Biodiversity Loss and Emerging Infectious Disease

ProMED
INTERNATIONAL SOCIETY FOR INFECTIOUS DISEASES

IMED 2018

International Meeting on Emerging Diseases and Surveillance

UCDAVIS VETERINARY MEDICINE
EpiCenter for Disease Dynamics

Christine Kreuder Johnson
Professor of Epidemiology
EpiCenter for Disease Dynamics
One Health Institute
University of California, Davis

Emerging Pandemic Threat

Common (most likely) features
1. New pathogen or a new strain of a pathogen
2. Initiated by effective contact with an animal
3. Propagated by human-to-human transmission
4. Humans lack prior immunity

Putting aside
Major infectious diseases of the 21st century

Endemic or seasonally epidemic zoonotic diseases

such as brucellosis, rabies, plague, salmonellosis, campylobacteriosis, leptospirosis, bovine tuberculosis, cysticercosis, echinococcosis, trypanosomiasis, toxoplasmosis, anthrax, cholera, Q fever, Chagas disease, Rift Valley fever, etc . . .

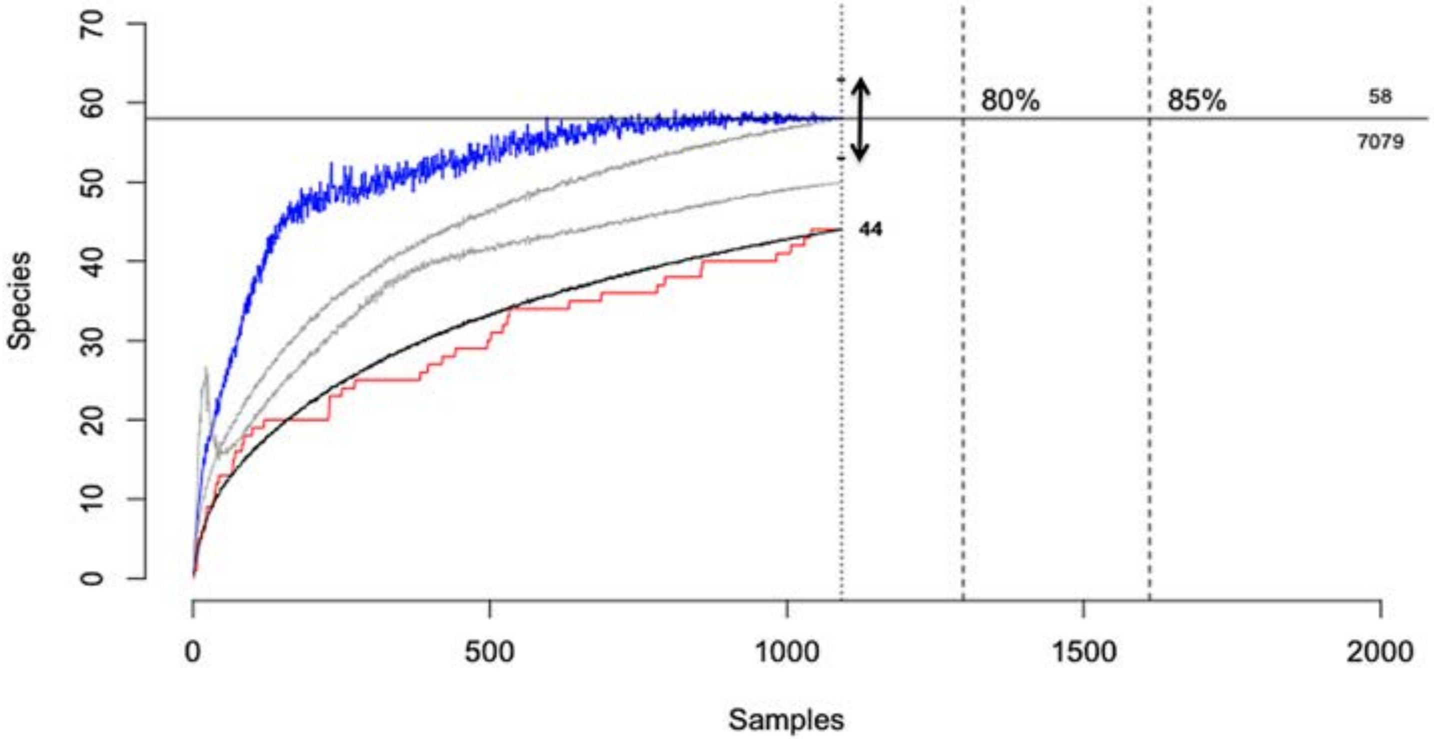
Routinely transmitted between animals and humans,
causing persistent and serious burden to public health and development,
not to mention millions of deaths every year

AMR

Mechanisms Underlying Emergence of a Pandemic Threat

Something NEW under the sun

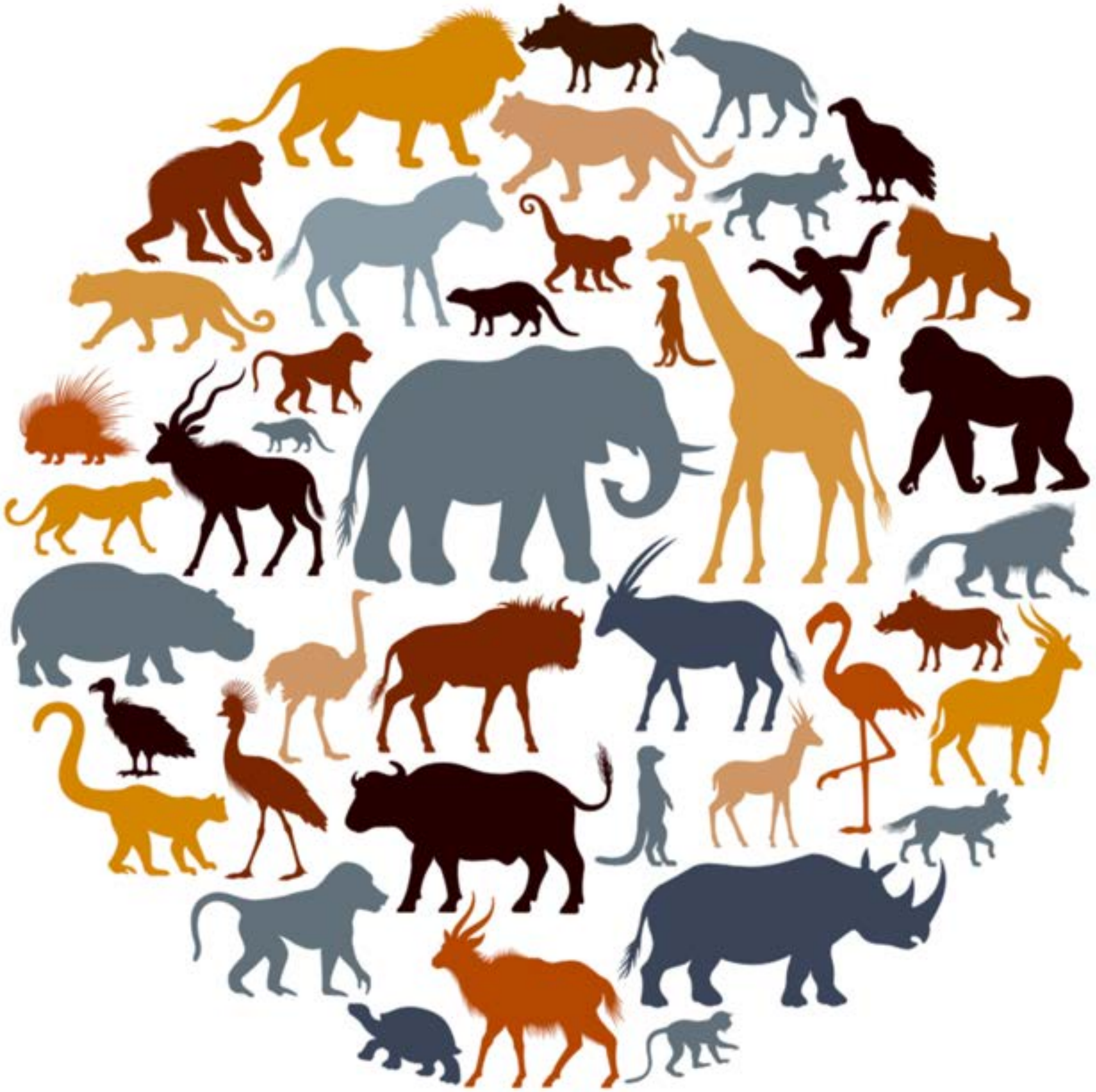
Or something old that just hasn't emerged into humans yet . . . . . .



Detected 55 viruses in nine viral families in *Pteropus giganteus* in this one mammal species
Estimate a minimum of 320,000 mammalian viruses awaiting discovery

Anthony SJ, Epstein JH, Murray KA, Navarrete-Macias I, Zambrana-Torrelio CM, Solovyov A, Ojeda-Flores R, Arrigo NC, Islam A, Ali Khan S, Hosseini P, Bogich TL, Olival KJ, Sanchez-Leon MD, Karesh WB, 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. doi:10.1128/mBio.00598-13.

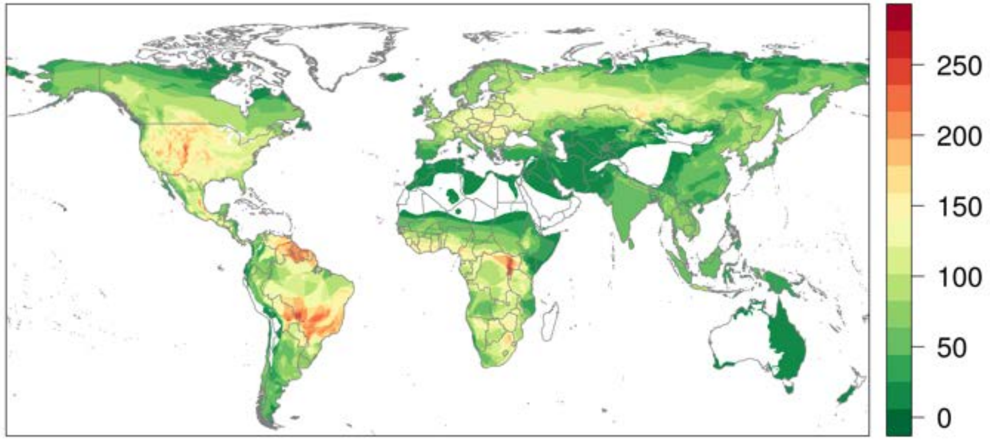
The "Zoonotic Pool"



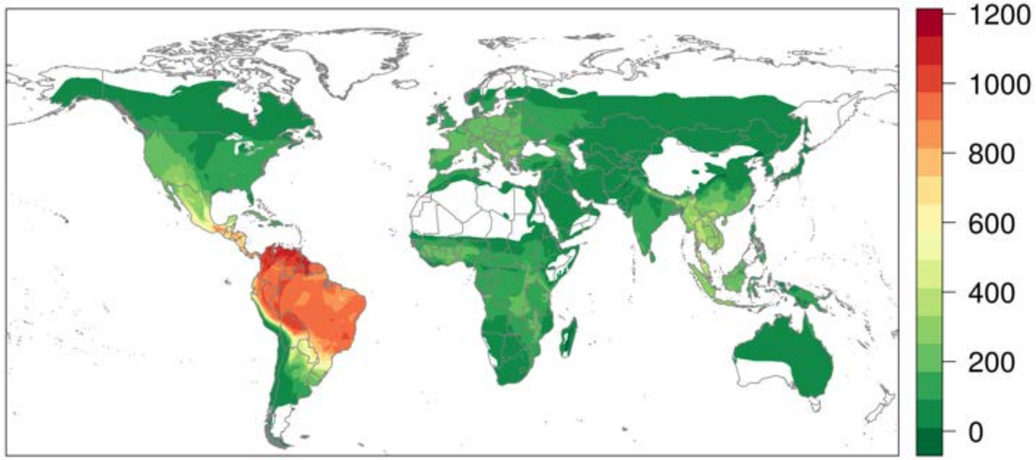
Millions of viruses, some of which could be pre-adapted to be zoonotic, or be evolving to be zoonotic

As yet undiscovered zoonoses

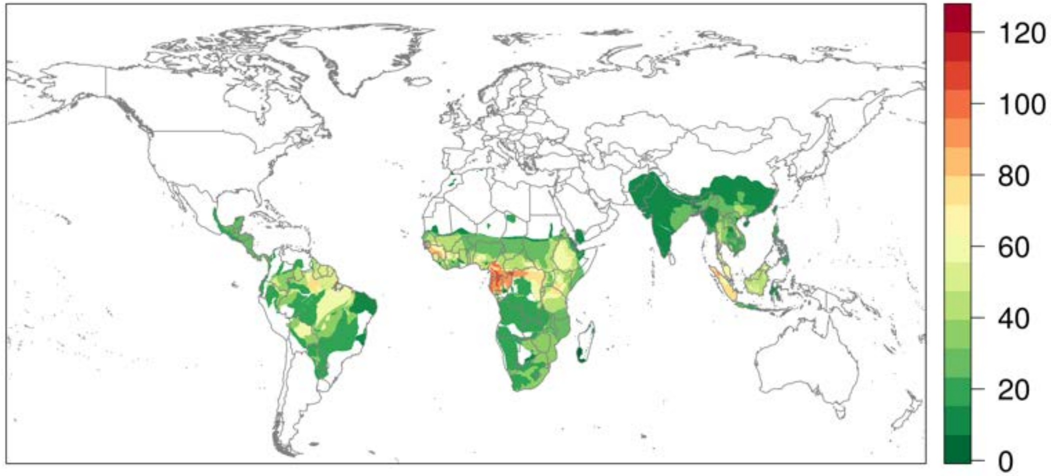
Rodent Missing Zoonoses



Bat Missing Zoonoses



Primate Missing Zoonoses



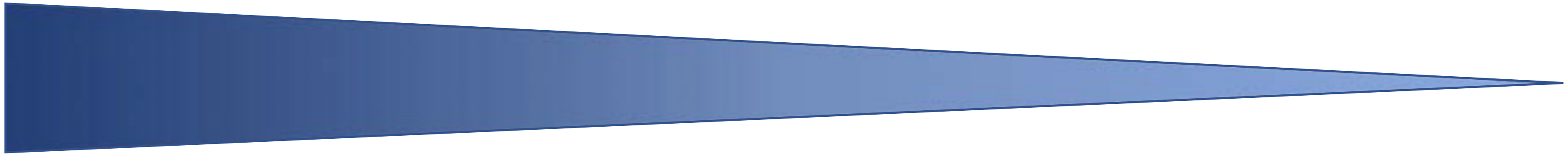
Olival *et al.* 2017, *Nature*

Theoretical relationship between

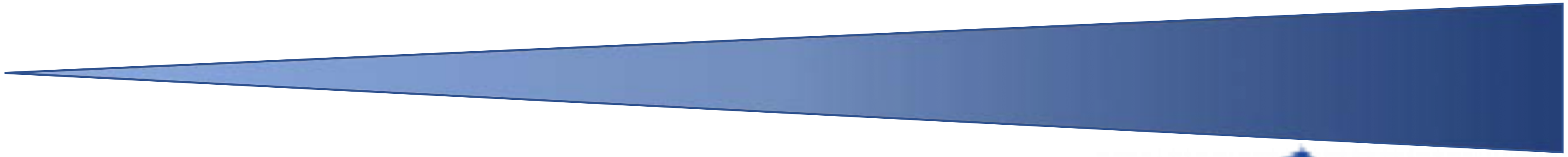
Biodiversity and Emerging Infectious Disease

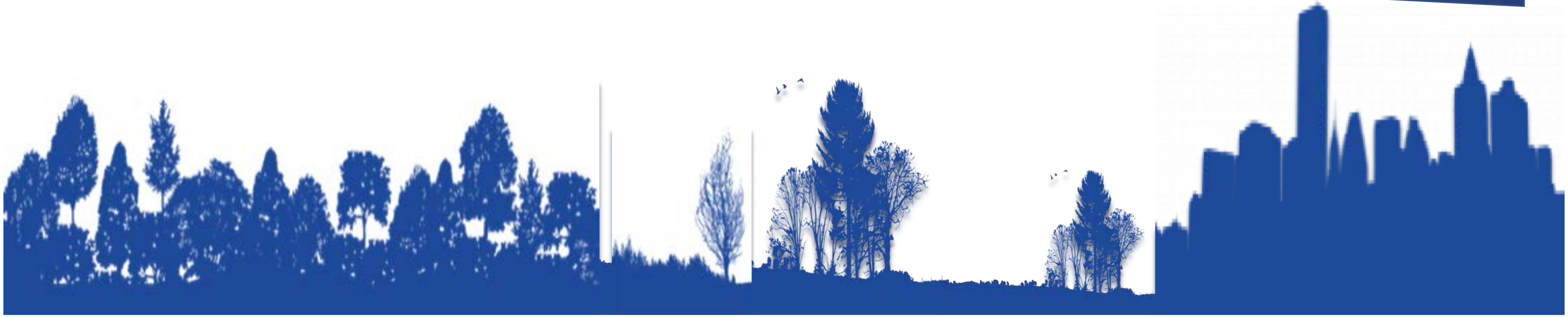
Biodiversity Loss and Emerging Infectious Disease

Biodiversity (presumably)



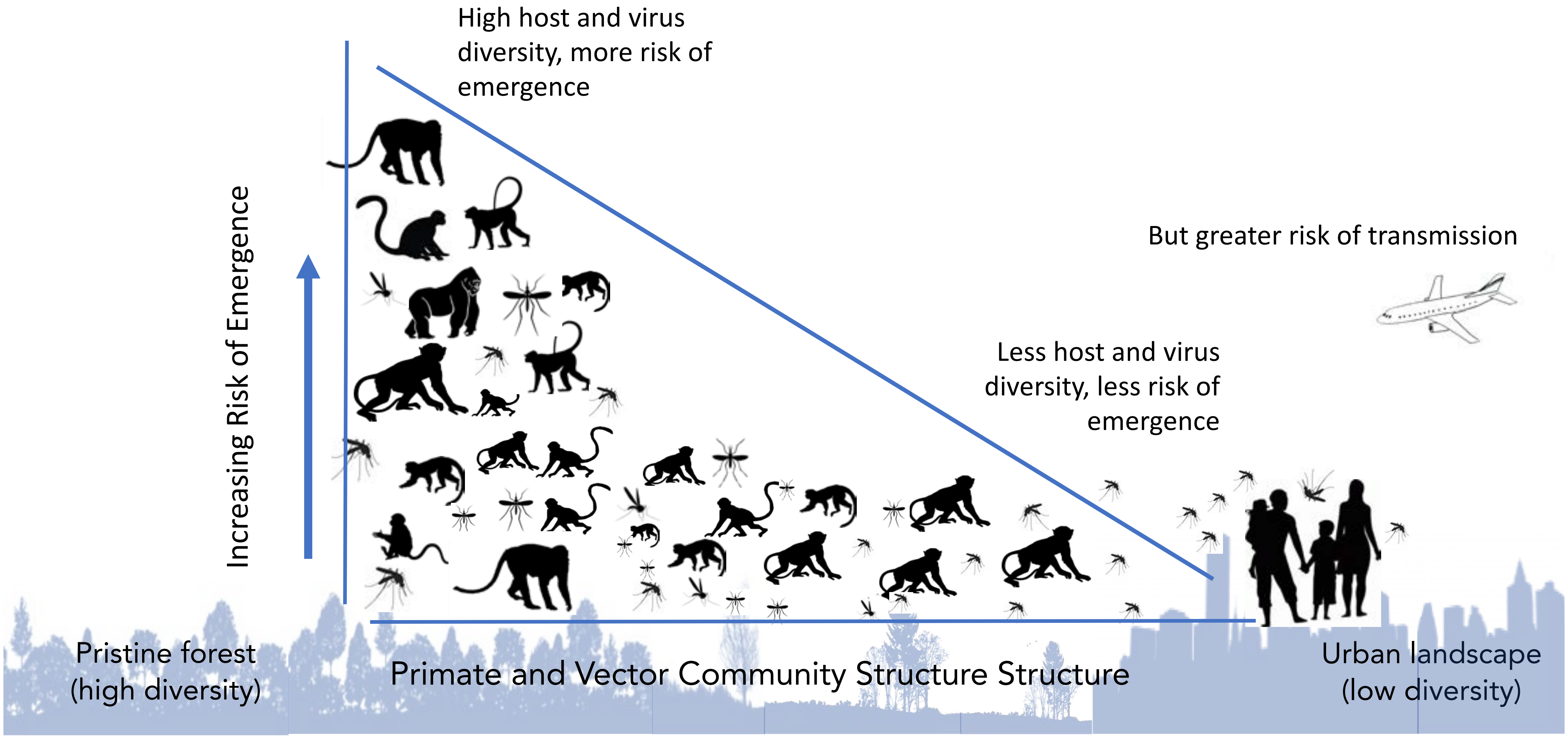
Human abundance (obviously)





Theoretical relationship between

Biodiversity and Emerging Infectious Disease



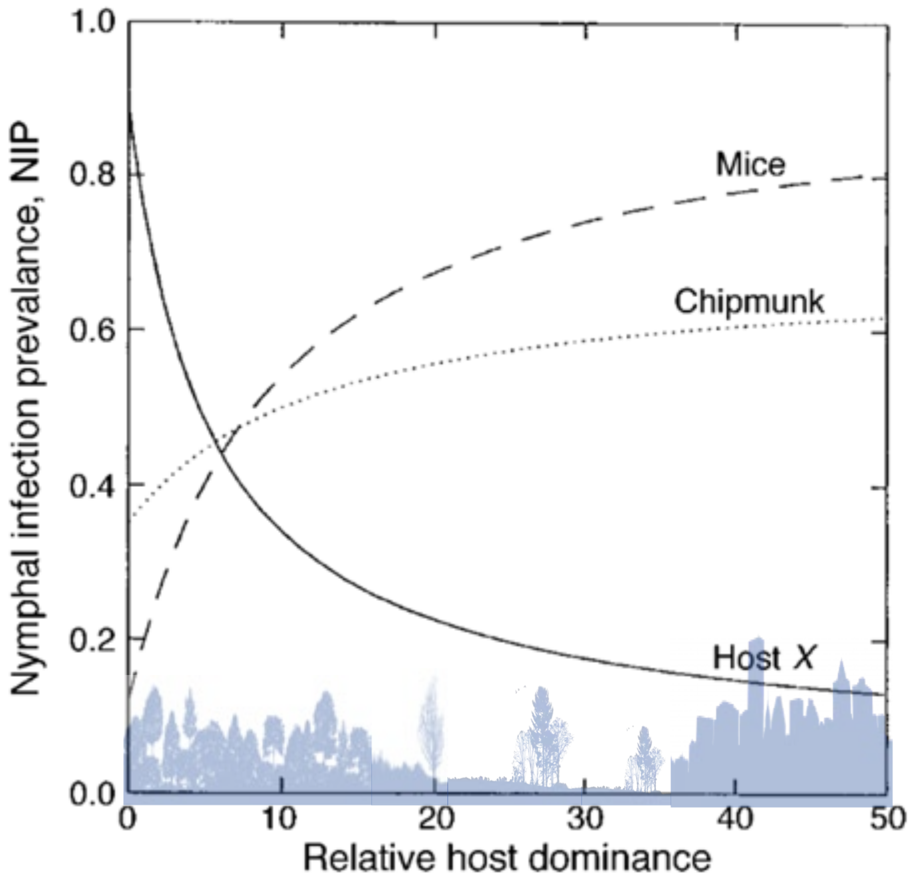
A Role for Biodiversity in Lowering Disease Risk

Community composed mainly of mice and chipmunks

The "Dilution Effect"

Risk of Lyme Disease in eastern New York, US

Loss of biodiversity, towards selection of a couple highly competent hosts (mice, chipmunks) in the community, results in greater tick infection prevalence; whereas, increasing the presence of Host X (eg an incompetent host), results in decreased tick infection prevalence

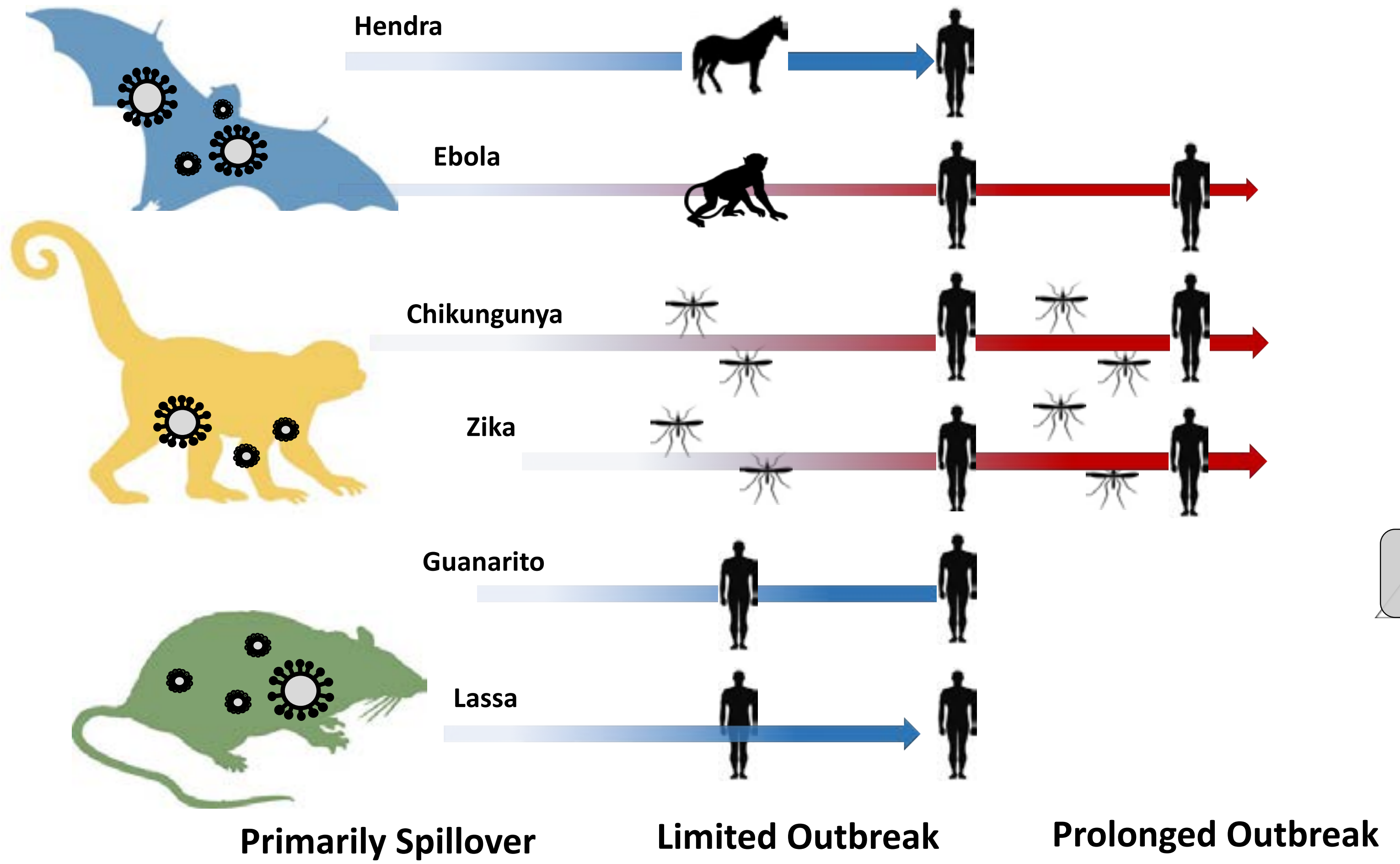


Ecology, 82(3), 2001, pp. 609–619

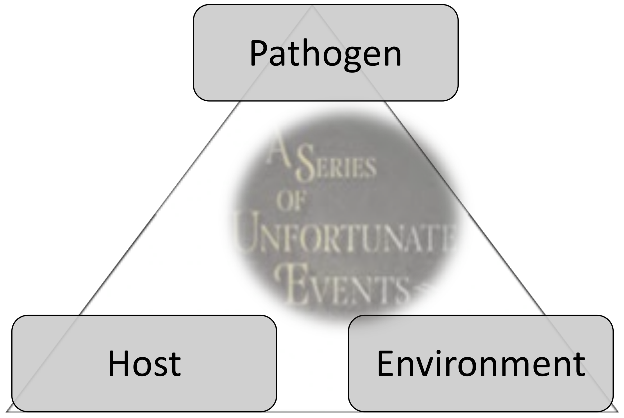
BIODIVERSITY AND THE DILUTION EFFECT IN DISEASE ECOLOGY

KENNETH A. SCHMIDT[1] AND RICHARD S. OSTFELD

Zoonoses: Variability in Potential for Spillover and Human-to-Human Spread

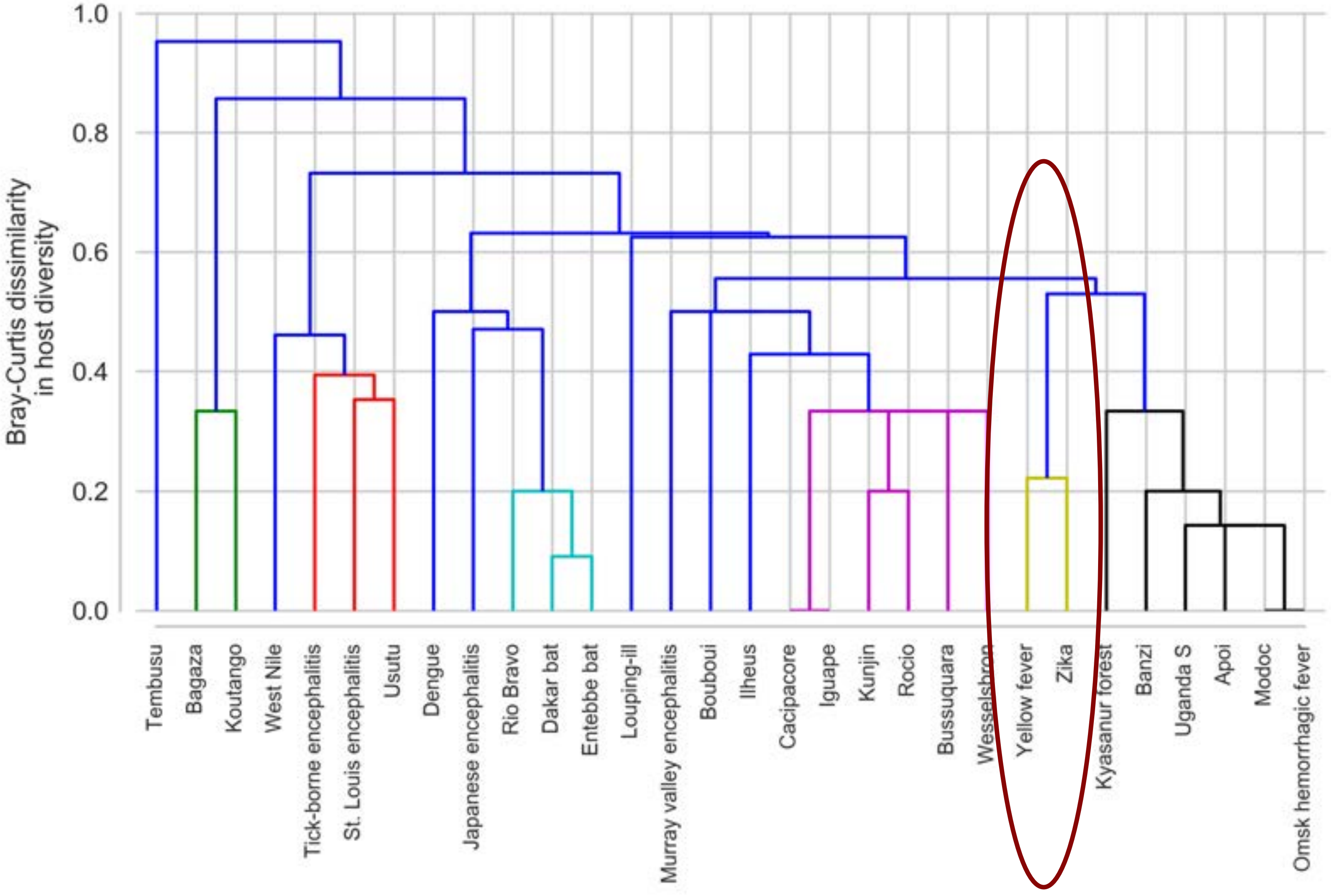


Each virus has unique characteristics



Viruses grouped according to their abilities to cause primary and secondary human cases (adapted from Wolfe et al, 2007)

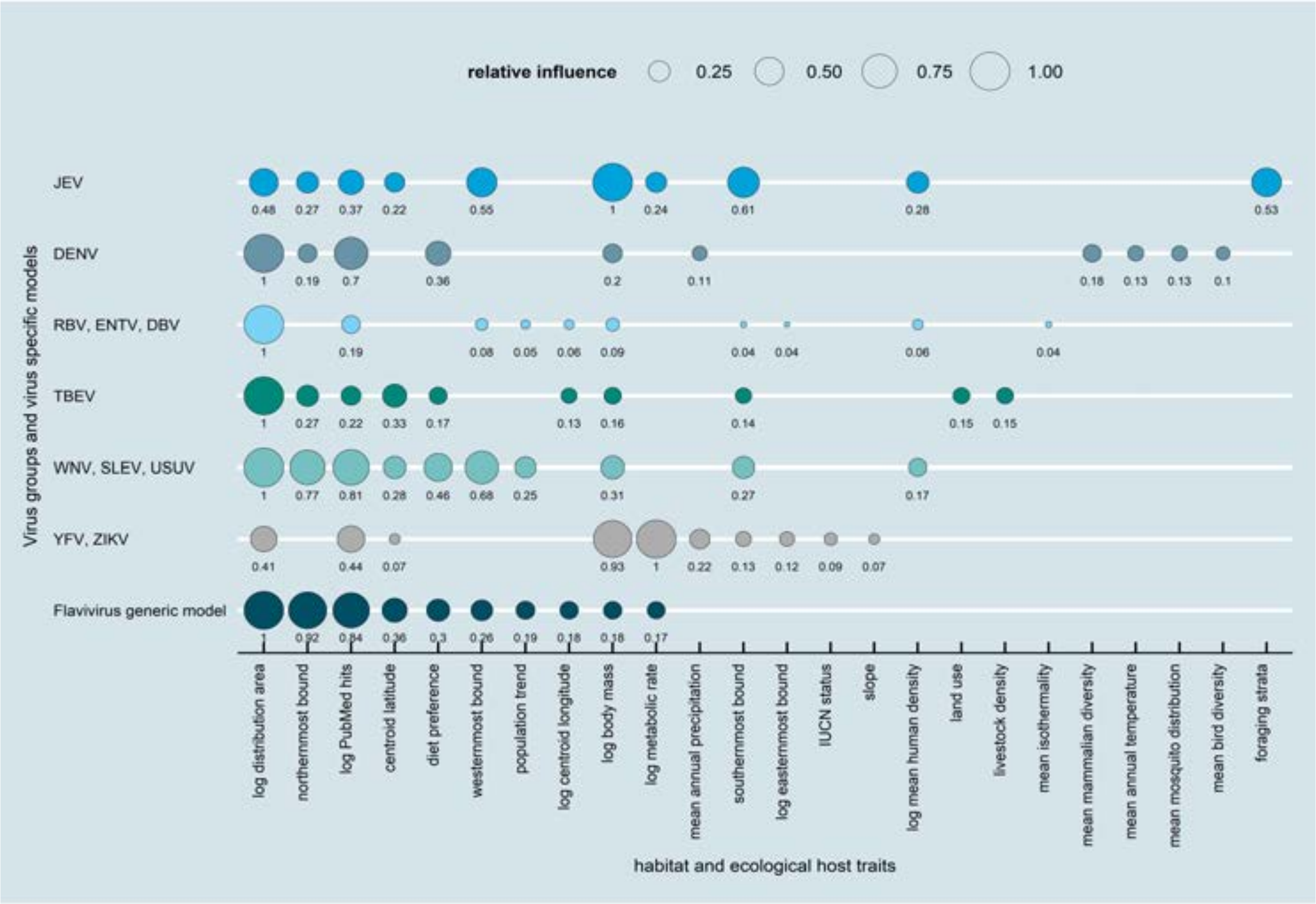
Looking at Similarities in Hosts across Flaviviruses



Predicting wildlife reservoirs and global vulnerability to zoonotic Flaviviruses

P. Pandit[1], M. Doyle[1], K. Smart[2], C. Young[1], G. Drape[2], C.K. Johnson[1]

Similarities across Flaviviruses: Commonalties of Host Traits

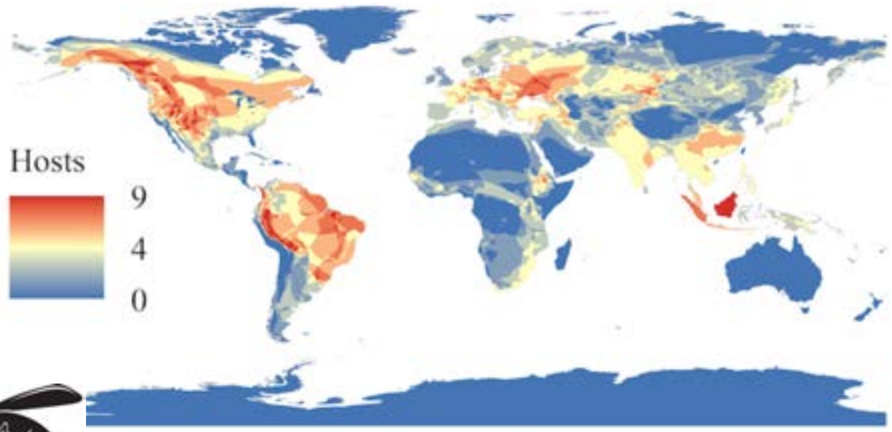


Predicting wildlife reservoirs and global vulnerability to zoonotic Flaviviruses

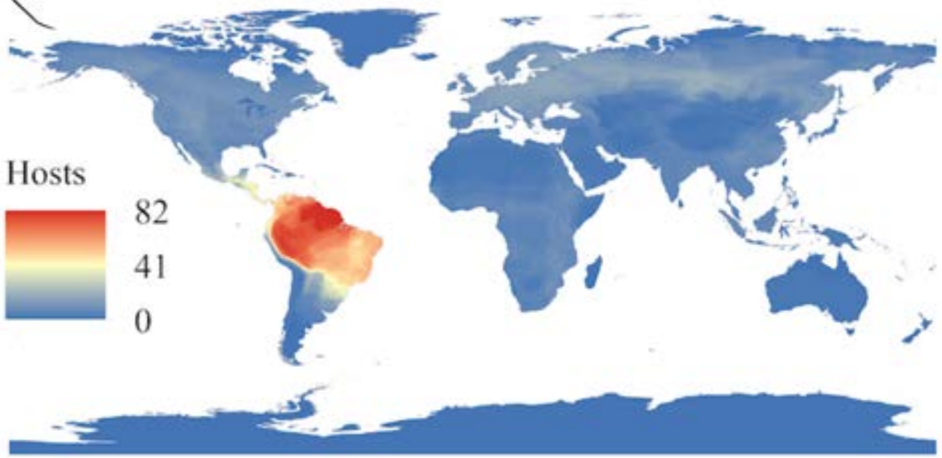
P. Pandit[1], M. Doyle[1], K. Smart[2], C. Young[1], G. Drape[2], C.K. Johnson[1]

Similarities across Flaviviruses: Co-occurrence of Potential Hosts

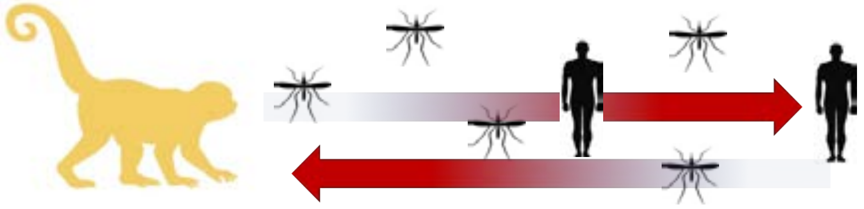
Yellow Fever and Zika Virus



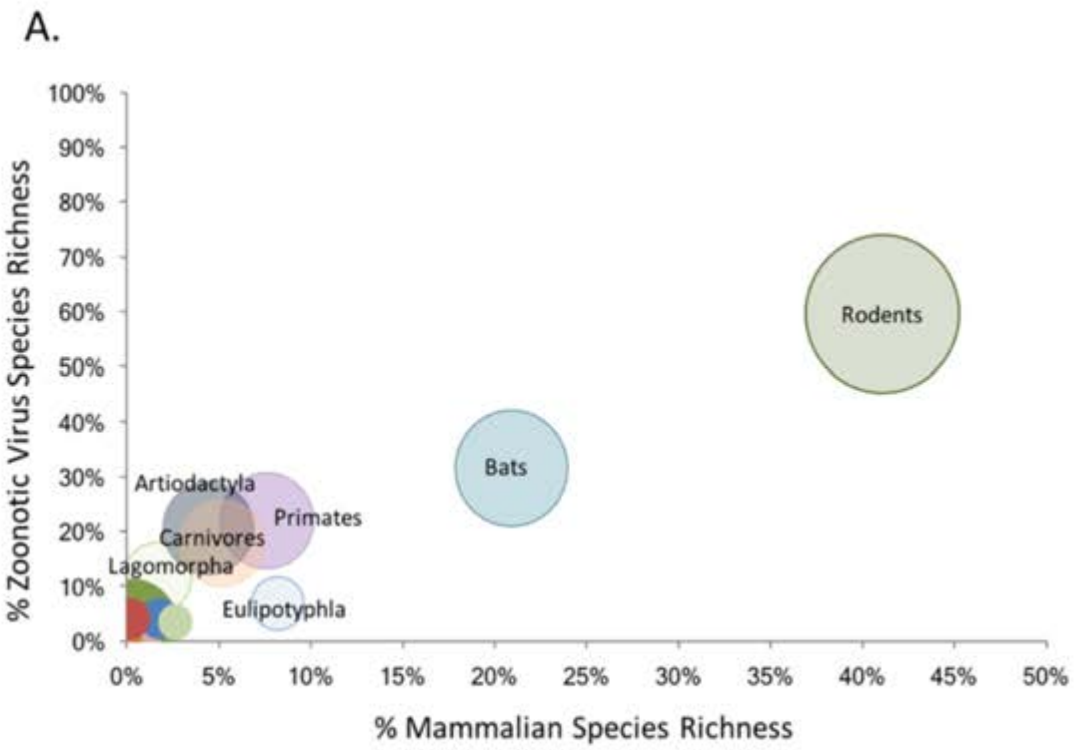
Dengue Virus



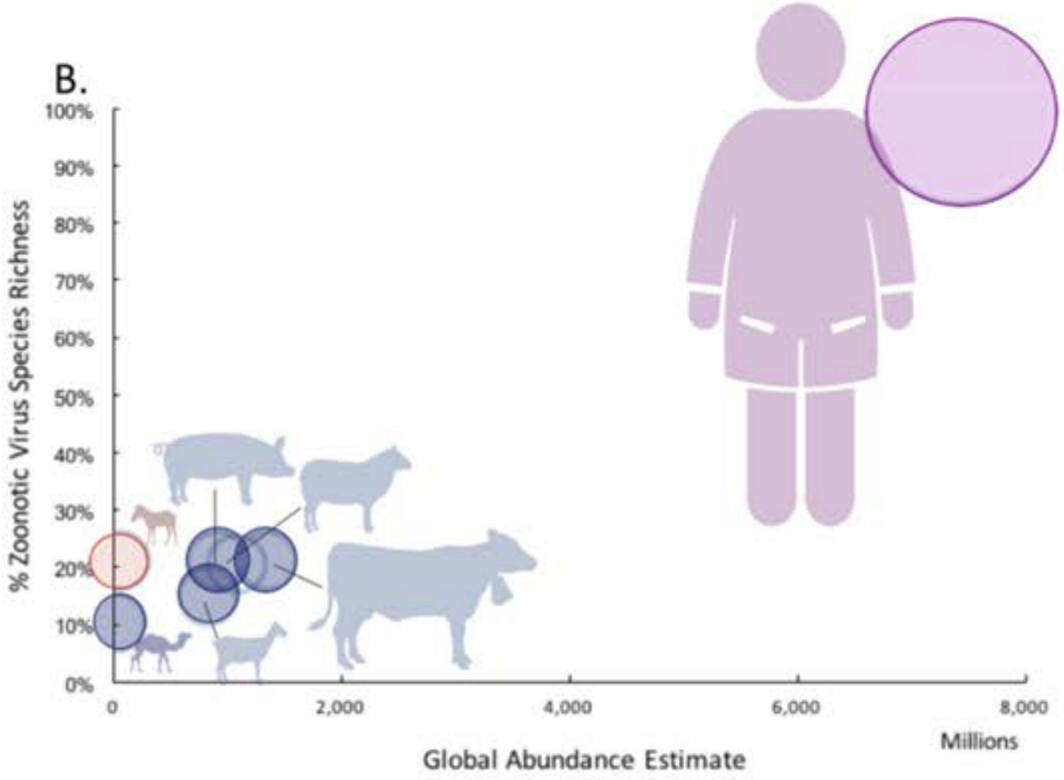
Based on significant host traits, what are the most likely hosts?
Where do these host co-occur?
Could they contribute to establishment of a sylvatic cycle given virus circulation in humans?



Similarities across all Zoonotic Viruses:
Propensities for Species to Share Viruses with People



Based on # of species in an order



Based on abundance

Variability in Risk of Spillover (in order of importance of effect)

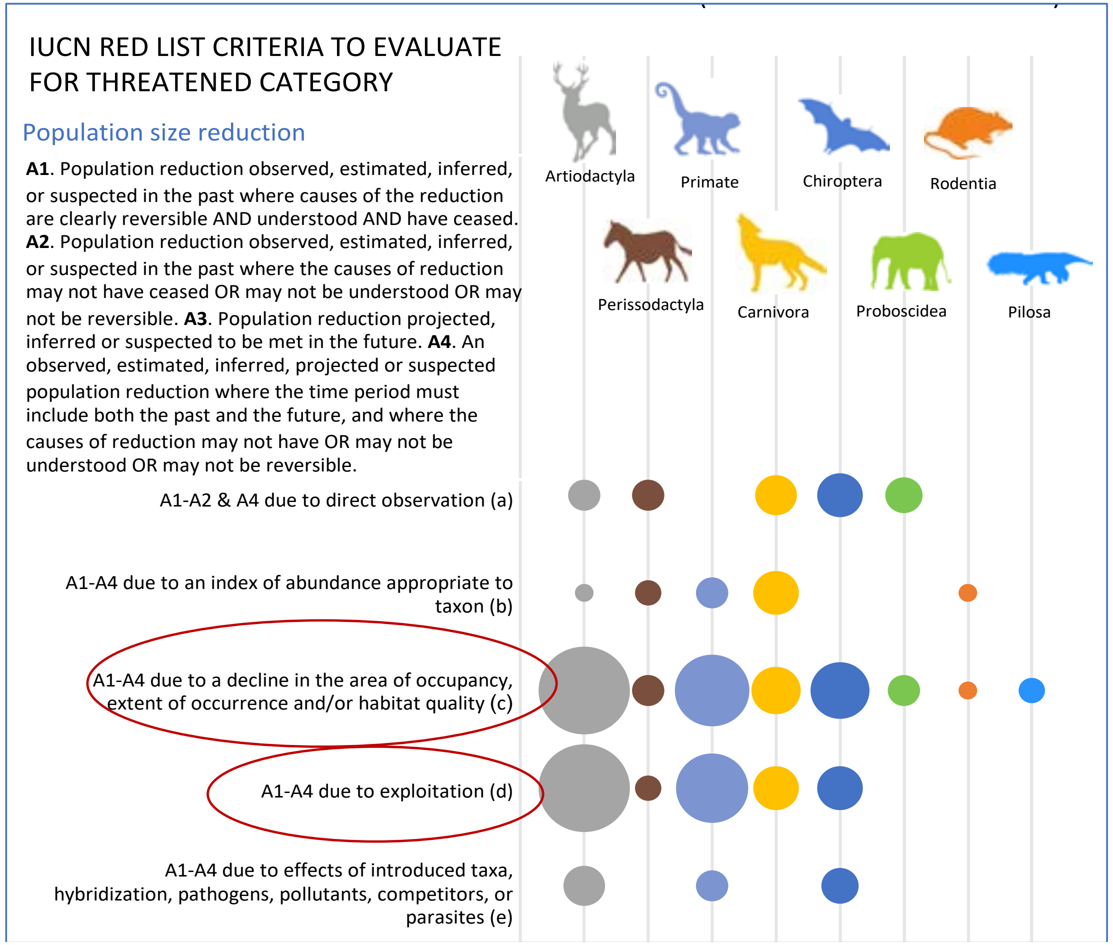
Variables	IRR**	95% CI	P-Value
Trends in Species Declines* **			
Least concern increasing	1.320	(1.03, 1.69)	0.026
Least concern decreasing	0.600	(0.47, 0.76)	< 0.001
Near threatened decreasing	0.365	(0.25, 0.54)	< 0.001
Vulnerable threatened status	0.110	(0.06, 0.19)	< 0.001
Endangered threatened status	0.107	(0.06, 0.19)	< 0.001
Critically endangered threatened status	0.049	(0.02, 0.11)	< 0.001
Data deficient/unknown population trend	0.511	(0.41, 0.63)	< 0.001
IUCN Criteria for Threatened Status****			
Population size reduction by direct observation (A1, A2, A4(a))	3.223	(2.00, 5.18)	< 0.001
Decline in area of occupancy or habitat quality (A1-4(c))	2.229	(1.27, 3.90	0.005
Population size reduction based on levels of exploitation (A1-4(d))	2.268	(1.35, 3.80)	0.002
Small extent of occurrence (B1)	0.230	(0.09, 0.60)	0.003
Taxonomic Order*****			
Primates	2.098	(1.73, 2.54)	< 0.001
Chiroptera	1.425	(1.22, 1.66)	< 0.001
Domesticated species	8.990	(6.92, 11.68)	< 0.001

- Most **common** species, especially species that are increasing in numbers, have shared more viruses with people
- Species that were less studied, had fewer zoonotic viruses (recognized)
- Species with small extent of occurrence had shared fewer viruses
- Primates and bats!
- Domesticated species

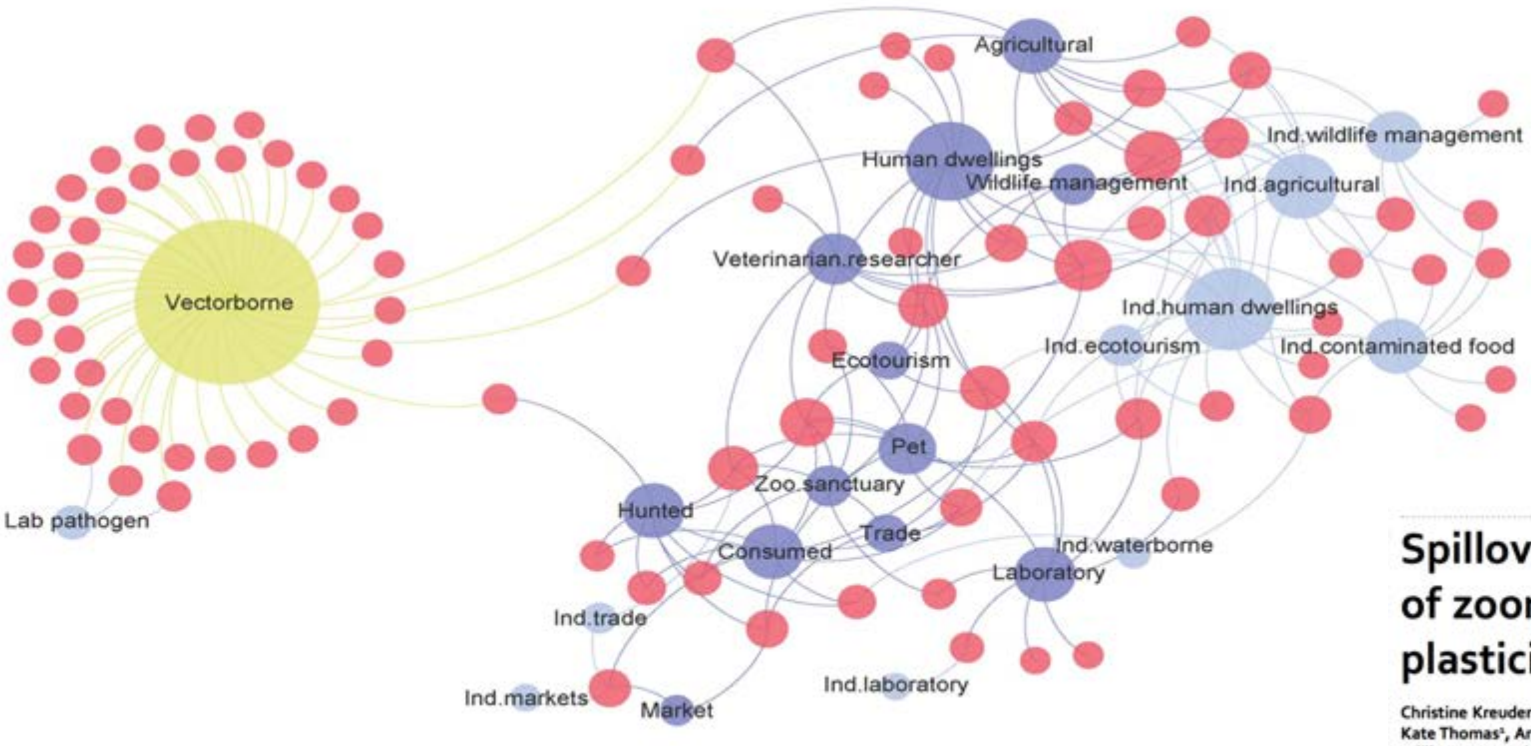
Variability in Spillover Risk –
due to animal-human interactions

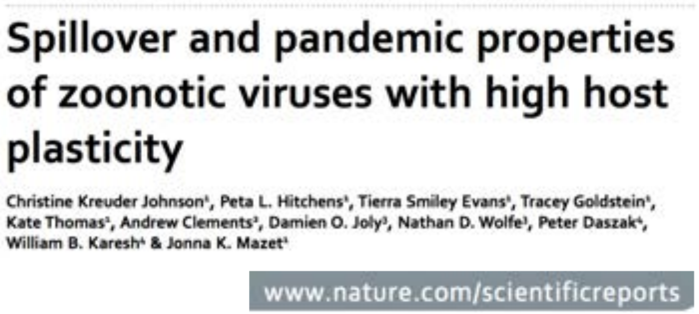
- Species that declined because of exploitation and habitat loss shared more viruses with people
- **Exploitation of wildlife** through hunting and the wild animal trade - increased opportunities for close contact between animals and humans
- **Anthropogenic activities causing declines in habitat quality**, such as deforestation, development, and conversion to cropland- increased opportunities for animal-human interactions

Number of zoonotic viruses among threatened species



Human Activities Implicated in Spillover Events




Spillover and pandemic properties of zoonotic viruses with high host plasticity

Christine Kreuder Johnson[1], Peta L. Hitchens[1], Tierra Smiley Evans[1], Tracey Goldstein[1], Kate Thomas[2], Andrew Clements[3], Damien O. Joly[3], Nathan D. Wolfe[3], Peter Daszak[4], William B. Karesh[4] & Jonna K. Mazet[1]

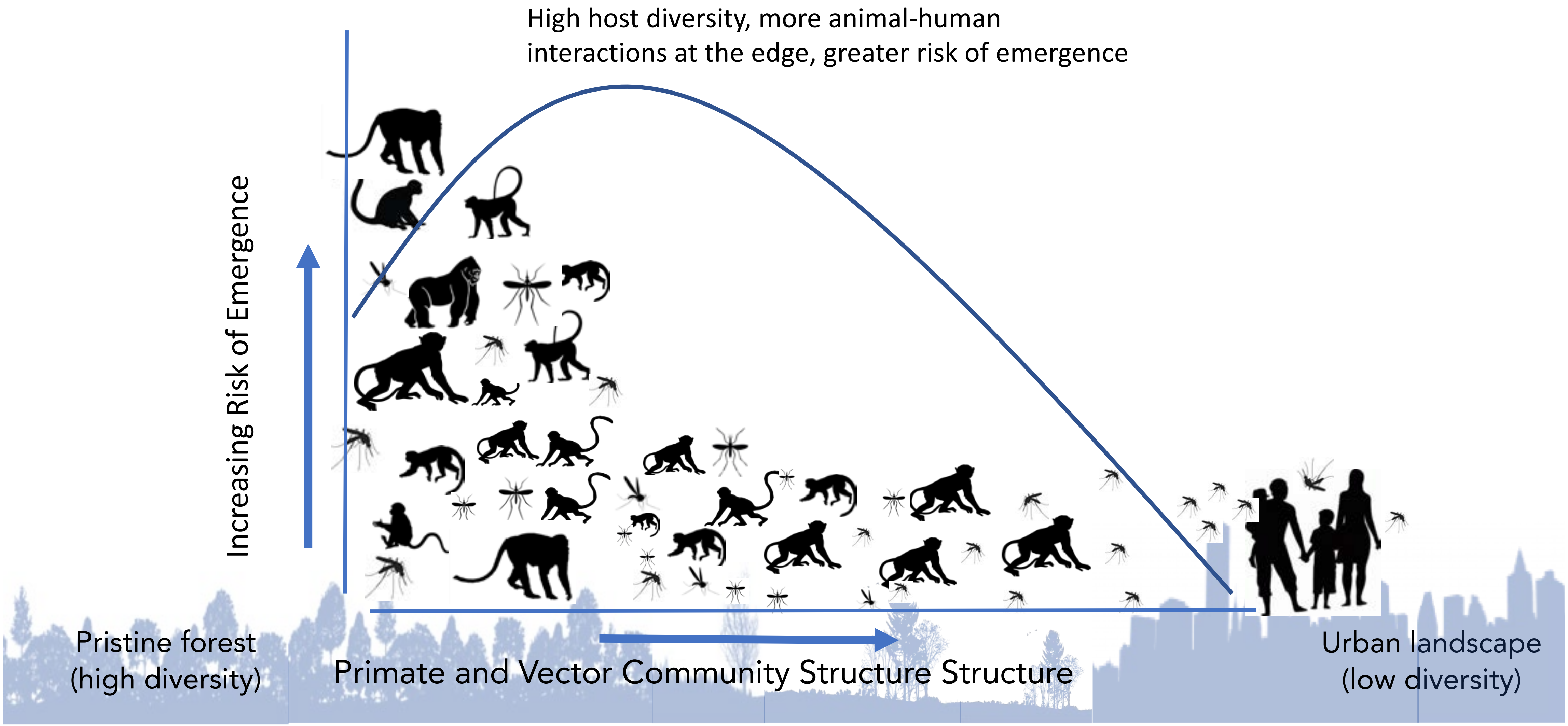
www.nature.com/scientificreports

Direct and indirect contact with wildlife

Bunyaviridae, Flaviviridae, Togaviridae, Arenaviridae, Rhabdoviridae, Poxviridae, Filoviridae, Paramyxoviridae, Retroviridae, Orthomyxoviridae, Picornaviridae, Reoviridae, Bornaviridae, Coronaviridae, Hepevirida, Herpesviridae

Relationship between

Biodiversity and Emerging Infectious Disease



Not to discount the urban environment

- Rapid trend toward urbanization over past half century
- Decreases biodiversity overall, increases abundance of adaptable species that benefit from close relationship with humans

Shenzhen business district and Mai Po marshes of Hong Kong (Karen Seto)

Most people are unaware of the wild animals living amongst us

Sam Hobson/NPL

Animal-Human Interactions and Evolution in the Urban Ecosystem

AMBIO 2015, 44:194–203
DOI 10.1007/s13280-014-0547-2

PERSPECTIVE

Adaptive evolution in urban ecosystems

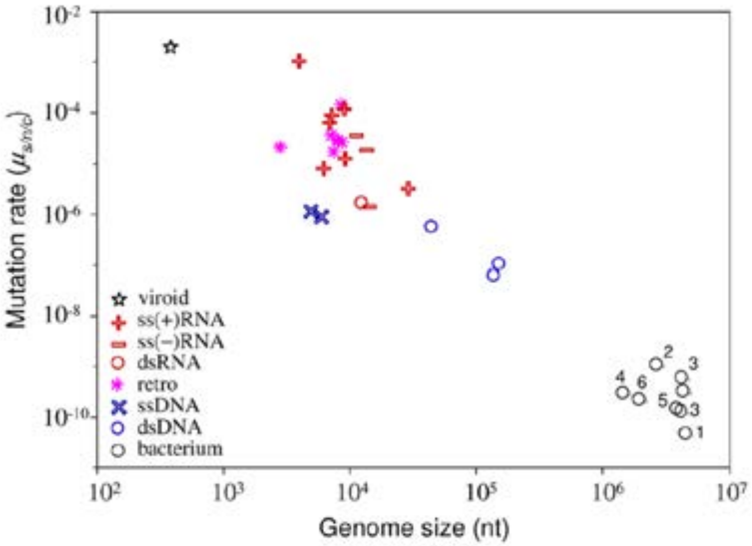
Colin M. Donihue, Max R. Lambert

Novel species interactions,
at high density

JOURNAL OF VIROLOGY, Oct. 2010, p. 9733–9748 Vol. 84, No. 19
0022-538X/10/$12.00 doi:10.1128/JVI.00694-10

Viral Mutation Rates▽

Rafael Sanjuán,[1*] Miguel R. Nebot,[2] Nicola Chirico,[3] Louis M. Mansky,[4] and Robert Belshaw[5]



Need for surveillance and monitoring in increasingly human-dominated landscapes

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The Challenge

Earlier detection of zoonotic diseases where they are most likely to emerge and re-emerge

Improved understanding of risk at the animal-human interface to inform mitigation

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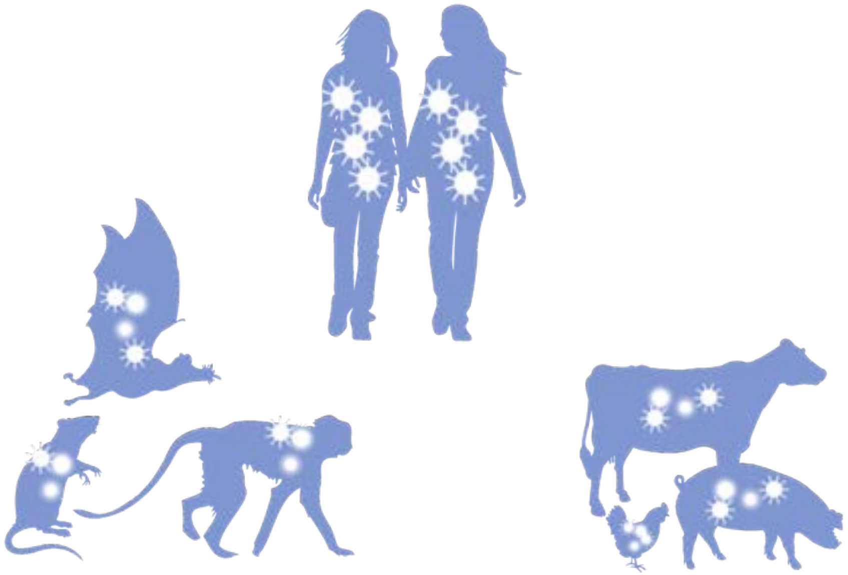
Emerging Pandemic Threats Program

Strengthening capacity for tackling emerging disease threats

Partnering with 30 countries
2014-2019

Coordinated One Health Surveillance

Concurrent sampling of wildlife, livestock, and people



Triangulation -
Identify viruses shared among species at high-risk animal-human interfaces

World Health Organization

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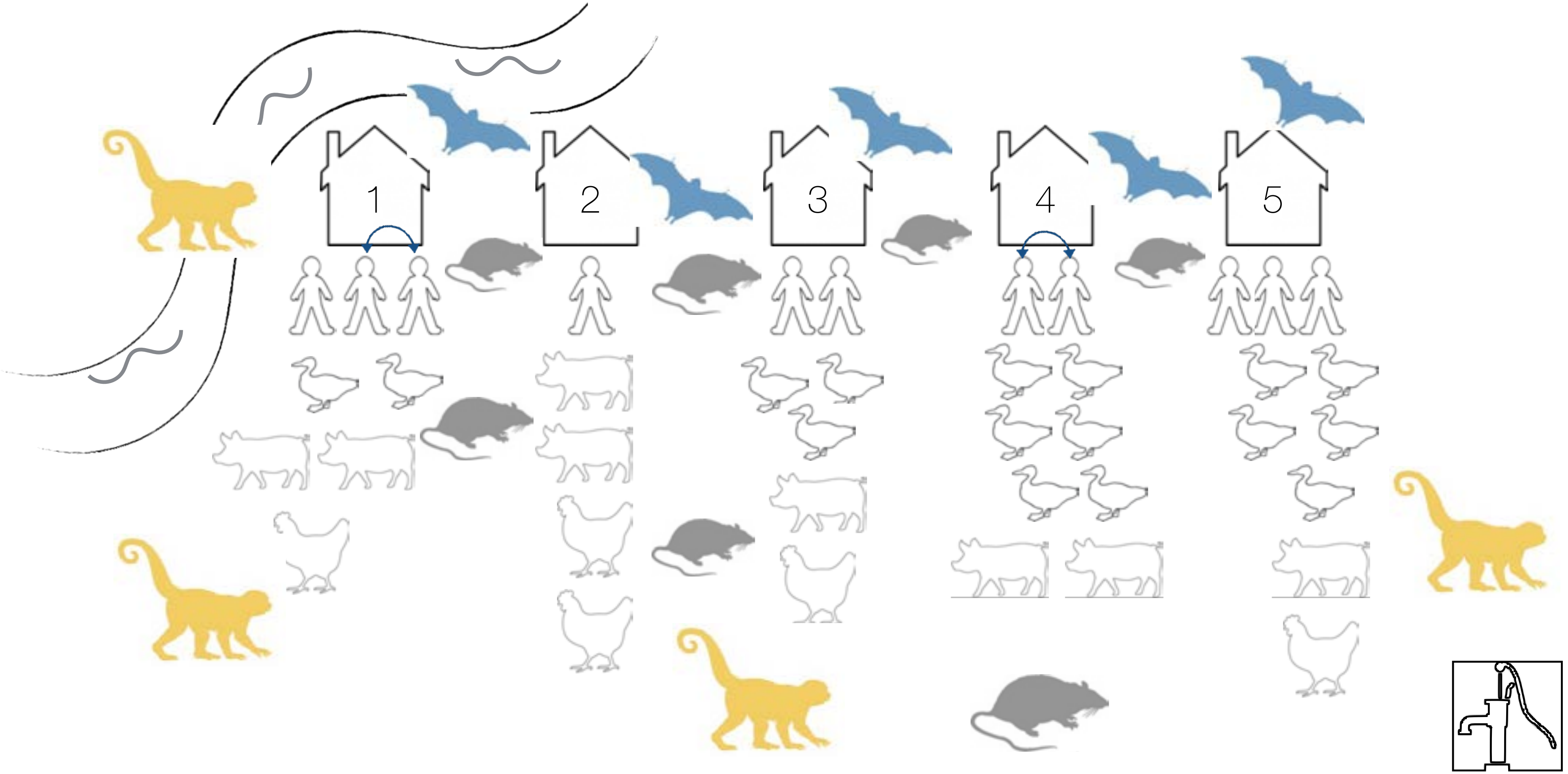
One Health Surveillance – in partnership with communities



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One Health Surveillance – in partnership with hospitals

Enrolling patients meeting clinical case definitions

Acute febrile illness

- Severe acute respiratory disease
- Acute encephalitis
- Hemorrhagic fevers

Clinics in rural high-risk areas

Referral hospitals

To inform on viral causes of fever of unknown origin in the community

Including livelihood, medical history, animal contact, and behavioral surveys

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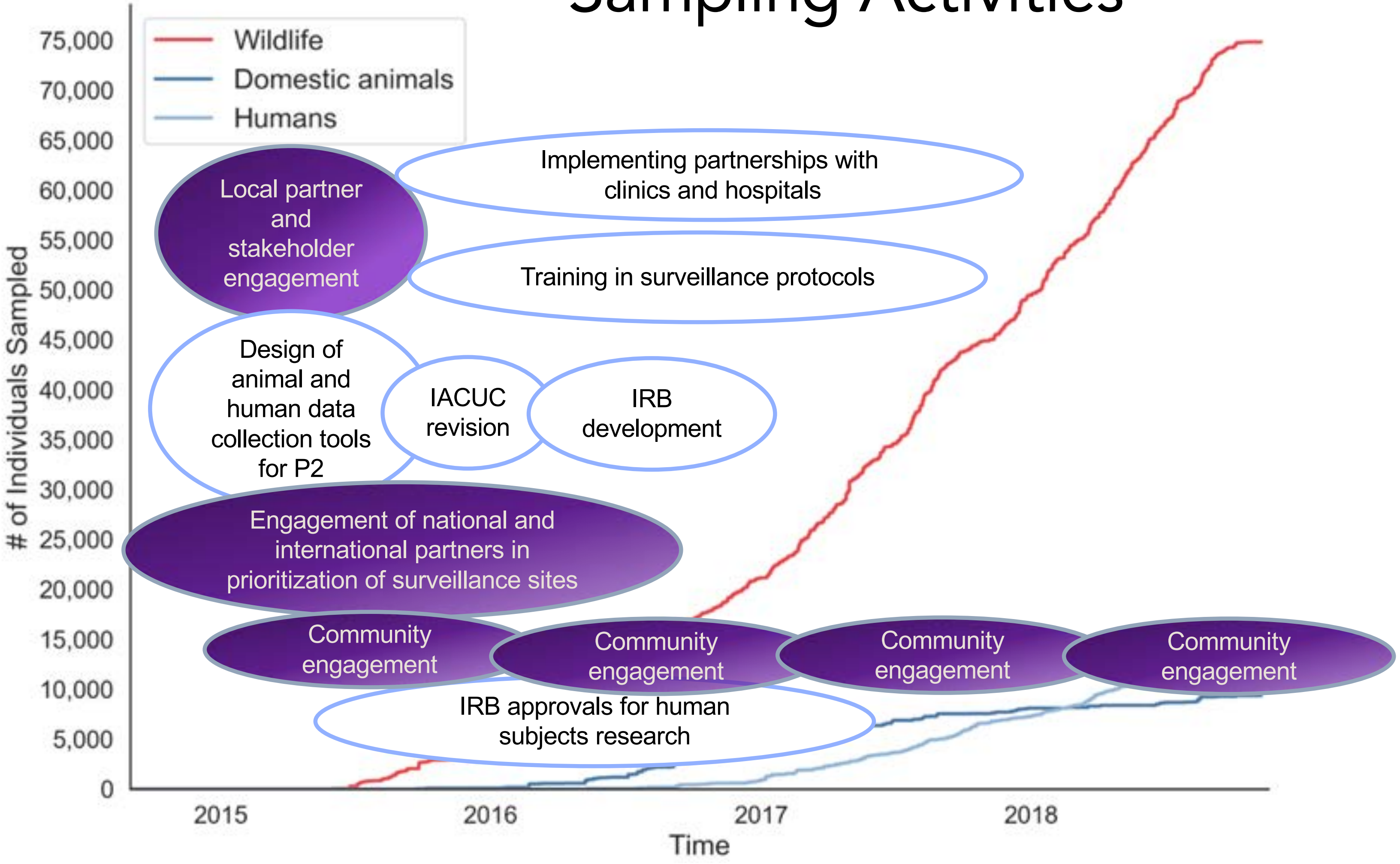
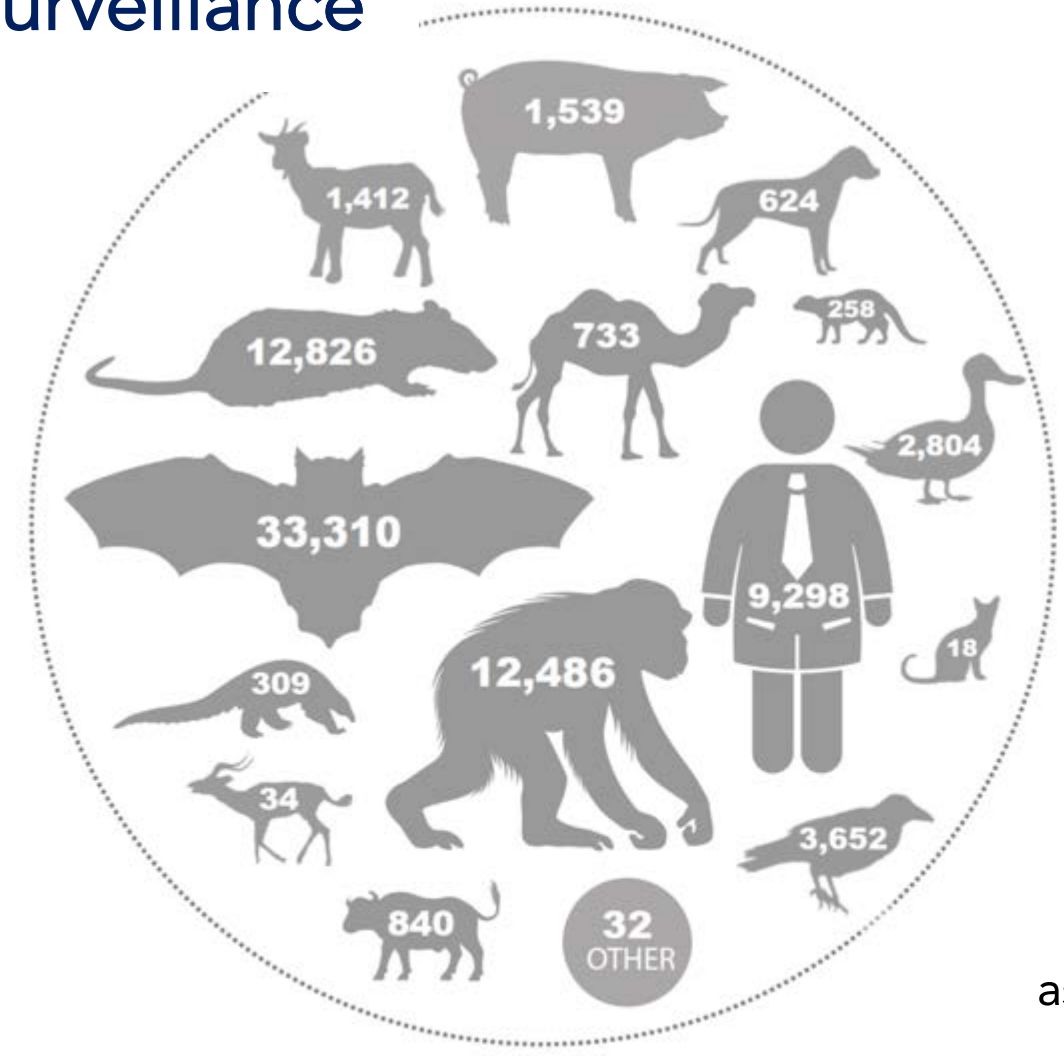
Sampling Activities



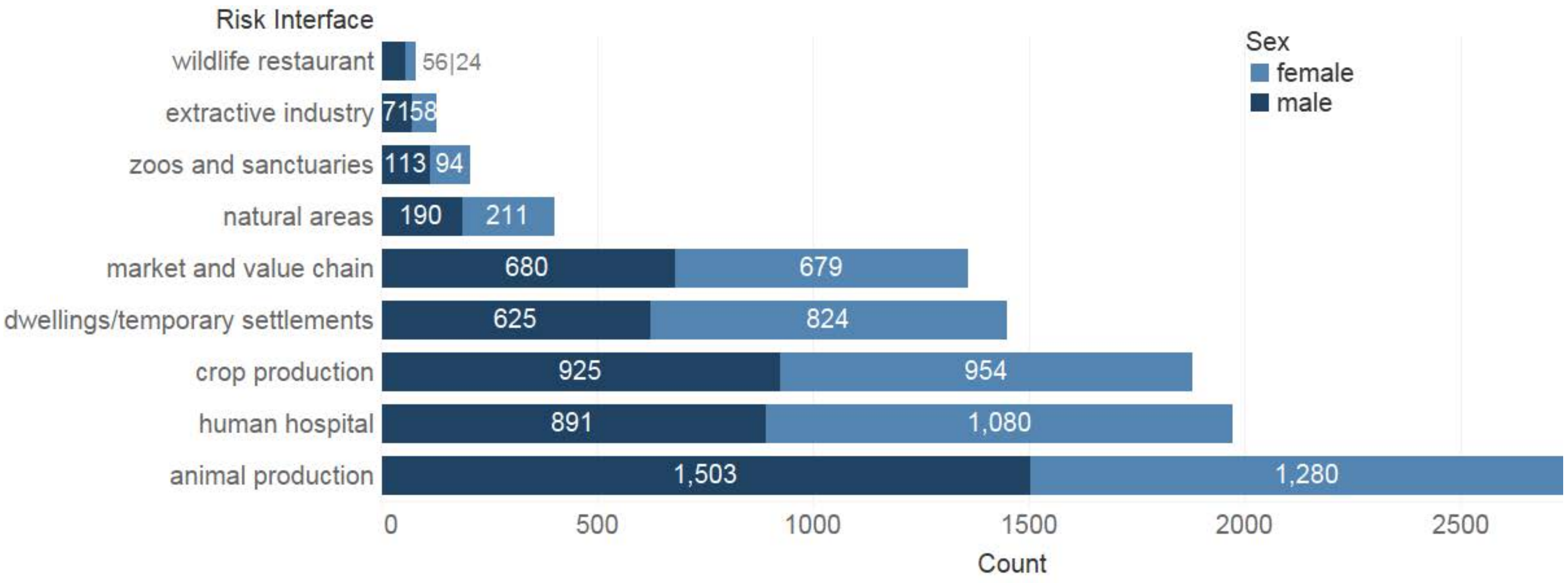
One Health Surveillance



as of June 2018

One Health Surveillance

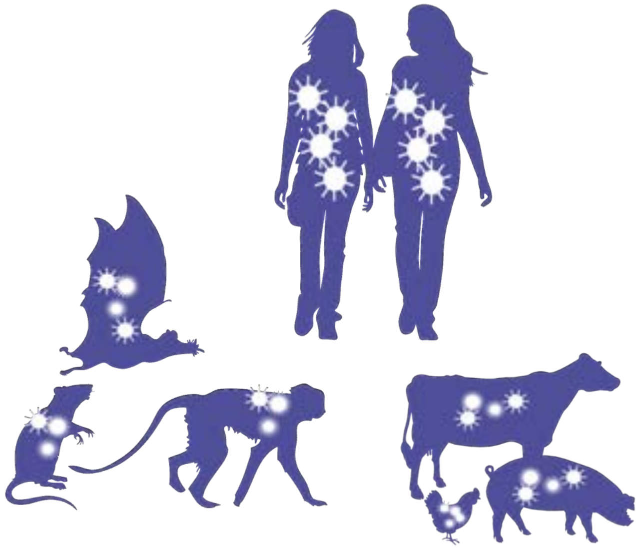
Humans sampled to date at high-risk interfaces (by gender)



One Health Testing Strategy

Priority Zoonotic Diseases with Pandemic Potential

Multi-valent testing platform
Standardized across wildlife, livestock, and people



Consensus PCR - detect known pathogens and variations that will be missed by real-time PCR
Next generation sequencing for unbiased detection and to further characterize novel viruses

- Filoviruses (Ebola, Marburg and new variants)
- Influenza viruses (Flu and new variants)
- Coronaviruses (MERS, SARS, and new variants)
- Flaviviruses (YFV, Zika, and new variants)
- Paramyxoviruses (Nipah, Hendra, and new variants)
- Arenaviruses, Bunyaviruses, Rhabdoviruses, Retroviruses

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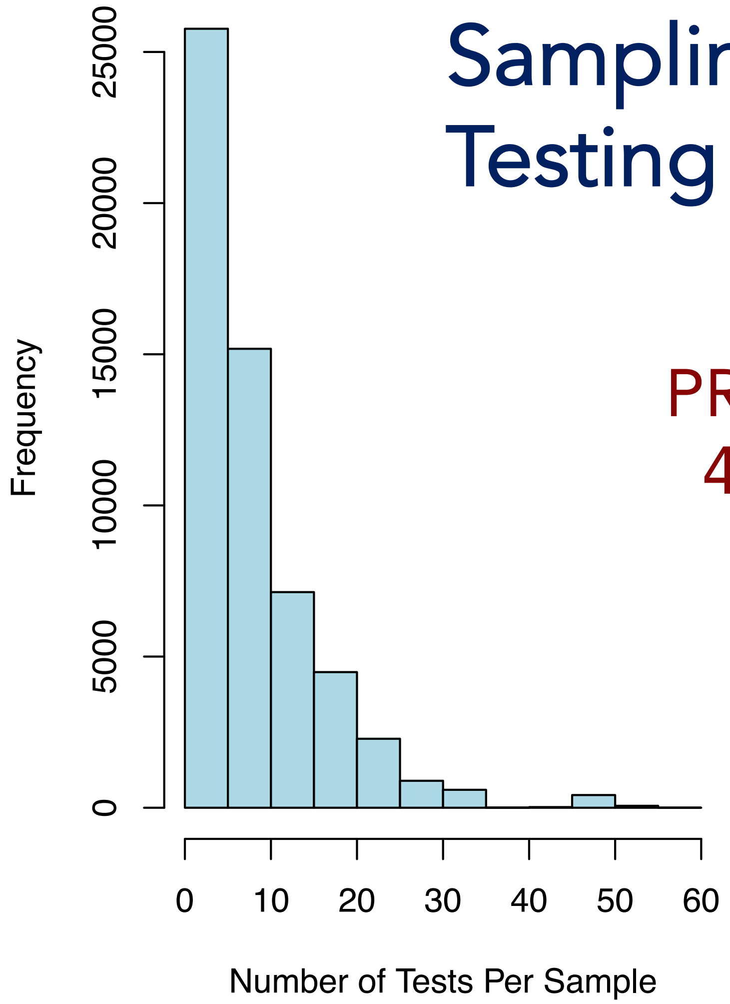
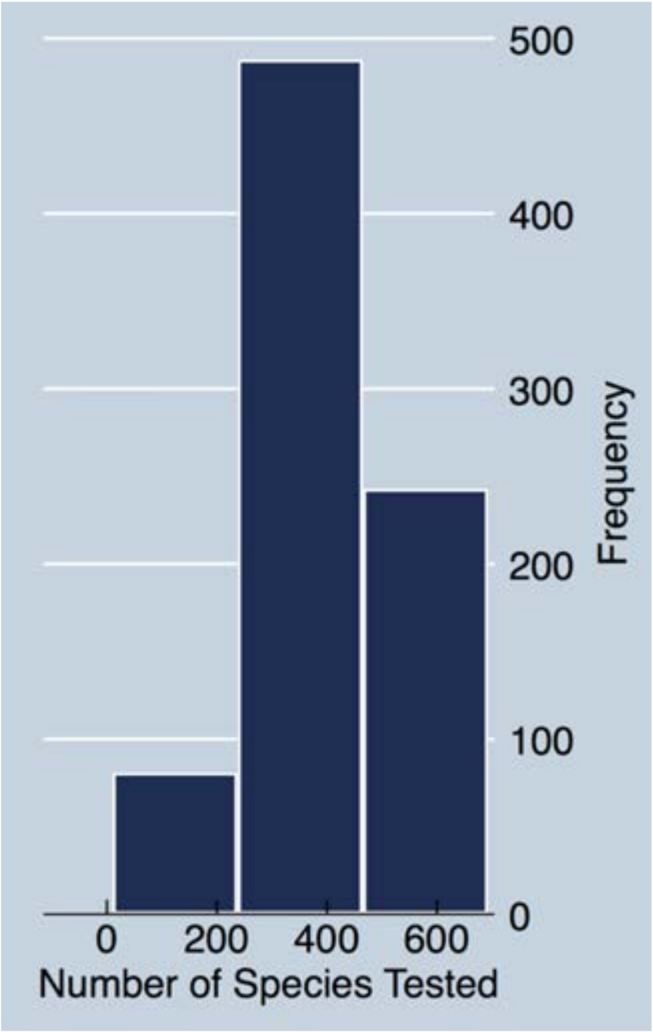
Sampling and Testing Effort



PREDICT 2009-2014
466,055 tests
180 known viruses
820 new viruses

Number of species tested for each virus detected



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BRIEF COMMUNICATION
https://doi.org/10.1038/s41564-018-0227-2
nature microbiology

The discovery of Bombali virus adds further support for bats as hosts of ebolaviruses

Tracey Goldstein[1,14*], Simon J. Anthony[2,3,4,14*], Aiah Gbakima[5], Brian H. Bird[1], James Bangura[5], Alexandre Tremeau-Bravard[1], Manjunatha N. Belaganahalli[1], Heather L. Wells[2], Jasjeet K. Dhanota[1], Eliza Liang[2,4], Michael Grodus[2], Rohit K. Jangra[6], Veronica A. DeJesus[6], Gorka Lasso[7], Brett R. Smith[1], Amara Jambai[8], Brima O. Kamara[9], Sorie Kamara[10], William Bangura[11], Corina Monagin[1,12], Sagi Shapira[7,13], Christine K. Johnson[1], Karen Saylors[12], Edward M. Rubin[12], Kartik Chandran[6], W. Ian Lipkin[2,3] and Jonna A. K. Mazet[1]

- Benefits and risks from bats
- Reducing risk and contact with bats
- Behavior change towards interventions

Bat Coronavirus 512/2005

Family: *Coronaviridae*

Genbank accession no. NC_009657

This is a strain of the known *alphacoronavirus* Bat coronavirus 512/2005 found previously in bats.

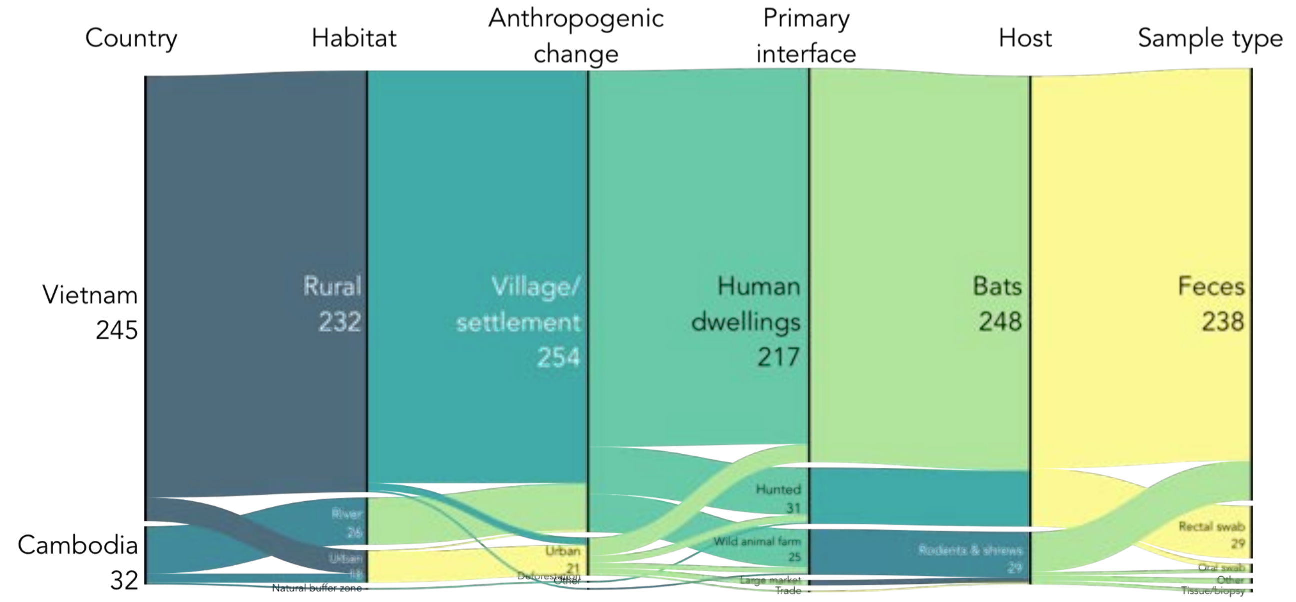
Through PREDICT, this strain was found 277 times out of 31,061 tests. There is no evidence at this time to suggest this virus poses a threat to human health.

These findings suggest risk of cross-species transmission, particularly in wild animal farms in Vietnam.

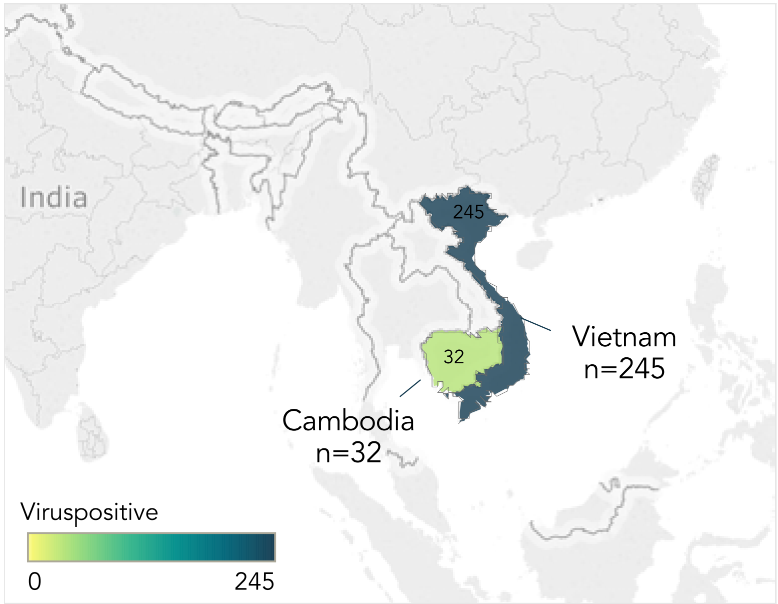
Positive samples found in species by primary interfaces

Primary Interface	Species: Coromandel pipistrelle	Lesser Asian house bat	Malayan porcupine	Microchiroptera sp.	Rattus sp.	Rhizomyinae bamboo rat	Grand Total
human dwellings		1		216			217
hunted	1	30					31
large market					3		3
trade					1		1
wild animal farm			21			4	25
Grand Total	1	31	21	216	4	4	277

Sum of samples positive broken down by species and primary interface. Color shows how many samples were found positive, which ranges from 1 to 216 (N=277).



Sankey diagram showing the flow of number of animals sampled at least once that tested positive for a virus (N=277) across five key variables (L to R): country, habitat, anthropogenic change, primary interface, taxa, and sample type.



PREDICT Consortium
Created June 2018
by Cristin Young, Julie Rushmore, Pranav Pandit, Christine K. Johnson

Preliminary Findings to Date

Across all animals sampled

- DNA viruses most commonly shed orally
- RNA viruses mostly shed in feces and urine

RNA viruses were most commonly found:

- in bats, primates
- in medium markets
- in large markets
- in wildlife restaurants
- near crop growing at site
- near road building at site

Positive for RNA Virus	Odds Ratio	P value	95% Confidence Interval
Bats	3.358	<0.001	(1.991 - 5.66)
Primates	3.434	<0.001	(2.026 - 5.820)
Blood sample (drop)	3.850	0.002	(1.617 - 9.165)
Feces	6.051	<0.001	(4.762 - 7.688)
Oral/Nasal swab	2.745	<0.001	(2.232 - 3.374)
Rectal swab	12.702	<0.001	(10.555- 15.285)
Urine	9.026	<0.001	(6.367-12.797)
Urogential swab	3.392	<0.001	(2.456 - 4.685)
Dead (> 48 hrs)	0.315	<0.001	(0.174 - 0.571)
Alive (and non-invasively sampled)	2.994	<0.001	(2.283 - 3.926)
Pristine habitat	0.406	<0.001	(0.293 - 0.564)
Crop growing	3.603	<0.001	(2.843 - 4.564)
Established village	2.092	<0.001	(1.794 - 2.440)
Ongoing road buildling	9.938	<0.001	(7.163 - 13.788)
Trade	3.803	<0.001	(2.814 - 5.140)
Medium Market	5.727	<0.001	(3.0134 - 10.885)
Large market	4.478	<0.001	(3.406 - 5.886)
Restaurants	4.971	<0.001	(3.745 - 6.598)
Veterinarians/Researcher	4.076	<0.001	(3.229 - 5.145)
Zoo/Sanctuary	2.009	<0.001	(1.421 - 2.842)
Urban unplanned settlement	0.398	0.001	(0.235 - 0.676)

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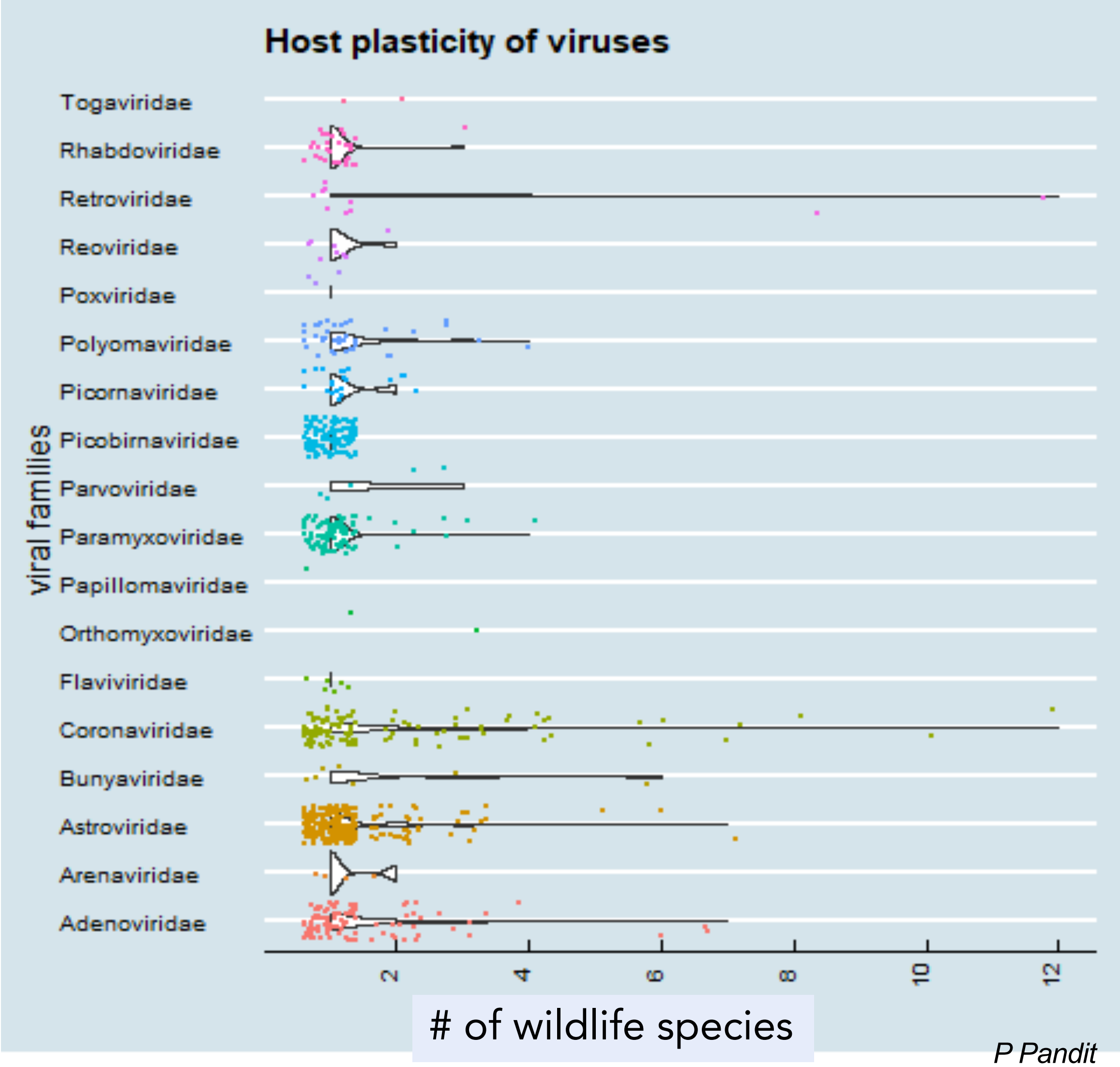
Preliminary Findings to Date



Virus with High Host Plasticity

Viruses detected in more than one species were most commonly from animals sampled in **large markets**, and **intensive holding facilities** for wildlife

TOWARD PANDEMIC PREPAREDNESS

Risk-based surveillance at animal-human interfaces

Standardized collaborative data collection

Multi-valent approach to detection

Data sharing across borders

Long-term longitudinal monitoring


Arctic Circle
CAN.
ICELAND
U.S.
BERM.
MRT.
MALI
NIGER
CHAD
ALG.
LIBYA
SUDAN
OMAN
KAZ.
CHINA
JAPAN
MALD.
PALAU
SYC.
BRAZIL
PERU
ST.H.
Tropic of Capricorn
WORLD
METEOROLOGICAL
ORGANIZATION
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USAID FROM THE AMERICAN PEOPLE | PREDICT Collaborative Disease Surveillance Workforce


250 ml
ISOFLURANE USP

USAID | PREDICT Collaborative Disease Detection Workforce

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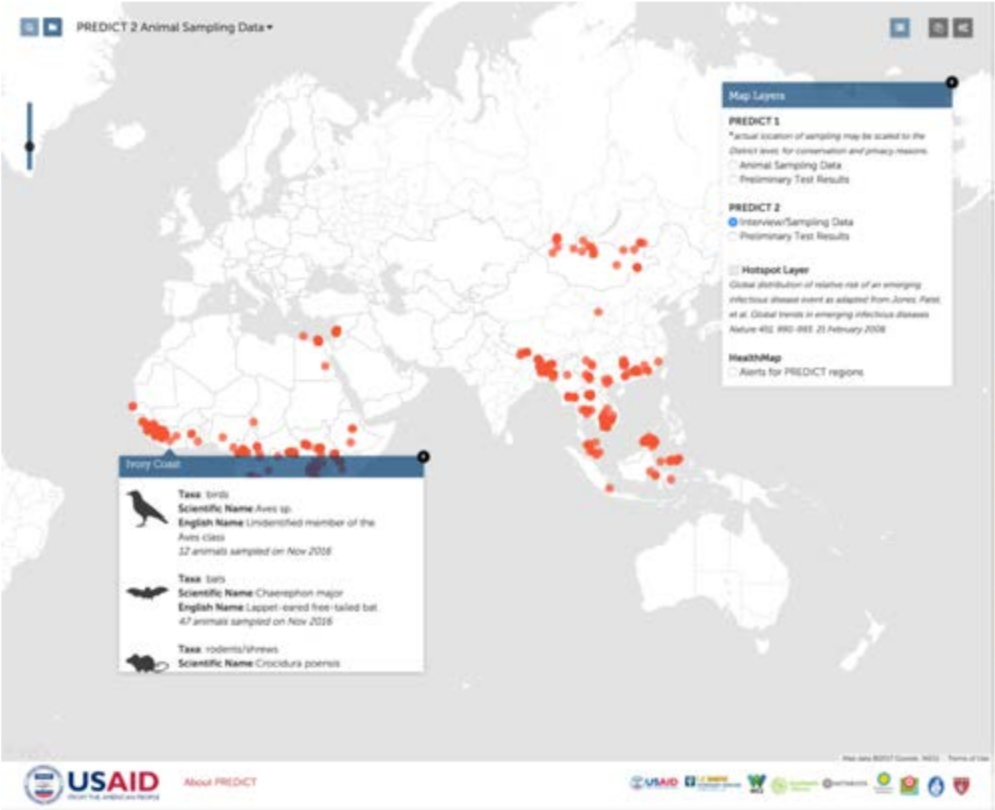
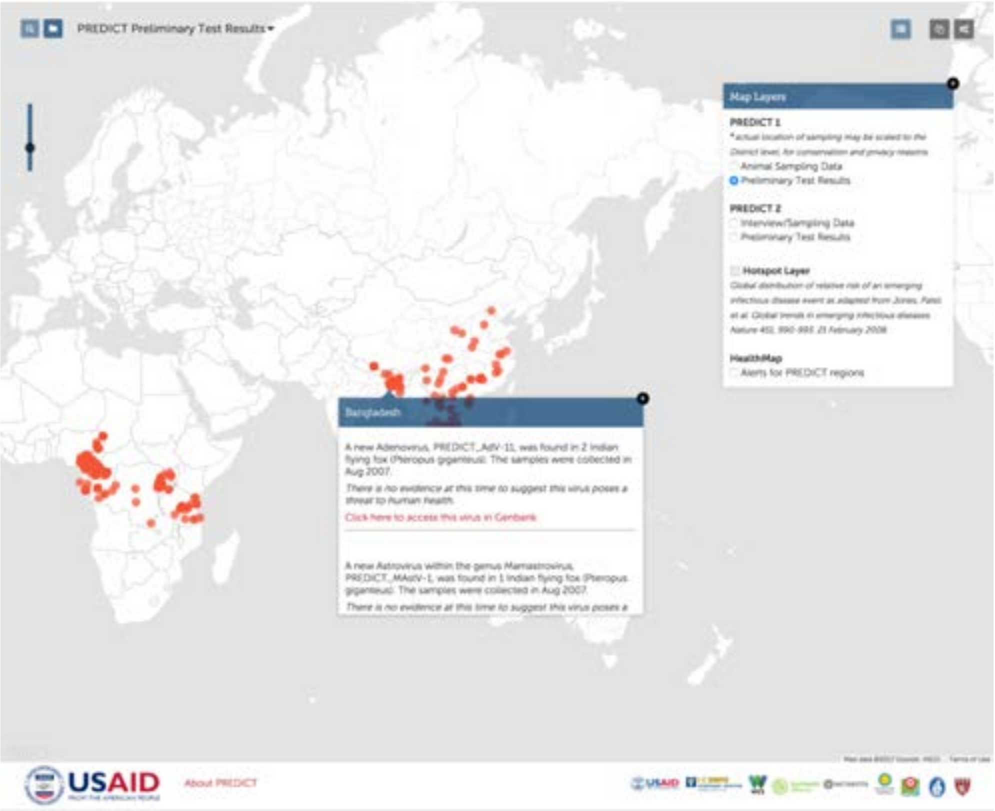
FROM THE AMERICAN PEOPLE

Government Engagement, Policy Change
Community Engagement, Behavior Change

Data Sharing





https://www.healthmap.org/predict/

Thank you, PREDICT CONSORTIUM

Ehab Abu-Basha, Mohamed Ahmed Ali, Laurentius Ambu, William Ampofo, Simon Anthony, Ungke Antonjaya, Ohnmar Aung, Joseph Awuni, Romain Bagamboula, James Bangura, Cale Basaraba, Manjunatha Belaganahalli, Samuel Bel-Nono, Ridzki MF Binol, Brian Bird, James Brandful, John Brownstein, Alpha Camara, Carolina Churchill, Dennis Carroll, Daniel Chai, Debapriyo Chakraborty, Aleksei Chmura, Andrew Clements, Emmanuel Couacy-Hymann, Julien Kalpy Coulibaly, Michael Cranfield, Peter Daszak, Patrick Dawson, Jasjeet Dhanota, Aristide Dionkounda, Kimberly Dodd, Megan Doyle, Prateep Duengkae, Veasna Duong, Philippe Dussart, Abel Ekiri, Enkhtuvshin Shiilegdamba, Jonathan H. Epstein, Jason Euren, Yasha Feferholtz, Amanda Fine, Taylor Gabourie, Aiah Gbakima, Kirsten Gilardi, Amethyst Gillis, Tracey Goldstein, Benoit Goossens, Denise Griieg, Emily Hagan, Qun He, Helen Lee, Thiravat Hemachudha, Mei Ho, Hong Duong, Paul Horwood, Junhua Hu, Tom Hughes, Vibol Hul, Diah Iskandriati, Ariful Islam, Shariful Islam, Jacques Iyanya, Amara Jambai, Christine Johnson, Erica Johnson, Damien Joly, Kate Jones, Joseph Rosario, Jusuf Kalengkongan , Douokoro Kalivogui, Joseph Kamau, Eddy Kambale, William Karesh, Kandeh Kargbo, Dibesh Karmacharya, Ghazi Kayali, Rudovick Kazwala, Changwen Ke, Lucy Ogg Keatts, Terra Kelly, Christopher Kilonzo, Kongsy Khammavong, Charles Kumakamba, Naing Tun Kyaw Yan, Christian Lange, Alice Latinne, Alice Latinne, Joseph Diffo Le Doux, Mat LeBreton, Jimmy Lee, Amara Leno, Neal Liang, Eliza Liang, Ian Lipkin, Ashley Lucas, Jean Paul Lukusa, Victor Lungay, Shongo Lushima, Wenjun Ma, Catherine Machalaba, Grace Maganga, Maria Makuwa, Patarapol Maneeorn, Martin Gilbert, Mathieu Pruvot, Jonna Mazet, Placide Mbala, Eric Mbunwe, David McIver, Maureen Miller, Happy Mkali, Debbie Mollard, Corina Monagin, Alphonce Msigwa, Antoine Mudakikwa, Prime Mulembakani, Suzan Murray, Pacifique Musabimana, Samson Mutura, Mwokozi Mwanzanilla, Sylivia Nakimera, Sen Nathan, Isamara Navarrete-Macias, Ipos Ngay, Nguyen Van Long, Nguyen Thi Thanh Nga, Fabien Niama, Schadrack Niyonzima, Felix Nkom, Rachmitasari Noviana, Julius Nziza, Ricky Okwir Okello, Kevin Olival, Sarah Olson, Bilal Omari, Vicotora Ontiveros, Tammie O'Rourke, Pranav Pandit, Joko Pamungkas, Alisa Pereira, Pham Thi Thu Ha, Jum Rafiah Abd Sukor, Noam Ross, Melinda Rostal, Eddy Rubin, Julie Rushmore, Uus Saepuloh, Dodi Safari, Zikankuba Sajali, Suryo Saputro, Karen Saylors, Soubanh Silithammavong, Sireeda Miller, Tierra Smiley Evans, Brett Smith, Woutrina Smith, Sokha Chea, Benard Ssebide, Richard Suu-Ire, Jean Michel Takuo, Hani Talafha, Aung Than Toe, Watthana Theppangna, Thuy Hoang, Tin Tin Myaing, Alexandre Tremeau-Bravard, Jean Claude Tumushime, Marcela Uhart, Cristin Young, Marc Valitutto, Megan Vodzak, Supaporn Wacharapluesadee, Brooke Watson, Heather Wells, Allison White, Anna Willoughby, Ageng Wiyatno, Nathan Wolfe, David Wolking, Carlos Zambrana-Torrelio, and Dawn Zimmerman