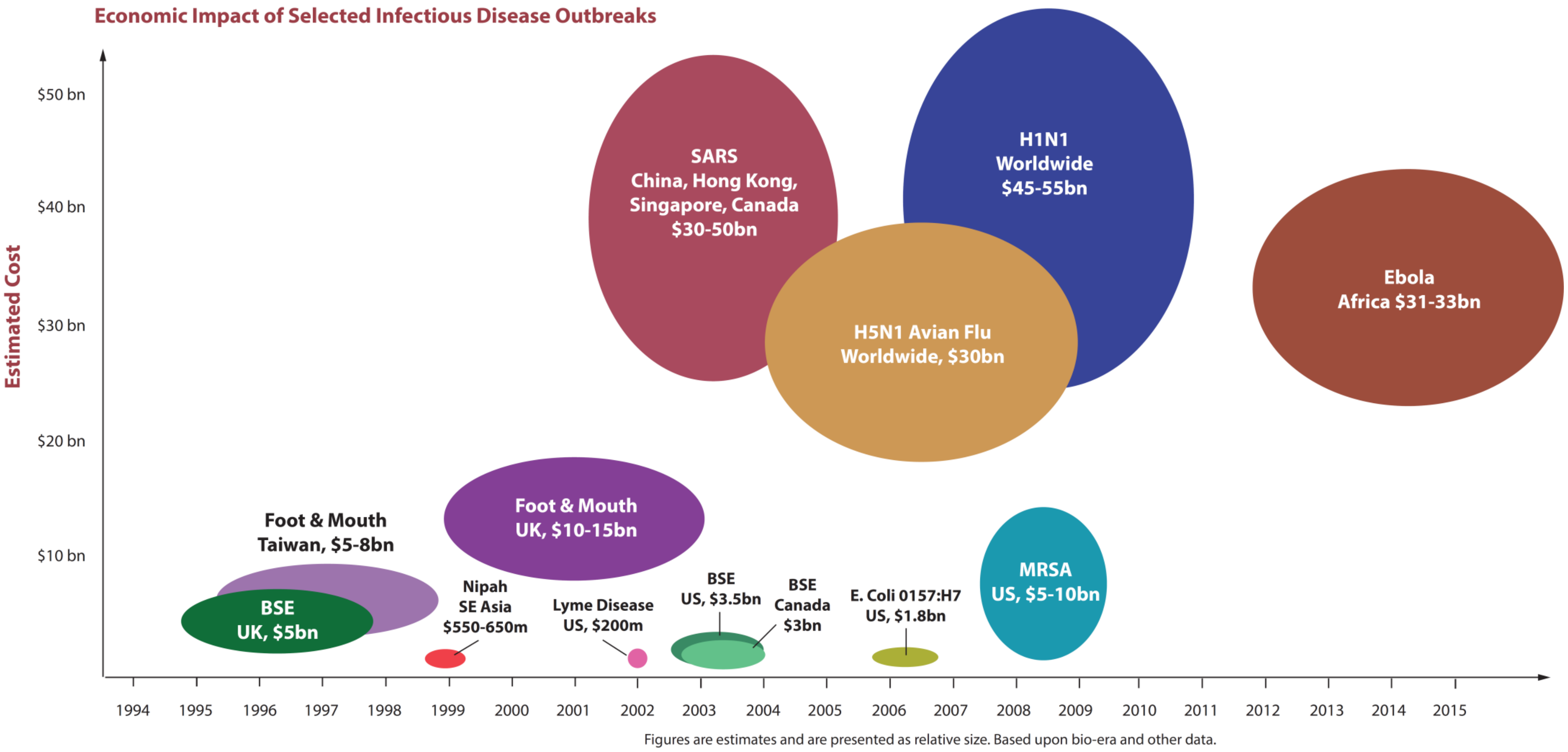
EcoHealth Alliance

Understanding the ecology and economics of pandemics

Peter Daszak
EcoHealth Alliance, New York, USA
www.ecohealthalliance.org

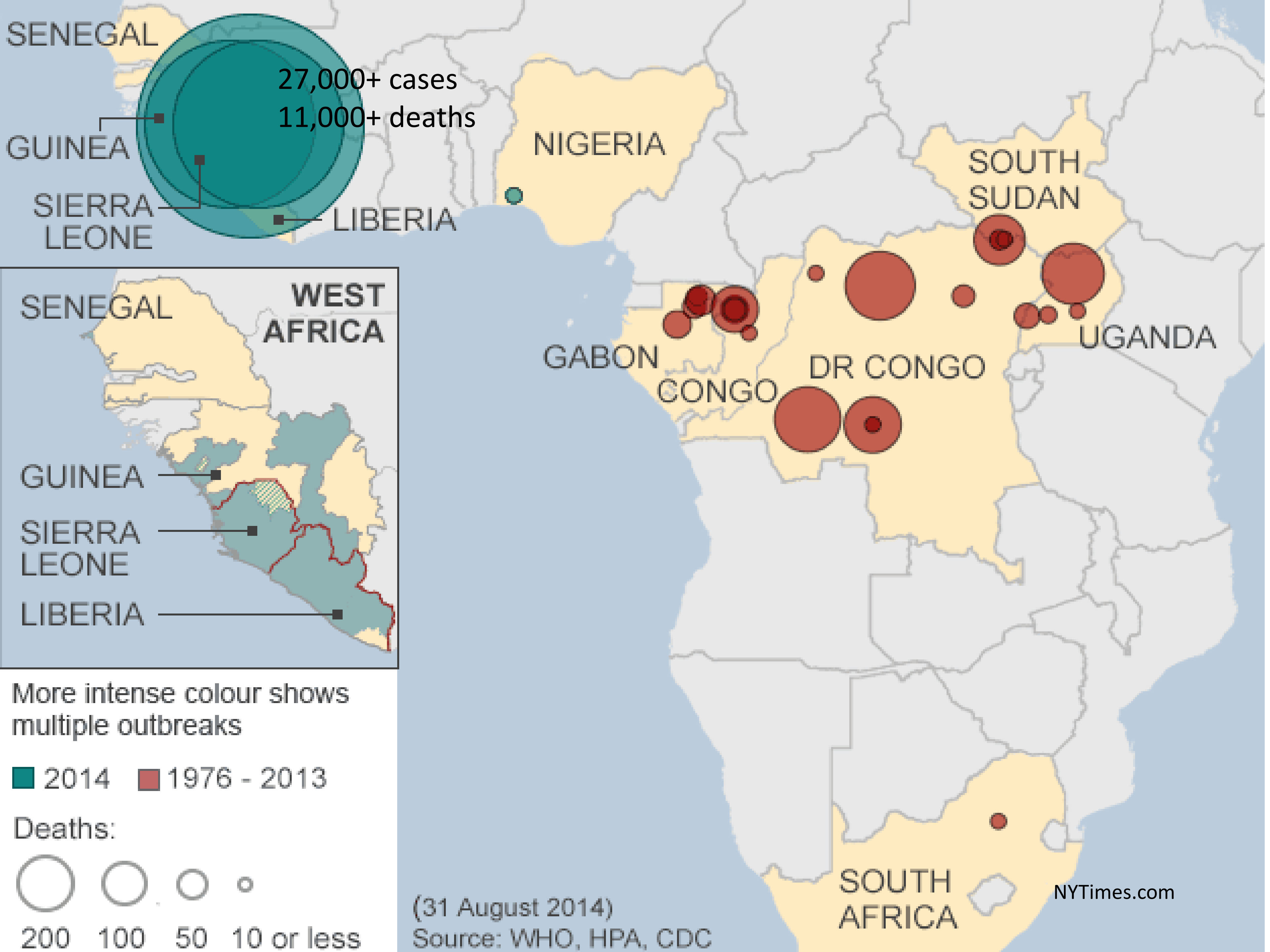
Local conservation.
Global health.

Economic Impact of Emerging Diseases



Figures are estimates and are presented as relative size. Based upon bio-era and other data.

W. African Ebola outbreak 2013-15



27,000+ cases
11,000+ deaths

(31 August 2014)
Source: WHO, HPA, CDC

NYTimes.com

USG ~$6.18 Billion Ebola Emergency Request

Immediate Response	
Department	Amount ($ in billions)
HHS	2.43
USAID	1.98
Department of State	0.127
Department of Defense	0.112
Contingency Fund (Long-term efforts)	
Department	Amount ($ in billions)
USAID and Department of Defense	0.792
HHS	0.751

USG ~$5.4 Billion Ebola Emergency Appropriation

Immediate Response	
Department	Amount ($ in billions)
HHS	2.742
USAID/Dept of State	2.5
Department of Defense	0.112
FDA	0.025
NIH	0.238

Contingency Fund (Long-term efforts)	
Department	Amount ($ in billions)
USAID and Department of Defense	-
HHS	-

Economic modeling

~$5 Billion is enough to significantly reduce risk of future event

$100M proposed by WHO is inadequate

To optimize prevention of future Ebola outbreaks:

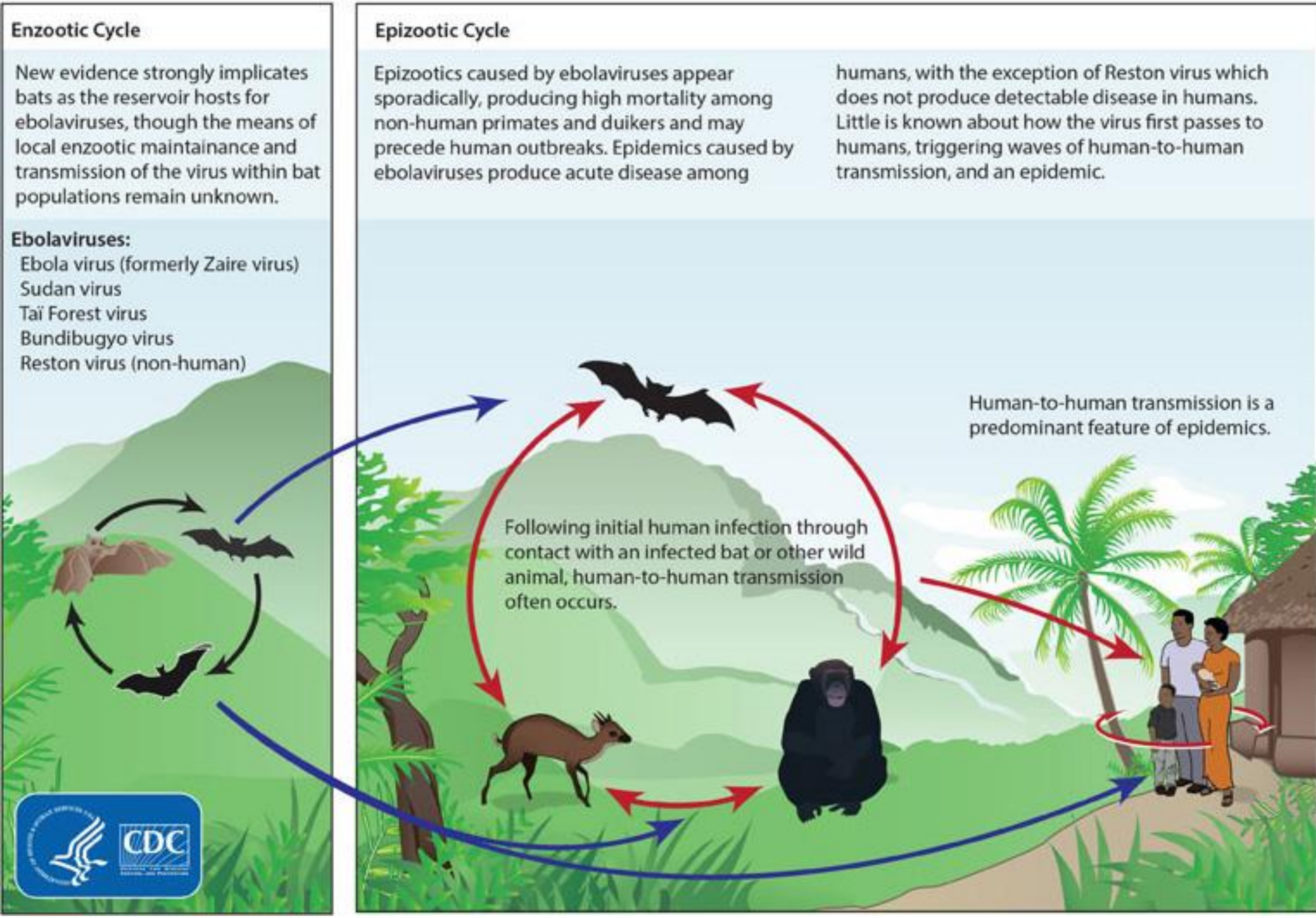
- $5 Billion as a reserve fund; $1Bn used to purchase equipment, train staff
- $4 Billion invested to produce annual return to fund reserve staff, logistics,

Reserve fund functions:

- Mobile laboratories, hospital beds within the region
- Trained nurses, doctors, within high risk countries
- Trained epidemiologists for contact tracing and behavioral risk mitigation
- Similar ethos as Dept of Defense, i.e. surge capacity and significant 'peace-time' redundancy of staff.

Berry et al. in review

Ebolavirus Ecology



Enzootic Cycle

New evidence strongly implicates bats as the reservoir hosts for ebolaviruses, though the means of local enzootic maintainance and transmission of the virus within bat populations remain unknown.

Ebolaviruses:

- Ebola virus (formerly Zaire virus)
- Sudan virus
- Taï Forest virus
- Bundibugyo virus
- Reston virus (non-human)

Epizootic Cycle

Epizootics caused by ebolaviruses appear sporadically, producing high mortality among non-human primates and duikers and may precede human outbreaks. Epidemics caused by ebolaviruses produce acute disease among humans, with the exception of Reston virus which does not produce detectable disease in humans. Little is known about how the virus first passes to humans, triggering waves of human-to-human transmission, and an epidemic.

Following initial human infection through contact with an infected bat or other wild animal, human-to-human transmission often occurs.

Human-to-human transmission is a predominant feature of epidemics.

Likely Ebola Virus Reservoirs

Epomops franqueti

Myonycteris torquata

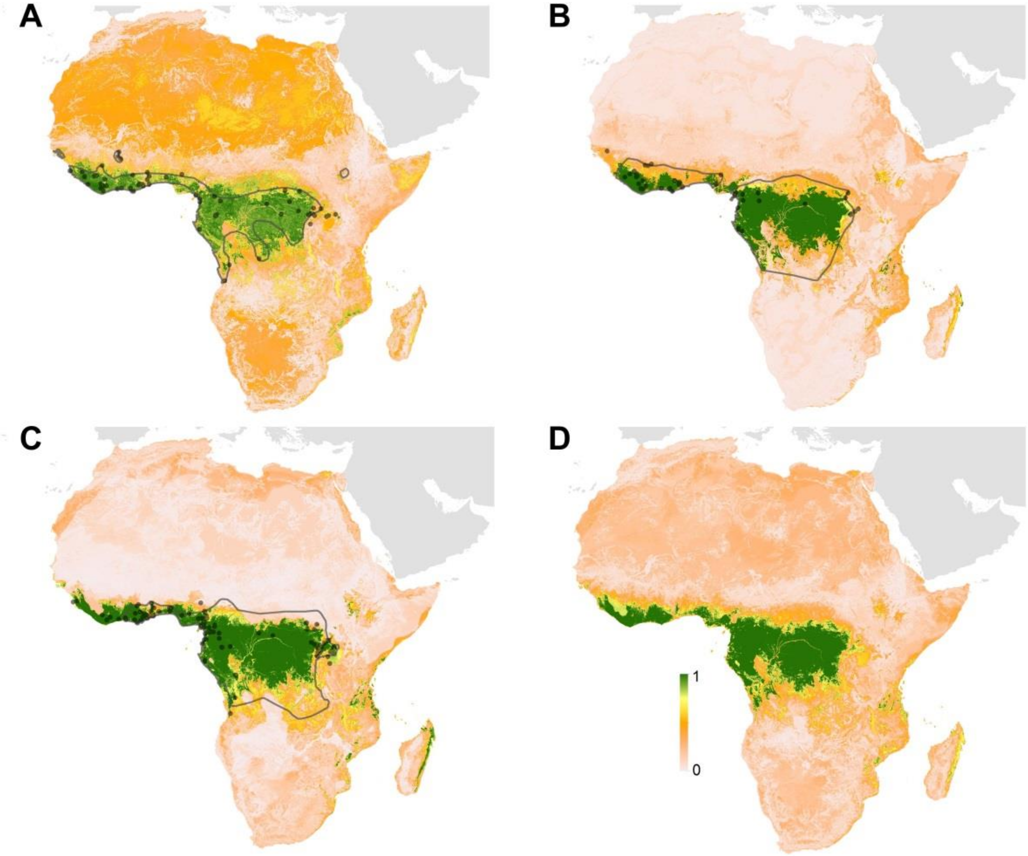
Hypsignathus monstrosus

Leroy et al. 2005 *Nature*

Paul Telfer, WCS

P. Reed / WCS

Predicted geographical distribution of the three species of Megachiroptera suspected to reservoir Ebola virus.(A) Shows the distribution of the hammer-headed bat (Hypsignathus monstrosus), (B) The little collared fruit bat (Myonycteris torquata) a...

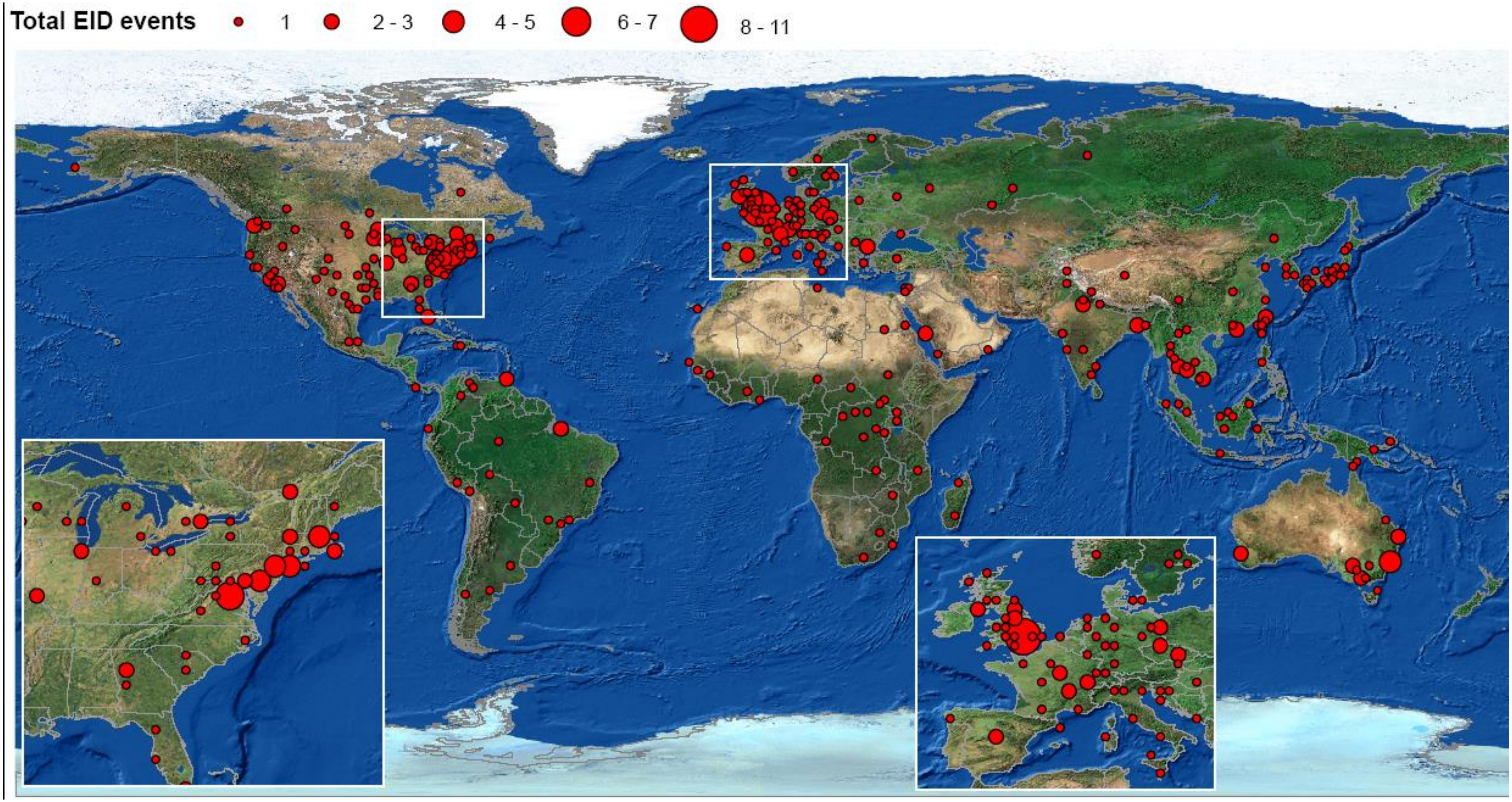


Pigott D M et al. eLife Sciences 2014;3:e04395

Big Questions for Pandemic Prevention

1. Are Emerging Infectious Diseases really on the rise?
2. Are there predictable patterns to disease emergence?
3. Where will the next pandemic originate?
4. Can we allocate resources to control them more strategically?
5. Is it more cost-effective to respond to pandemics or to try and pre-empt them?

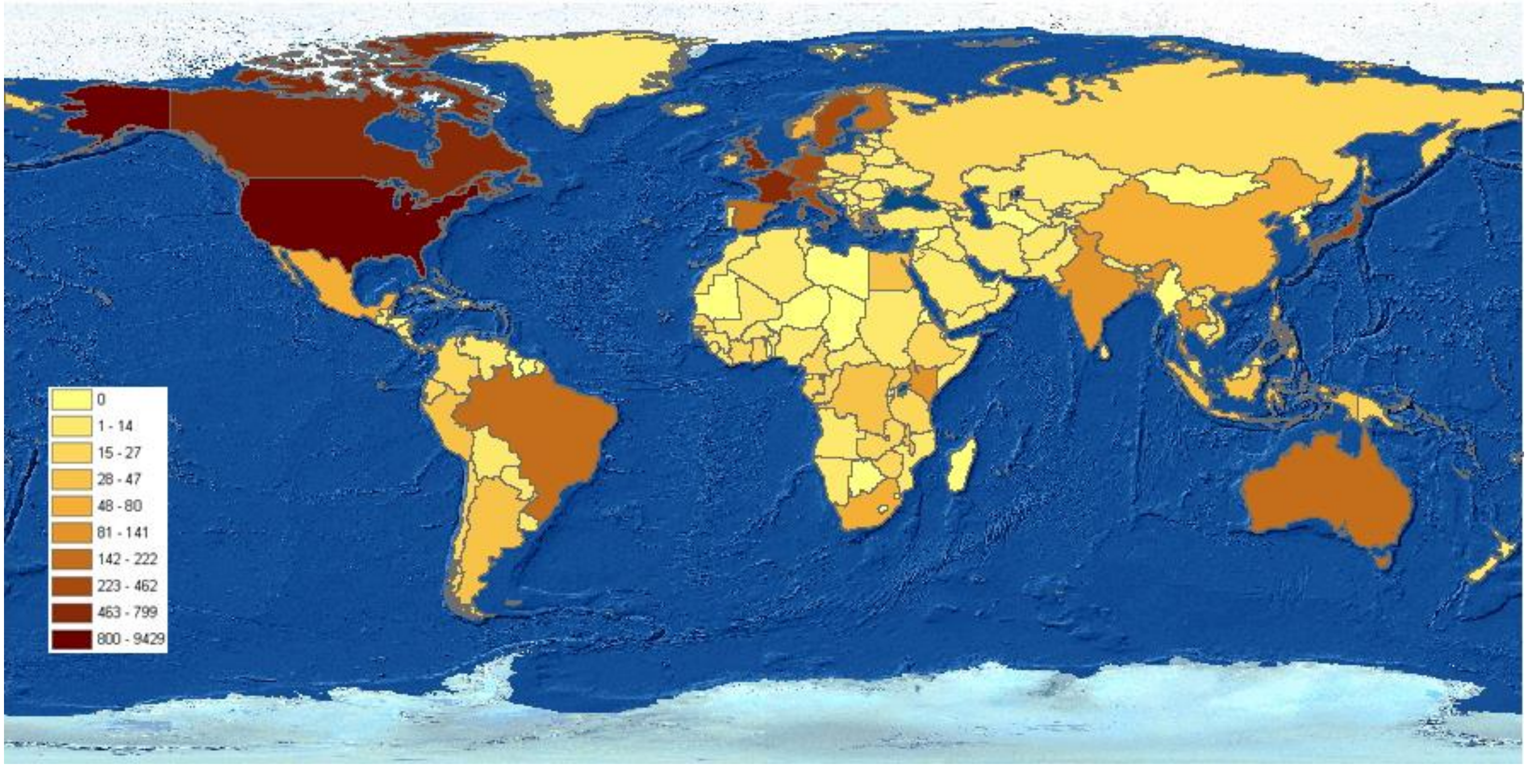
EcoHealth Alliance



Local conservation.
Global health.

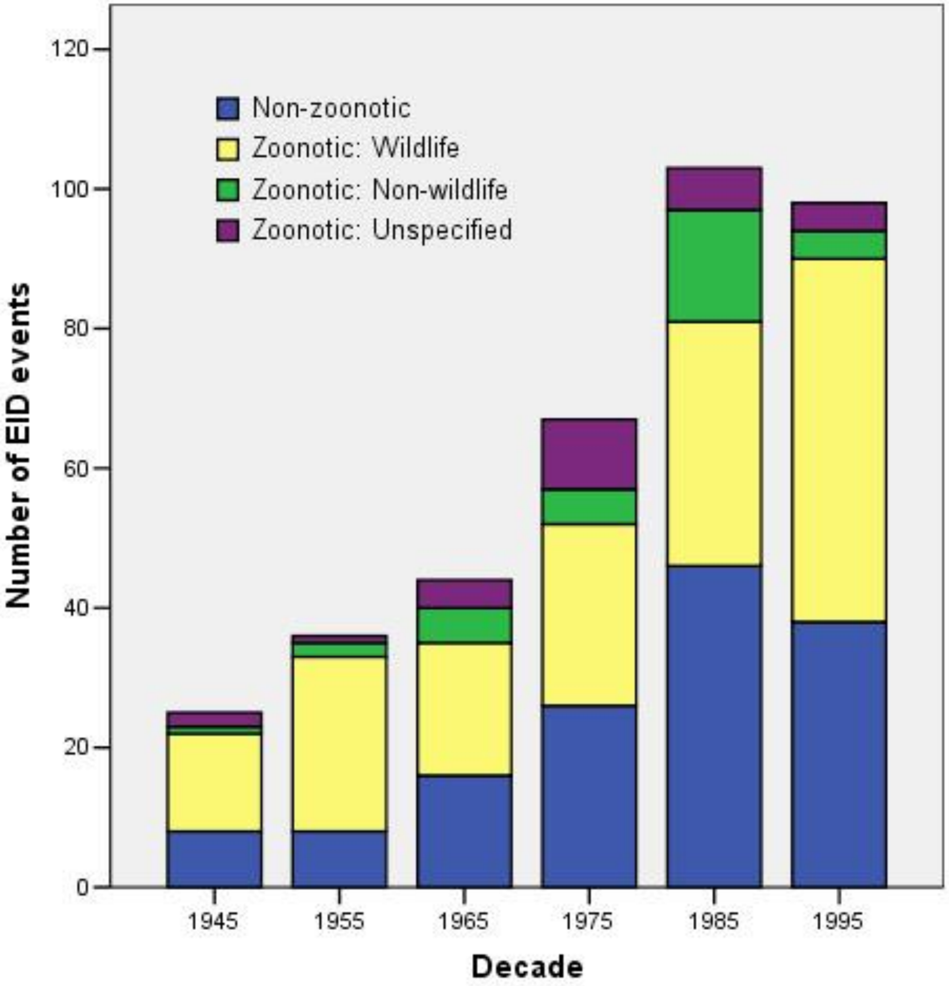
Jones *et al*. 2008 *Nature*

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 ($GLM_{P,JID}$ 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

Jones *et al*. Nature 2008

Quantifying the drivers of EID events

Dependent:

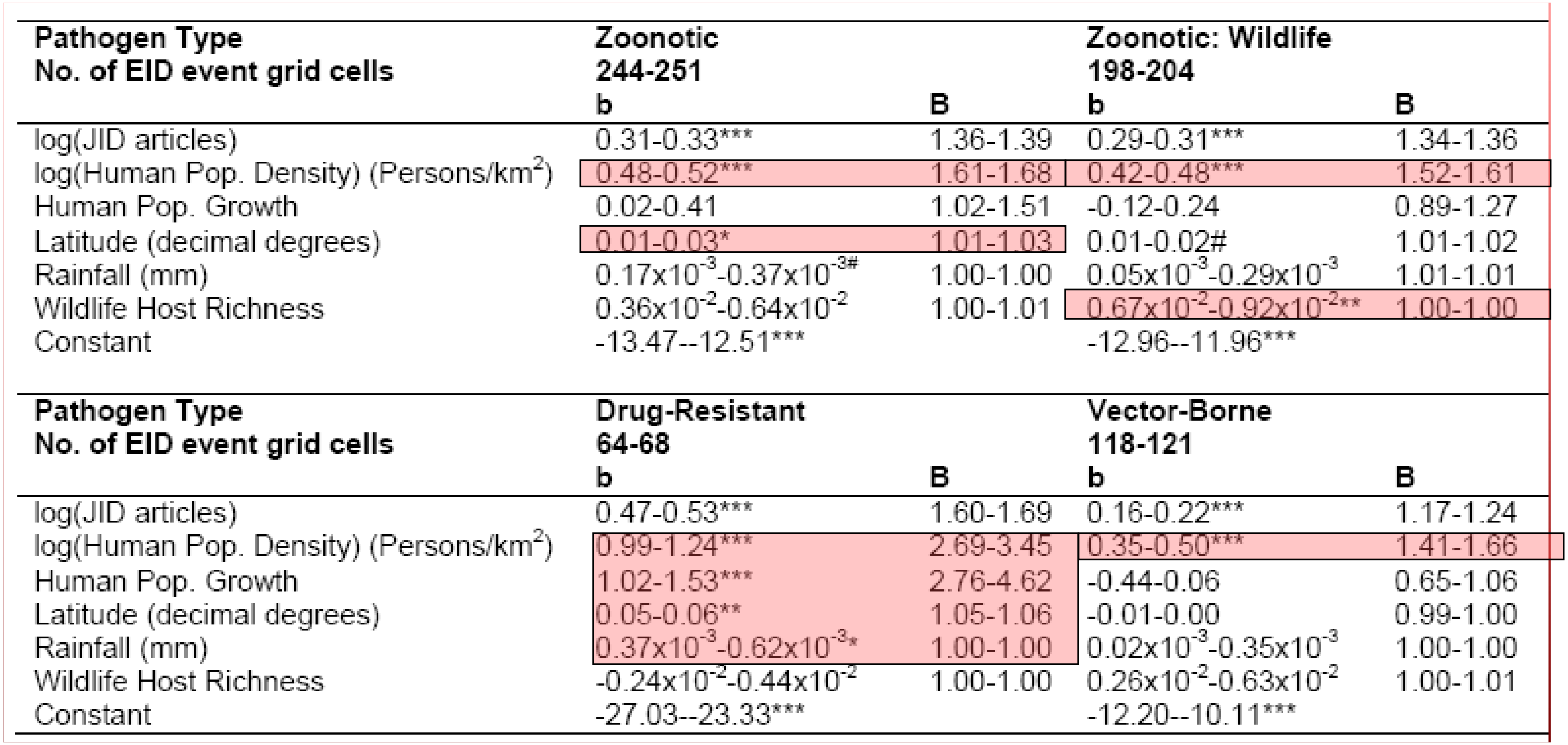
1. Presence/absence of an EID event in 1 degree grids (using data from 1940-2004)

Independents (calculated over 1990-2000 period):

1. Human population density & growth
2. Rainfall
3. Latitude
4. Mammal diversity
5. Journal of Infectious Disease reports (reporting bias measure)

Multivariate spatial logistic regressions split by EID event type

Assumes each mammal species has equal number of potential zoonoses

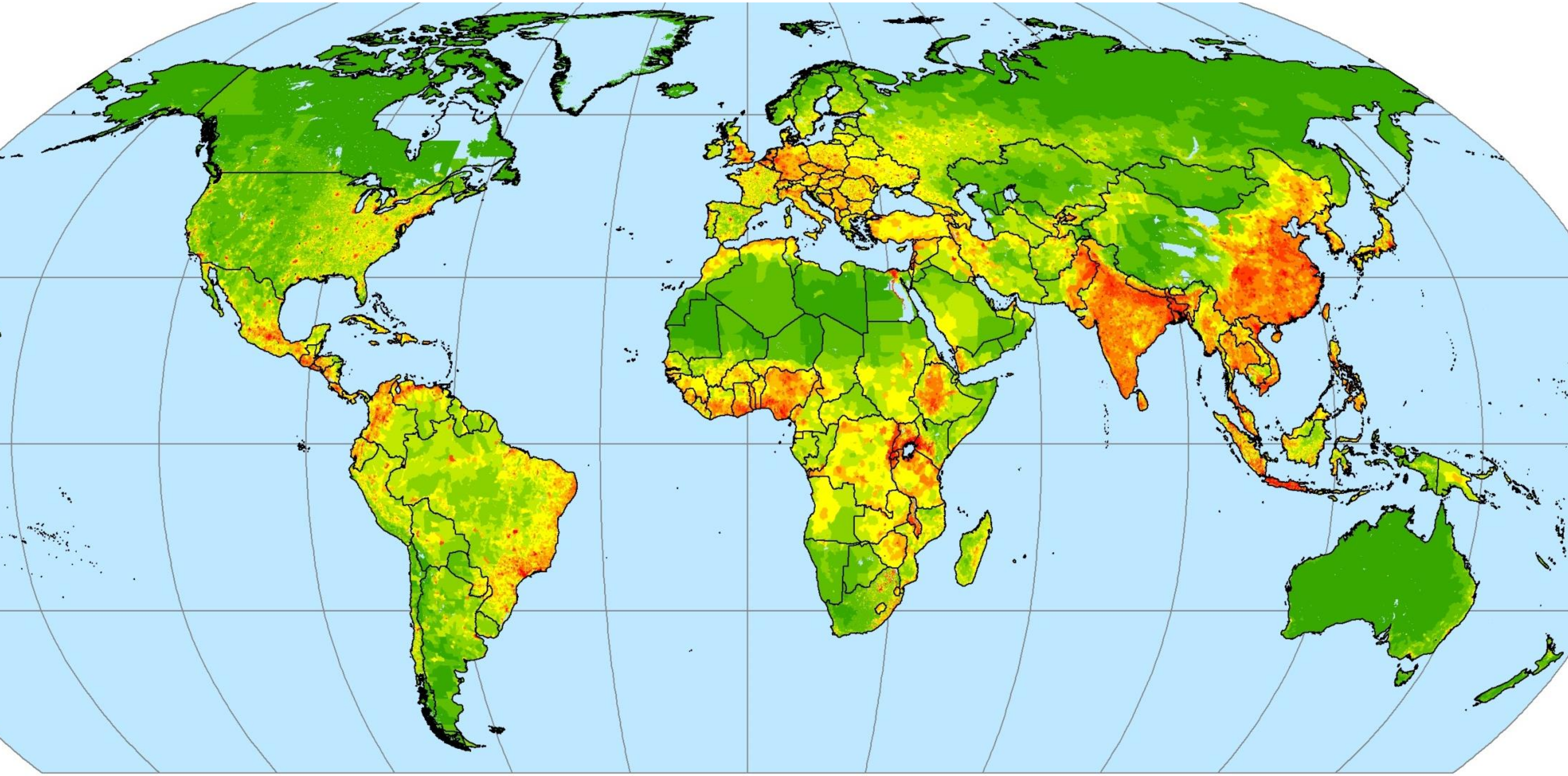


Pathogen Type	Zoonotic		Zoonotic: Wildlife	
No. of EID event grid cells	244-251		198-204	
	b	B	b	B
log(JID articles)	0.31-0.33***	1.36-1.39	0.29-0.31***	1.34-1.36
log(Human Pop. Density) (Persons/km^2)	0.48-0.52***	1.61-1.68	0.42-0.48***	1.52-1.61
Human Pop. Growth	0.02-0.41	1.02-1.51	-0.12-0.24	0.89-1.27
Latitude (decimal degrees)	0.01-0.03*	1.01-1.03	0.01-0.02#	1.01-1.02
Rainfall (mm)	0.17x10^{-3}-0.37x10^{-3}#	1.00-1.00	0.05x10^{-3}-0.29x10^{-3}	1.01-1.01
Wildlife Host Richness	0.36x10^{-2}-0.64x10^{-2}	1.00-1.01	0.67x10^{-2}-0.92x10^{-2}**	1.00-1.00
Constant	-13.47--12.51***		-12.96--11.96***	

Pathogen Type	Drug-Resistant		Vector-Borne	
No. of EID event grid cells	64-68		118-121	
	b	B	b	B
log(JID articles)	0.47-0.53***	1.60-1.69	0.16-0.22***	1.17-1.24
log(Human Pop. Density) (Persons/km^2)	0.99-1.24***	2.69-3.45	0.35-0.50***	1.41-1.66
Human Pop. Growth	1.02-1.53***	2.76-4.62	-0.44-0.06	0.65-1.06
Latitude (decimal degrees)	0.05-0.06**	1.05-1.06	-0.01-0.00	0.99-1.00
Rainfall (mm)	0.37x10^{-3}-0.62x10^{-3}*	1.00-1.00	0.02x10^{-3}-0.35x10^{-3}	1.00-1.00
Wildlife Host Richness	-0.24x10^{-2}-0.44x10^{-2}	1.00-1.00	0.26x10^{-2}-0.63x10^{-2}	1.00-1.01
Constant	-27.03--23.33***		-12.20--10.11***	

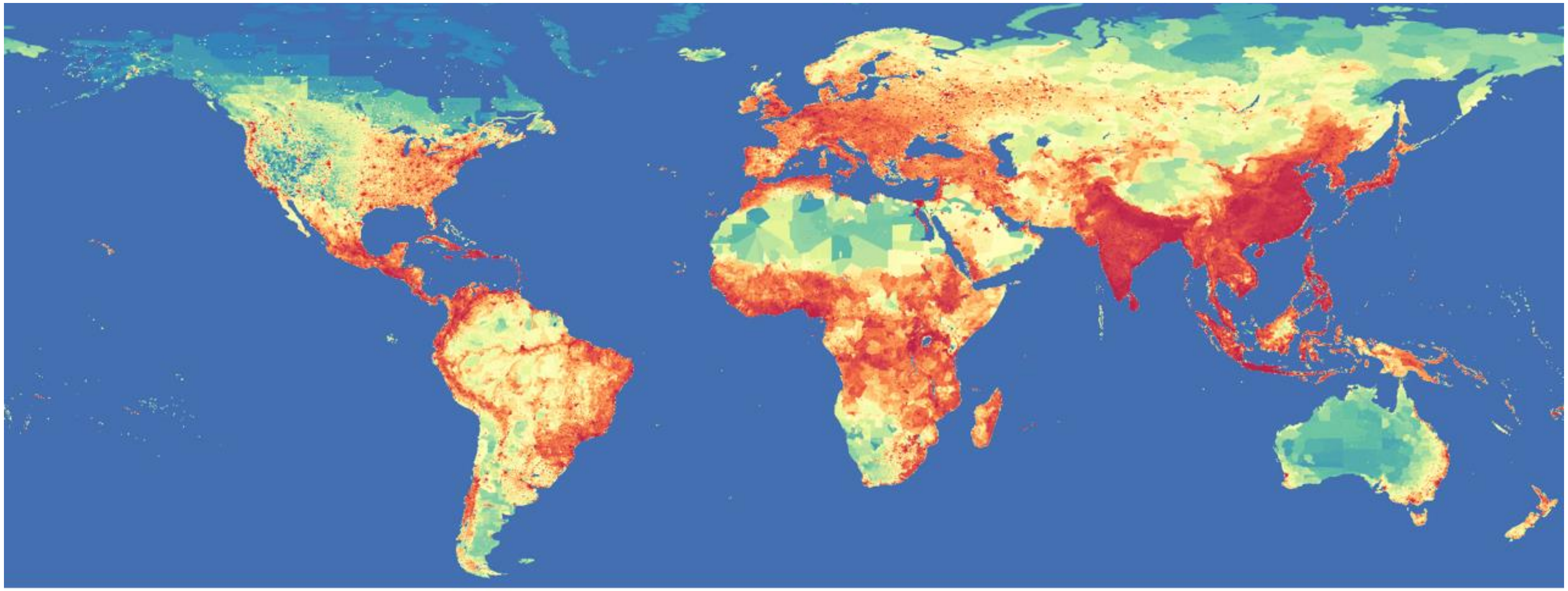
Jones *et al*. Nature 2008

Global emerging disease ‘hotspots’

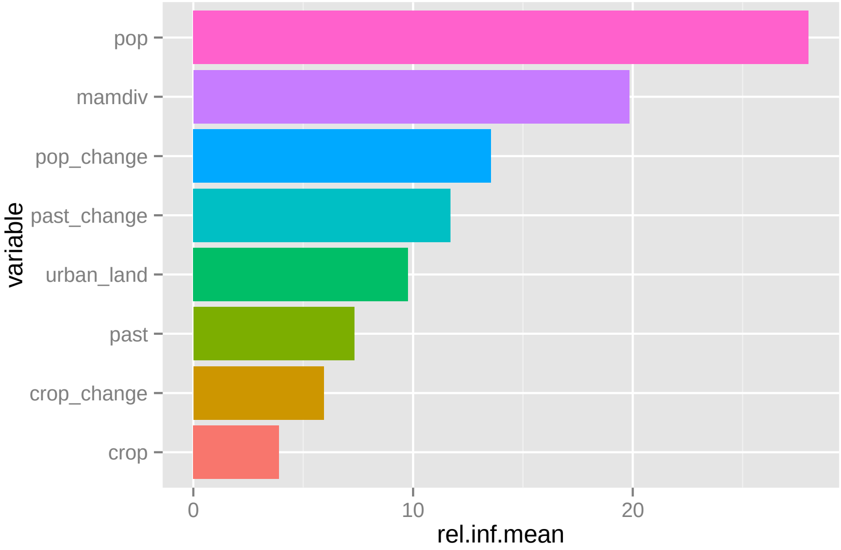


Jones *et al.* *Nature* 2008

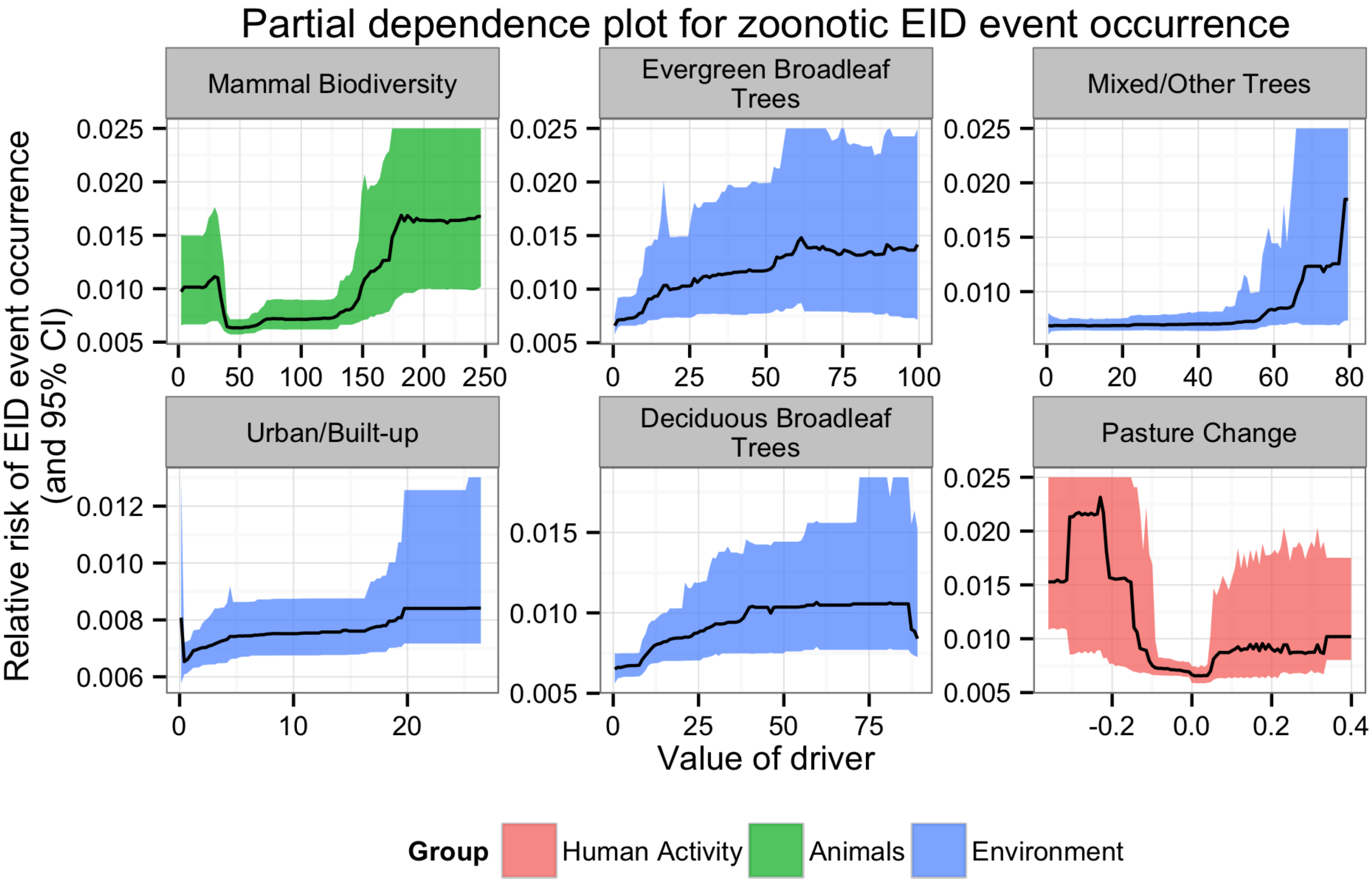
Hotspots II – new variables and methods



	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

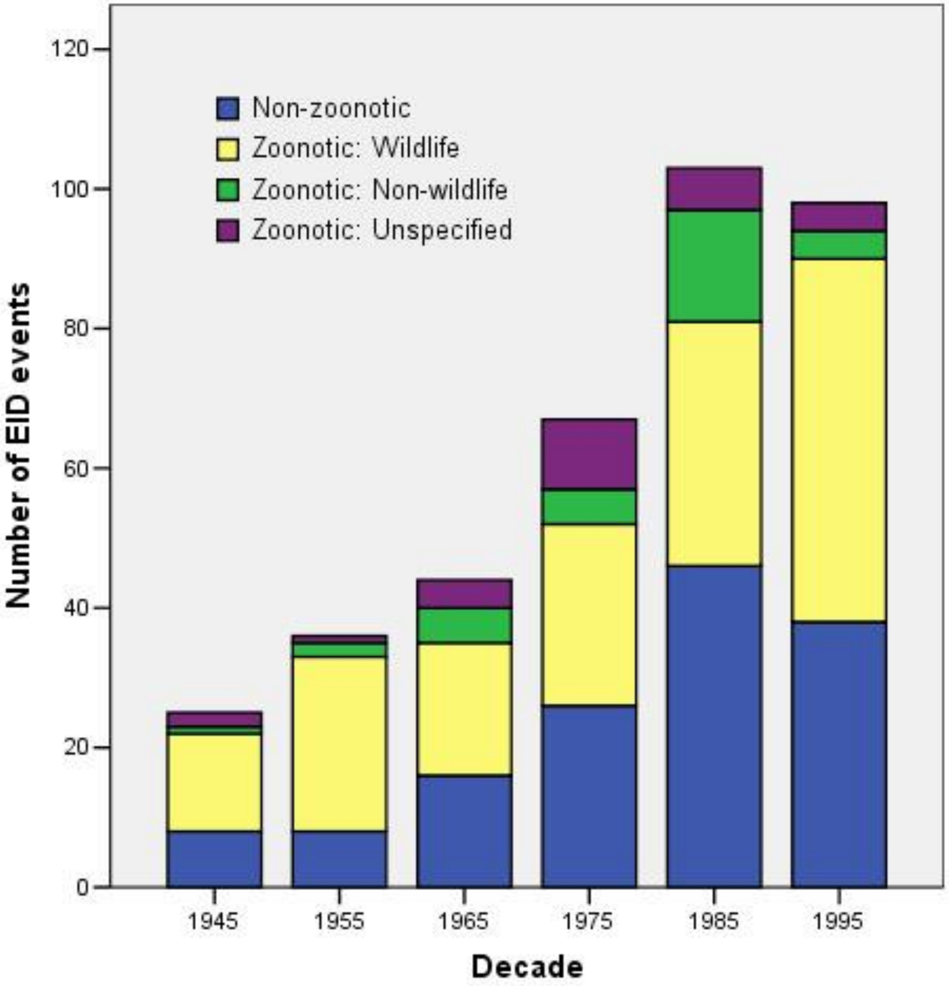


Hotspots II – influence of each variable



Allen et al., in prep

Temporal patterns in EID events



- EID events have increased over time, correcting for reporter bias ($GLM_{P,JID}$ F = 86.4, $p < 0.001$, d.f.=57)

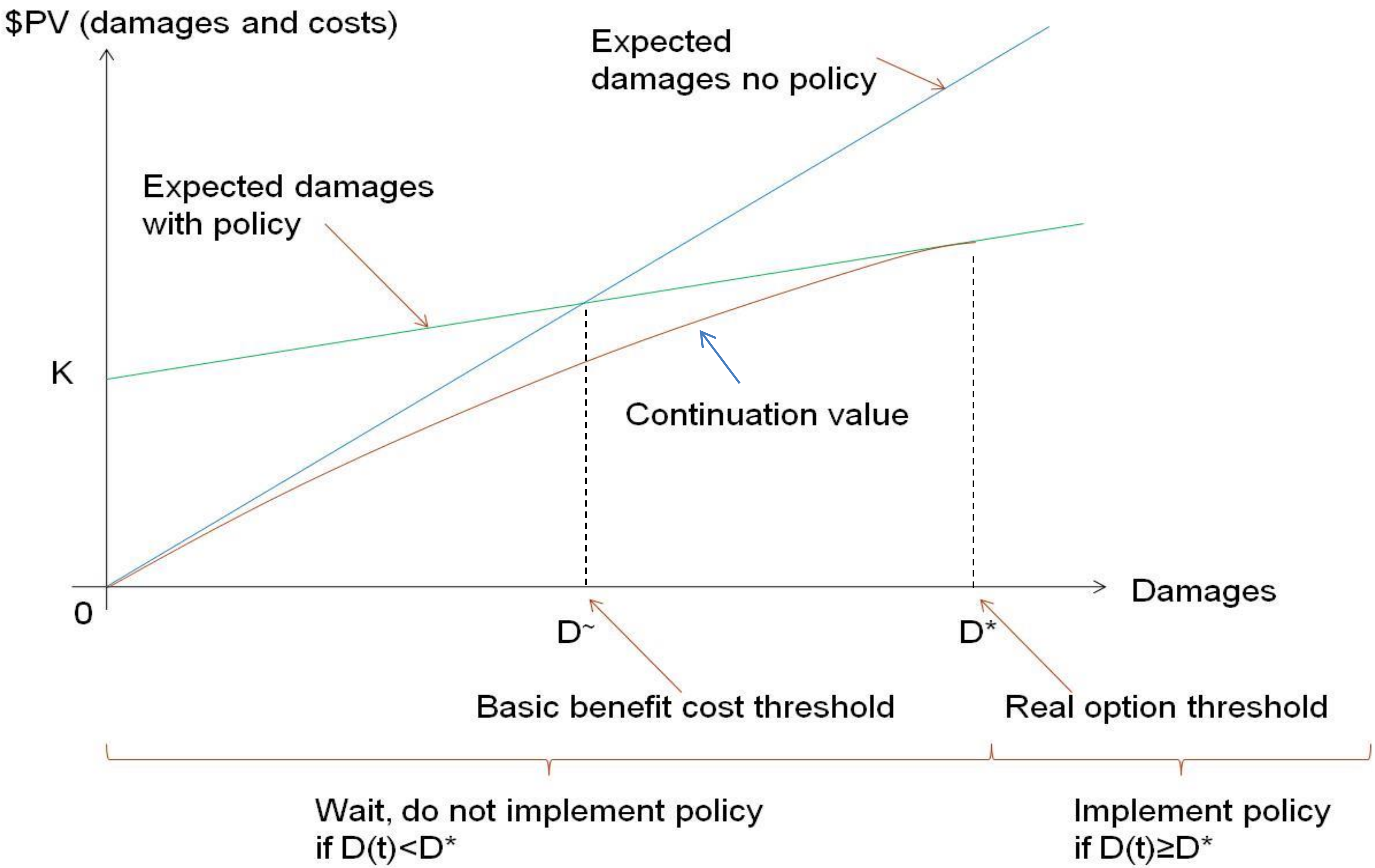
- ~5 new EIDs each year

- ~3 new Zoonoses each year

- **Zoonotic EIDs from wildlife** reach highest proportion in recent decade

Jones *et al*. 2008

Optimal Stopping Problem



Pike *et al.* PNAS 2014

Simulation results

Critical Damage Level, D*, Mean EID Event Trigger, Z*, Expected First-Passage Time, t*, option value, OV, and Expected Net Present Cost

	Policy option A	*Policy option B*	*Policy option C*	*Policy option D*
	$m_2 = 2.8857$	$m_2 = 2.5651$	$m_2 = 1.9238$	$m_2 = 0.8016$
	K = $56.3B	*K = $112.5B*	*K = $225.0B*	*K = $562.5B*
*D**	*$17.1B*	*$20.0B*	*$25.7B*	*$47.6B*
*Z**	*237.74*	*252.61*	*276.90*	*336.64*
*t**	*3*	*8*	*15*	*34*
OV	*$98.1B*	*$156.2*	*$215.2*	*$215.1*
*E**	*$808.7*	*$790.0*	*$712.4*	*$743.4*

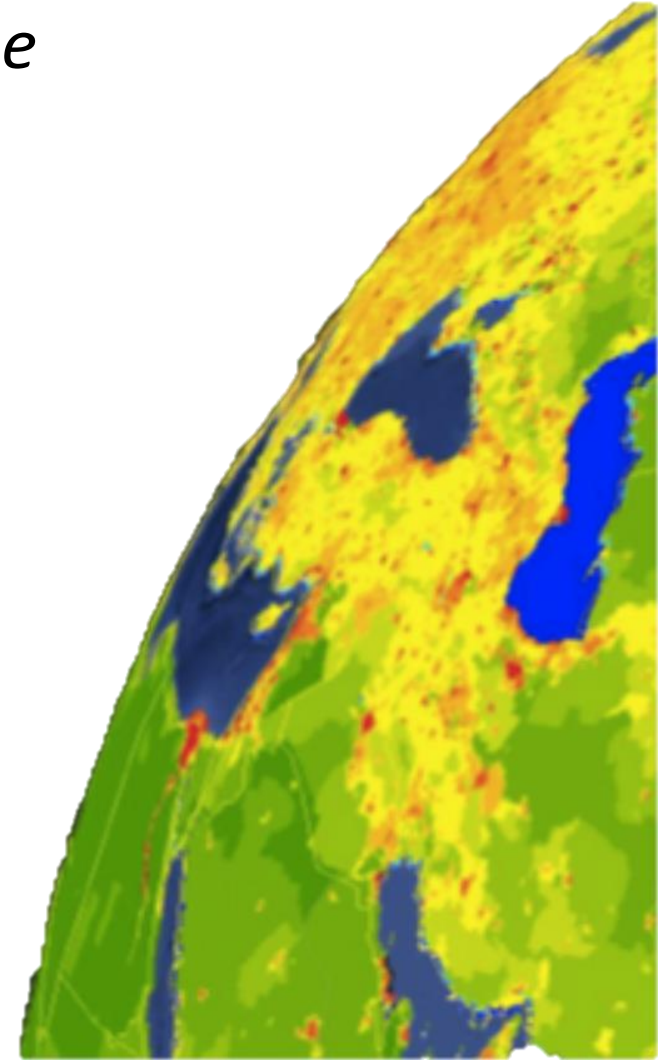
Conclusion: Mitigating pandemics is cost-effective, but we need to act rapidly

Pike *et al.* PNAS 2014

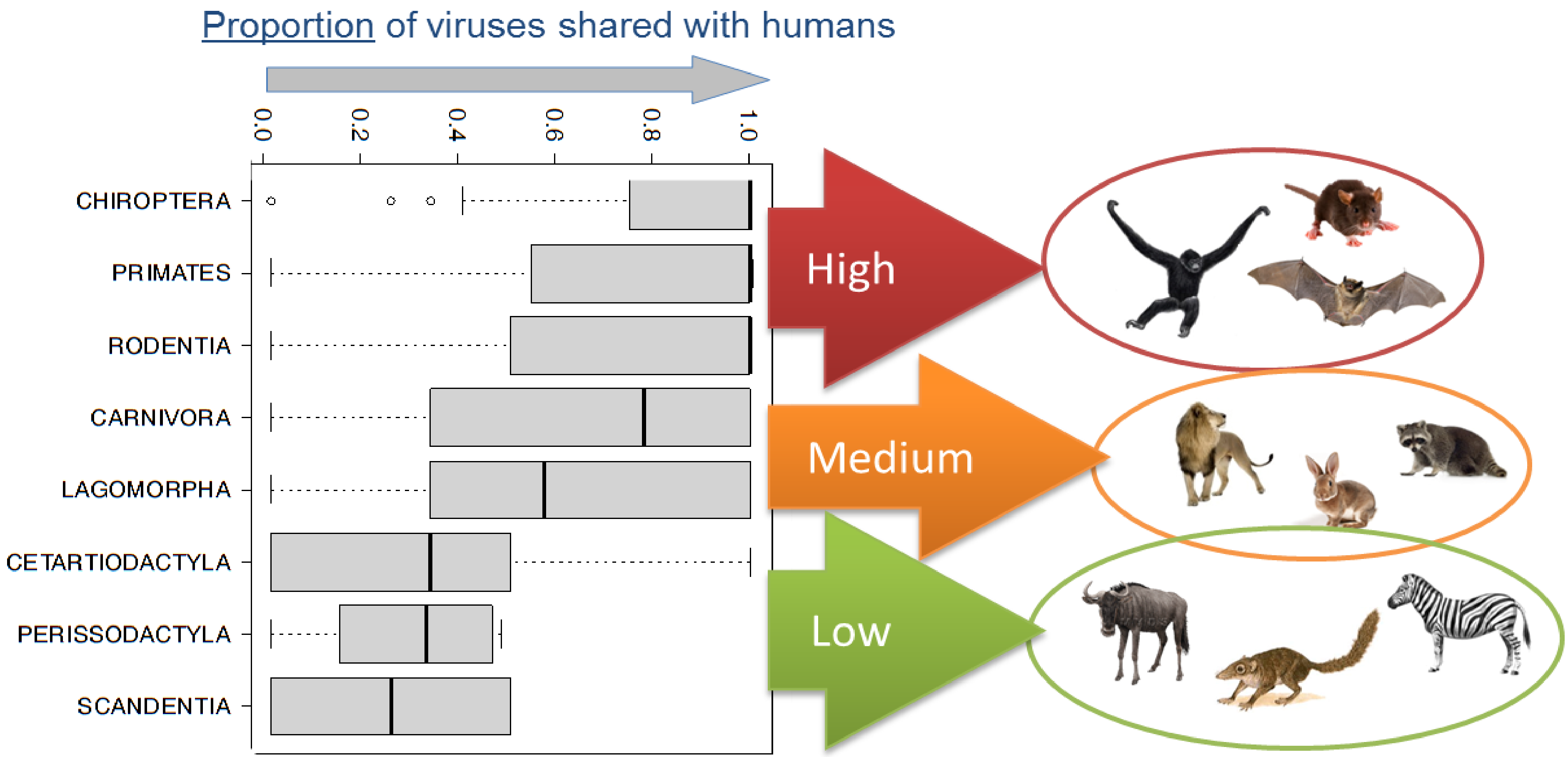
Global energy-related CO_2 emissions

IEA analysis for 2015 shows renewables surged, led by wind, and improvements in energy efficiency were key to keeping emissions flat for a second year in a row

Pre-empt or combat, at their source, the first stage of emergence of zoonotic diseases



Which species will the next pandemic emerge from?



PREDICT

THE WORLD'S MOST COMPREHENSIVE ZOONOTIC DISEASE SURVEILLANCE & CAPACITY DEVELOPMENT PROGRAM

TRAINED 2,500 government personnel, physicians, veterinarians, resource managers, laboratory technicians, hunters, and students on biosafety, surveillance, lab techniques, and disease outbreak investigation.

SAMPLED 56,000+ nonhuman primates, bats, rodents, and other wild animals (including bushmeat samples) at human-wildlife interfaces with high-risk and opportunity for viral spillover from wildlife hosts to humans.

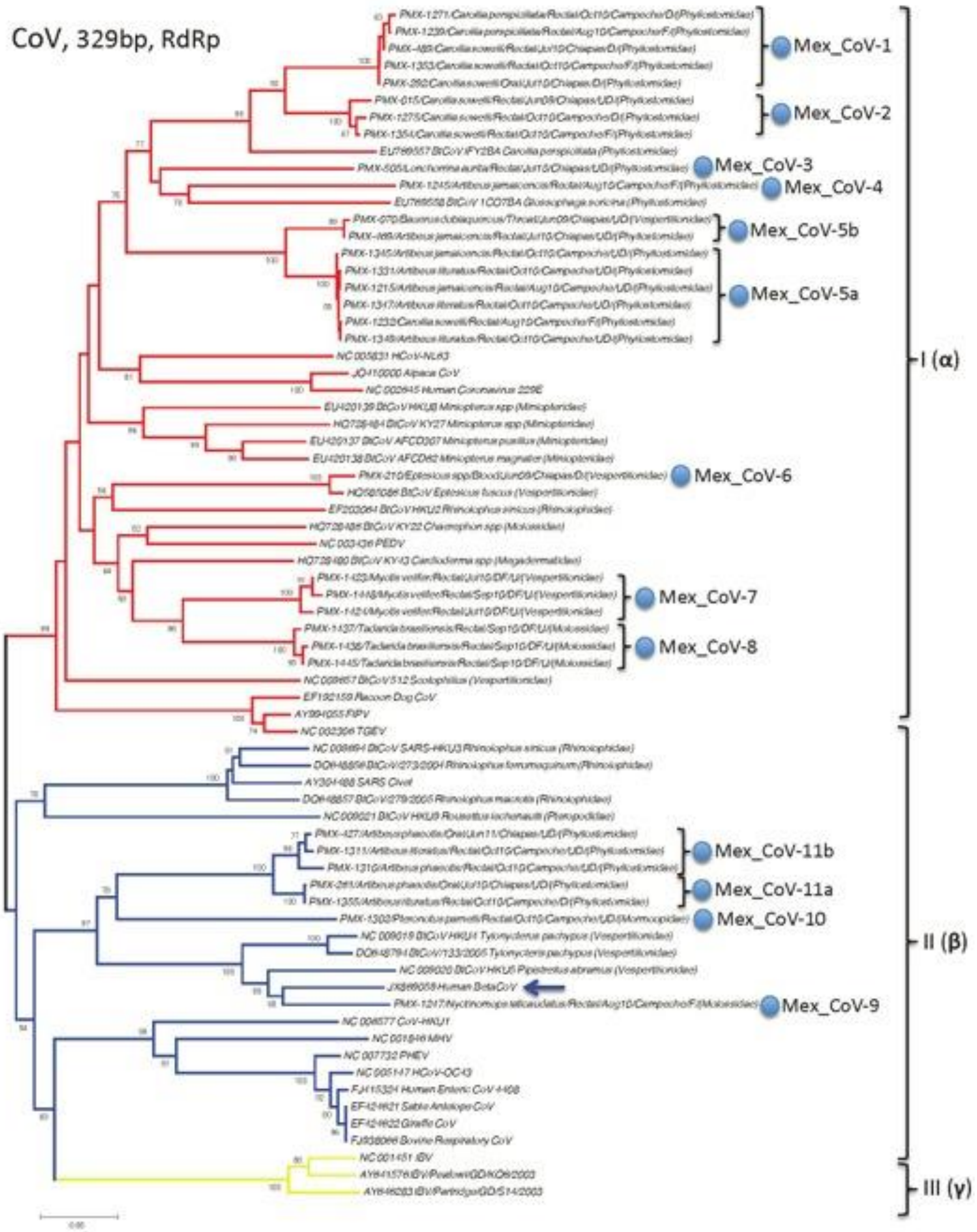
DEVELOPED & OPTIMIZED low-cost viral family level consensus PCR methods and synthetic controls for the detection and discovery of new viruses from the target viral families in 32 labs in 20 developing countries around the world.

DETECTED a total of 984 unique viruses in wild animals and humans: 815 novel viruses and 169 known viruses – the most comprehensive viral detection and discovery effort to date.

815 NOVEL

169 KNOWN

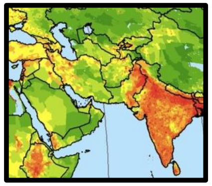
New Coronaviruses from bats in Mexico



Anthony et. al. 2013 *J. Gen Virol.*

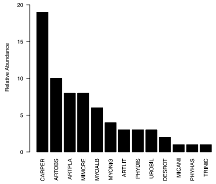
Ranking risk for zoonotic potential of novel viruses

VIRUS-INDEPENDENT TRAITS + VIRUS-SPECIFIC TRAITS = RISK OF SPILLOVER



Geographic hotspots for emergence

Host species traits, geographic range, relatedness

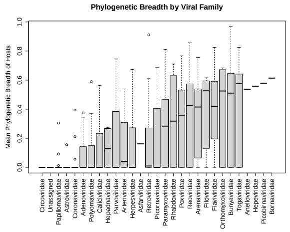


Host abundance

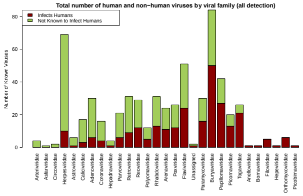
% pos

Viral prevalence in host

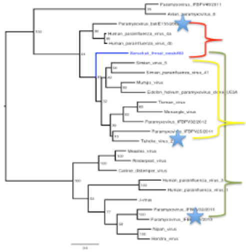
Epidemiological/ contact interface



Host breadth/plasticity



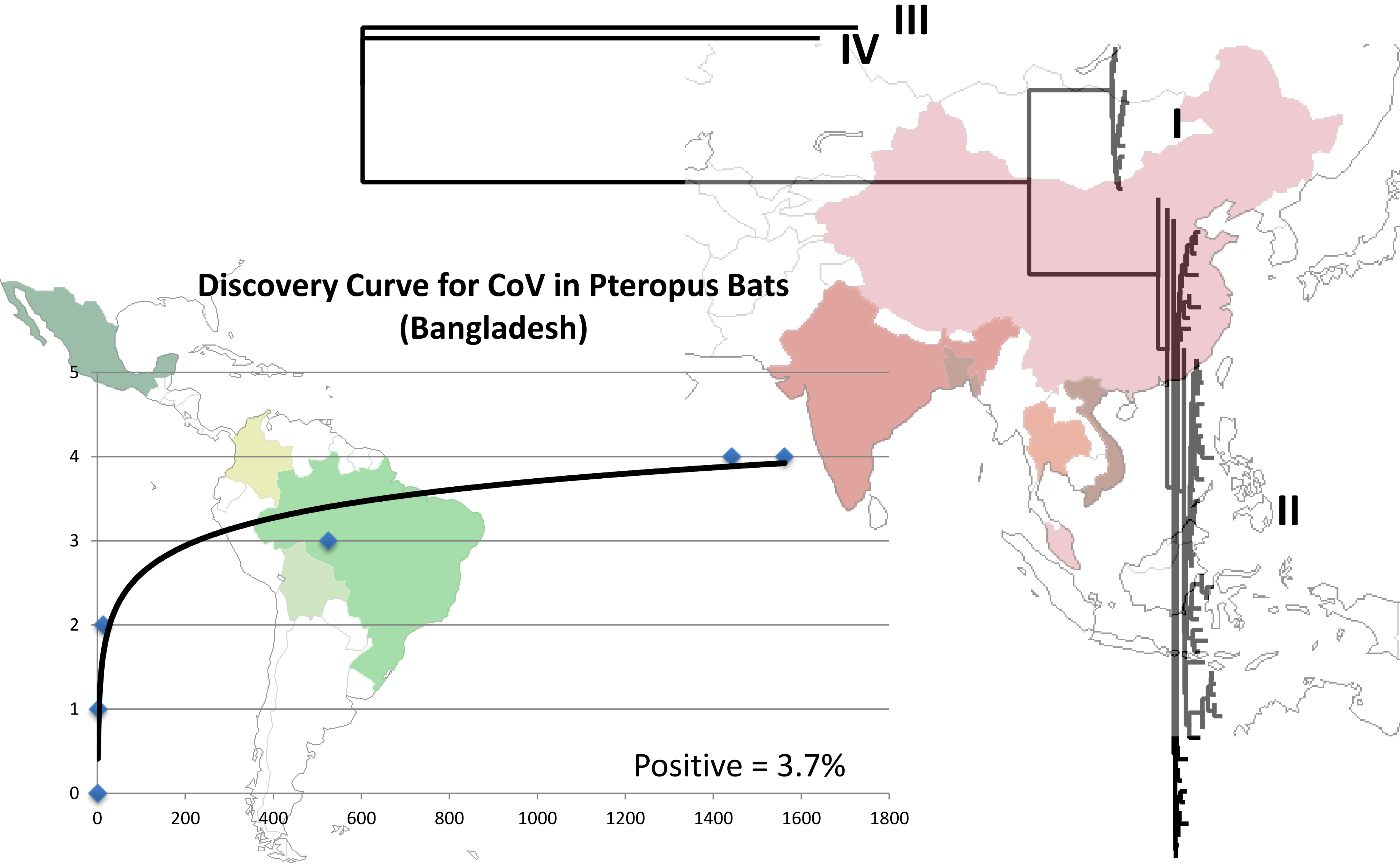
Proportion known zoonoses in virus family



Phylogenetic relatedness to known zoonoses

Other virus-specific traits

Coronavirus



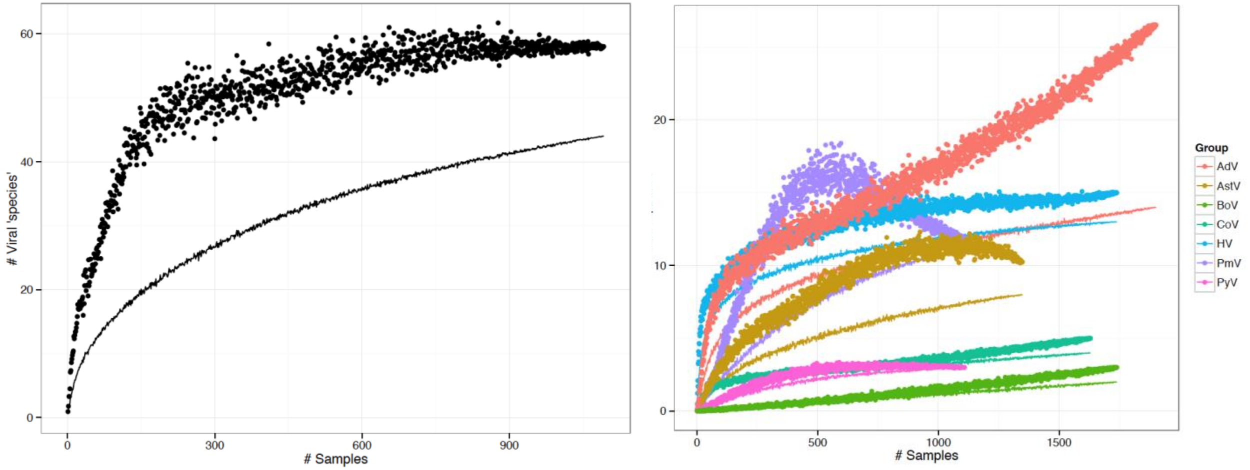
Discovery Curve for CoV in Pteropus Bats (Bangladesh)

Positive = 3.7%

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-Torrelio,[b] Alexander Solovyov,[a] Rafael Ojeda-Flores,[c] Nicole C. Arrigo,[a] Ariful Islam,[b] Shahneaz Ali Khan,[d] Parviez 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 #

Anthony et al. *mBio* 2013

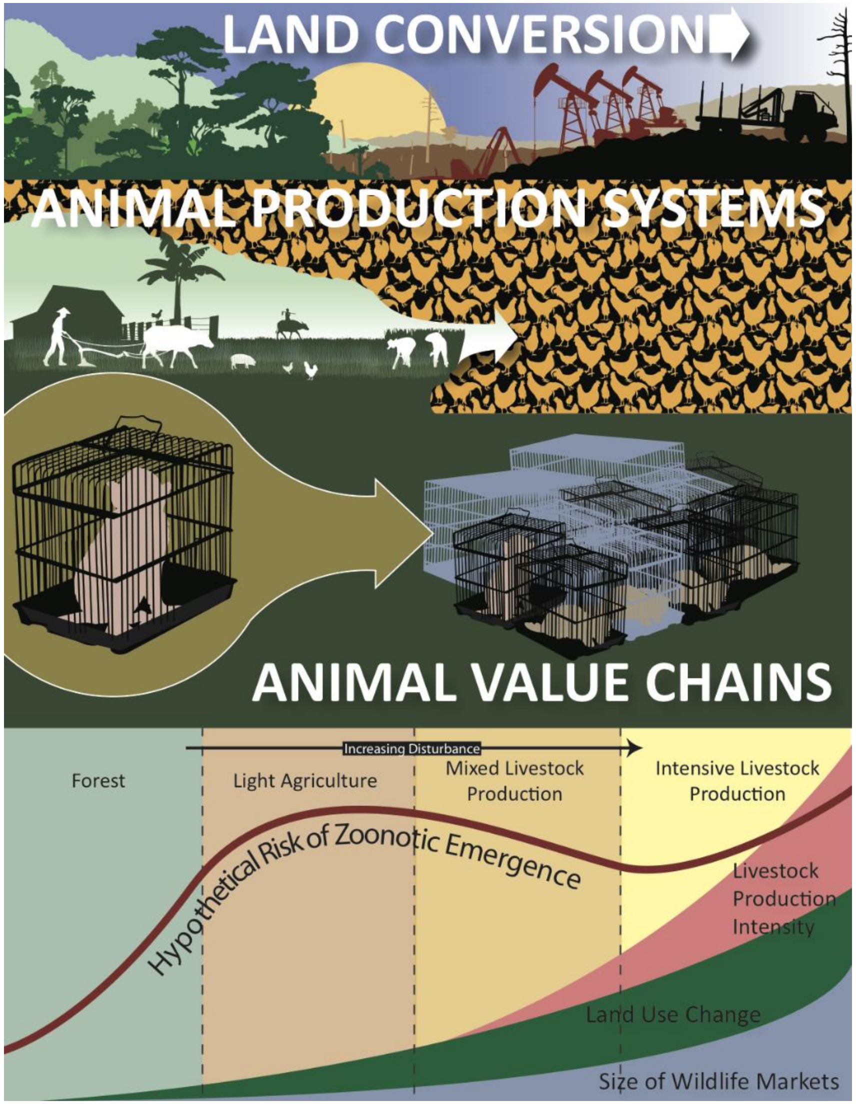
Local conservation.
Global health.

USAID PREDICT-2

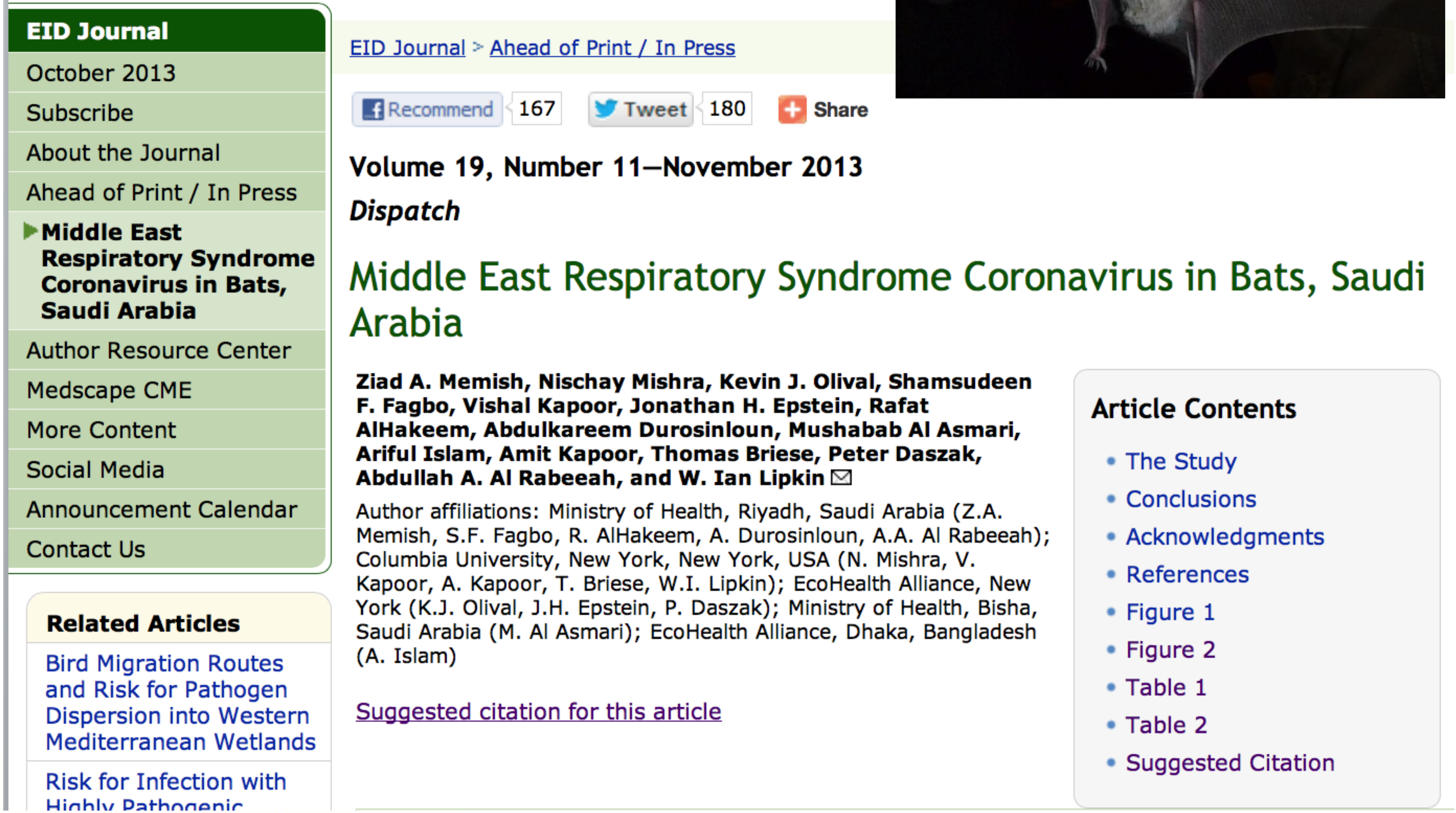
Geographic Focus

Asia
Bangladesh
Cambodia
China
Lao PDR
N. India
Indonesia
Nepal
Malaysia
Myanmar
Thailand
Vietnam

Africa
Cameroon
Gabon
DR Congo
Republic of Congo
Rwanda
Tanzania
Uganda
Liberia
Guinea
Sierra Leone
Kenya
Ethiopia
Egypt
Jordan
Sudan & S. Sudan



EMERGING INFECTIOUS DISEASES®



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Risk for Infection with Highly Pathogenic

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Dispatch

Middle East Respiratory Syndrome Coronavirus in Bats, Saudi Arabia

Ziad A. Memish, Nischay Mishra, Kevin J. Olival, Shamsudeen F. Fagbo, Vishal Kapoor, Jonathan H. Epstein, Rafat AlHakeem, Abdulkareem Durosinloun, Mushabab Al Asmari, Ariful Islam, Amit Kapoor, Thomas Briese, Peter Daszak, Abdullah A. Al Rabeeah, and W. Ian Lipkin ✉

Author affiliations: Ministry of Health, Riyadh, Saudi Arabia (Z.A. Memish, S.F. Fagbo, R. AlHakeem, A. Durosinloun, A.A. Al Rabeeah); Columbia University, New York, New York, USA (N. Mishra, V. Kapoor, A. Kapoor, T. Briese, W.I. Lipkin); EcoHealth Alliance, New York (K.J. Olival, J.H. Epstein, P. Daszak); Ministry of Health, Bisha, Saudi Arabia (M. Al Asmari); EcoHealth Alliance, Dhaka, Bangladesh (A. Islam)

Suggested citation for this article

Article Contents

- The Study
- Conclusions
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- Table 2
- Suggested Citation

Global health.

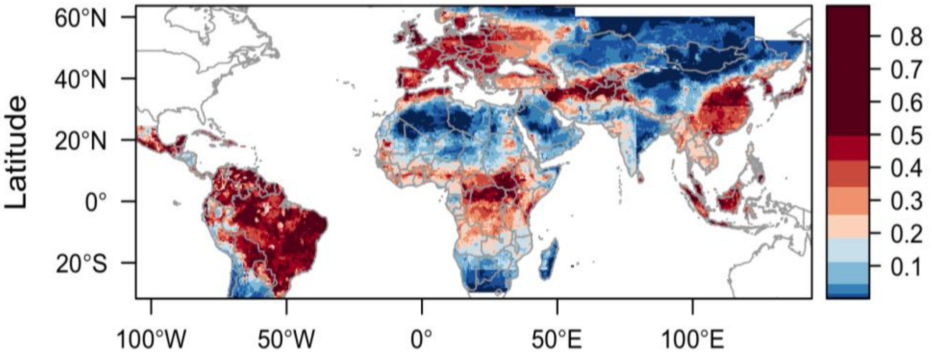
Human-Camel Interface

Photo: K.J. Olival

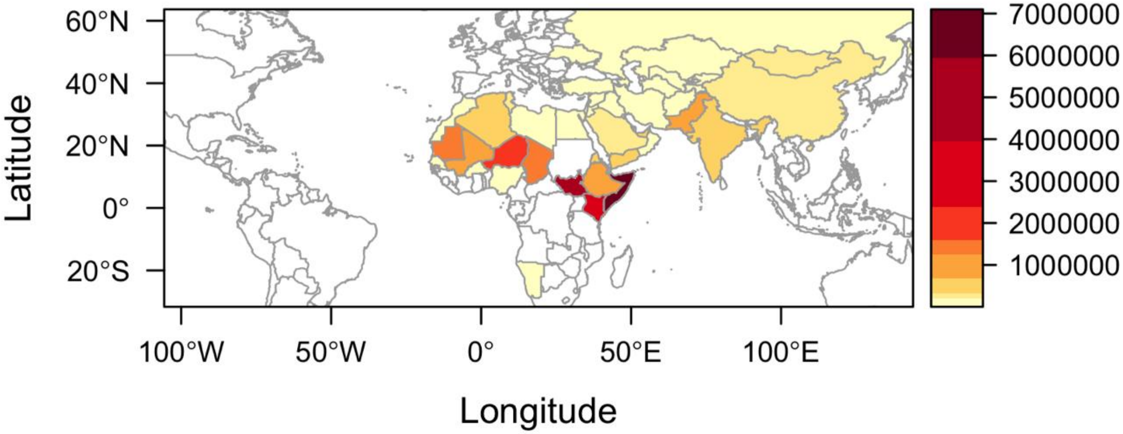
http://www.efratnakash.com

Where did MERS originate?

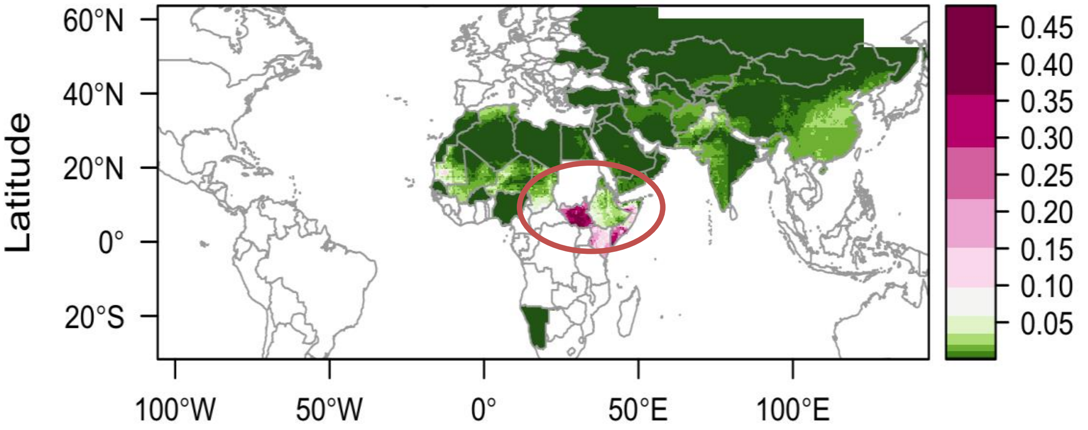
- Modeled distribution of MERS-CoV bats



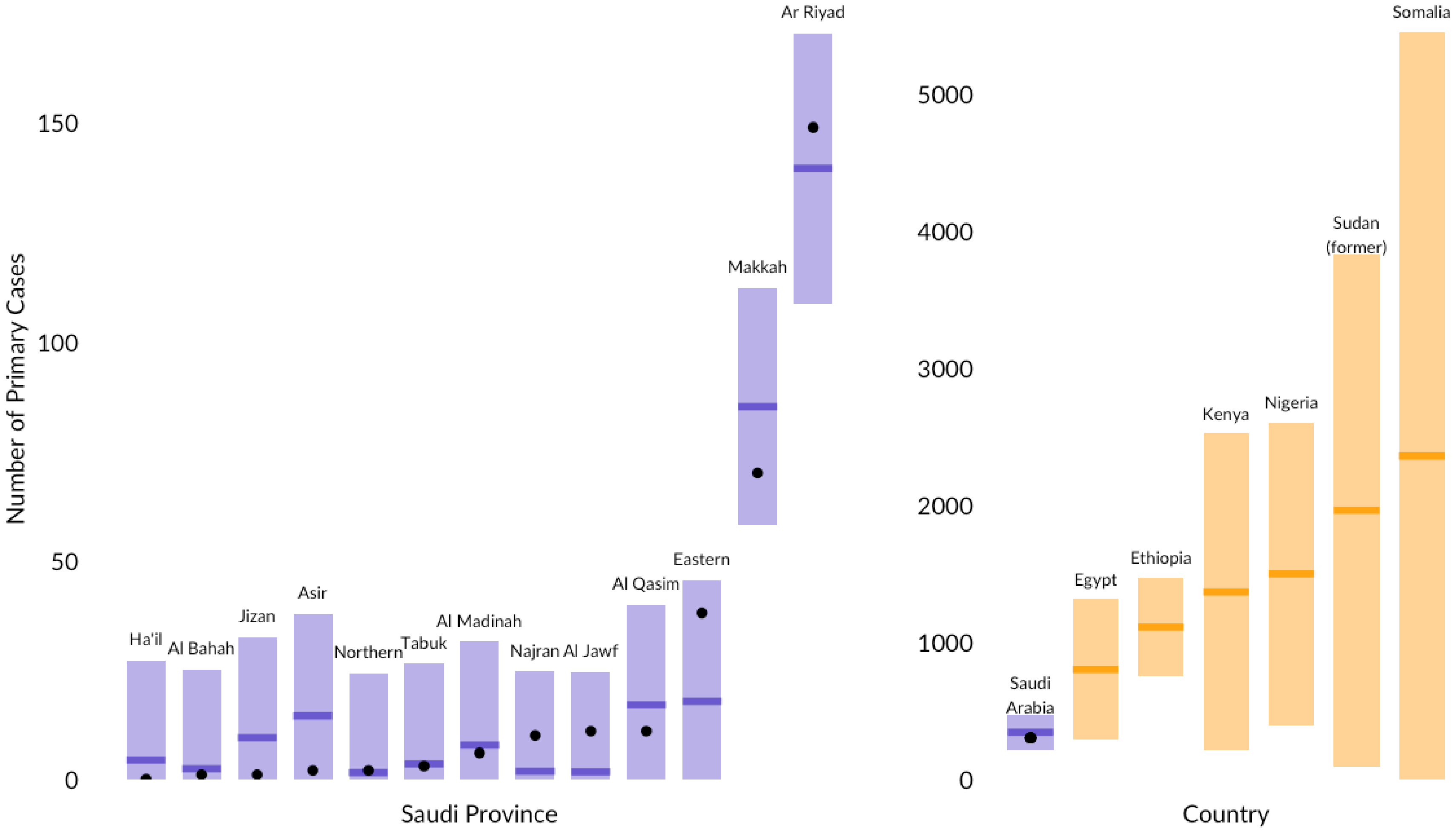
- Camel production (FAO)



- Modeled risk of MERS spillover (horn of Africa)



Unidentified MERS-CoV cases:



PREDICT 2: Behavioral Research

- Linking specific behaviors and practices with evidence of spillover
  - Identify relationships between exposure and outcome
  - What are the mechanisms of spillover transmission

- Understand the communities and context within which risk occurs
  - What are the circumstances that increase or decrease risk

Observational Research

- Introduction of research to target community
- Identify individuals of power and influence/barriers to access
- Evaluation of settings of possible disease transmission from animals to humans
- Does not require IRB approval to conduct

Focus group discussions

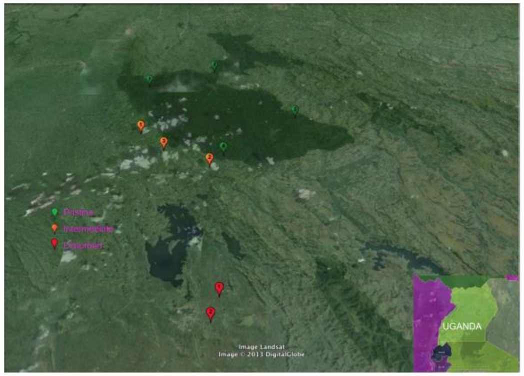
- Carefully planned and guided discussion
- Captures ideas that people agree on in public
- Targets ‘experts’ with regular animal contact
- Requires IRB approval and informed consent

Ethnographic interviews

- One-to-one semi-structured interviews
- Learn about daily and household life
- Assess privately held beliefs and experiences
- Requires IRB approval and informed consent

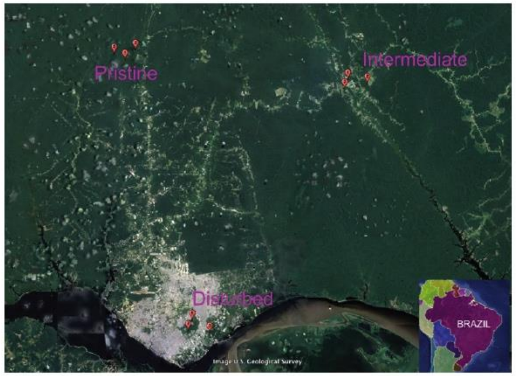
DEEP FOREST

Uganda

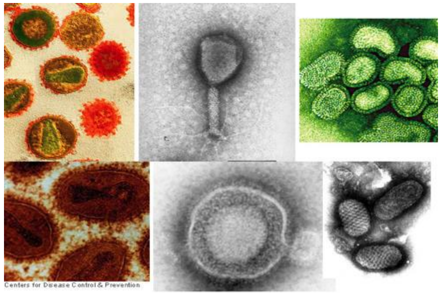


Malaysia

Brazil



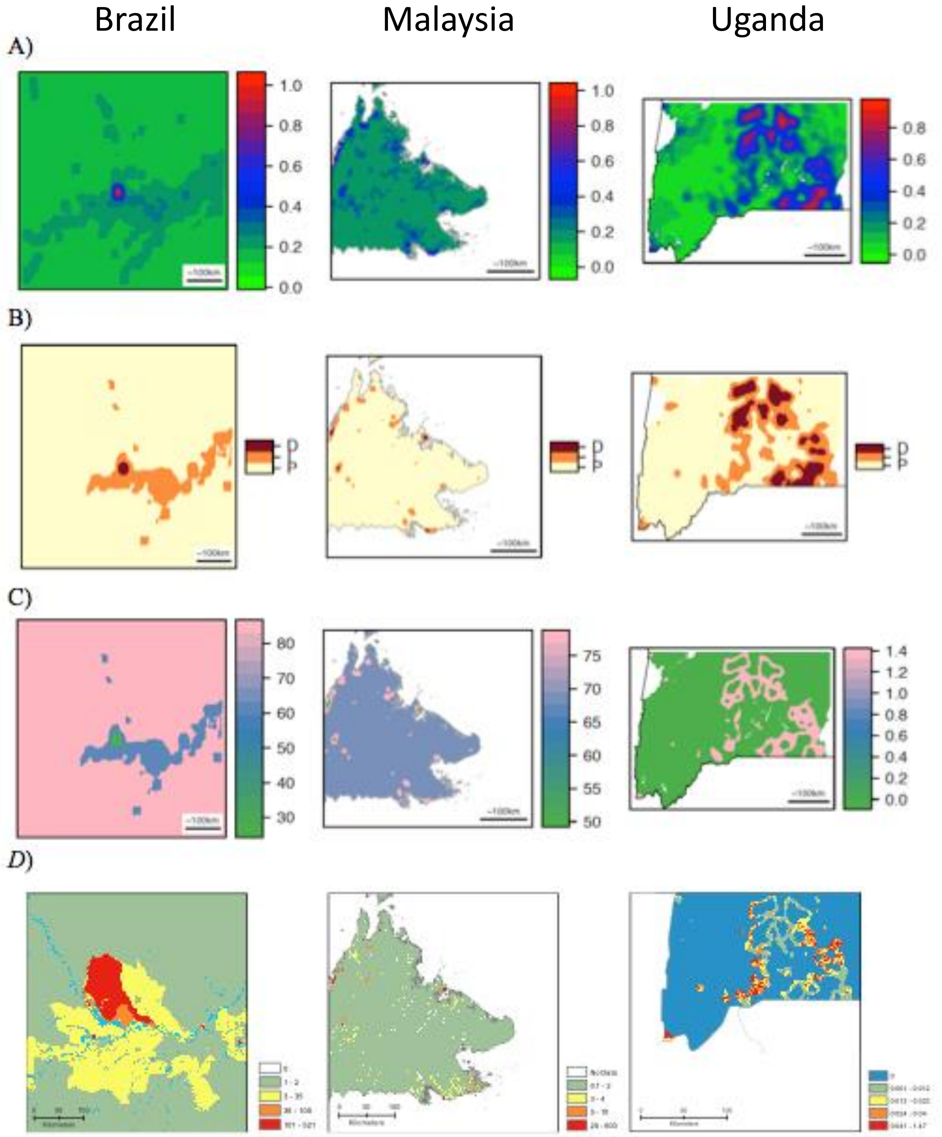

Pristine
Intermediate
Urban



- Systematic animal sampling
- Broad viral screening
- Human behavioral data collection

USAID | PREDICT
FROM THE AMERICAN PEOPLE

Mapping human-animal contact from behavioral surveys



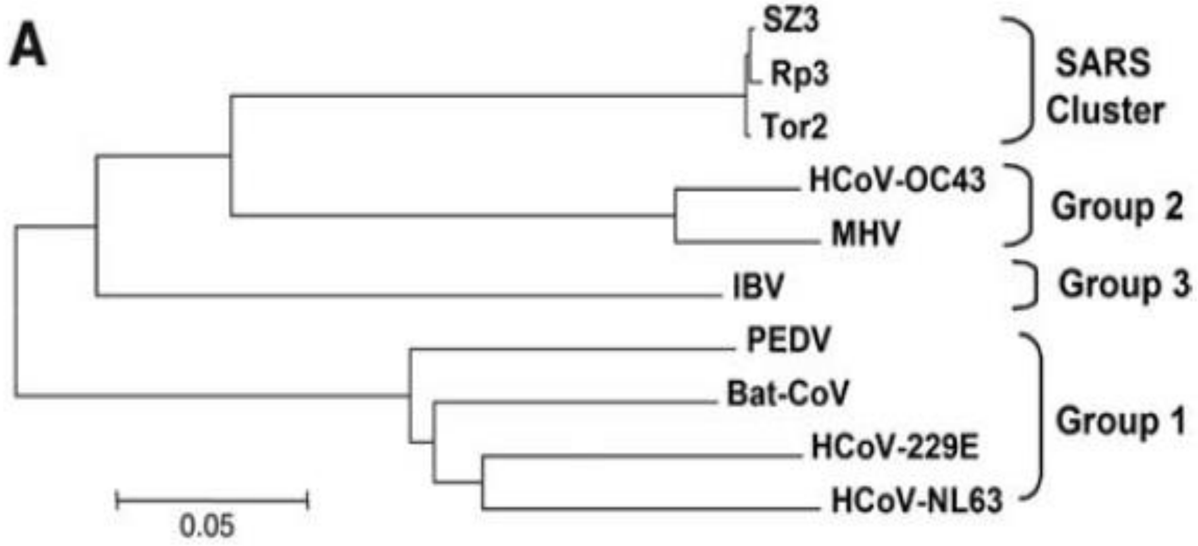
A) **Raw Landscape Development Intensity (LDI) Index**
(0=pristine, 1=highly disturbed)

A) **Reclassified LDI** (P=Pristine, I=Intermediate, D=disturbed)

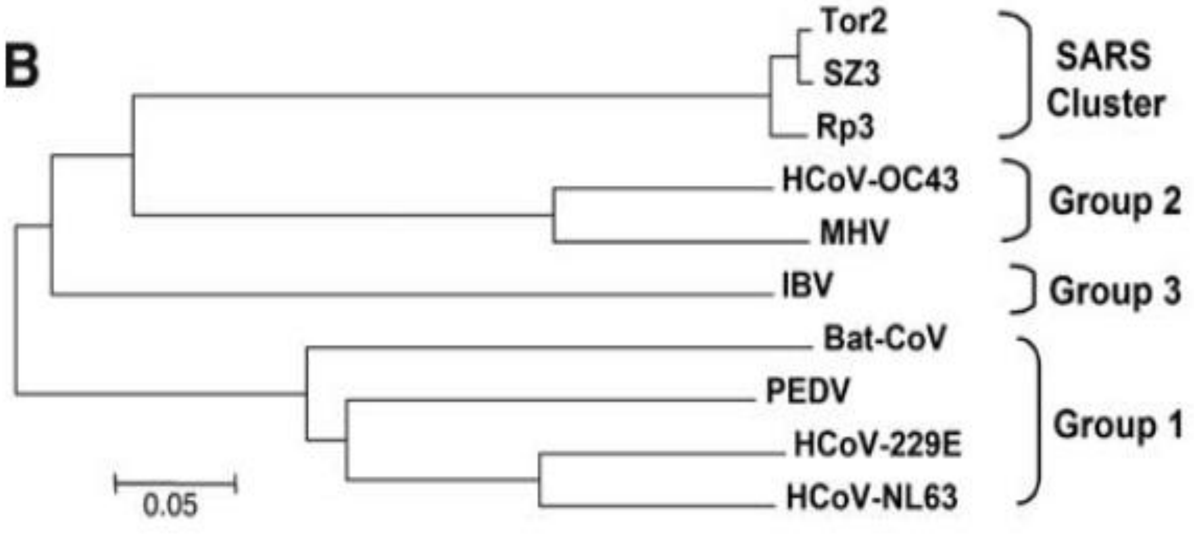
A) **Percentage of respondents reporting wildlife consumption**

B) **Relative human-animal contact rate**

SARS-like CoV locate within SARS cluster



P1b



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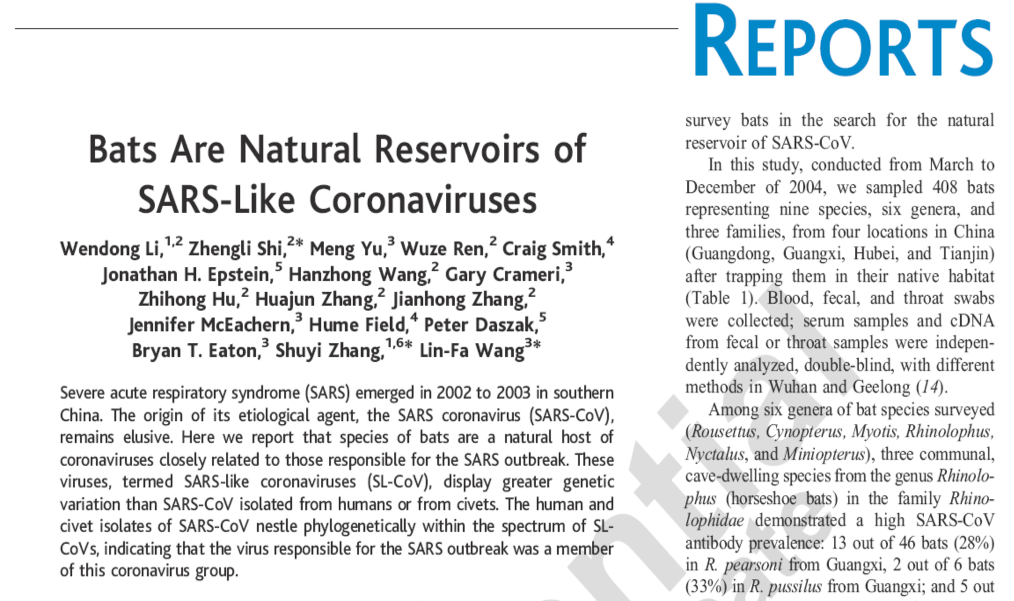


Bats Are Natural Reservoirs of SARS-Like Coronaviruses

Wendong Li,[1,2] Zhengli Shi,[2*] Meng Yu,[3] Wuze Ren,[2] Craig Smith,[4]
Jonathan H. Epstein,[5] Hanzhong Wang,[2] Gary Crameri,[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*]

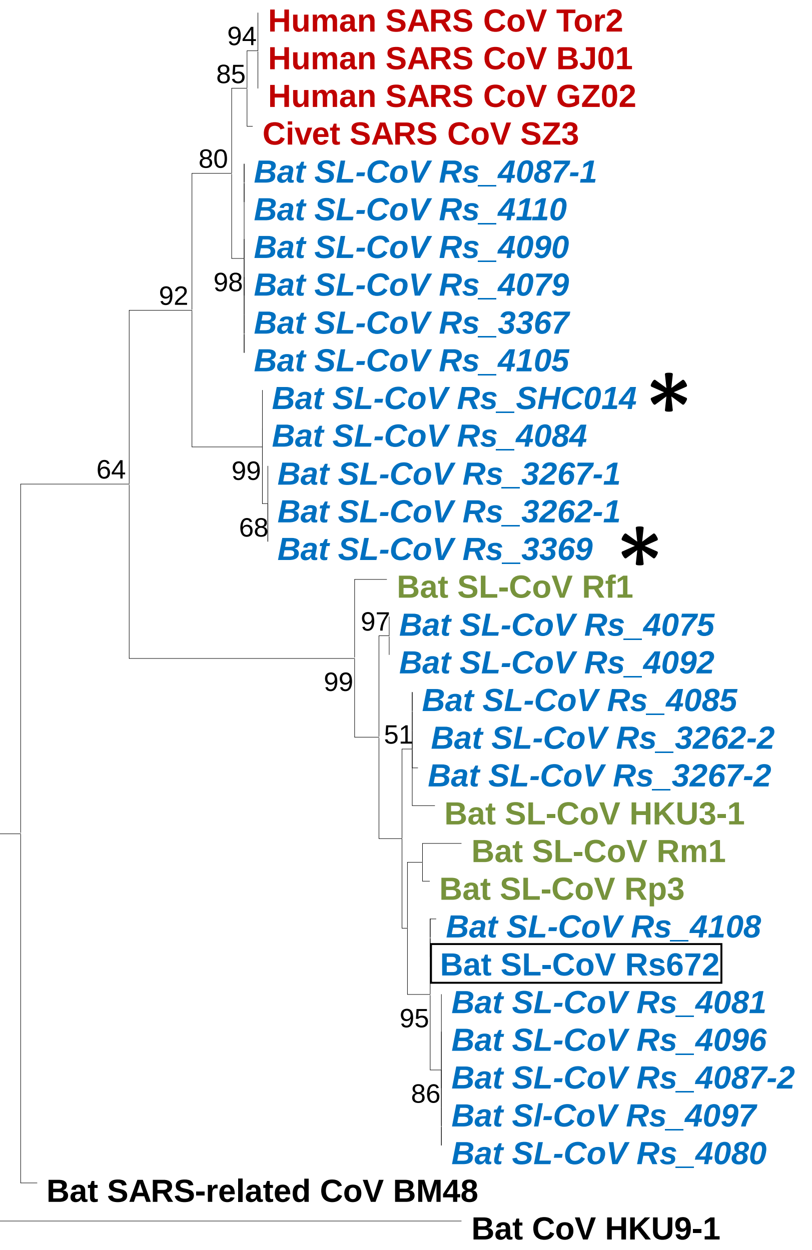
Severe acute respiratory syndrome (SARS) emerged in 2002 to 2003 in southern China. The origin of its etiological agent, the SARS coronavirus (SARS-CoV), remains elusive. Here we report that species of bats are a natural host of coronaviruses closely related to those responsible for the SARS outbreak. 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.

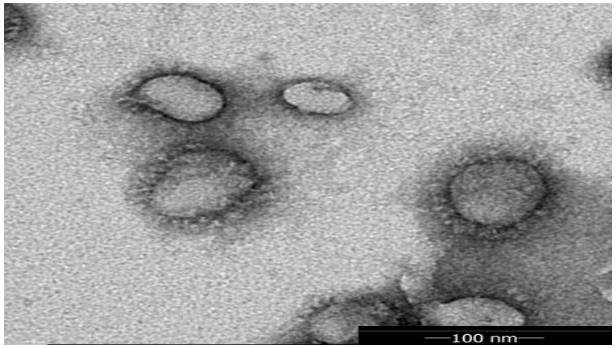
survey bats in the search for the natural reservoir of SARS-CoV.

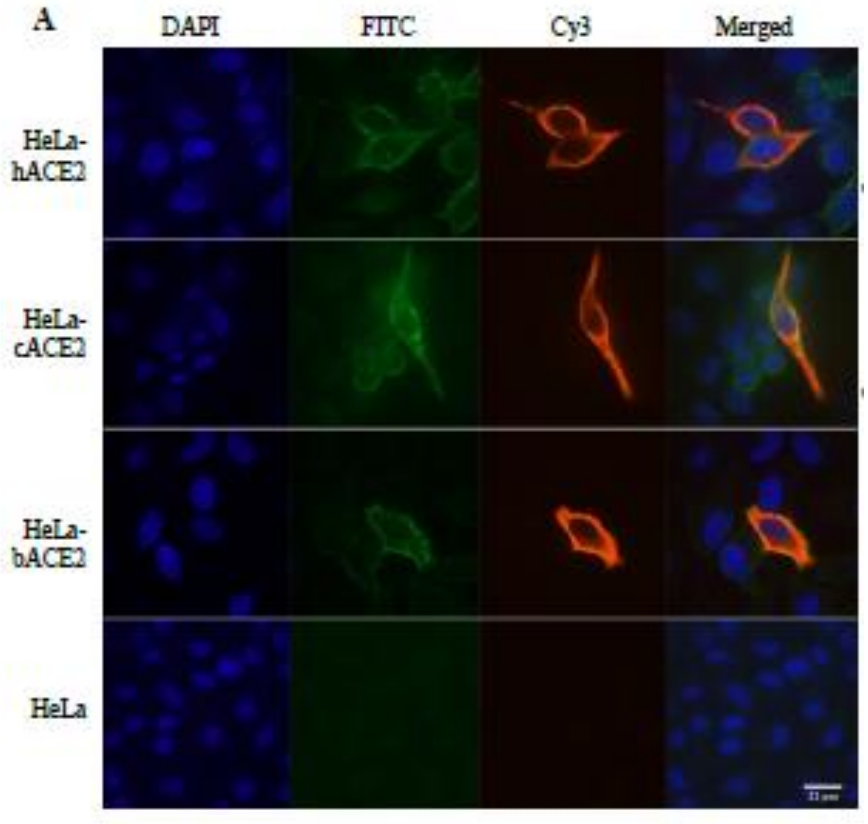
In this study, conducted from March to December of 2004, we sampled 408 bats representing nine species, six genera, and three families, from four locations in China (Guangdong, Guangxi, Hubei, and Tianjin) after trapping them in their native habitat (Table 1). Blood, fecal, and throat swabs were collected; 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. pussilus* from Guangxi; and 5 out

Li *et al.* (2005) *Science* 310: 676-679







Ge *et al.* (2013) *Nature*

EcoHealth Alliance

Wildlife Trade in China

Local conservation.
Global health.

Presumed medicinal properties

- Reduces blood viscosity
- Anti-inflammatory

With local township hospital president

Field Investigation Phase

Human investigation

Questionnaire Implementation

Field Investigation Phase

Human investigation

oropharyngeal swab samples collection

Field Investigation Phase

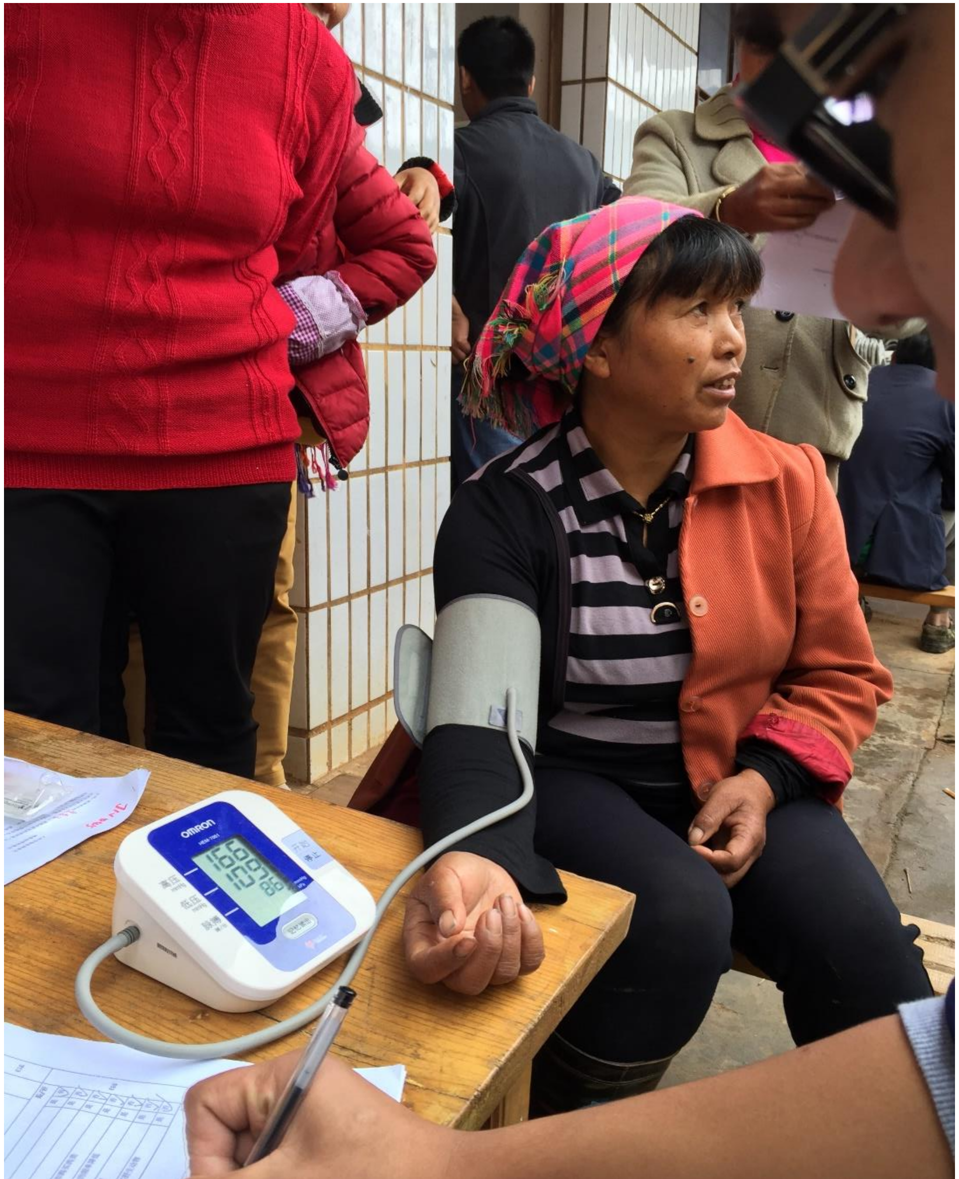
Human investigation

Blood samples collection

Field Investigation Phase

Human investigation

Blood pressure test



Field Investigation Phase

Human investigation

provided a container for stool samples

instructions for collecting uncontaminated samples


广西师范大学教学科研实习基地


VARTA

广西陆生野生动物
驯养繁殖许可证

桂野动繁（　　）号

经审核，允许驯养繁殖广西陆生野生动物。特发此证。

（准许驯养繁殖种类见副本）

发证机关

EcoHealth Alliance

**MILLIONS OF ANIMALS
ARE SMUGGLED EACH YEAR –
ENDANGERING THEIR LIVES
AND YOURS.**

**PLEASE JOIN ECOHEALTH ALLIANCE IN
STOPPING ILLEGAL WILDLIFE TRADE.**

**Visit
EcoHealthAlliance.org/trade**

EcoHealthy Pets Program:
www.ecohealthypets.com

- Nearly 28 million households own 45 million exotic pets in the U.S. (205 million including fish)

PETWATCH: CHOOSING THE RIGHT EXOTIC PET

PetWatch is a consumer information website developed from scientific research on global wildlife trade into the U.S. Our aim is to protect natural resources, native wildlife, global biodiversity, and public health by offering consumers a list ranking the Best, Worst and Fair exotic pet options for you and your home.

Promotin
for famili
the envir

EcoHealthy Pets

A program of EcoHealth Alliance

We aim to protect U.S. natural resources, native wildlife, global biodiversity, and public health by offering you a science-based list of Best, Worst, and Fair Choice pet species.

Valuing Ecosystem Services

If we convert forest, diseases emerge.

These diseases cost billions of dollars annually.

Can we include these costs in decision making to reduce deforestation?

Conversion: Benefits

Benefits

- Meet global demand for goods and services
- Generate household income
- Regional/national economic growth

Conversion: Costs

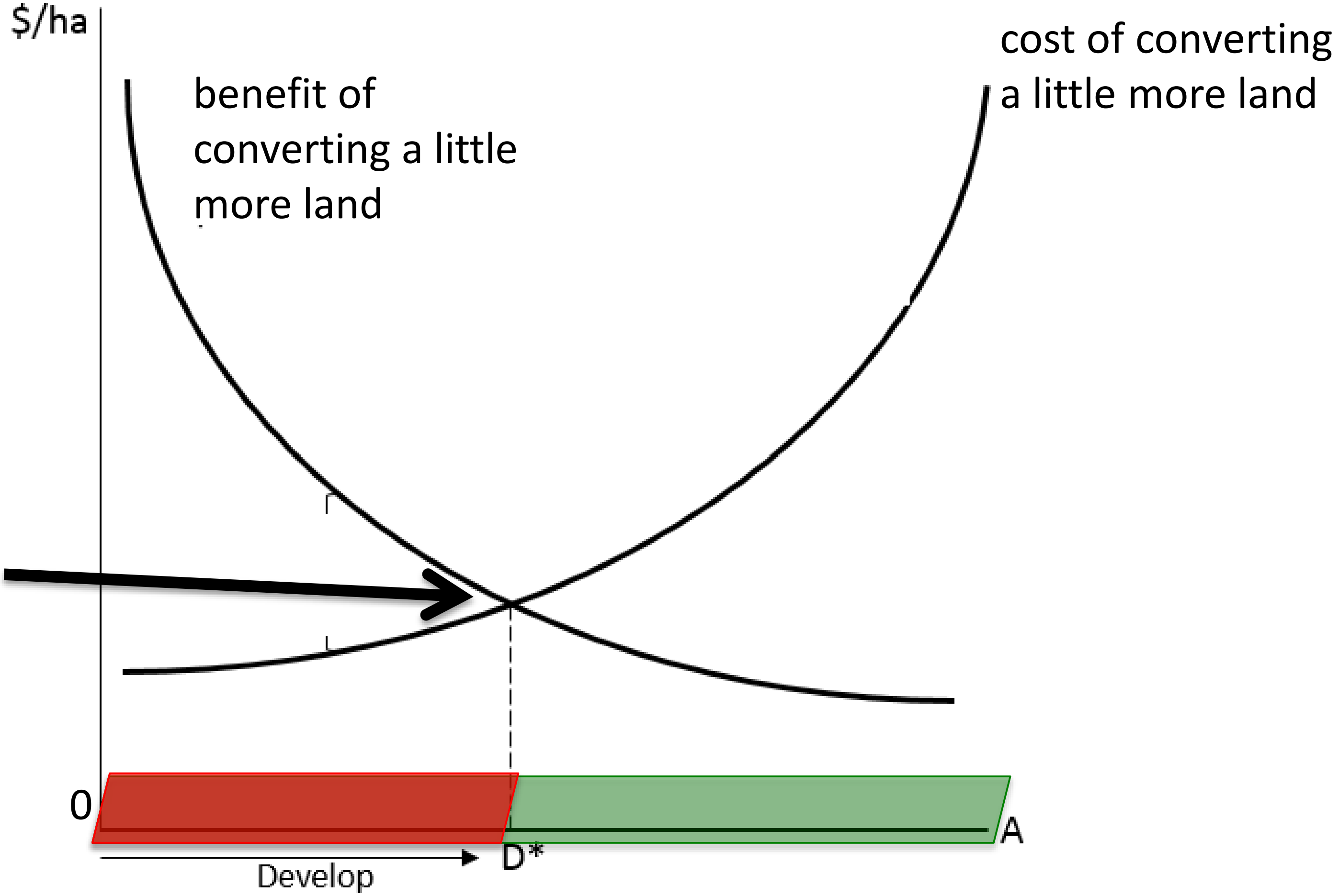
Costs

- Converting land costs money
  - clearing forest
  - cultivating field

- Maintaining land productivity
  - fertilizer
  - irrigation

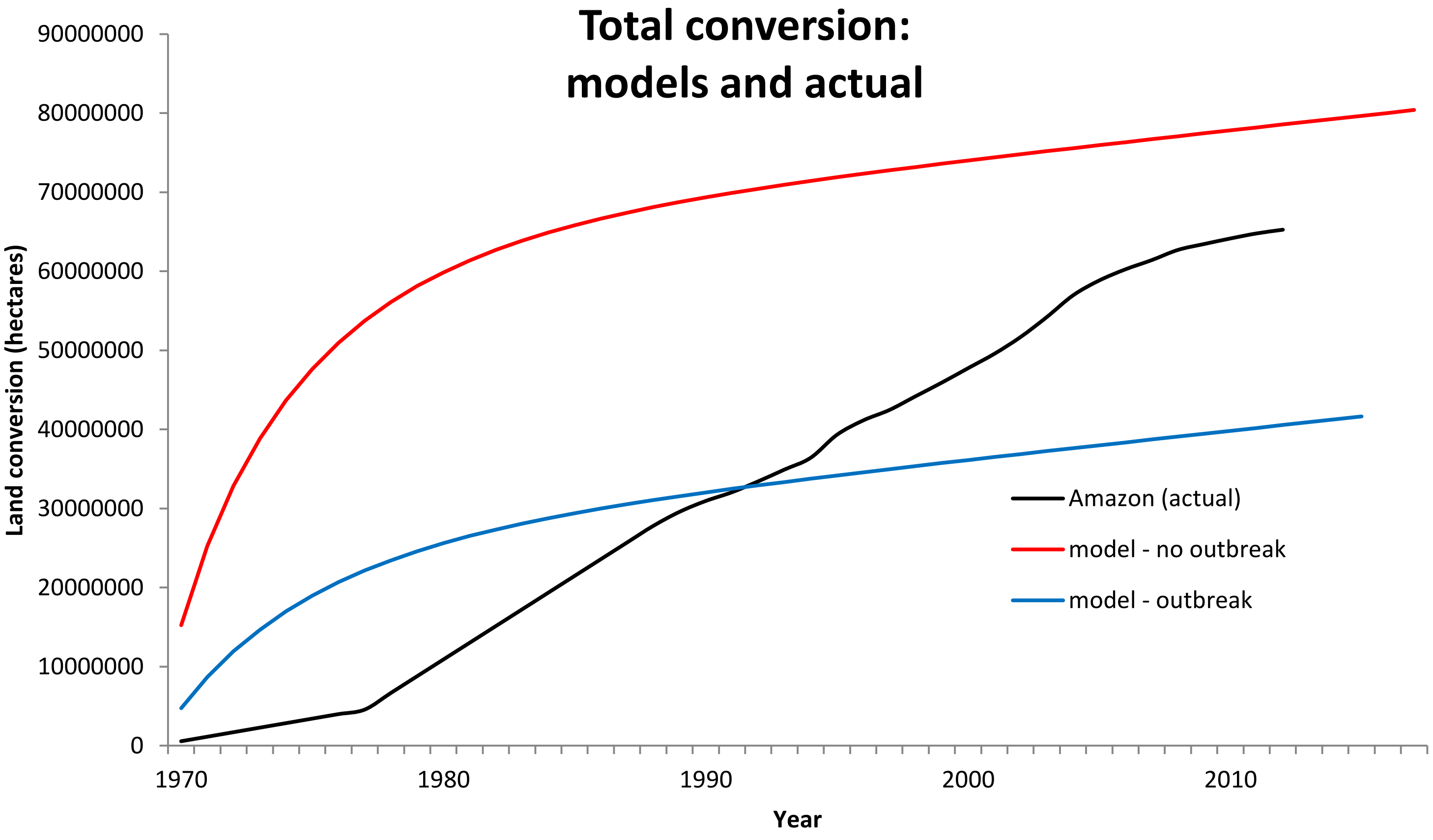
- Lost ecosystem benefits
  - Abiotic and biotic services
  - Naturally derived products
  - **Exposure to disease**

How much to convert?

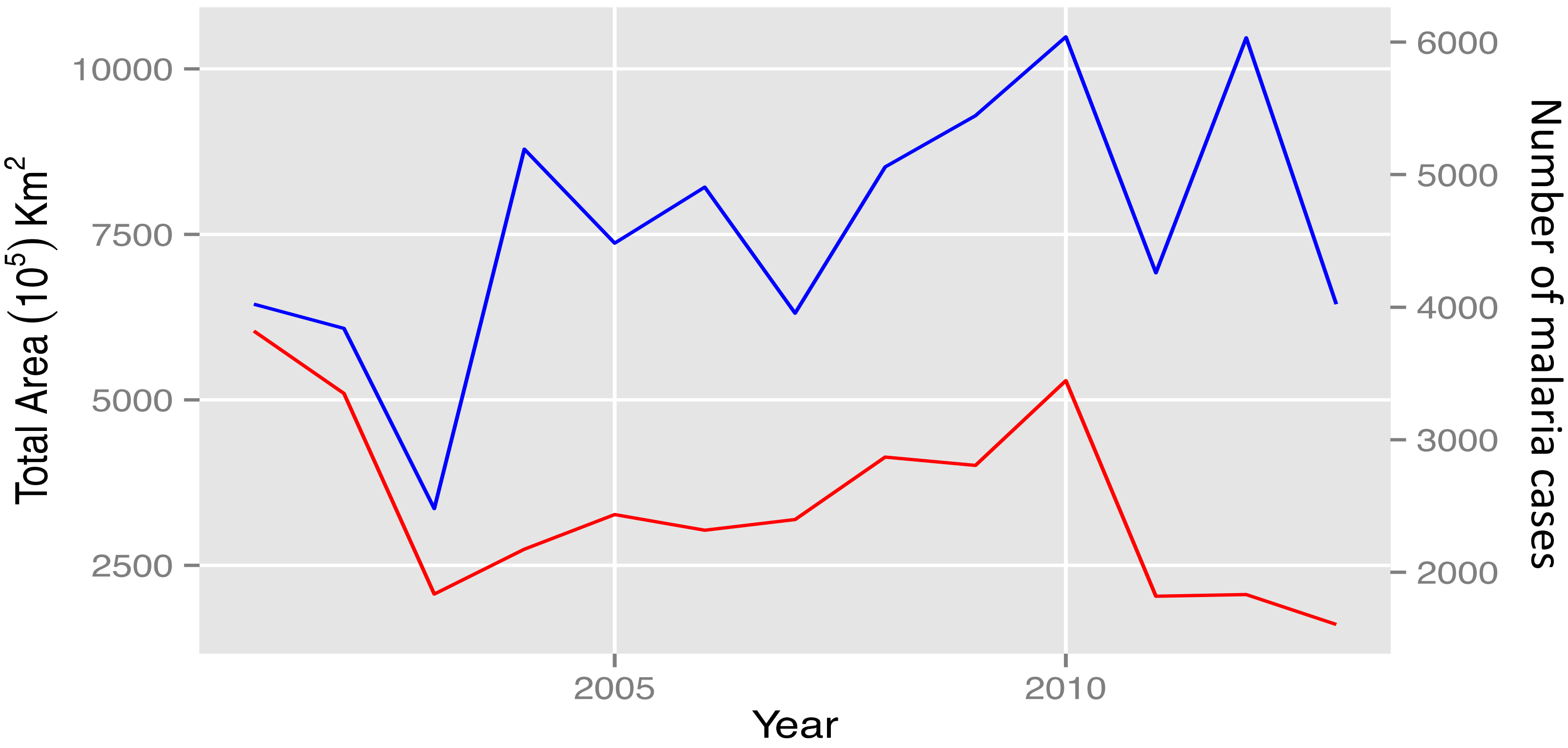


no difference between benefits and costs

Brazilian Amazon



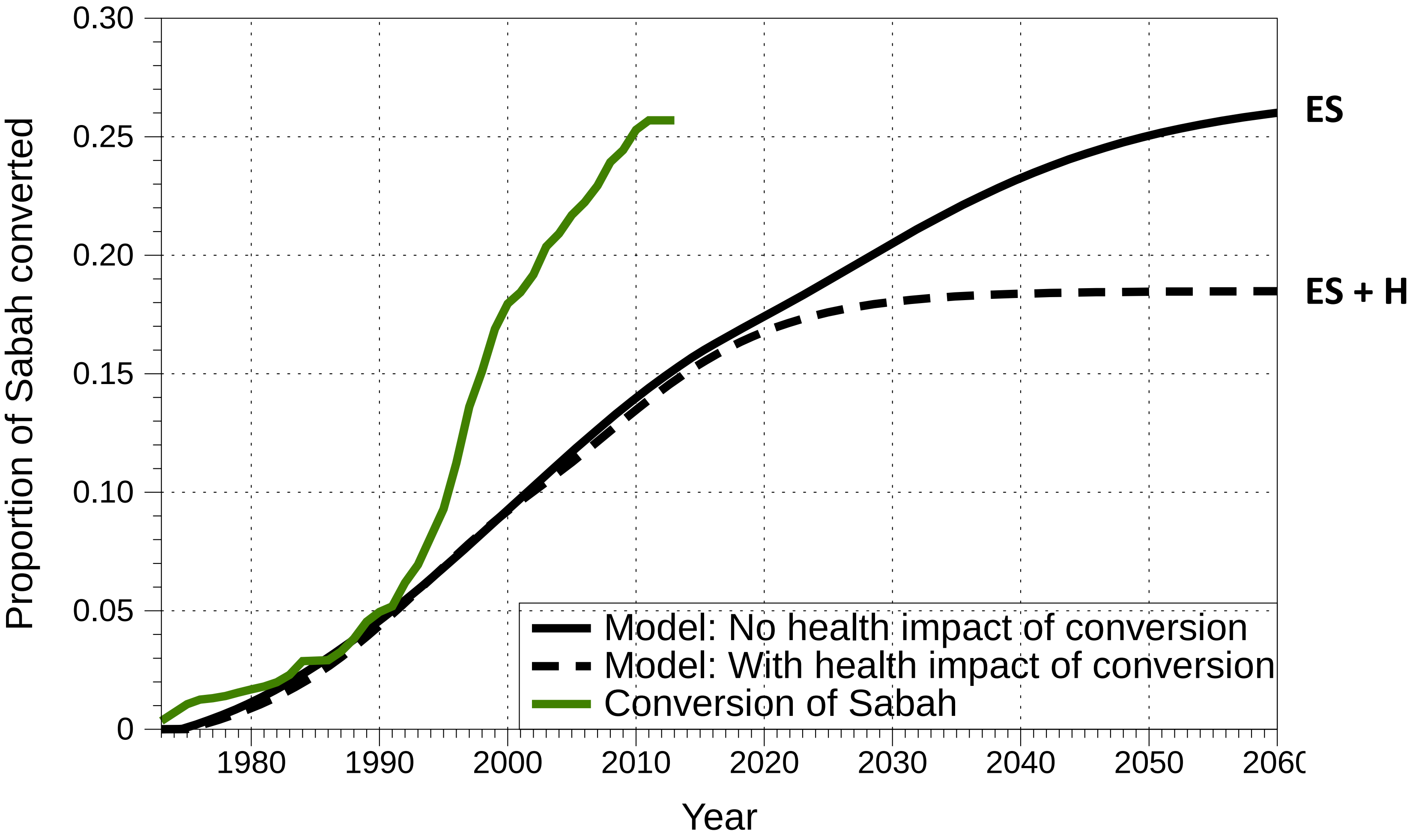
deforestation and malaria in Sabah, MY

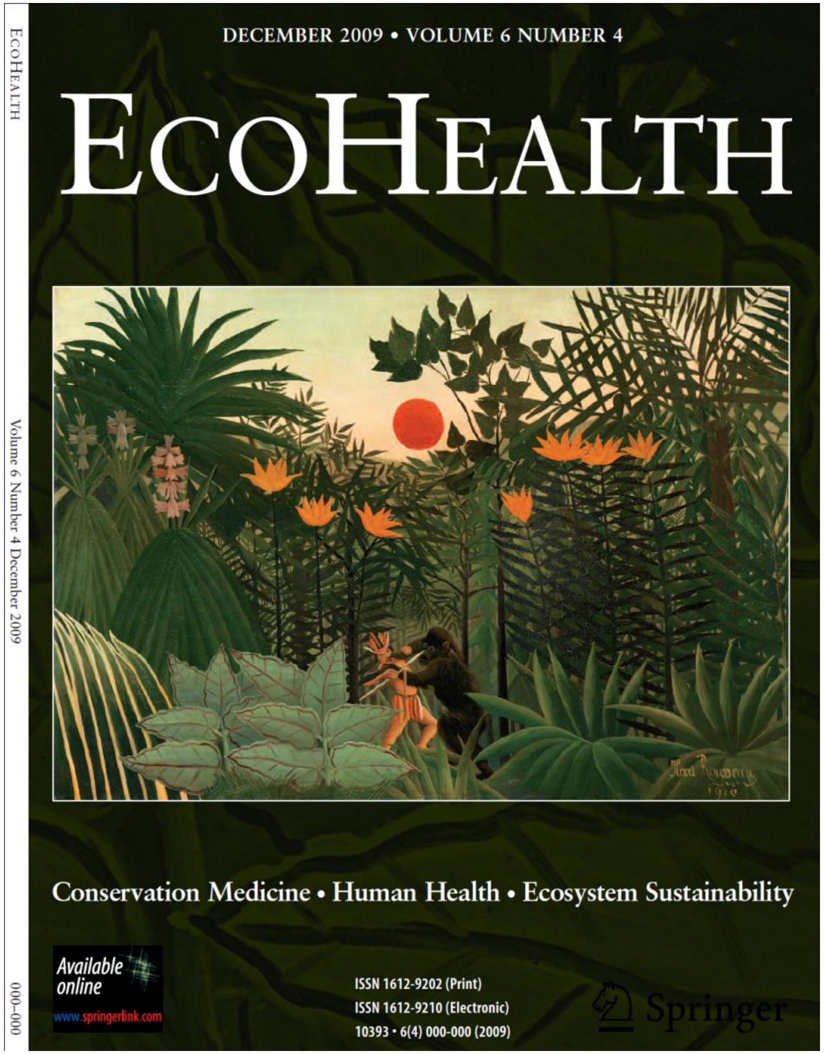


Deforested area in Sabah – Malaysia (red) and the number of cases of Malaria in blue (2001 – 2013) (Zambrana-Torrelio unpub. data)

Similar trends observed in Brazil (Olson et al. 2010) and Indonesia (Garg 2015)

Simulations: Sabah

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- 100+ partners in 24 countries
- Wuhan Inst. Virol.: Zhengli Shi, Ben Hu, Xingye Ge
- Yunnan CDC: Yunzhe Zhang
- Wuhan CDC: Shiyue Li
- Columbia Univ. (Ian Lipkin, Simon Anthony)
- UC Davis, Metabiota, WCS, Smithsonian
- Universiti Malaysia Sabah, Sabah Wildlife Dept.

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