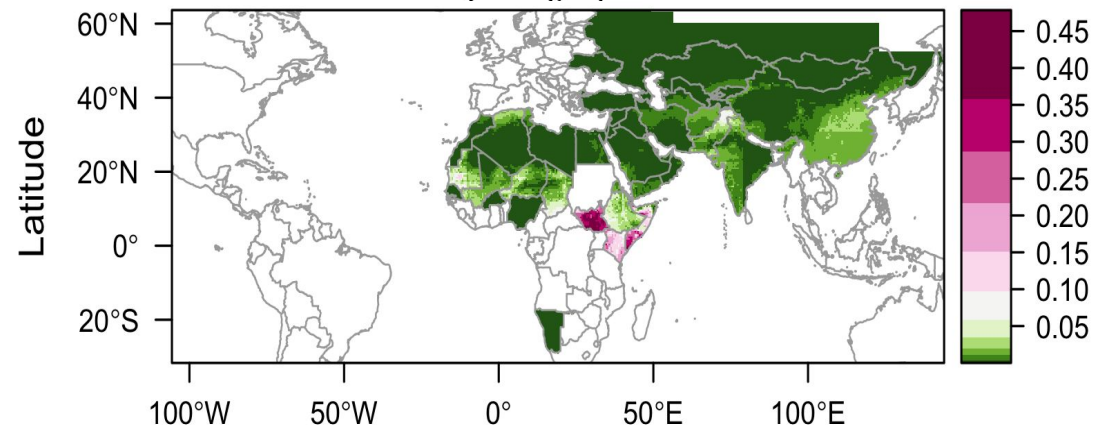
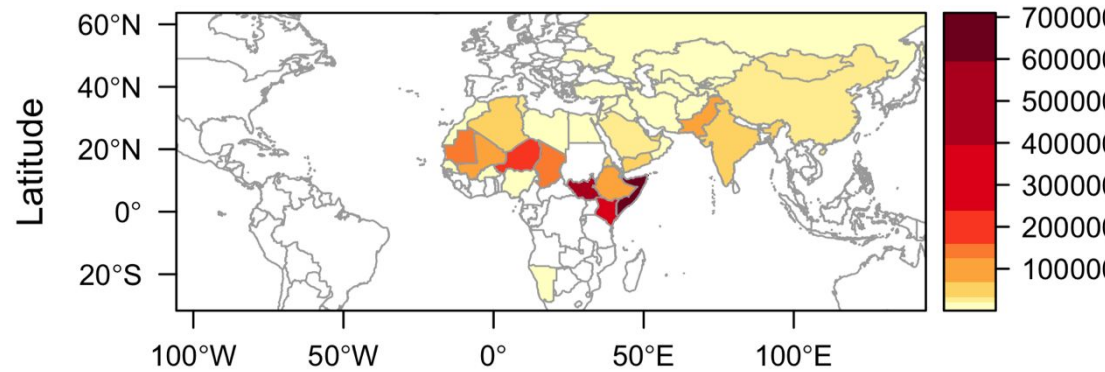
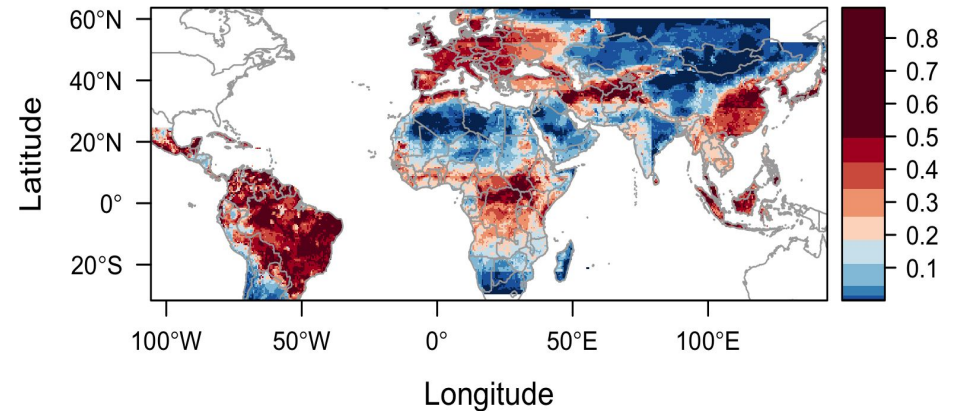


Bats: missing zoonoses



Where to look for specific pathogen groups

- Modeled distribution of MERS-CoV bats
- Camel production (FAO)
- Modeled risk of MERS spillover (horn of Africa)



The Great Donald Rumsfeld

“There are known knowns; there are things we know that we know.

There are known unknowns; that is to say, there are things that we now know we don't know.

But there are also unknown unknowns – there are things we do not know we don't know.”

*US Secretary of Defense Donald Rumsfeld,
Press briefing on links between Iraq and
WMD, February 12, 2002*

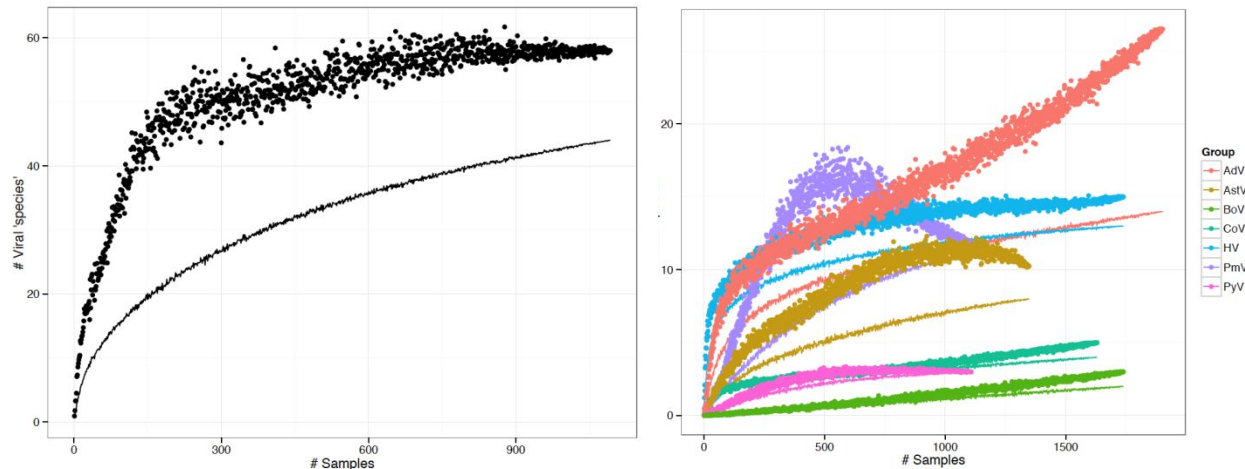


A Strategy To Estimate Unknown Viral Diversity in Mammals



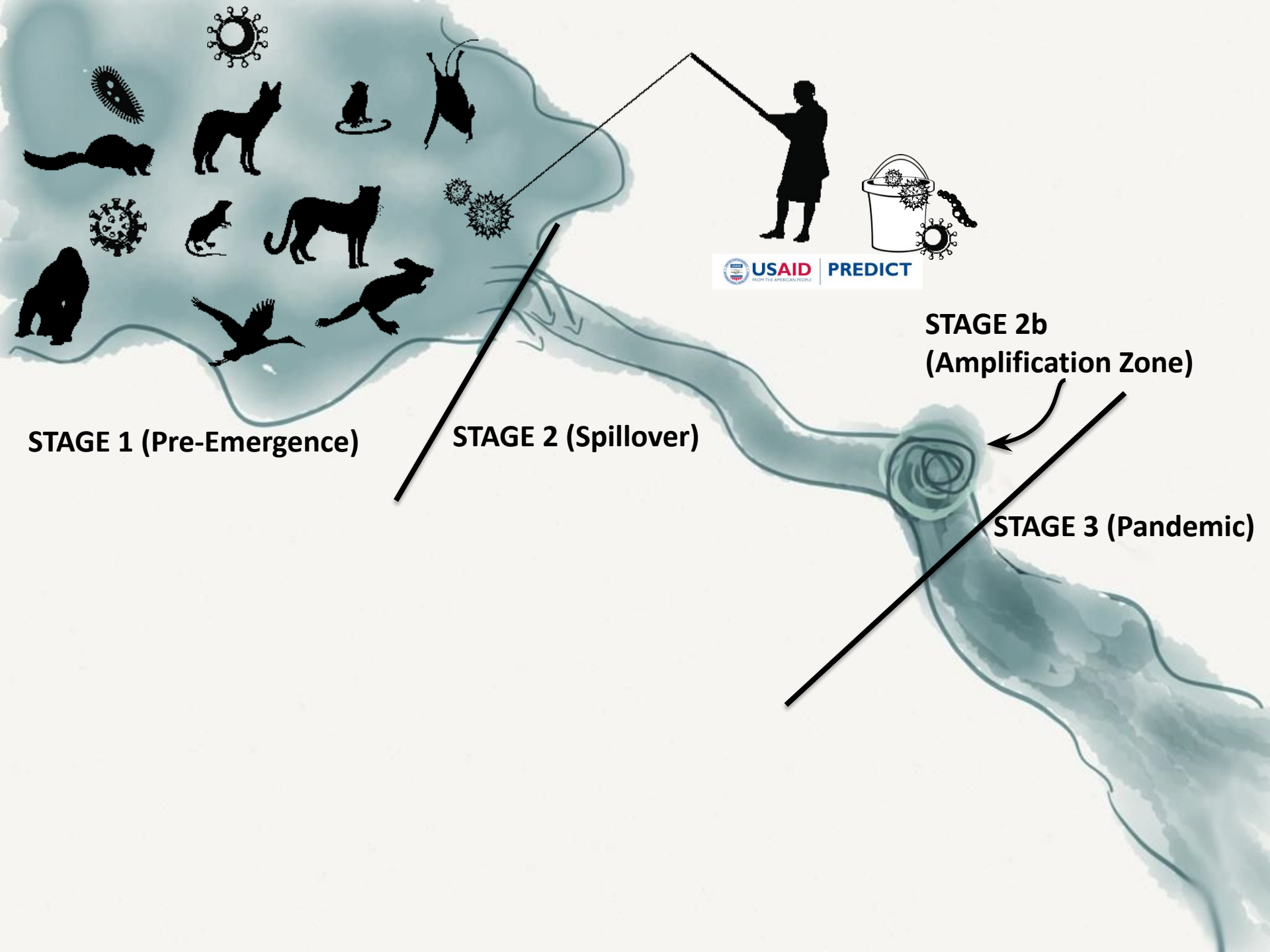
Simon J. Anthony,^{a,b} Jonathan H. Epstein,^b Kris A. Murray,^b Isamara Navarrete-Macias,^a Carlos M. Zambrana-Torrel,^b Alexander Solovyov,^a Rafael Ojeda-Flores,^c Nicole C. Arrigo,^a Ariful Islam,^b Shahneaz Ali Khan,^d Parvize Hosseini,^b Tiffany L. Bogich,^{e,f} Kevin J. Olival,^b Maria D. Sanchez-Leon,^{a,b} William B. Karesh,^b Tracey Goldstein,^g Stephen P. Luby,^h Stephen S. Morse,^{g,i} Jonna A. K. Mazet,^g Peter Daszak,^b W. Ian Lipkin^a

Center for Infection and Immunity, Mailman School of Public Health, Columbia University, New York, New York, USA^a; EcoHealth Alliance, New York, New York, USA^b; Facultad de Medicina Veterinaria and Zootecnia, Universidad Nacional Autónoma de México, Ciudad Universitaria, Mexico City, Distrito Federal, Mexico^c; Chittagong



- ~58 unknown viruses in *Pteropus giganteus*
- ~320,000 unknown viruses in all mammals; ~72,152 in the 1,244 known bat species
- One-off cost to identify 100% = \$6.8 Billion
- One-off cost to identify 85% = \$1.4 Billion
- Cost of SARS = \$10-50 Billion
- ~250 bat viruses in last 5 years, 530 total = 7% of the estimated #





Follow up Genetic and Experimental studies (post-PREDICT) to Further Assess Spillover Potential

With each step, increased risk possible

- Virus isolation
- Sequence whole genome
- With temporally sampled viruses, measure mutation rates and phylodynamics
- Sequence receptor binding domain, if known
- Structural comparison with human receptors (e.g. 3D models, *In silico*)
- Cell line infection experiments (*in vitro*)
- Humanized mice and other animal experiments

Ranking risk for zoonotic potential of novel viruses

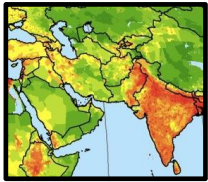
**VIRUS-INDEPENDENT
TRAITS**

+

VIRUS-SPECIFIC TRAITS

=

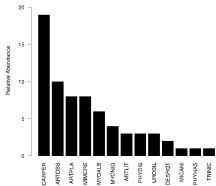
RISK OF SPILLOVER



Geographic hotspots for emergence



Host species traits, geographic range, relatedness

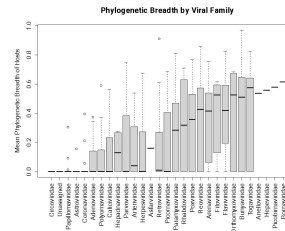
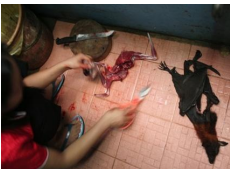


Host abundance

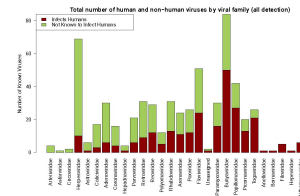
% pos

Viral prevalence in host

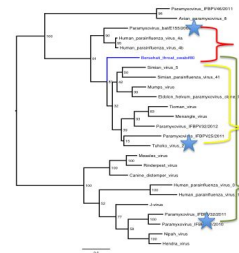
Epidemiological/
contact interface



Host breadth/plasticity



Proportion known zoonoses in virus family

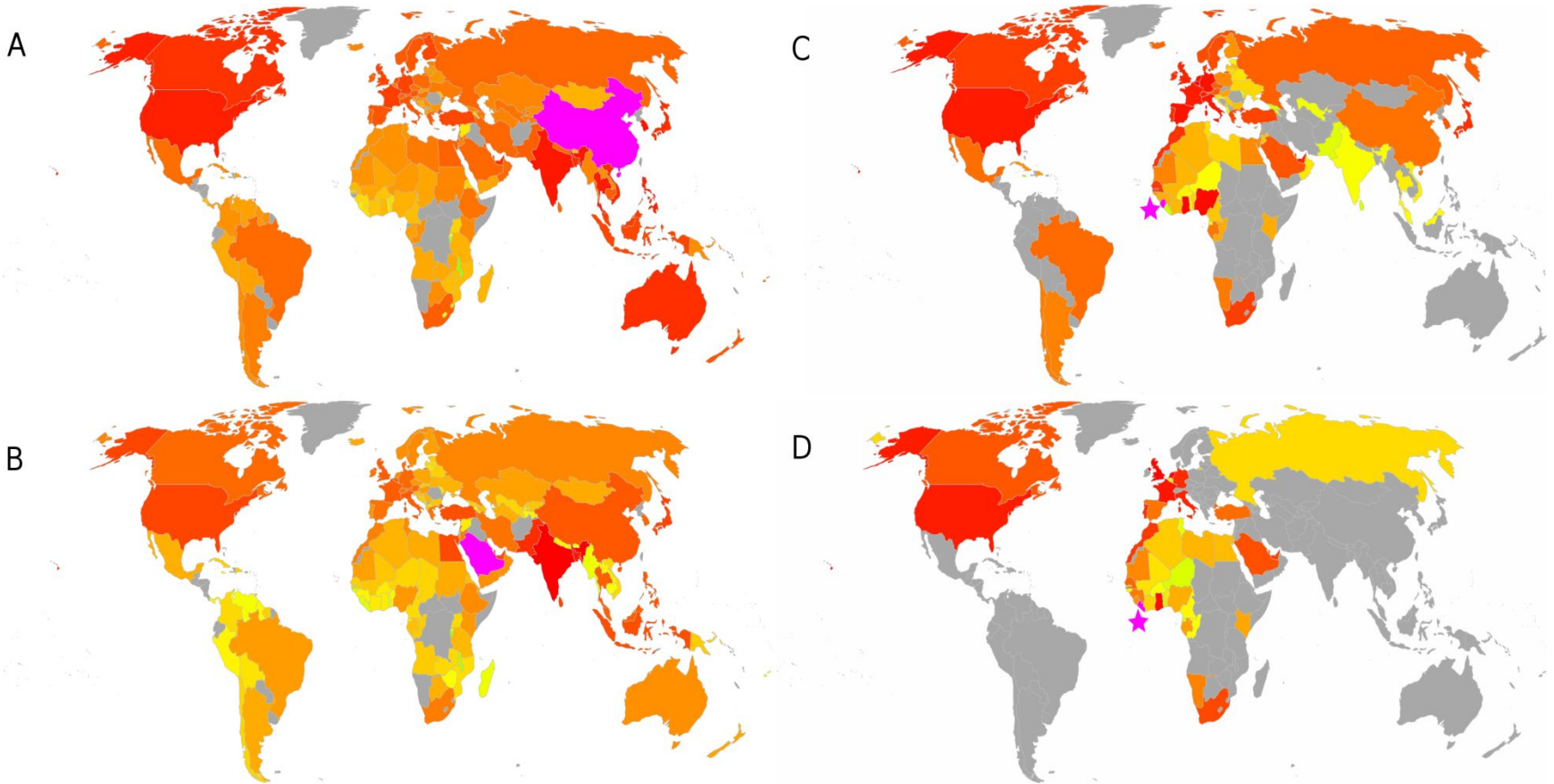


Phylogenetic relatedness to known zoonoses



Other virus-specific traits

Where would a new virus travel to?



(A) Influenza A/H7N9, China; (B) MERS, S. Arabia; (C) Ebola virus, S. Leone; (D) Ebola, Liberia

Bats Are Natural Reservoirs of SARS-Like Coronaviruses

Wendong Li,^{1,2} Zhengli Shi,^{2*} Meng Yu,³ Wuze Ren,² Craig Smith,⁴ Jonathan H. Epstein,⁵ Hanzhong Wang,² Gary Cramer,³ Zhihong Hu,² Huajun Zhang,² Jianhong Zhang,² Jennifer McEachern,³ Hume Field,⁴ Peter Daszak,⁵ Bryan T. Eaton,³ Shuyi Zhang,^{1,6*} Lin-Fa Wang^{3*}

Severe acute respiratory syndrome (SARS) emerged in 2002 to 2003 in southern China. The origin of its etiological agent, the SARS coronavirus (SARS-CoV), remains elusive. Here we report that species of bats are a natural host of coronaviruses closely related to those responsible for the SARS outbreak. These viruses, termed SARS-like coronaviruses (SL-CoV), display greater genetic variation than SARS-CoV isolated from humans or from civets. The human and civet isolates of SARS-CoV nestle phylogenetically within the spectrum of SL-CoVs, indicating that the virus responsible for the SARS outbreak was a member of this coronavirus group.

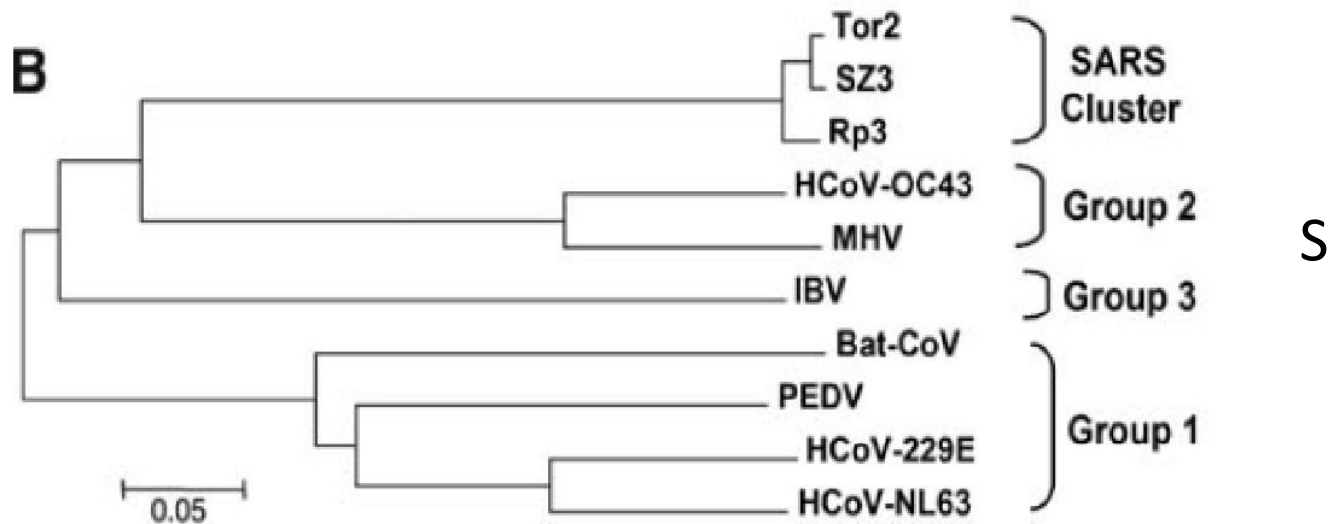
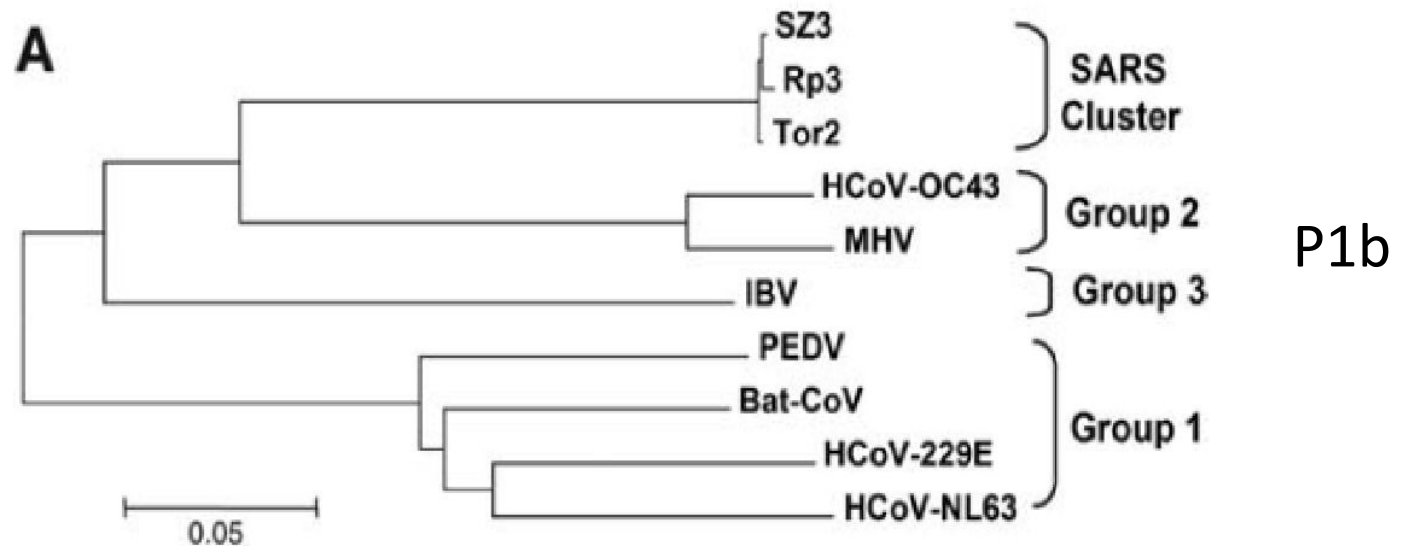
survey bats in the search for the natural reservoir of SARS-CoV.

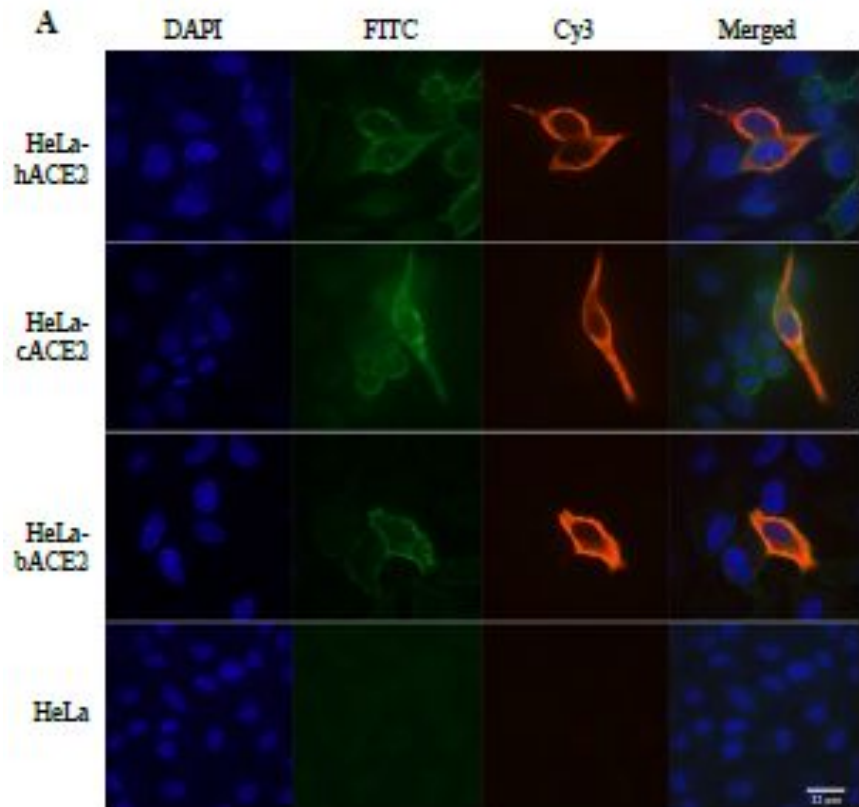
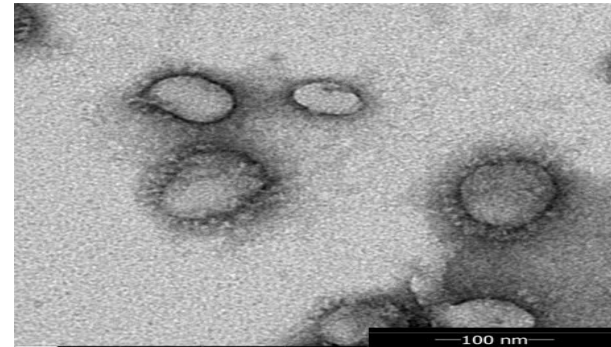
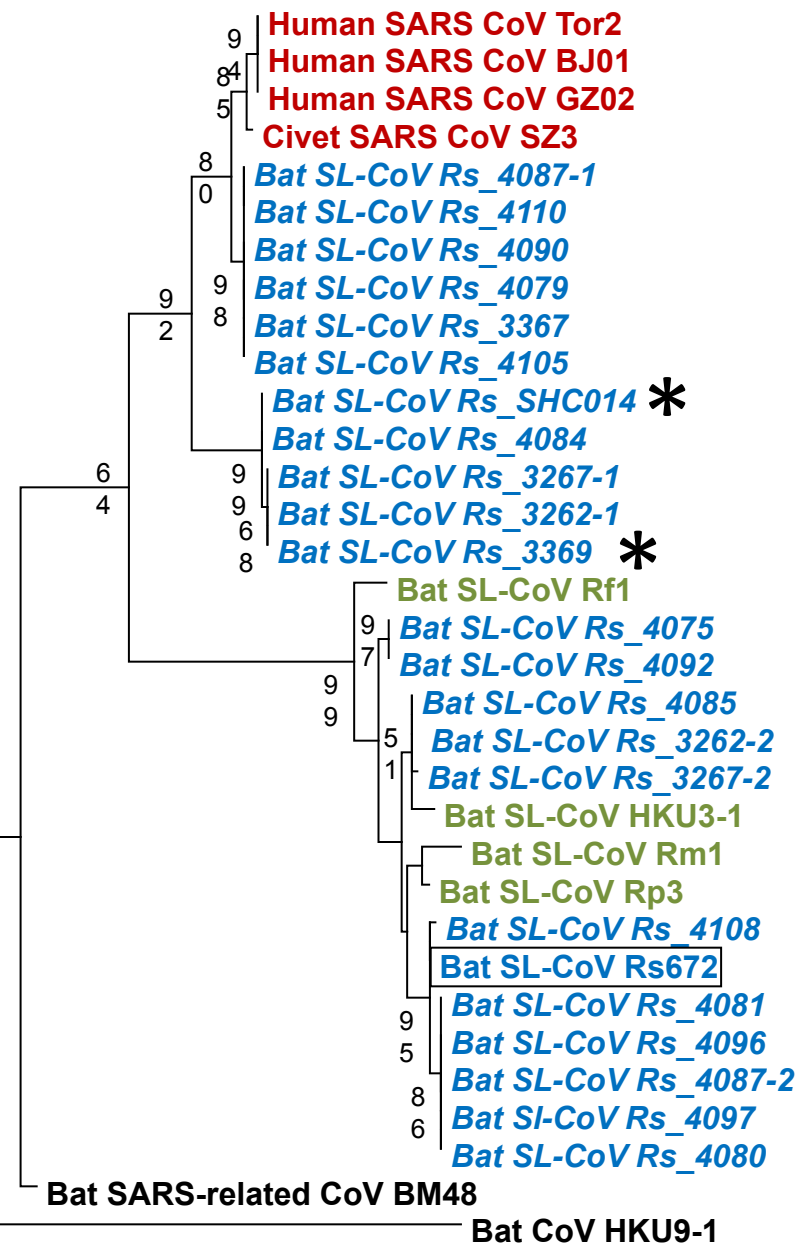
In this study, conducted from March to December of 2004, we sampled 408 bats representing nine species, six genera, and three families, from four locations in China (Guangdong, Guangxi, Hubei, and Tianjin) after trapping them in their native habitat (Table 1). Blood, fecal, and throat swabs were collected; serum samples and cDNA from fecal or throat samples were independently analyzed, double-blind, with different methods in Wuhan and Geelong (14).

Among six genera of bat species surveyed (*Rousettus*, *Cynopterus*, *Myotis*, *Rhinolophus*, *Nyctalus*, and *Miniopterus*), three communal, cave-dwelling species from the genus *Rhinolophus* (horseshoe bats) in the family *Rhinolophidae* demonstrated a high SARS-CoV antibody prevalence: 13 out of 46 bats (28%) in *R. pearsoni* from Guangxi, 2 out of 6 bats (33%) in *R. pusillus* from Guangxi; and 5 out



Human and Civet SARS-CoV nestle phylogenetically within Bat SL-CoV cluster







Global Rapid Identification Tool (GRITS)

- Automated diagnosis from online feeds
- Validated via Amazon Mechanical Turk



Web platform built for the One Health community to collect, share, and visualize information from human, animal, and environmental health.

Emerging Infectious Disease Repository (EIDR)



Centralized web-application dedicated to the improvement, storage, display, dissemination, and discussion of current knowledge on historical disease emergence.

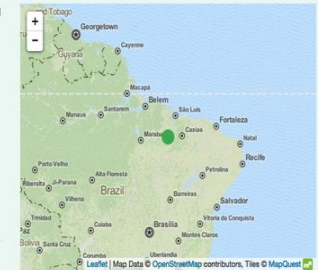


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Anajatuba virus

March 2000

In May 2000, a 19 year old female student was home. She was helping her parents with field work in a rural village in Anajatuba, Brazil. On May 20, this young student became seriously ill, presenting with a fever of 39 °C, shivering, intense generalized myalgia predominating in the lumbar region, persistent dry cough. She was treated with diclofenac and gentamicin, but developed intense dyspnea, cyanotic extremities, tachycardia and profuse diarrhea. She died shortly after being transferred to a hospital in São Luís. Serological testing confirmed infection by a novel sub-species of hantavirus and a diagnosis of hantavirus pulmonary syndrome (HPS). Two suspected cases occurred within 8 miles of the confirmed case, in two men of first-degree relation, ages 19 and 25 respectively. Rodents are a known host for HPS and transmission occurs by, "inhalation of aerosols containing the virus, by contact with a rodent's saliva during a bite, or by contact of non-intact skin with rodent excreta" (Mendes et al. 2001). A serious rodent infestation occurred during the time of these outbreaks, which may have been caused by seasonal flooding. It is likely that this infestation, coupled with the storage of rice and corn within the households of all three cases, facilitated infection. In this outbreak, the emergence of HPS developed in a new region.



Maranhão, Brazil
This represents the most specific location information found for the event.

Emergence Type	Driver	Disease
New Region, Evolution an existing organism	Human Behavior, Climate and Weather, Ecosystem Change	Hantavirus pulmonary syndrome
Event Transmission	Pathogen Host(s)	Specific Host Involved in the Event
	Rodents	Rodent

Collaborators

- UC Davis, Metabiota, WCS, Smithsonian
- Univ. Wyoming (David Finnoff)
- Columbia Univ. (Ian Lipkin, Simon Anthony)
- 100+ partners in 24 countries
- Wuhan Institute of Virology, Yunnan CDC
- Universiti Malaysia Sabah, Sabah Wildlife Dept.

Funders



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