USAID FROM THE AMERICAN PEOPLE | PREDICT

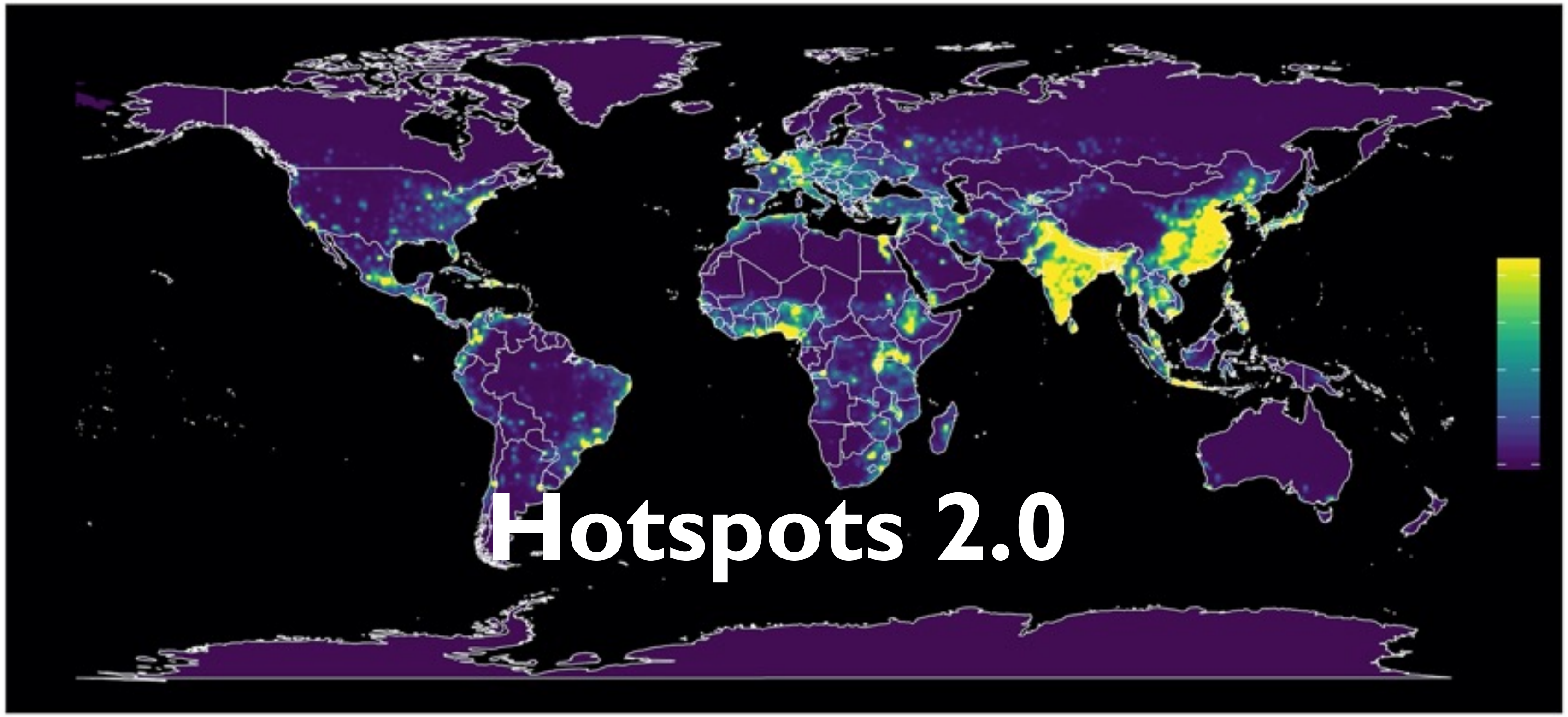
PANDEMIC PREPAREDNESS FOR GLOBAL HEALTH SECURITY

USAID BRIEFING, MARCH 17, 2020

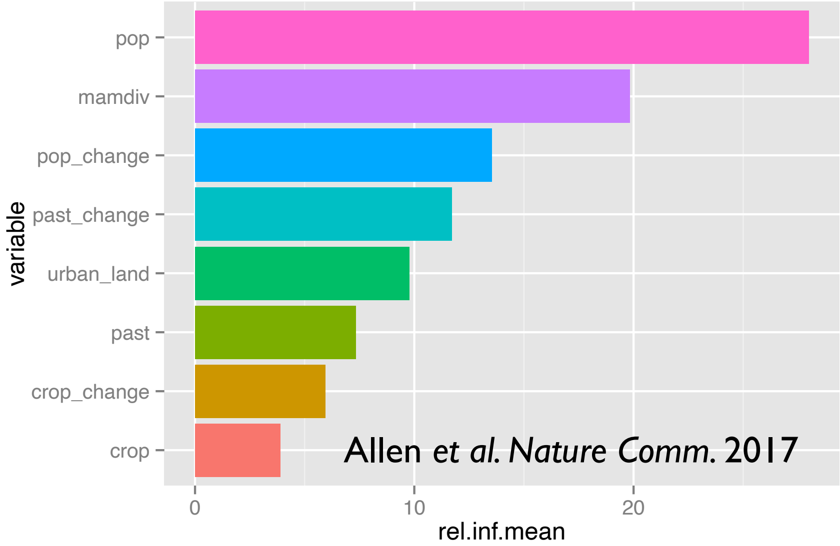
Guiding Light: Modeling & Analytics Insights

Models answer key questions to predict and prevent pandemics

1. Where will the next pandemic originate?
2. What's causing the rise in pandemics?
3. Which wildlife species harbors the most potentially pandemic viruses?
4. How can we *prevent* pandemics, and can we afford it?



	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

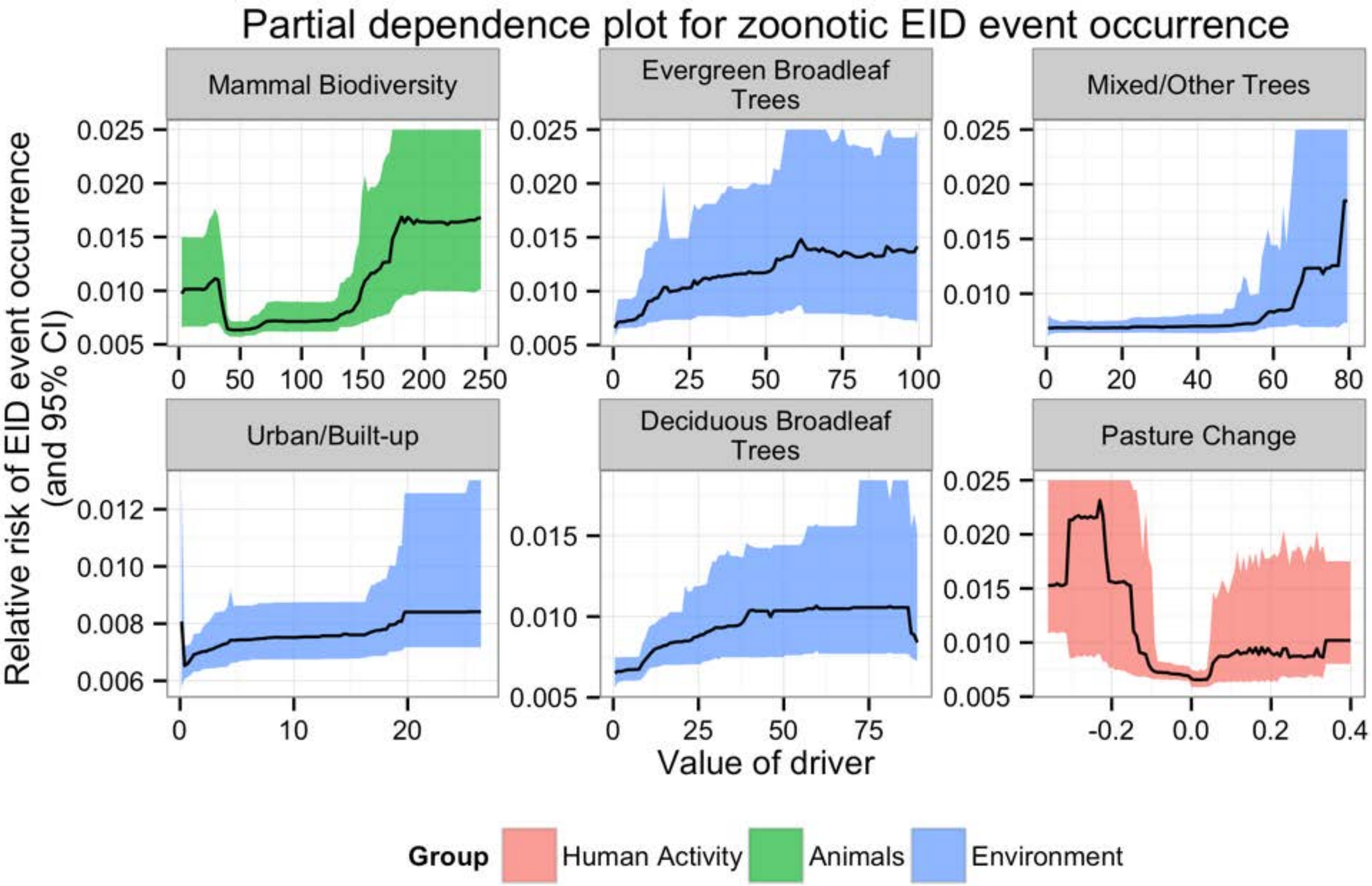


y-axis: relative probability of an EID event in a grid cell with this characteristic

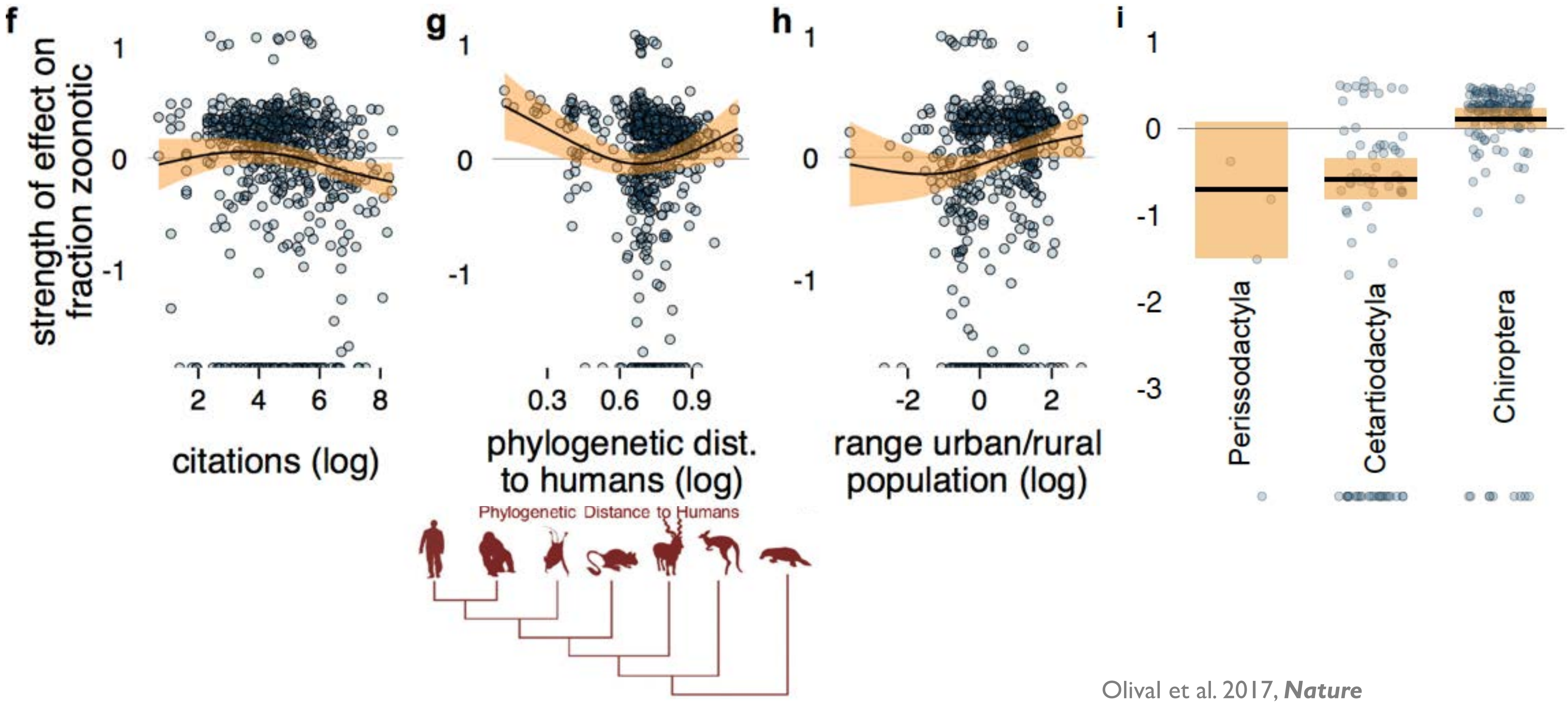
x-axis: min. to max. values of each driver (except 'Pasture Change')

The plots show effect relative to human pop. distribution, factoring out reporting bias

Model: 2 levels of interaction between drivers

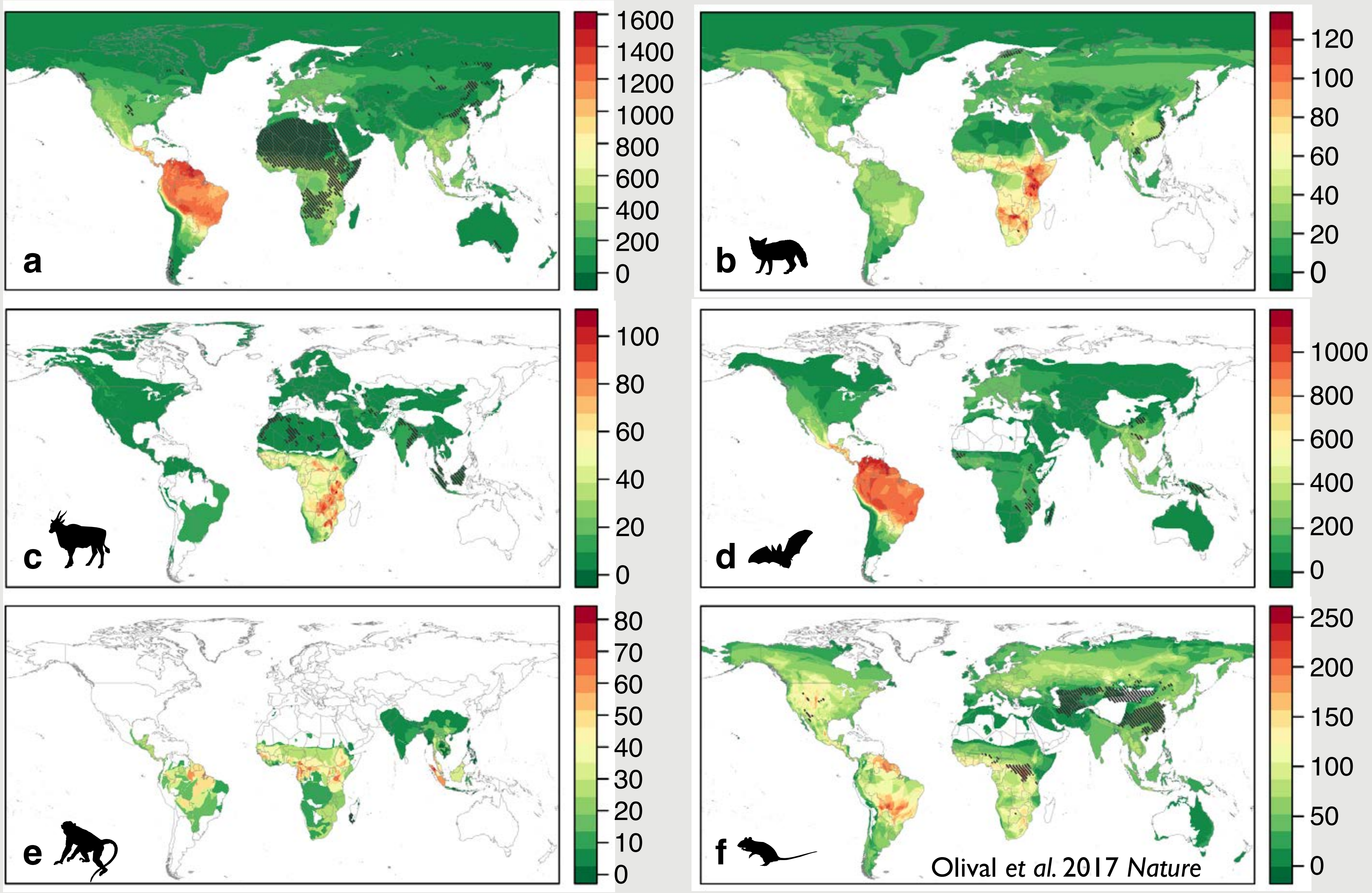


Which species will the next pandemic spillover from?



Olival et al. 2017, ***Nature***

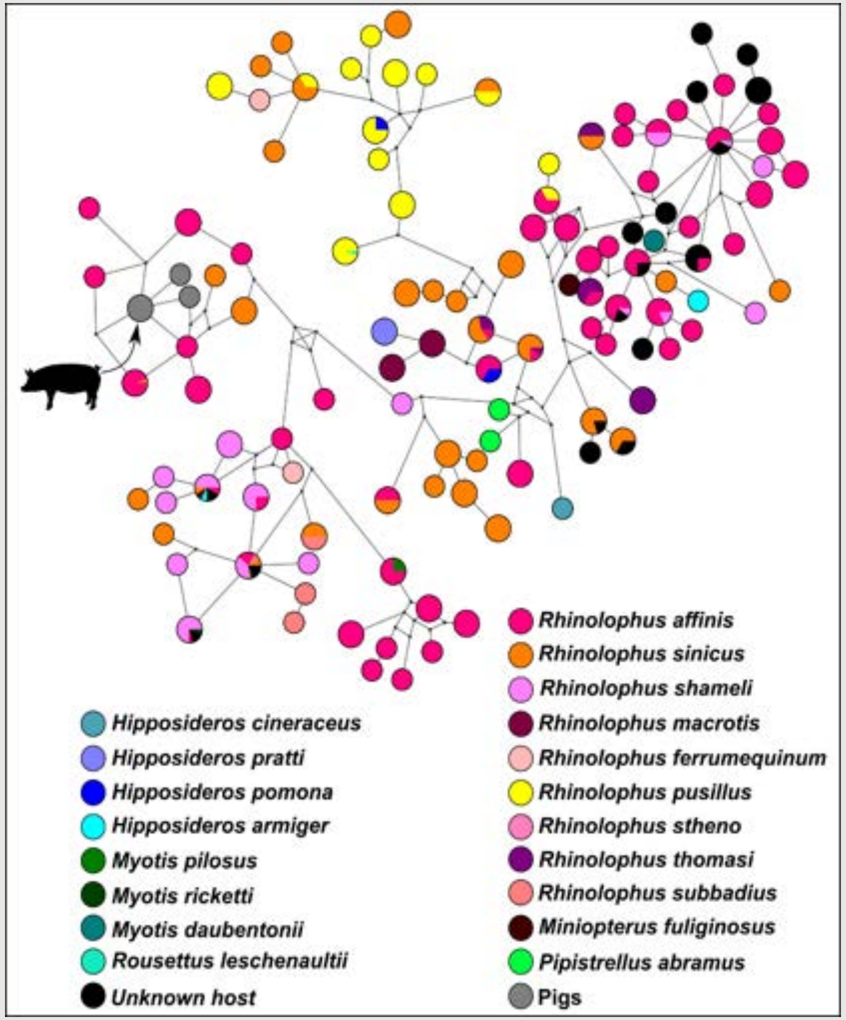
Missing Zoonoses - Mammals



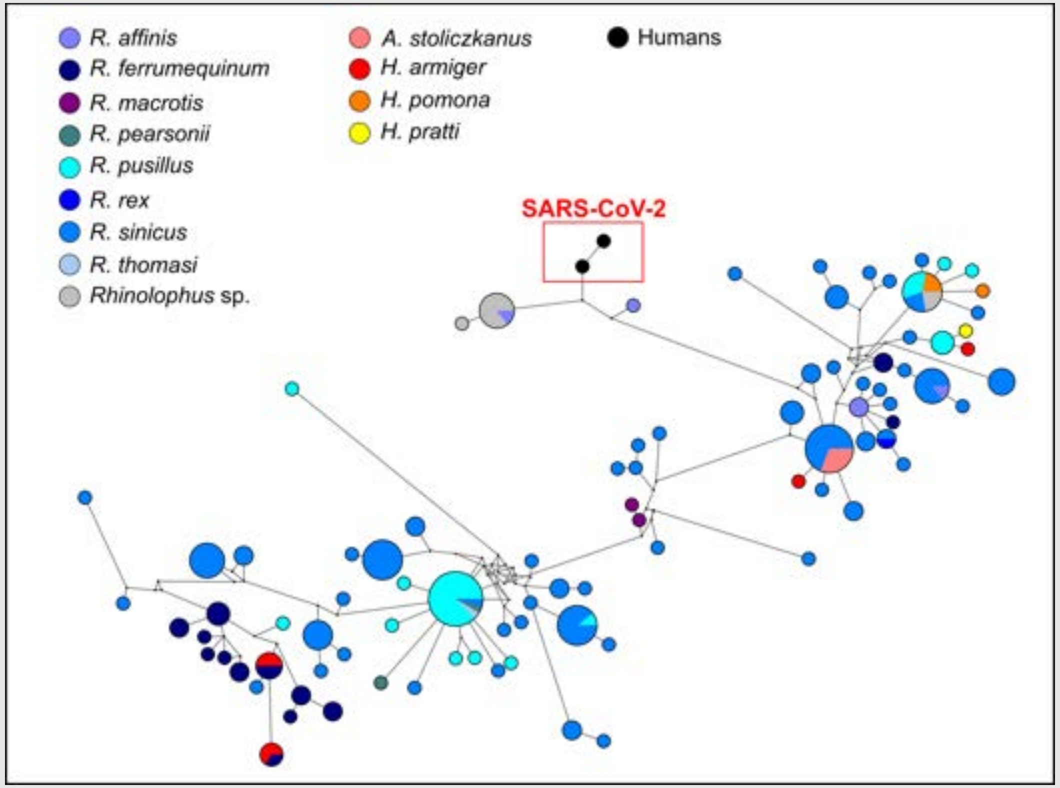
PREDICT/NIAID work discovered >500 bat-CoVs in China

RdRp partial gene sequence.
Size of circle proportional to the number of samples with identical viral sequences.

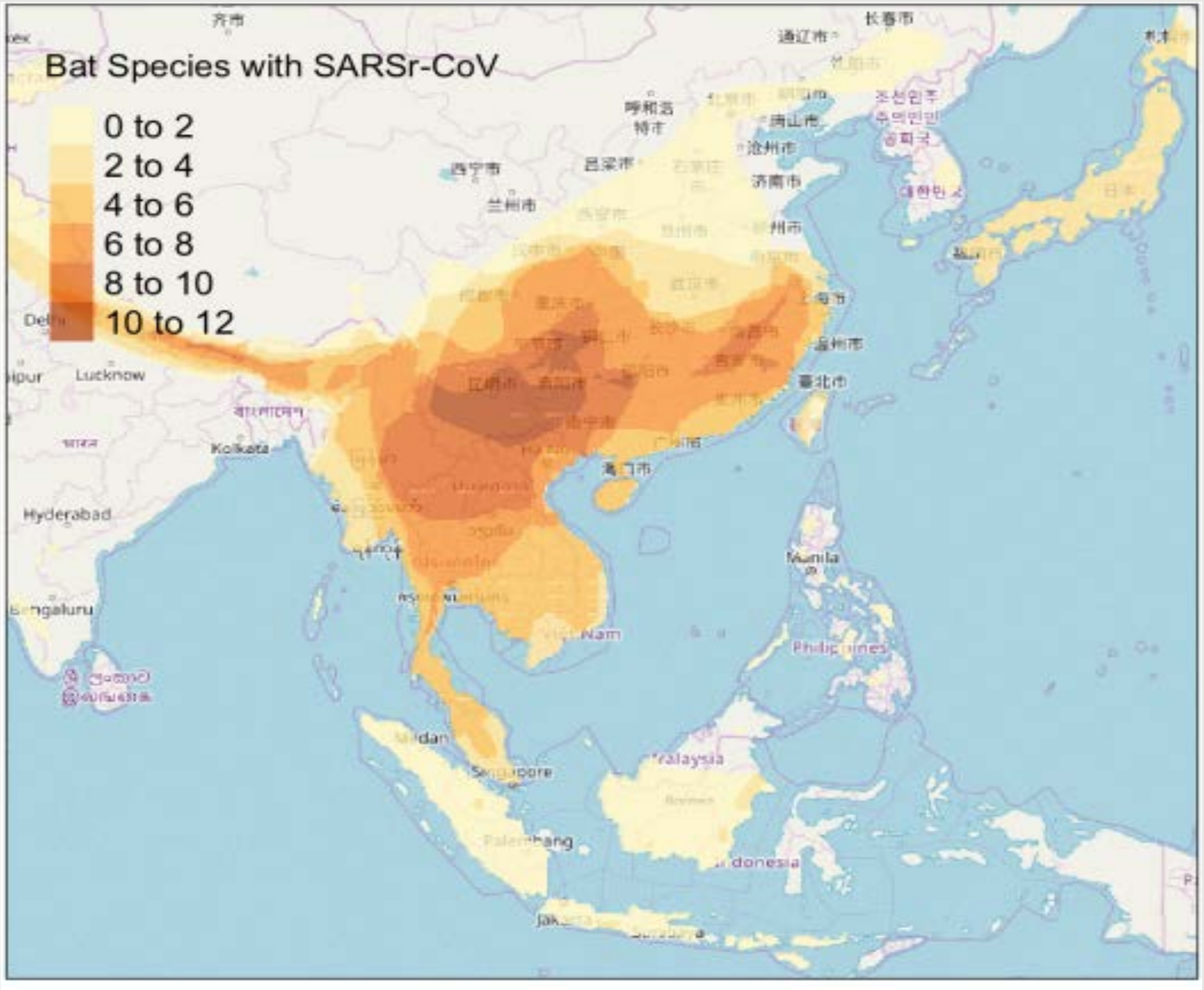
405 β – CoVs (SADSr), 361 from China



α – CoVs Clade 2b (SARSr-CoVs)



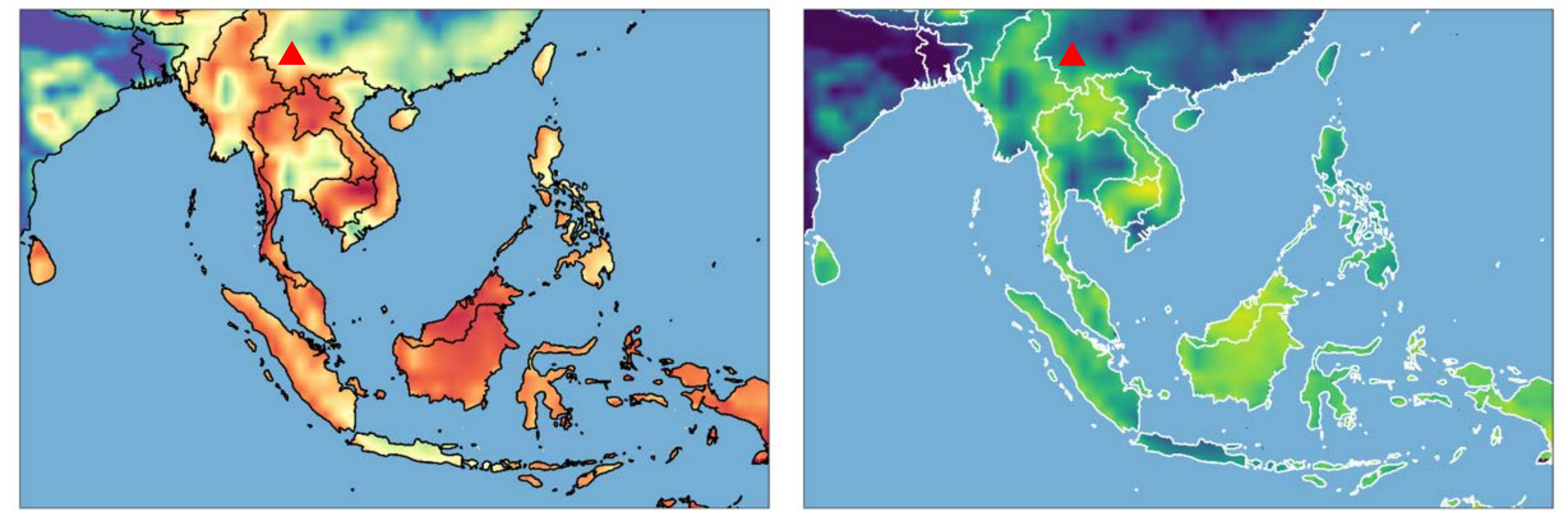
Bat-CoV risk is regional, not restricted to China



Distribution of bats harboring SARSr-CoVs

Distribution of *Rhinolophus affinis*

Bat coronavirus risk is regional, not restricted to China



▲ = Site in SW Yunnan where we conducted surveillance

Evidence of community exposure to bat CoVs (0.45% - 2.9% seropositive)

Across Southeast Asia: **1 - 7 million people likely exposed <u>every year</u> across the region**

Bat coronaviruses are a "clear and present danger"

"Our study provides **the first serological evidence of likely human infection by bat SARSr-CoVs or, potentially, related viruses.**"
(Wang et al., 2018)

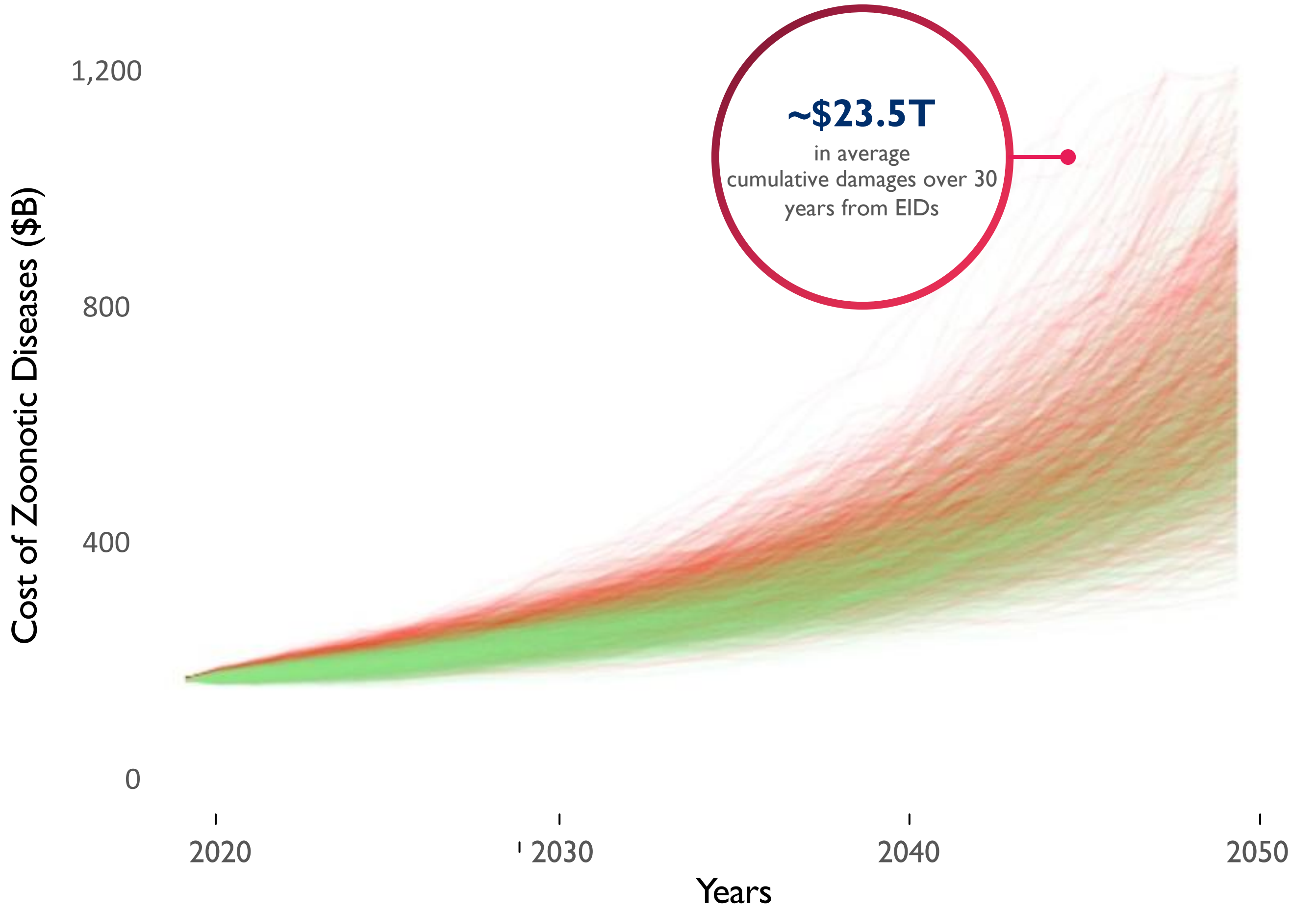
"We report the isolation and characterization of a novel bat coronavirus which is much closer to the SARS-CoV...this virus can use ACE2 as a receptor and infect animal and human cell lines. Our results provide further evidence of the bat origin of the SARS-CoV and ***highlight the likelihood of future bat coronavirus emergence in humans***."
(Yang et al., 2015)

Out of >20 PREDICT publications on bat CoV research in China and SE Asia

"Cell entry studies demonstrated that three newly identified SARSr-CoVs with different S protein sequences are all able to use human ACE2 as the receptor, further exhibiting the close relationship between strains in this cave and SARS-CoV. This work provides new insights into the origin and evolution of SARS-CoV and ***highlights the necessity of preparedness for future emergence of SARS-like diseases***." (Hu et al., 2017)

"We demonstrate that **bats harbour a significantly higher proportion of zoonotic viruses than all other mammalian orders.**"
(Olival et al., 2017)

Costs and Return on Investments for Disease Emergence



~60% due to reduction in outbreak **severity**

~40% due to reduction in number of outbreaks

1. Key model assumptions: Reduction in the cost of zoonotic outbreaks from GVP grows from 1% in 2020 to 10% in 2035 and remains at 10% through 2050; global GDP starts at $73.4T and increases 2.4% annually (World Bank 2015 analyses); Annual number of EID events starts at 2.6 and increases 1.2% annually (Jones et al. 2008; Pike et al. 2014)

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Surveillance
where it matters

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Coordinated Disease Surveillance Workforce

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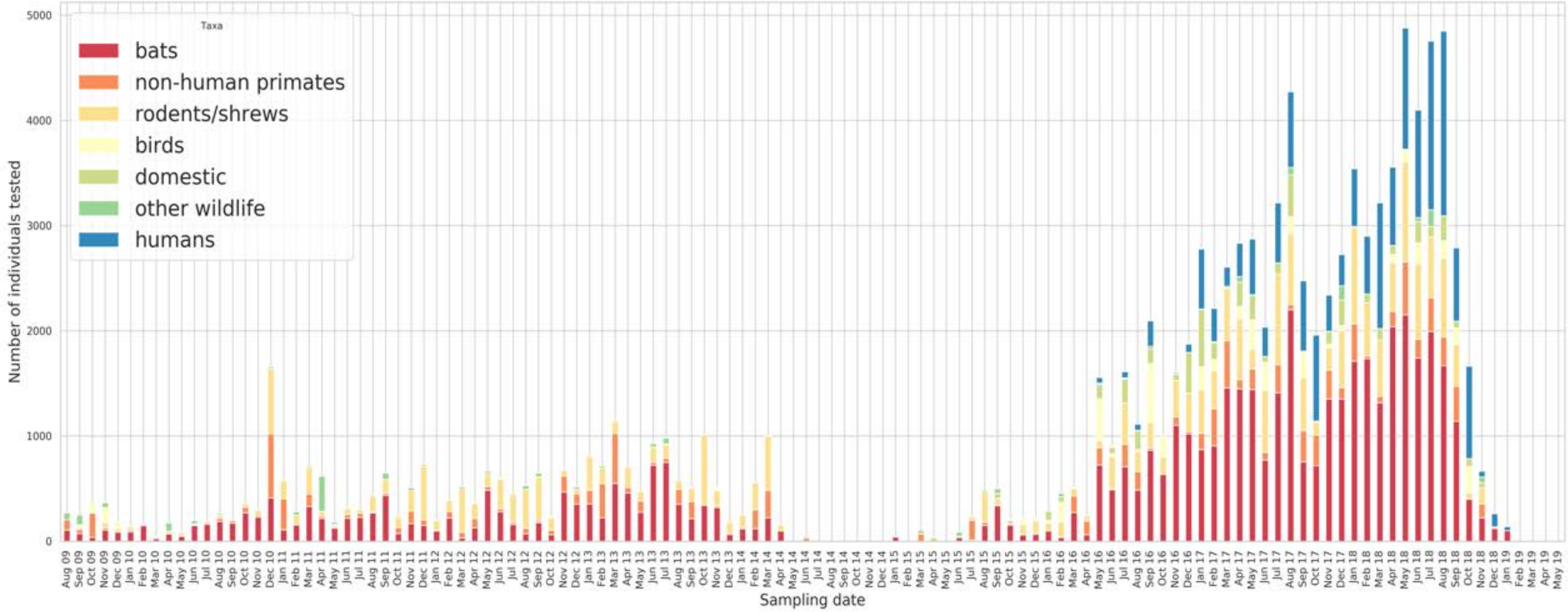
Collaborative Disease Detection Workforce

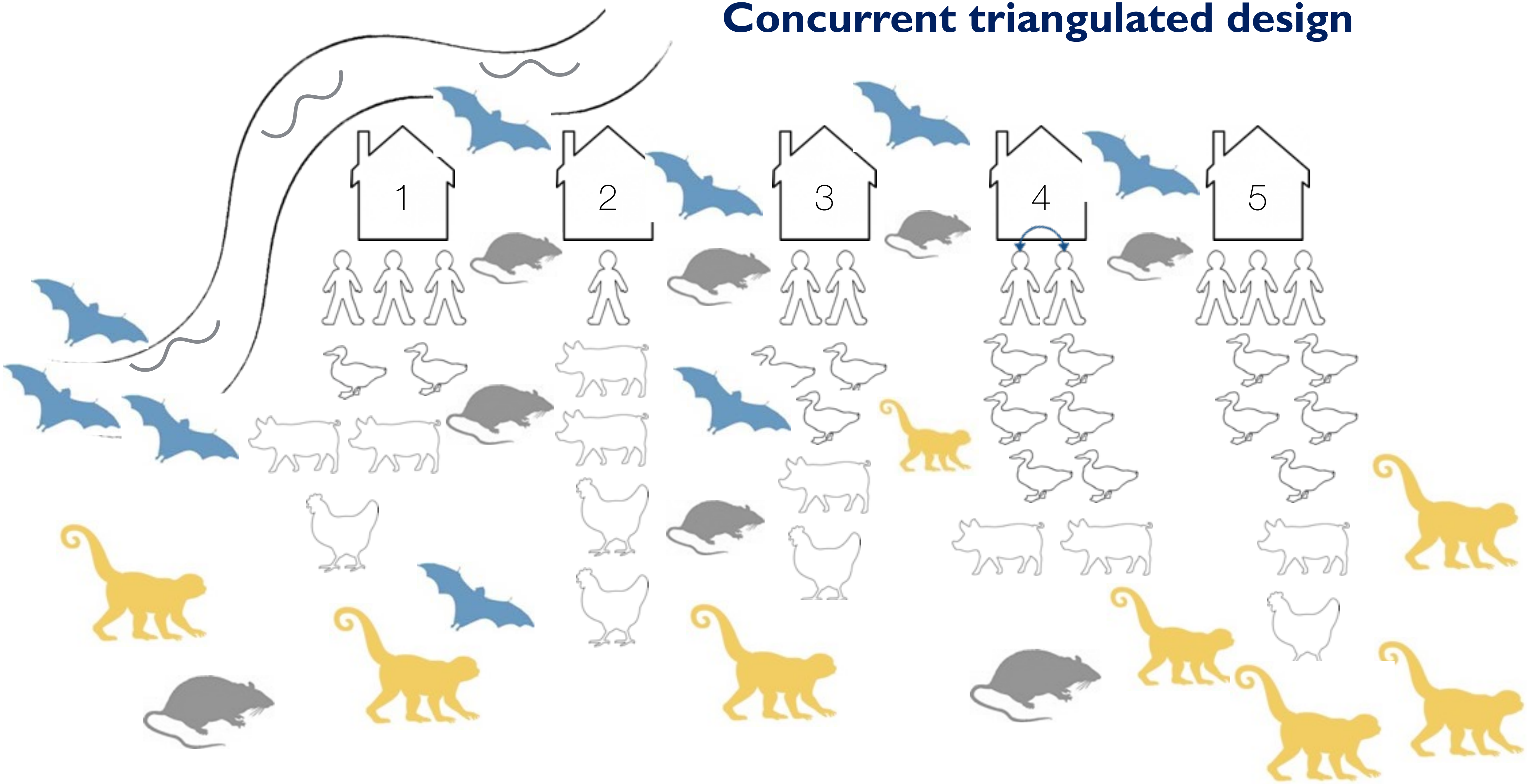
PREDICT 2009-2019

PREDICT 2 only
Animals tested n = 67,679
Humans tested n = 16,499



One Health Surveillance

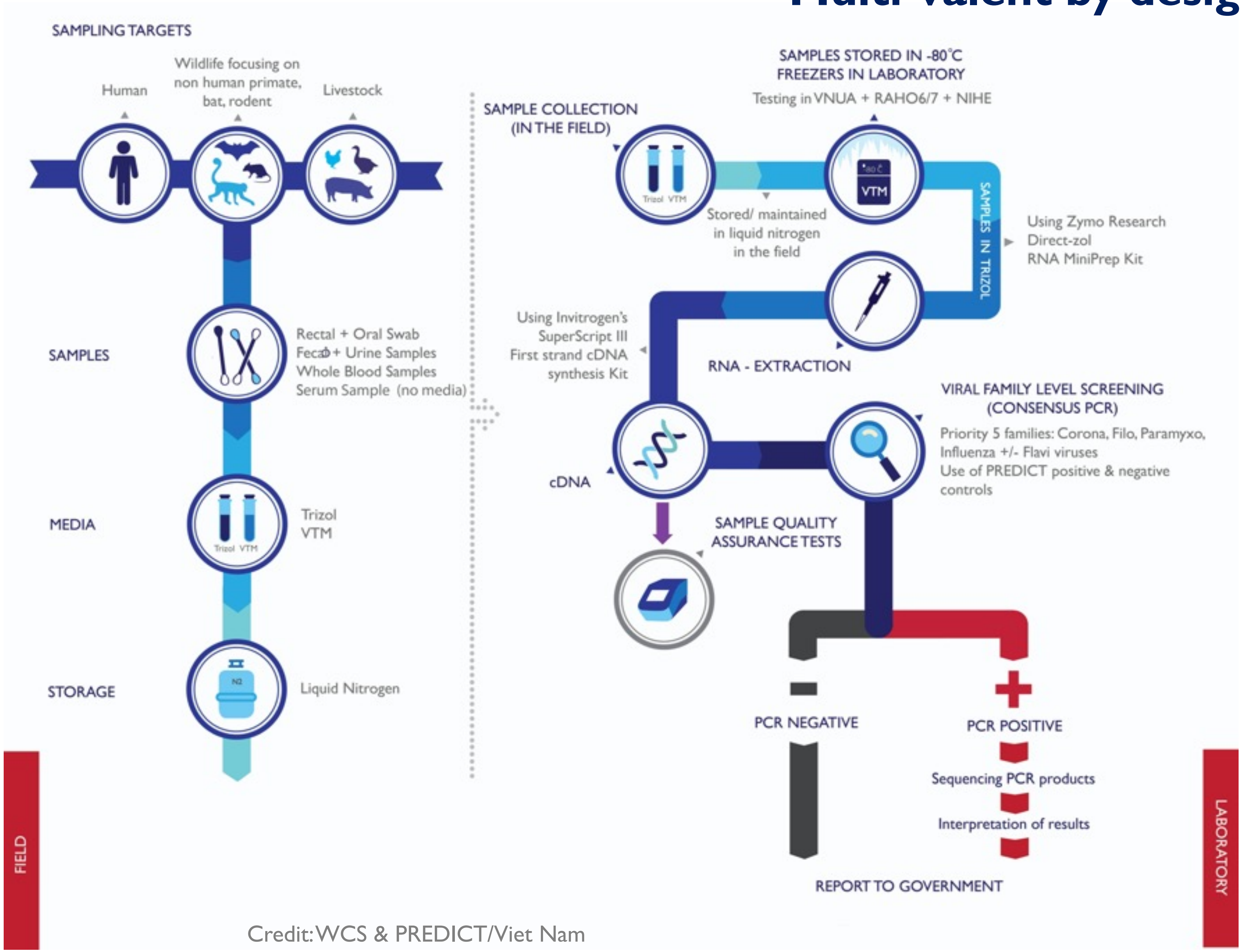
Concurrent triangulated design



Partnership between wildlife, livestock, and human health experts

One Health Surveillance

Multi-valent by design



Credit: WCS & PREDICT/Viet Nam

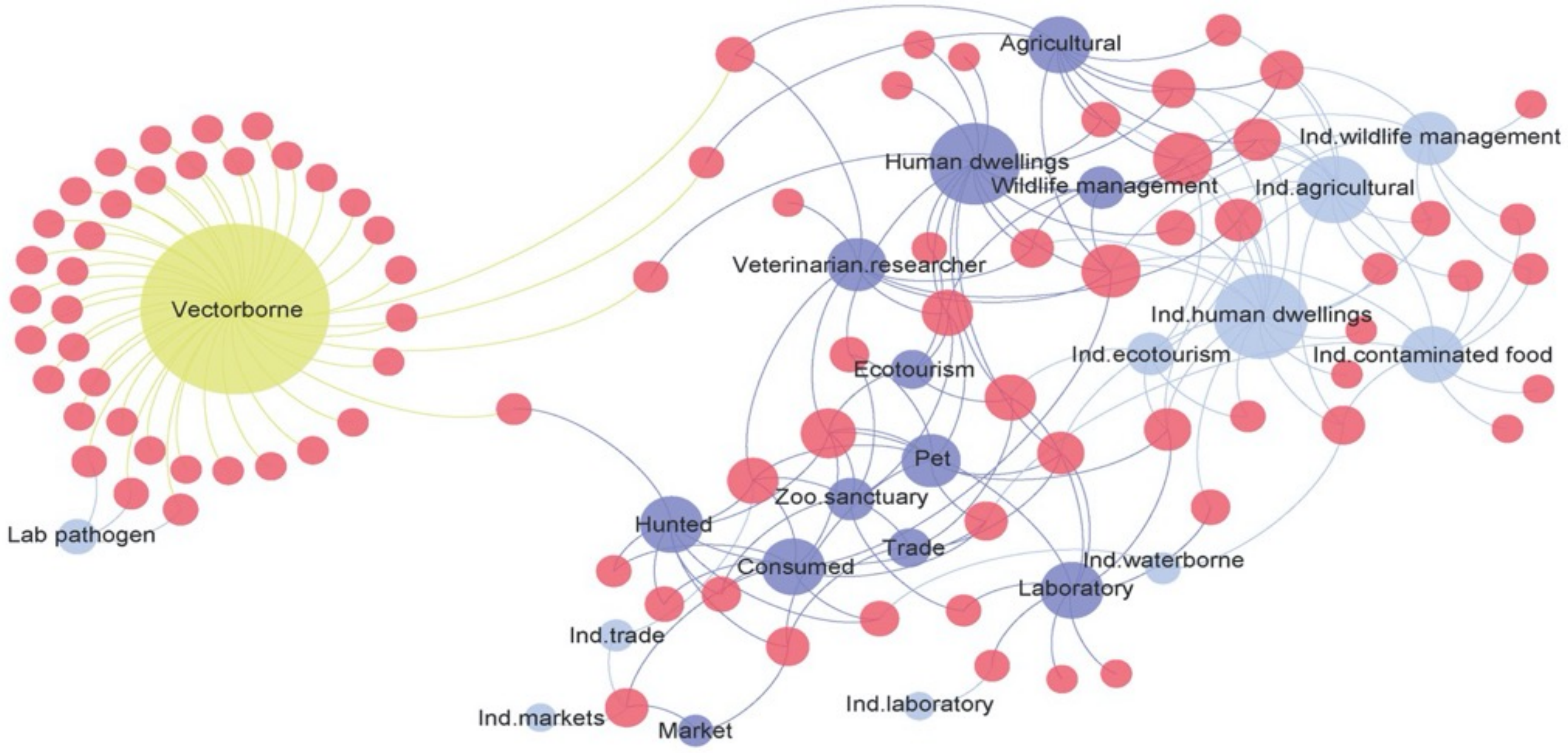
PREDICT FINDINGS in 14 Africa and 12 Asia countries (2009-2019)

	Coronaviruses		Paramyxoviruses		Influenzaviruses		Flavivirus		Overall Total*	
	% positive	n positive	% positive	n positive	% positive	n positive	% positive	n positive	n positive	n tested
bats	4.80%	3,070	0.78%	500	0.08%	50	0.01%	6	4,630	63,959
rodents & shrews	2.71%	1,021	0.37%	140	0.02%	6	0.00%	0	1,602	37,643
non-human primates	0.03%	4	0.01%	2	0.00%	0	0.00%	0	445	13,751
birds	0.48%	23	0.17%	8	4.31%	205	0.00%	0	230	4,755
ungulates	0.39%	1	0.00%	0	0.00%	0	0.00%	0	10	255
camels	0.00%	0	0.00%	0	0.00%	0	0.00%	0	0	602
carnivores	0.10%	1	0.10%	1	0.00%	0	0.00%	0	4	1,026
pangolins	0.00%	0	0.00%	0	0.00%	0	0.00%	0	0	649
other mammals	0.00%	0	0.00%	0	0.00%	0	0.00%	0	7	710
cats	0.00%	0	0.00%	0	0.00%	0	0.00%	0	0	113
dogs	0.28%	4	0.42%	6	0.00%	0	0.00%	0	10	1,414
cattle/buffalo	0.21%	2	0.00%	0	0.00%	0	0.00%	0	2	932
goats/sheep	0.00%	0	0.67%	4	0.00%	0	0.00%	0	4	601
poultry/other fowl	10.43%	258	1.46%	36	1.94%	48	0.16%	4	309	2,473
swine	12.42%	99	0.88%	7	3.01%	24	0.00%	0	125	797
Total		4,483		705		333		10	7,379	129,734

* varied by test type

based on number of samples tested

High-risk Interfaces for Virus Spillover (published through 2011)

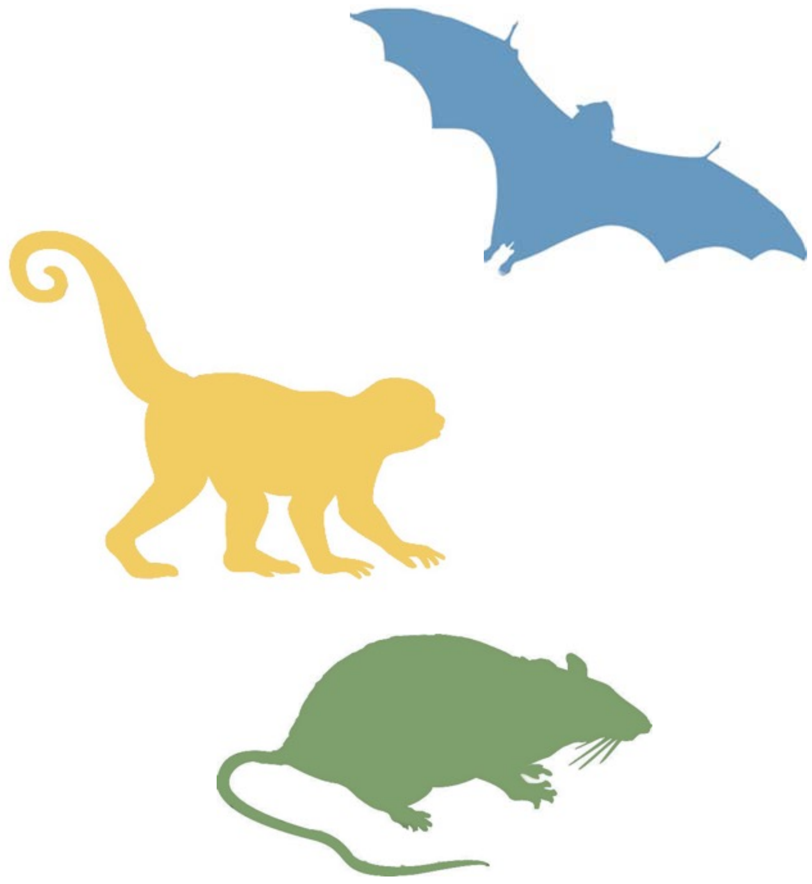


Direct and indirect contact with wildlife resulting in disease spillover

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

PREDICT Surveillance 2009-2019

Where have we been most likely to find viruses with zoonotic potential in wild animals?

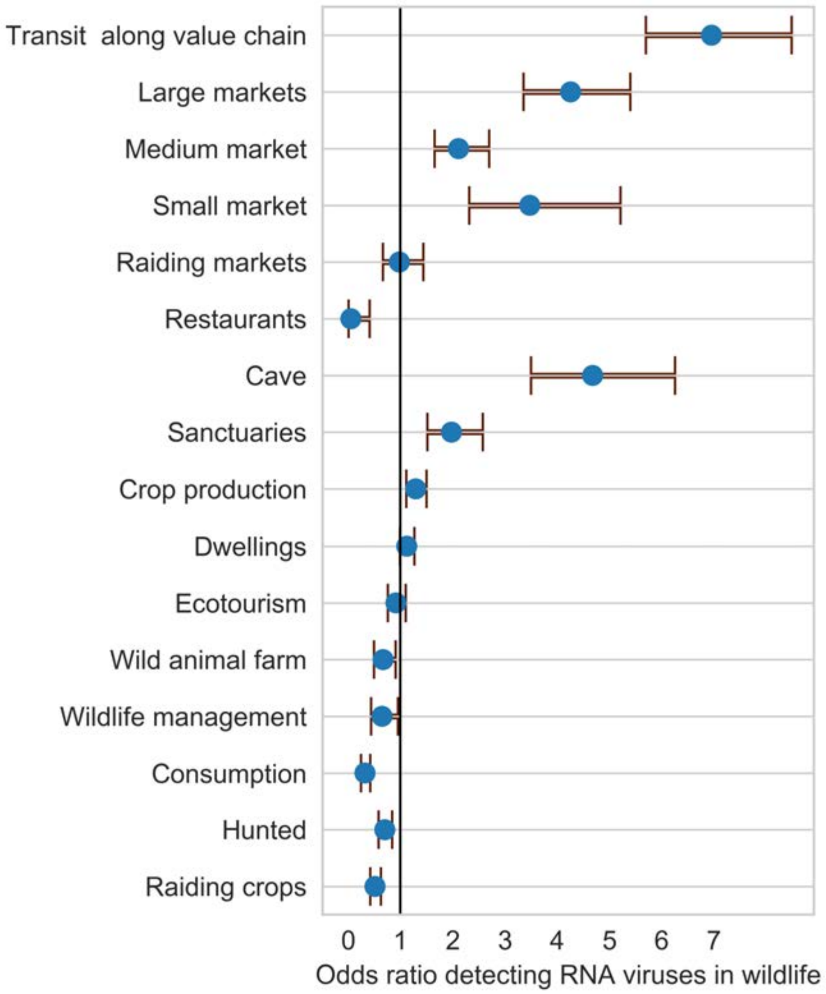


- Bats, primates, rodents and shrews more likely than other species to shed viruses among species targeted in PREDICT 1 and 2
- Detections in specimen type highlight important animal-human interfaces for disease transmission
  - DNA viruses most commonly shed orally
  - RNA viruses most commonly shed in urine and feces

PREDICT Surveillance 2014-2019

Where have are we most likely to find RNA viruses with zoonotic potential in wild animals?

- **Bats, primates, rodents, shrews, and birds** more likely than other species to shed RNA viruses in urine and feces
- **Wildlife-human interfaces** with **more frequent** detection of RNA viruses (in order of magnitude of association, compared to situations where contact with animals is not likely)
  - in transit along value chain
  - caves
  - for sale in large markets
  - for sale in small markets
  - for sale in medium markets
  - wildlife sanctuary/confiscation, extractive industry, crop production
- **Wildlife-human interfaces** with **less frequent** detection of RNA viruses
  - wildlife restaurants, wildlife destined for consumption, wildlife in management settings, hunted wildlife, wildlife raiding crops, wild animal farms, private sale of wildlife



PREDICT Surveillance 2009-2019

Where have we been most likely to find coronaviruses with zoonotic potential in wild animals?

- **Bats, birds, rodents and shrews** more likely than other species to shed coronaviruses in urine and feces
- **Wildlife-human interfaces** with **more frequent** detection of coronaviruses (in order of magnitude of association):
  - in transit along value chain
  - for sale in large, medium, and small markets

Where have we been most likely to find paramyxoviruses with zoonotic potential in wild animals?

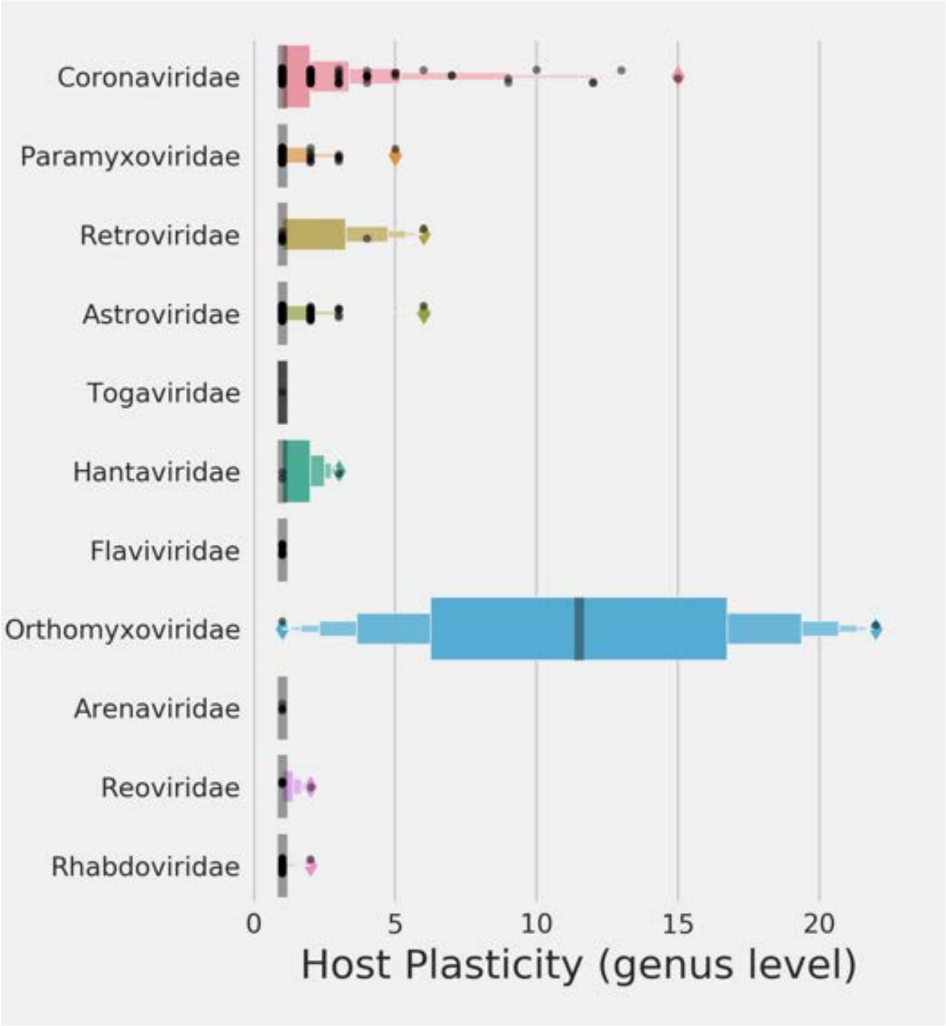
- No strong species predilections, paramyxoviruses were more likely to be shed in urine
- Wildlife-human interfaces with **more frequent** detection of paramyxoviruses (in order of magnitude of association):
  - wild animal farms
  - guano farms

Virus Host Plasticity

Zoonotic Viruses
Reported through 2011

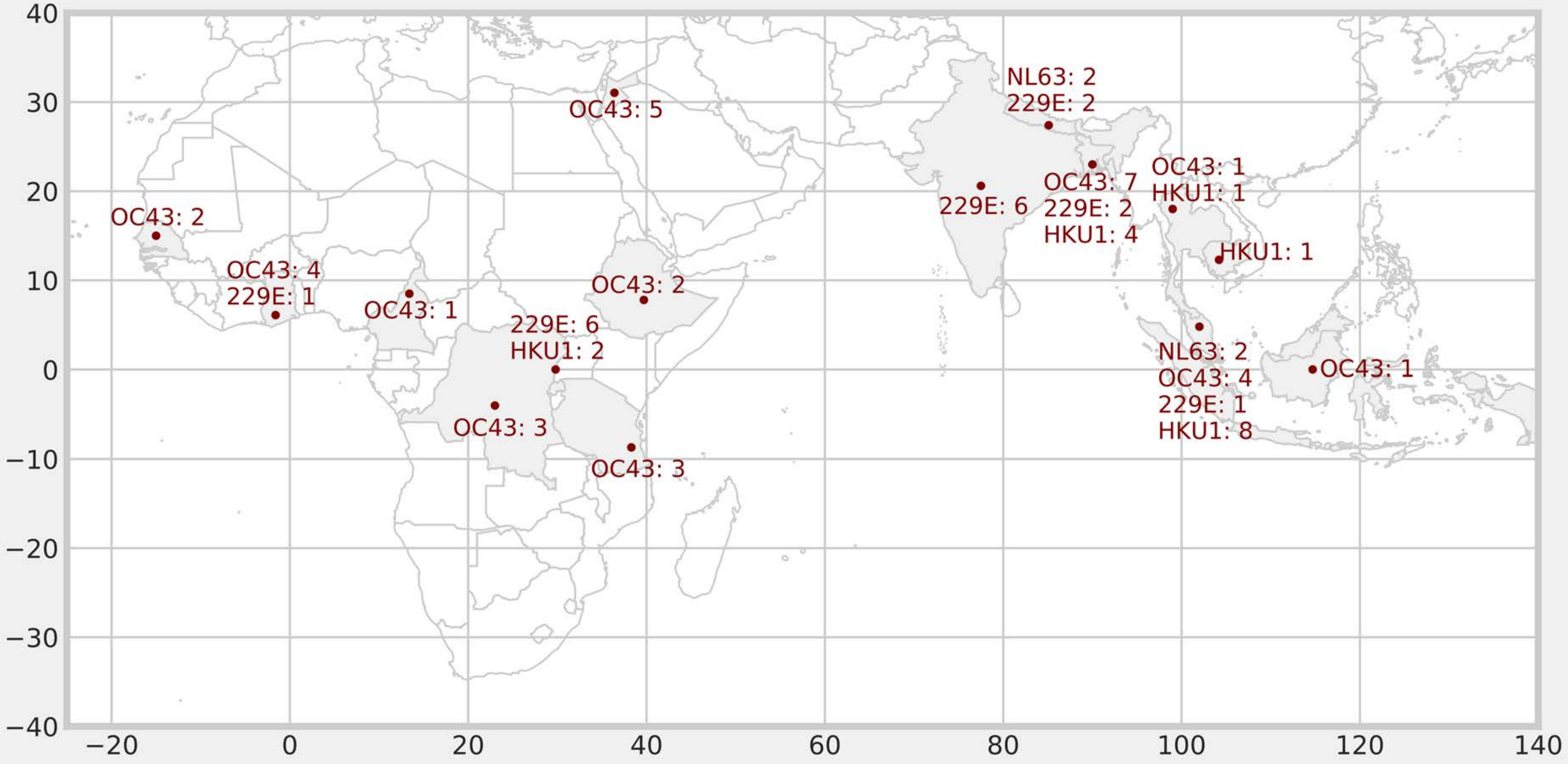
- 65% of zoonotic viruses in 3 or more taxonomic orders
- 45% of zoonotic viruses in 5 or more taxonomic orders
- High-risk interfaces with increased host plasticity
    - Situations that facilitate close contact between diverse hosts of wild animals, such as wildlife sold at markets, kept in sanctuaries

Viruses with Zoonotic Potential Detected by PREDICT 2009-2019



Human coronaviruses

Coronaviruses detected in people during PREDICT surveillance (2014-2019)



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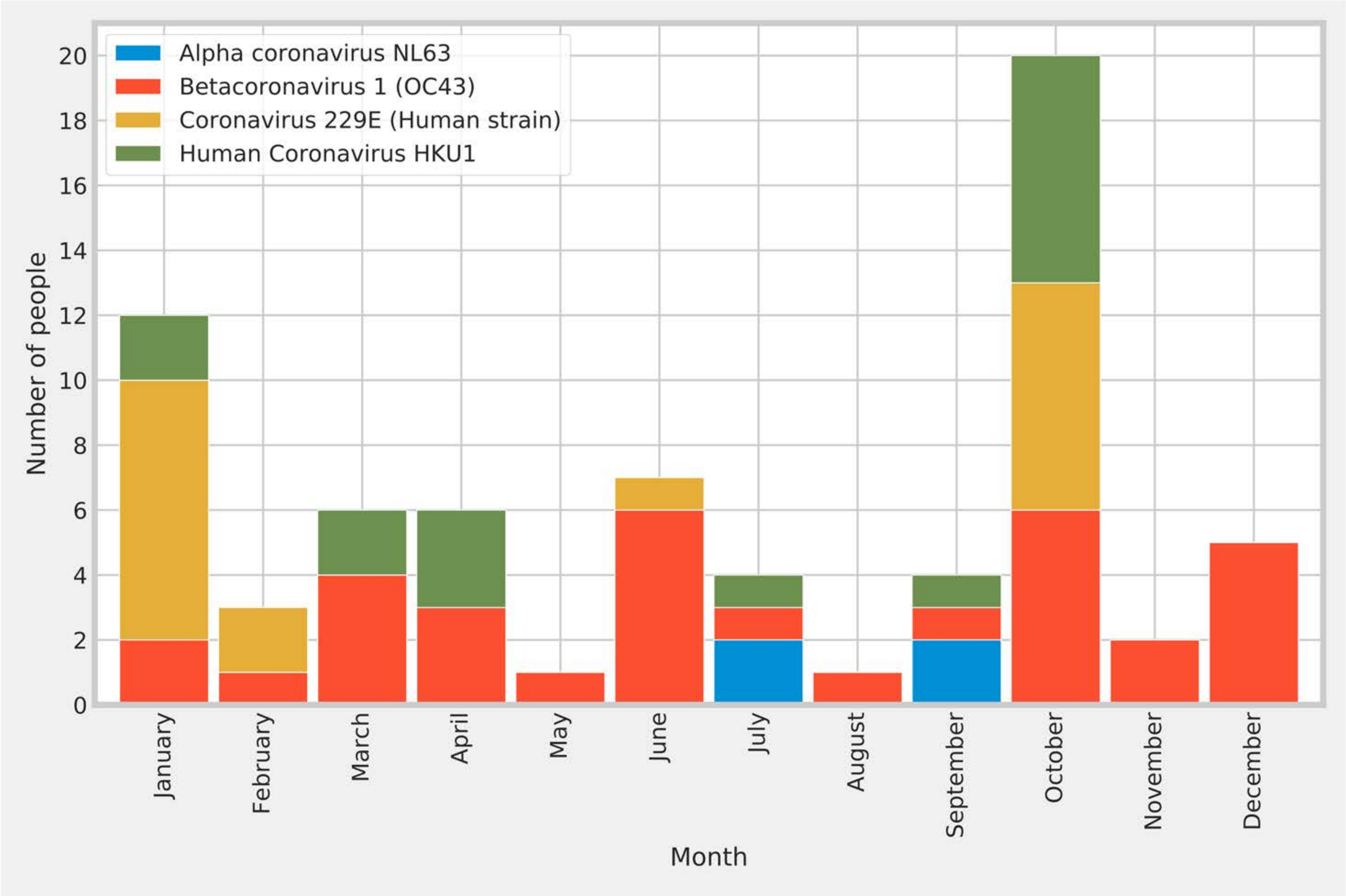
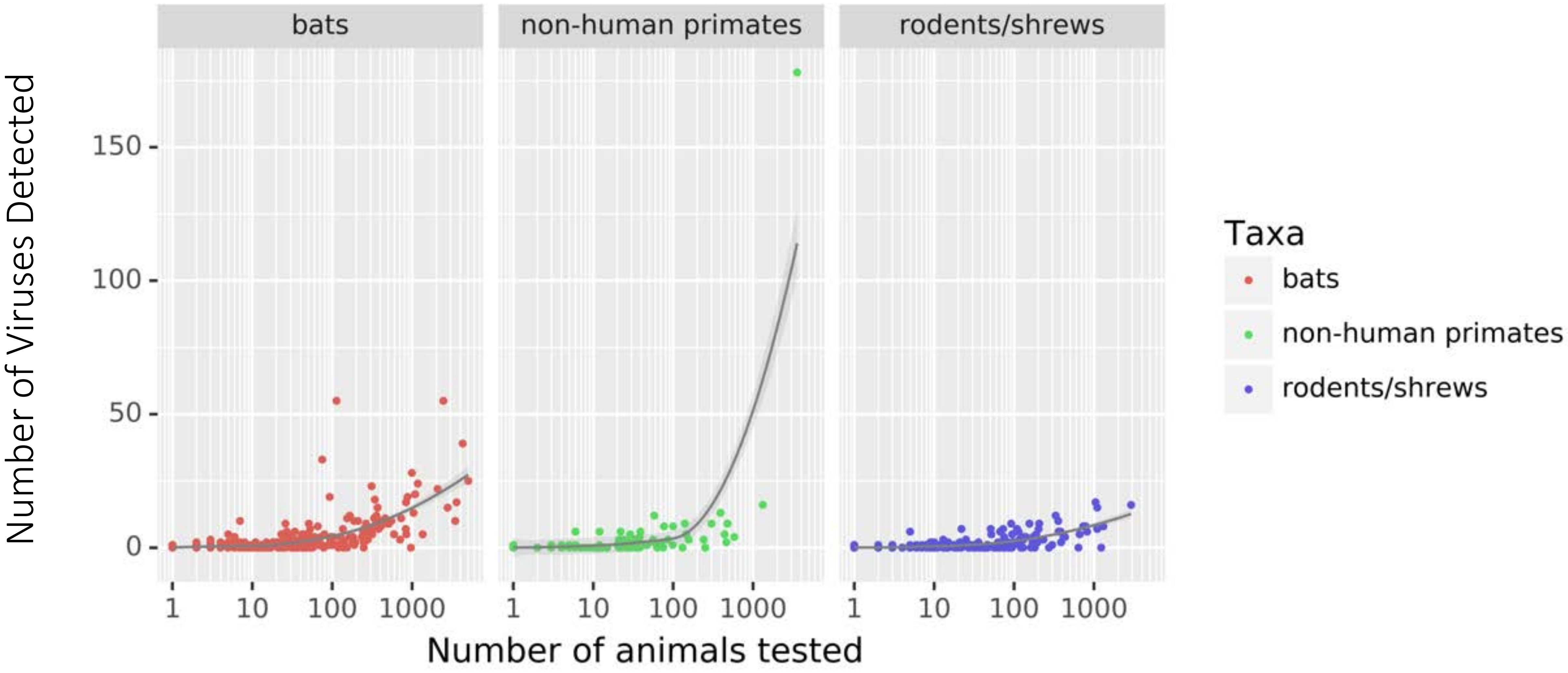
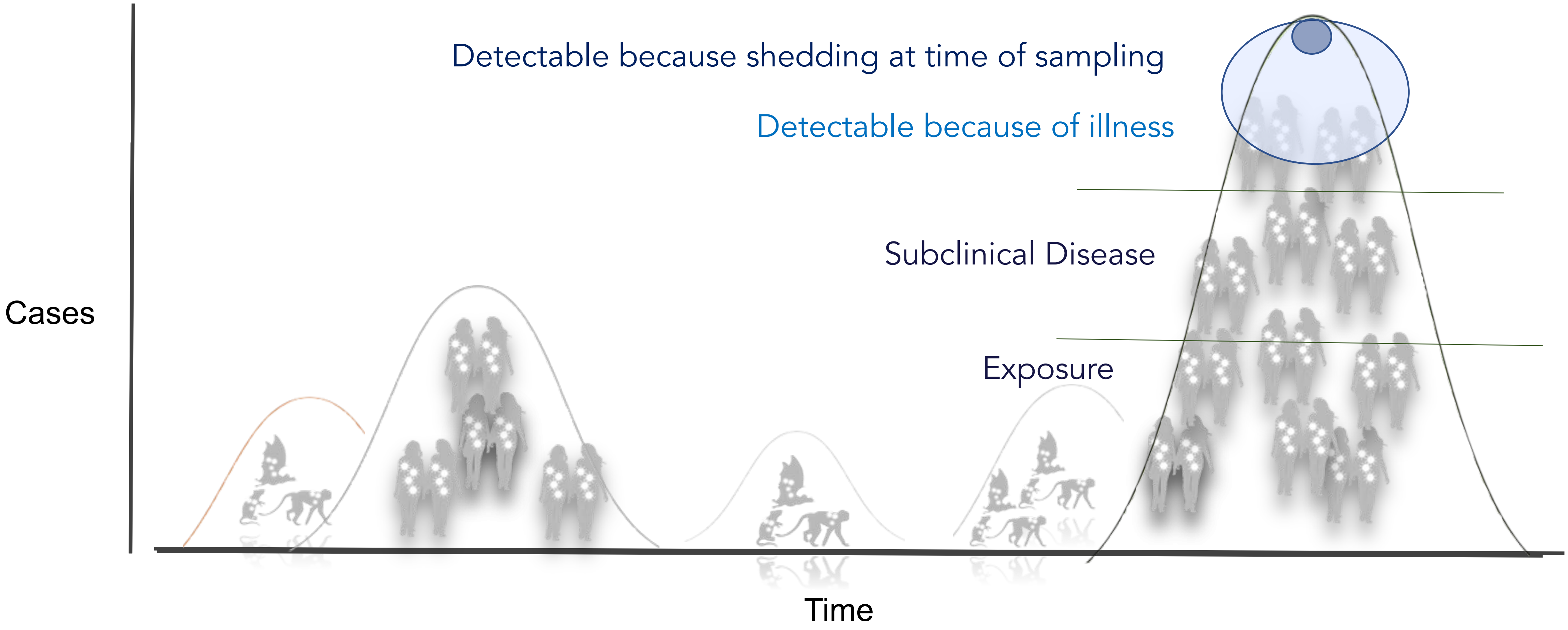


Emerging Threats Surveillance

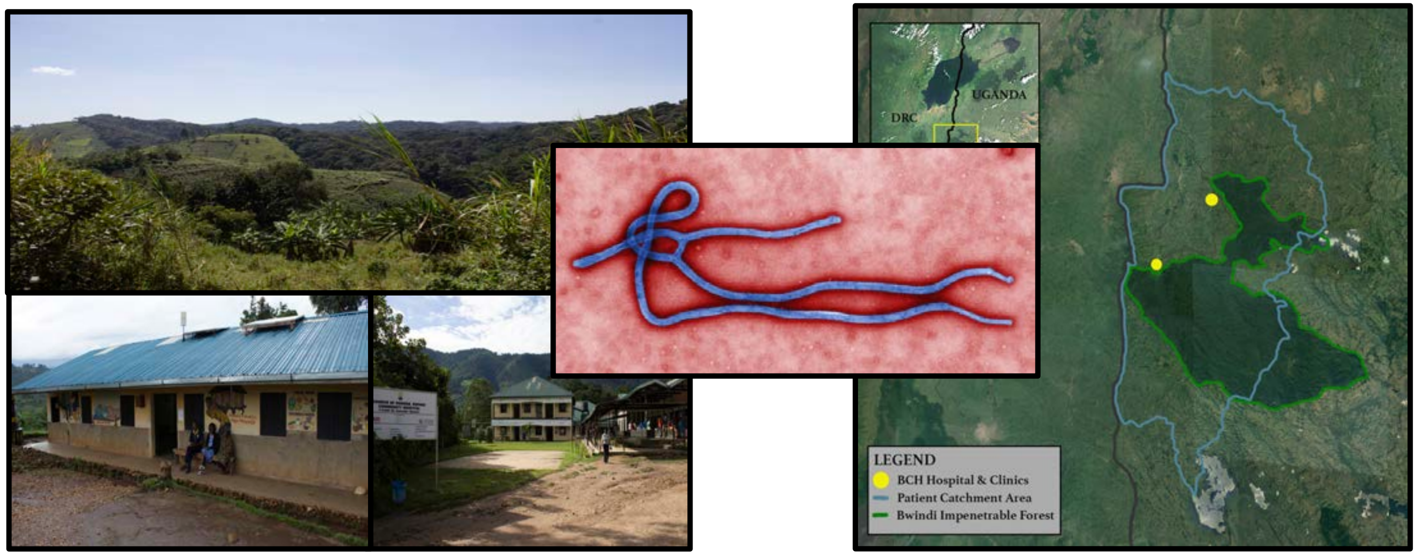


Emerging Threats Surveillance



Wildlife contact associated with human exposure to ebolaviruses

Secondary wild animal spillover hosts remain important sources of human exposure to Ebola virus and Sudan virus, two causes of hemorrhagic fever.



We enrolled 331 febrile patients presenting two healthcare facilities near the Bwindi Impenetrable Forest, Uganda, a hotspot for primate diversity in East / Central Africa. Specimens were tested using PCR and Western blot for Ebola virus (EBOV), Sudan virus (SUDV), Bundibugyo virus (BDBV) and Marburg virus and questionnaires were used to collect information on interactions with wildlife. We did not detect active infection in patients by PCR but found evidence for past exposure to ebolaviruses in this population.

The Journal of Infectious Diseases

IDSA Infectious Diseases Society of America
hivma hiv medicine association

Suspected Exposure to Filoviruses Among People Contacting Wildlife in Southwestern Uganda

Tierra Smiley Evans,[1] Leonard Tutaryebwa,[6] Kirsten V. Gilardi,[1] Peter A. Barry,[2] Andrea Marzi,[5] Meghan Eberhardt,[2] Benard Ssebide,[3] Michael R. Cranfield,[3] Obed Mugisha,[6] Emmanuel Mugisha,[6] Scott Kellermann,[4] Jonna A. K. Mazet,[1] and Christine K. Johnson[1]

[1]One Health Institute, School of Veterinary Medicine, and [2]Center for Comparative Medicine, Department of Pathology and Laboratory Medicine, University of California, Davis; and [3]Gorilla Doctors, Mountain Gorilla Veterinary Project, Inc., Kampala, Uganda; [4]University of San Francisco, California; [5]Laboratory of Virology, Division of Intramural Research, National Institute of Allergy and Infectious Diseases, National Institutes of Health, Hamilton, Montana; and [6]Bwindi Community Hospital, Buhoma, Uganda

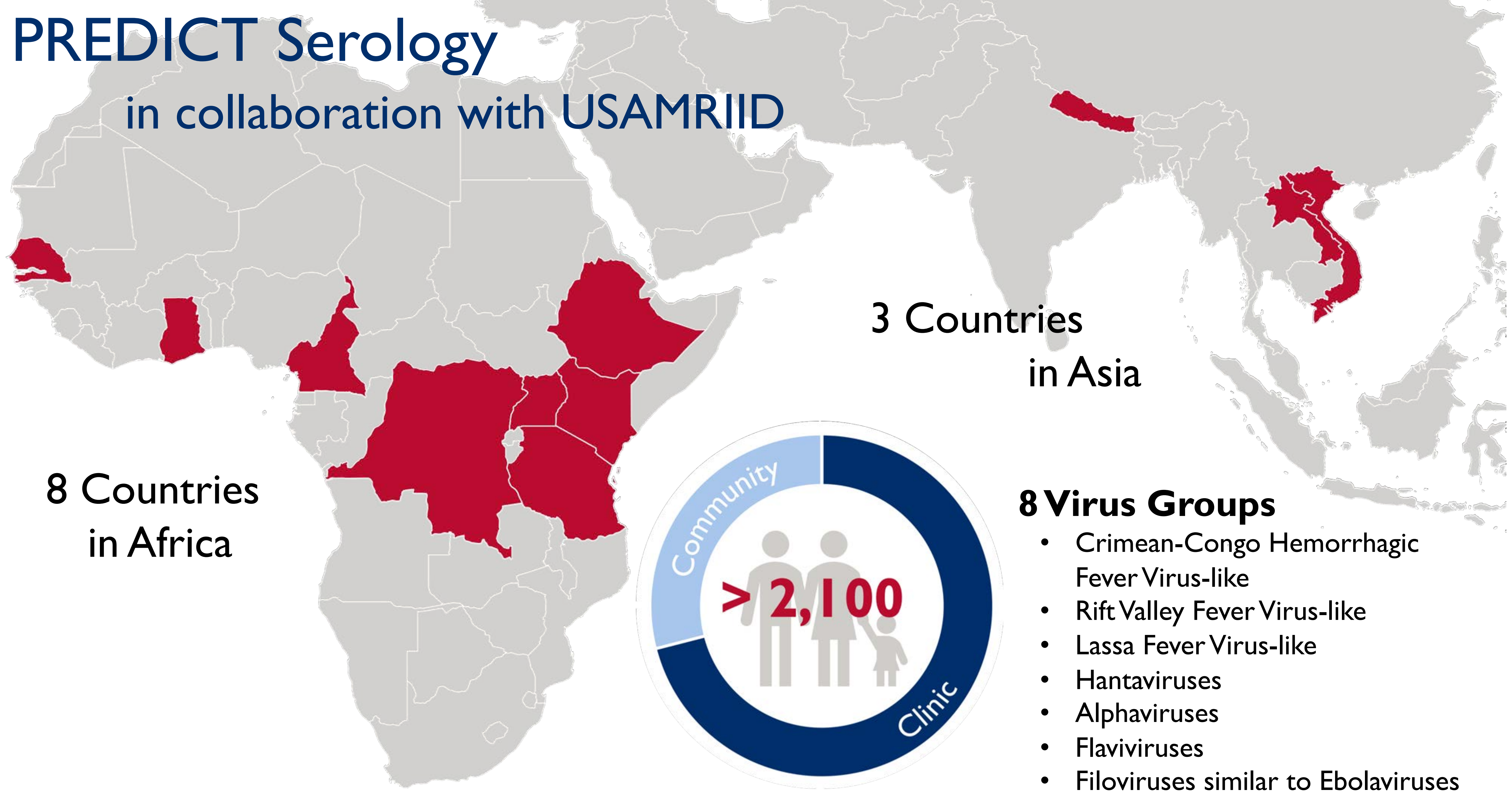
Hunting primates (increased risk 38 fold)

Contact with duiker (Increased risk 6 fold)

Contact with cane rats (Increased risk 11 fold)

PREDICT Serology

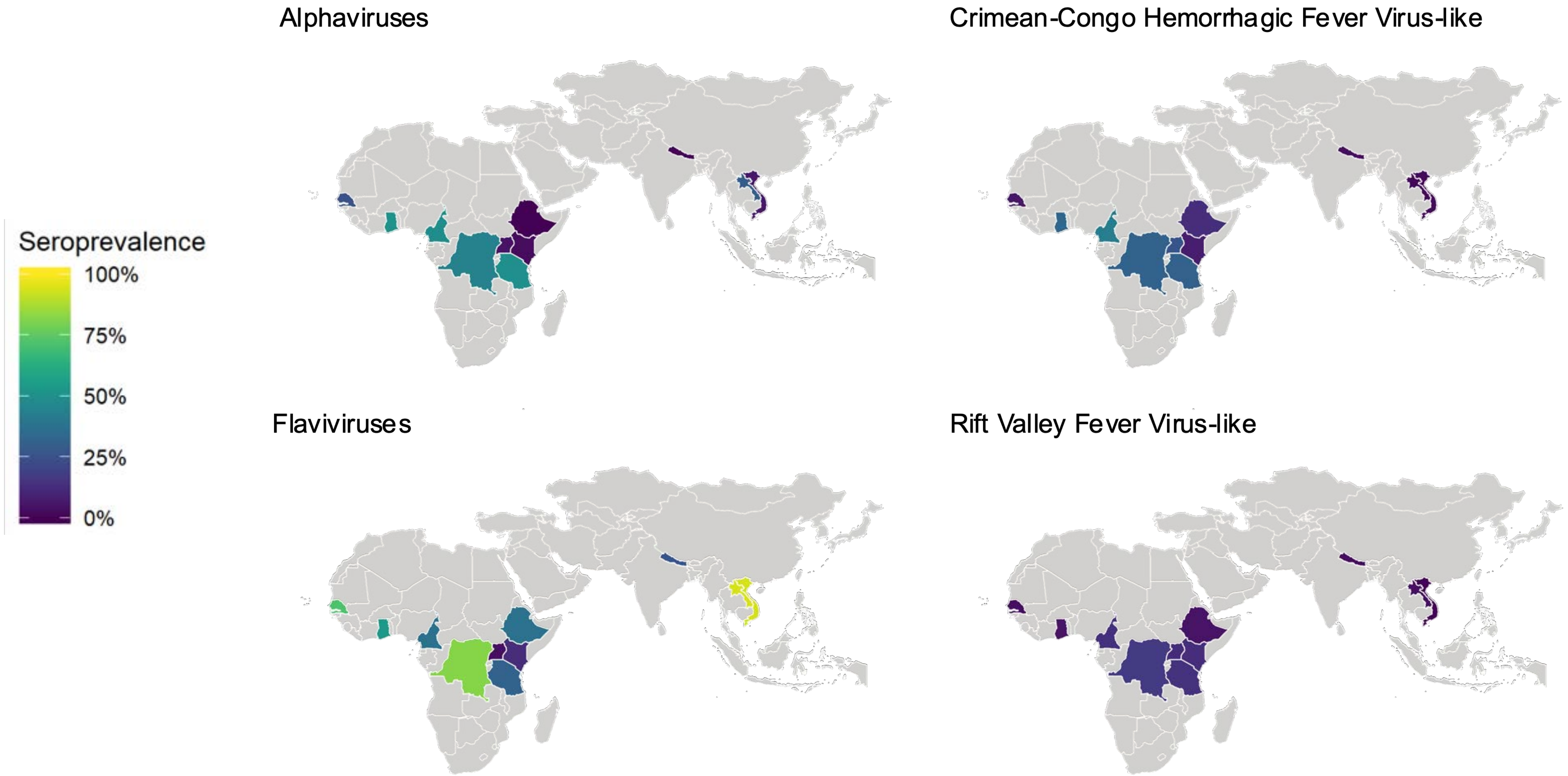
in collaboration with USAMRIID



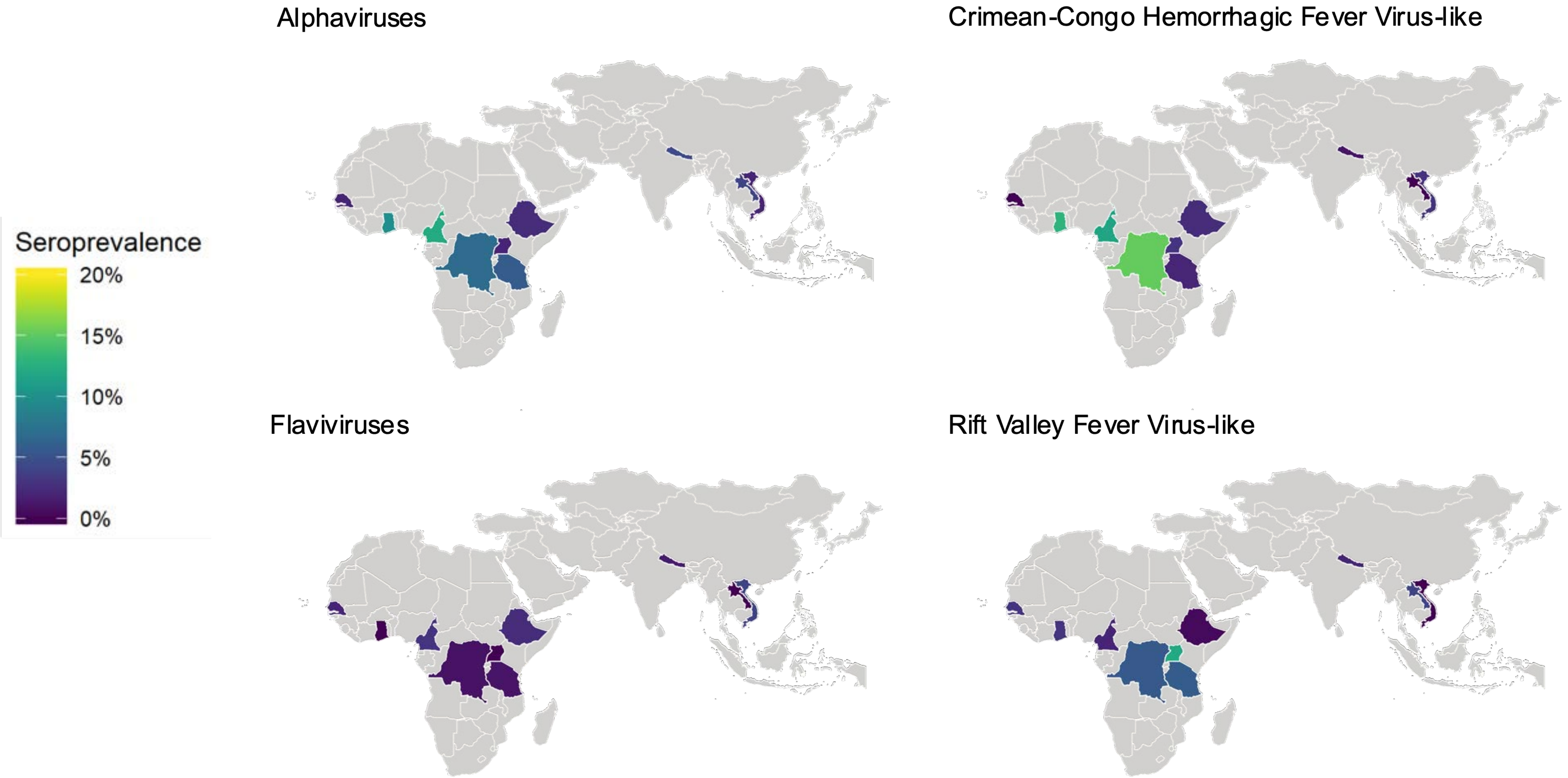
8 Virus Groups

- Crimean-Congo Hemorrhagic Fever Virus-like
- Rift Valley Fever Virus-like
- Lassa Fever Virus-like
- Hantaviruses
- Alphaviruses
- Flaviviruses
- Filoviruses similar to Ebolaviruses
- Filoviruses similar to Marburgvirus

IgG Seroprevalence



IgM Seroprevalence



Improved Awareness for Zoonotic Diseases = Pandemic Preparedness

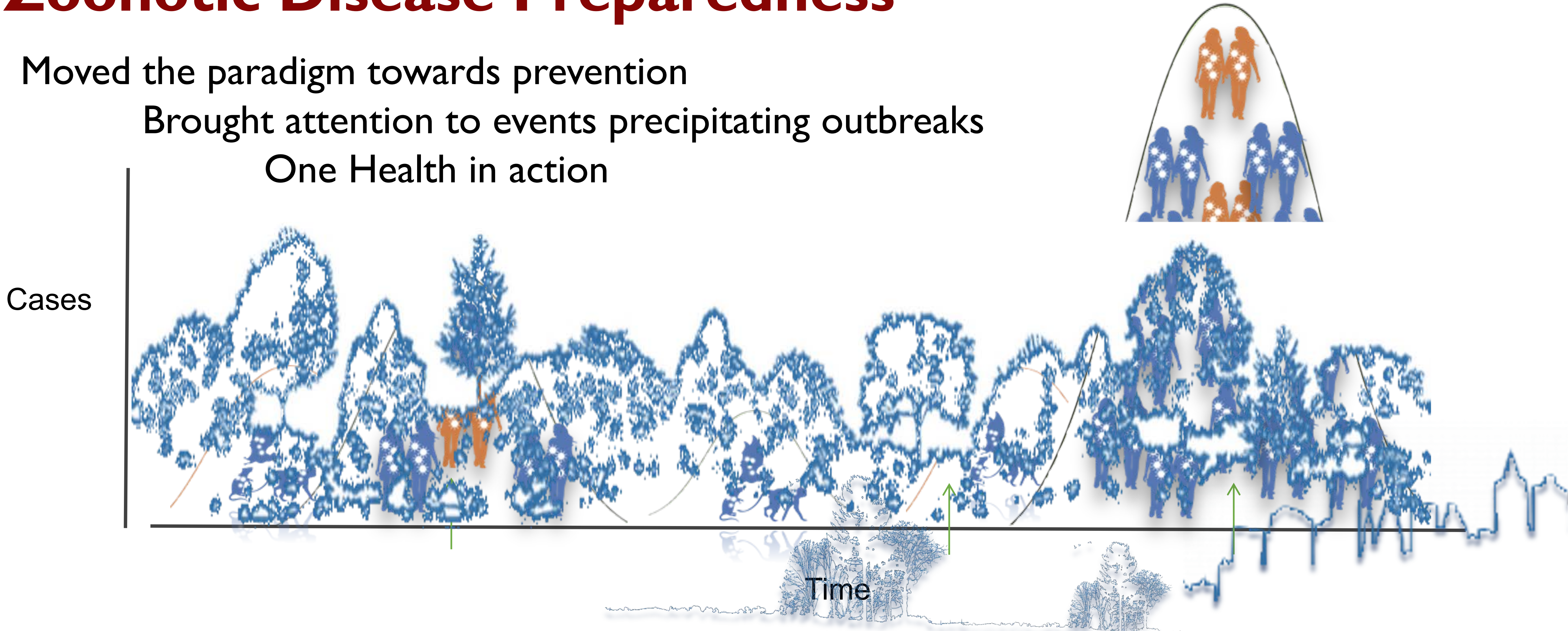
First detection of zoonotic disease outbreaks

Zoonotic Disease Preparedness

Moved the paradigm towards prevention

Brought attention to events precipitating outbreaks

One Health in action



Virus Detection and Discovery

- Overview of PREDICT strategy
- Summary of virus findings
- Highlights from priority virus families

Virus Detection and Discovery

- **Overview of PREDICT strategy**
- Summary of virus findings
- Highlights from priority virus families

Casting a Wide Net

①	**Sample**	wildlife, livestock, humans
②	**Detect**	consensus PCR - corona, filo, paramyxo, influenza (other)
③	**Characterize**	full-genome sequencing
④	**Assess risk**	experimental (specific viruses); eco-epidemiological (broad)

Virus Detection and Discovery

- Overview of PREDICT strategy
- **Summary of virus findings**
- Highlights from priority virus families

Viral Family	Number of known viruses found in P1	Number of novel viruses found in P1	Number of additional known viruses found in P2	Number of additional novel viruses found in P2	Total
Coronaviruses	37	73	29	40	**179**
Paramyxoviruses	13	79	14	104	**210**
Filoviruses	0	0	2	1	**3**
Influenza viruses	1	0	1	0	**2**
Influenza virus subtypes	1	1	10	0	**12**
Flaviviruses	1	5	7	1	**14**

Country	Total	Filo	Corona	Paramyxo	Influenza	Flavi
Bangladesh	54		23	29	1	1
Bolivia	9		3	4	1	1
Brazil	11		10	1		
Cambodia	33		18	11	2	2
Cameroon	46		22	21	2	1
China	76		42	33	1	
DR Congo	11	1	8	1	1	
Egypt	11		3	7	1	
Ethiopia	11		5	4	2	
Gabon	5		2	1		2
Ghana	16		6	8	2	
Guinea	16	1	10	5		
India	6		1	3	1	1
Indonesia	37		11	23	2	1
Ivory Coast	3		2		1	
Jordan	12		11	1		
Kenya	2		2			
Lao PDR	13		8	3	1	1
Liberia	1	1				
Malaysia	39		19	17	1	1
Mexico	12		10	2		
Mongolia	1				1	
Myanmar	10		7	2	1	
Nepal	15		8	5	1	1
Peru	2		2			
Republic of Congo	21		13	6		2
Rwanda	20		14	4	2	
Senegal	14		5	7	2	
Sierra Leone	6	2	2	2		
South Sudan	3		1	2		
Tanzania	36		15	19	2	
Thailand	57		25	28	2	2
Uganda	16		10	5	1	
Vietnam	29		14	12	2	1

Priority Virus Families

Human 16, Domestic species 14

Virus Detection and Discovery

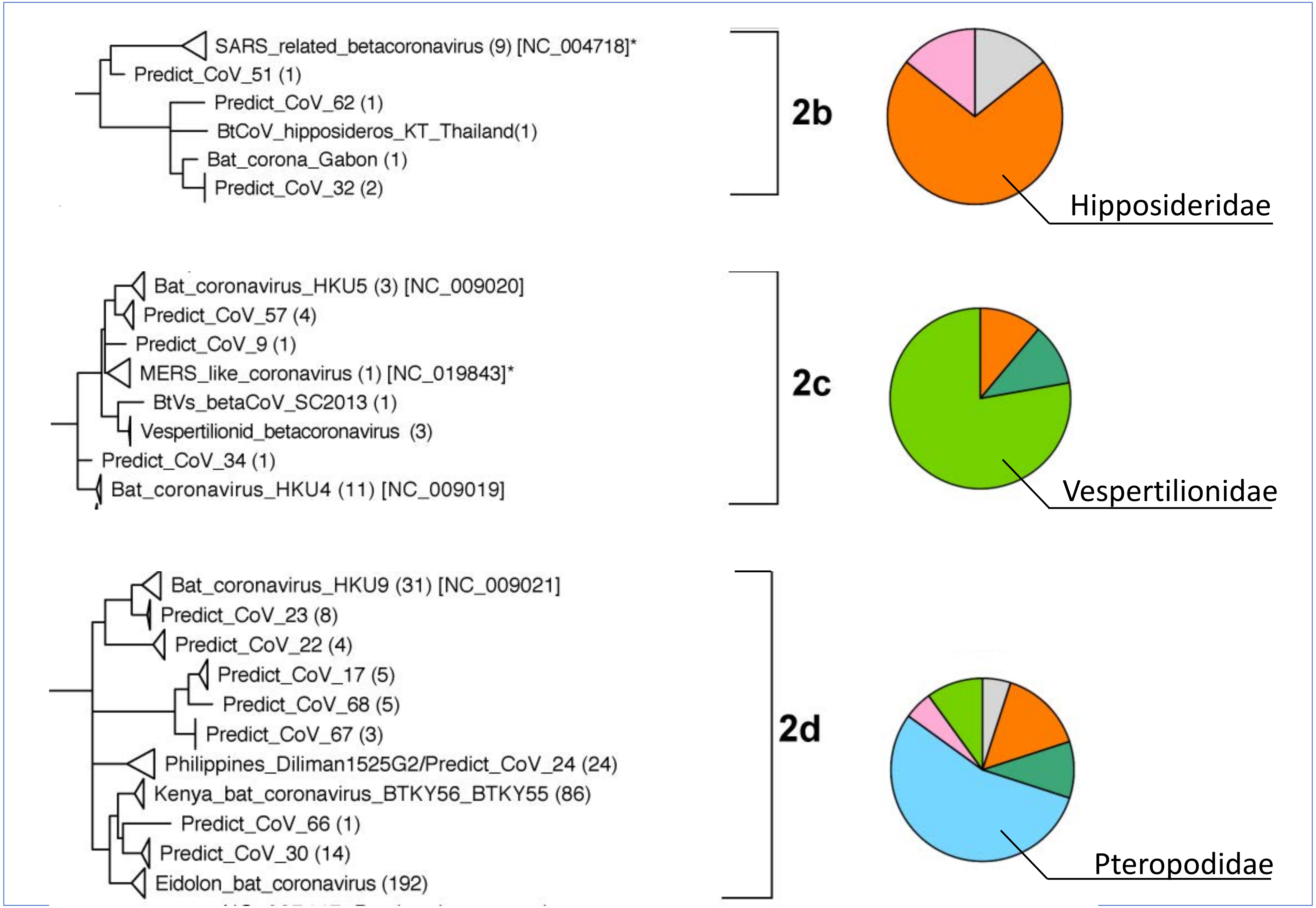
- Overview of PREDICT strategy
- Summary of virus findings
- **Highlights from priority virus families**

Coronaviruses

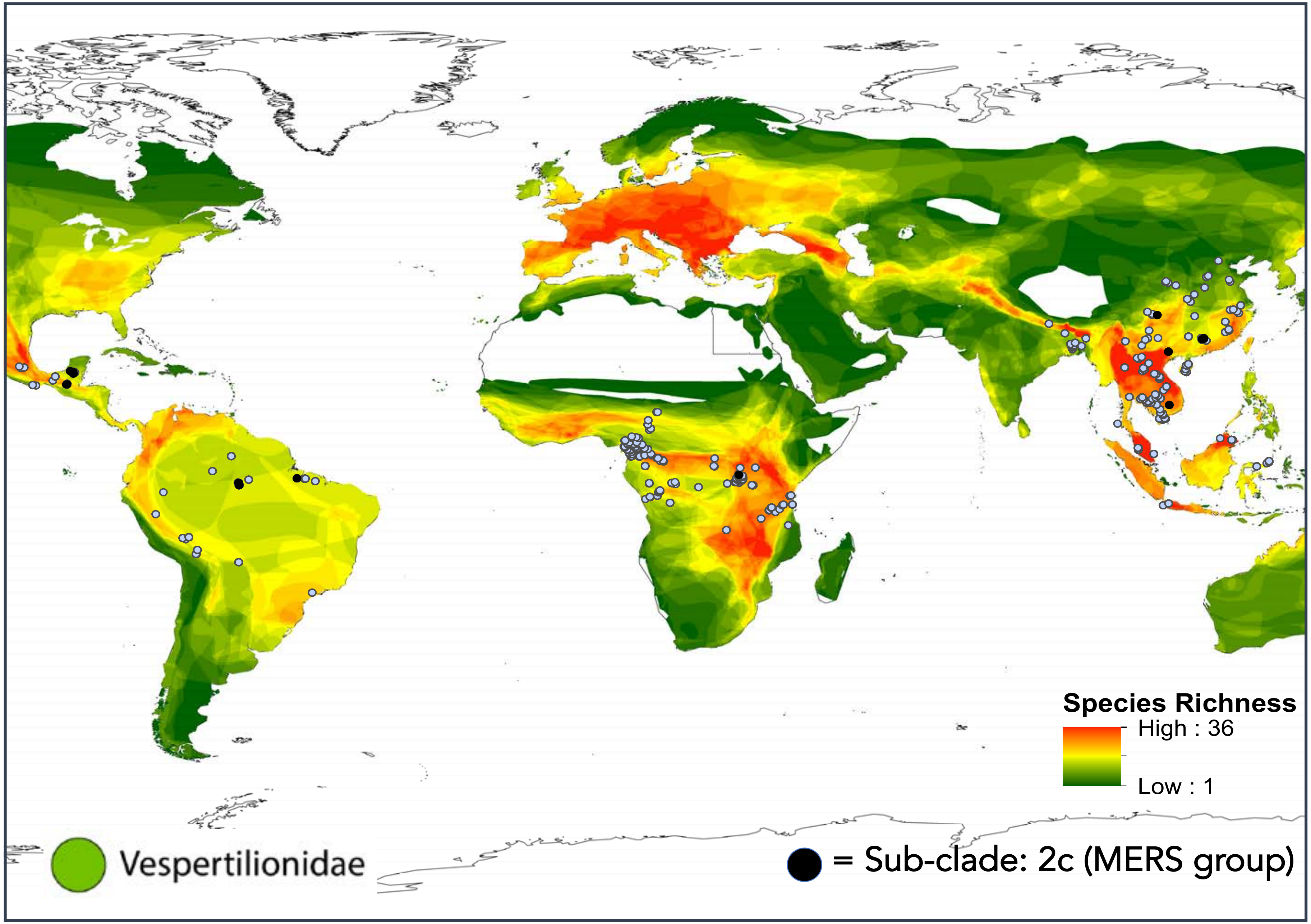
Coronavirus Results

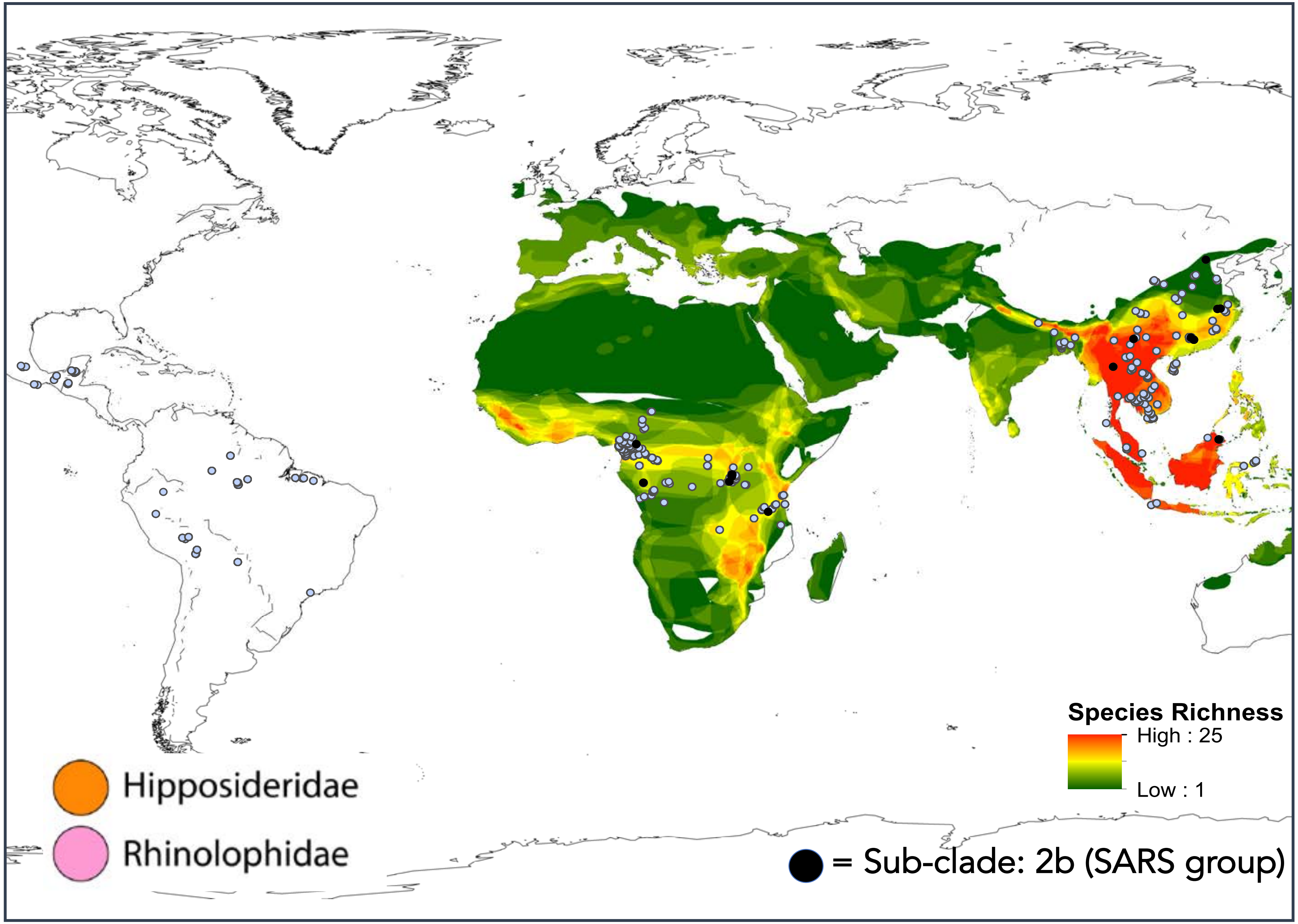
Taxa	# tested	# Pos	# Neg	% Pos
Bats	35857	2929	32928	8.2
Rodents and Shrews	17844	814	17030	4.6
Non-human Primates	9527	4	9523	0.04
Humans	16101	71	16030	0.4
Total	**79329**	**3818**	**75511**	

based on number of individuals

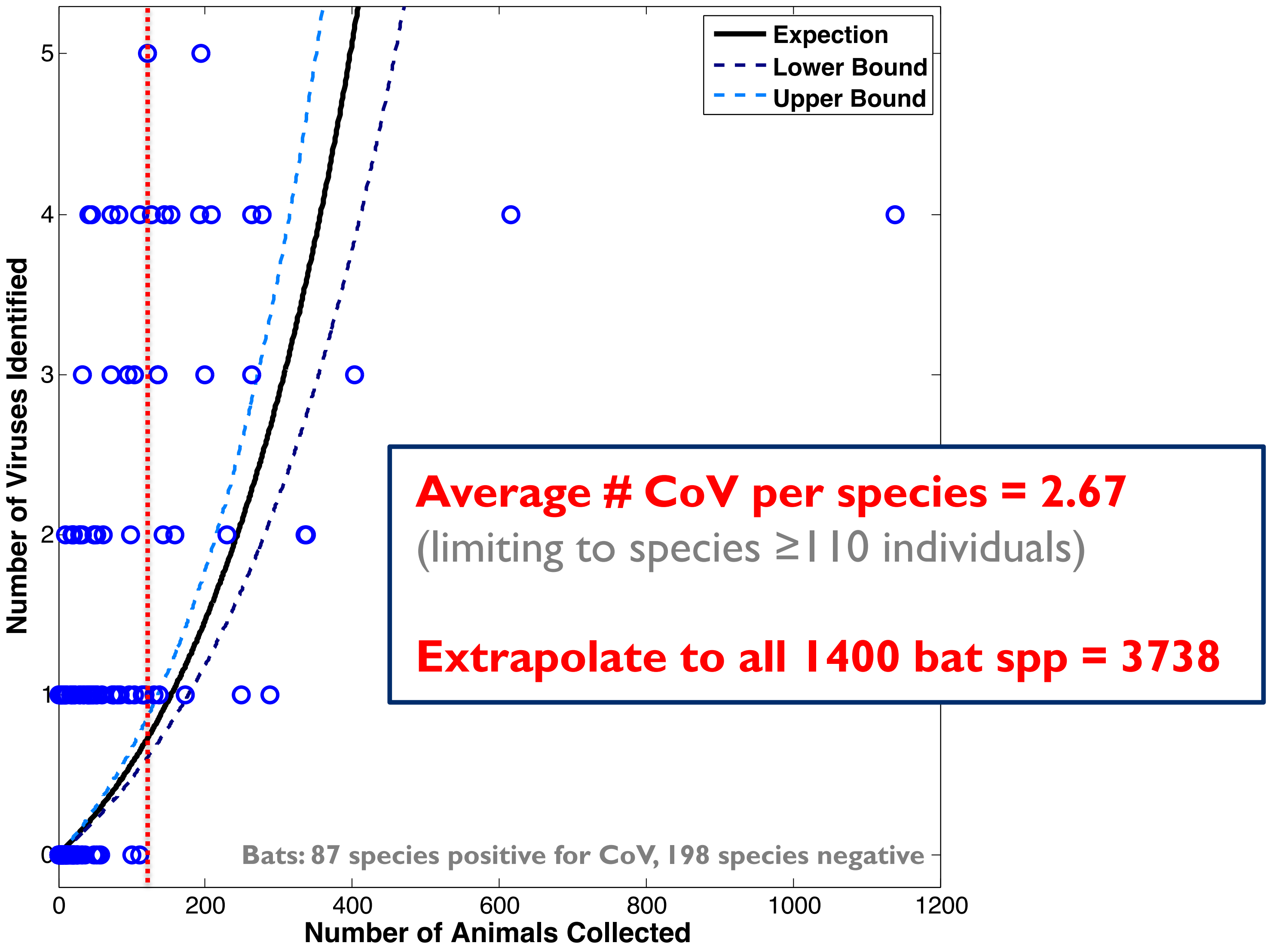


SARS_related_betacoronavirus (9) [NC_004718]*
Predict_CoV_51 (1)
Predict_CoV_62 (1)
BtCoV_hipposideros_KT_Thailand(1)
Bat_corona_Gabon (1)
Predict_CoV_32 (2)
2b
Hipposideridae
Bat_coronavirus_HKU5 (3) [NC_009020]
Predict_CoV_57 (4)
Predict_CoV_9 (1)
MERS_like_coronavirus (1) [NC_019843]*
BtVs_betaCoV_SC2013 (1)
Vespertilionid_betacoronavirus (3)
Predict_CoV_34 (1)
Bat_coronavirus_HKU4 (11) [NC_009019]
2c
Vespertilionidae
Bat_coronavirus_HKU9 (31) [NC_009021]
Predict_CoV_23 (8)
Predict_CoV_22 (4)
Predict_CoV_17 (5)
Predict_CoV_68 (5)
Predict_CoV_67 (3)
Philippines_Diliman1525G2/Predict_CoV_24 (24)
Kenya_bat_coronavirus_BTKY56_BTKY55 (86)
Predict_CoV_66 (1)
Predict_CoV_30 (14)
Eidolon_bat_coronavirus (192)
2d
Pteropodidae


Species Richness
High : 36
Low : 1
Vespertilionidae
= Sub-clade: 2c (MERS group)

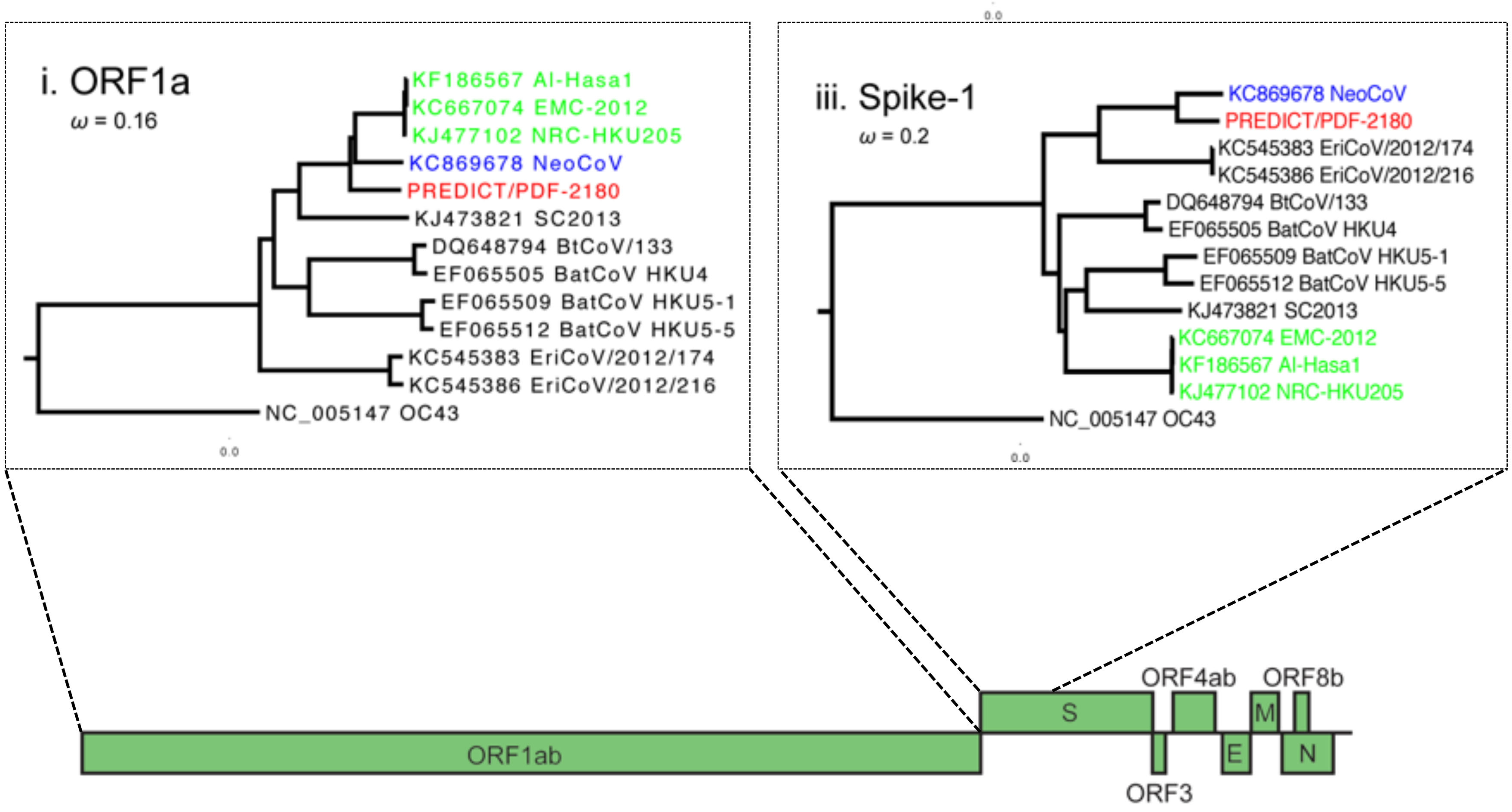

Species Richness
High : 25
Low : 1
Hipposideridae
Rhinolophidae
= Sub-clade: 2b (SARS group)

There are >3738 coronaviruses in bats



MERS-CoV is a recombinant

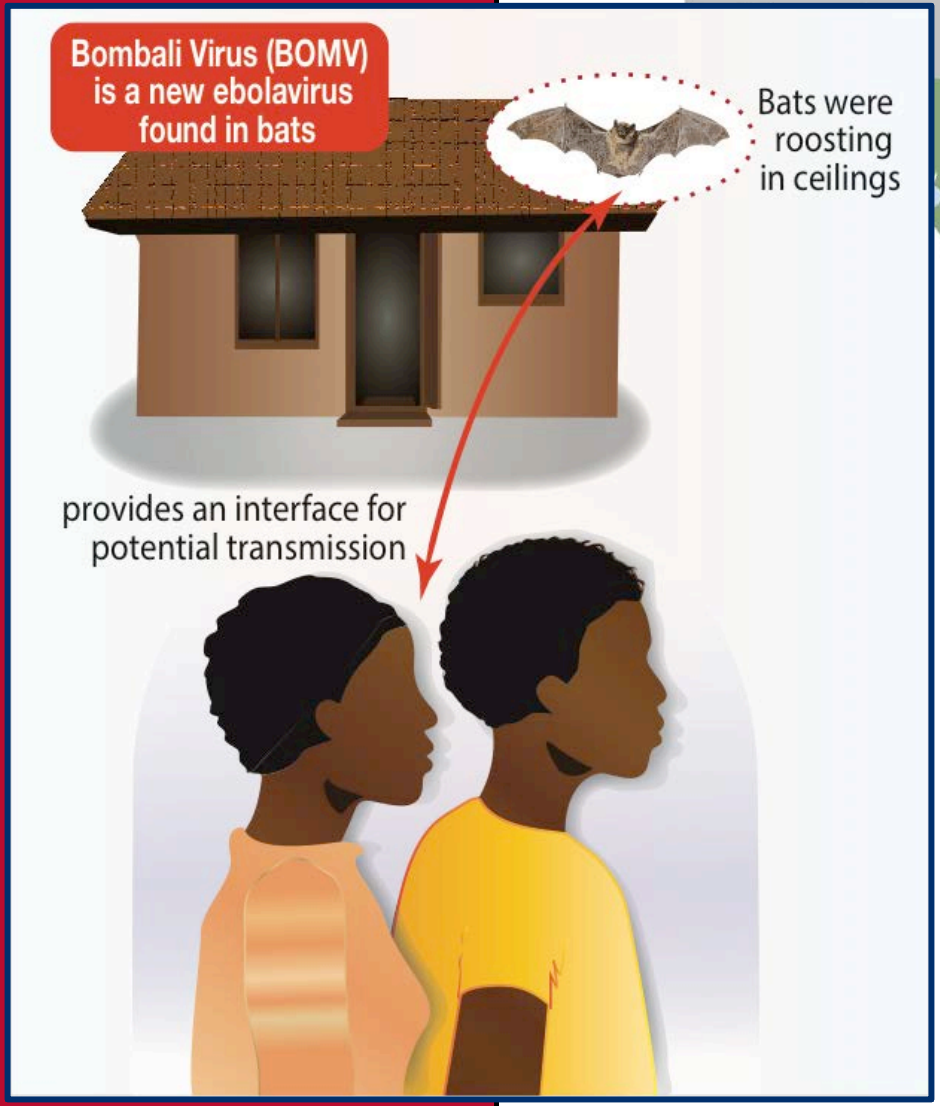
Recombination is an evolutionary driver of host-switching

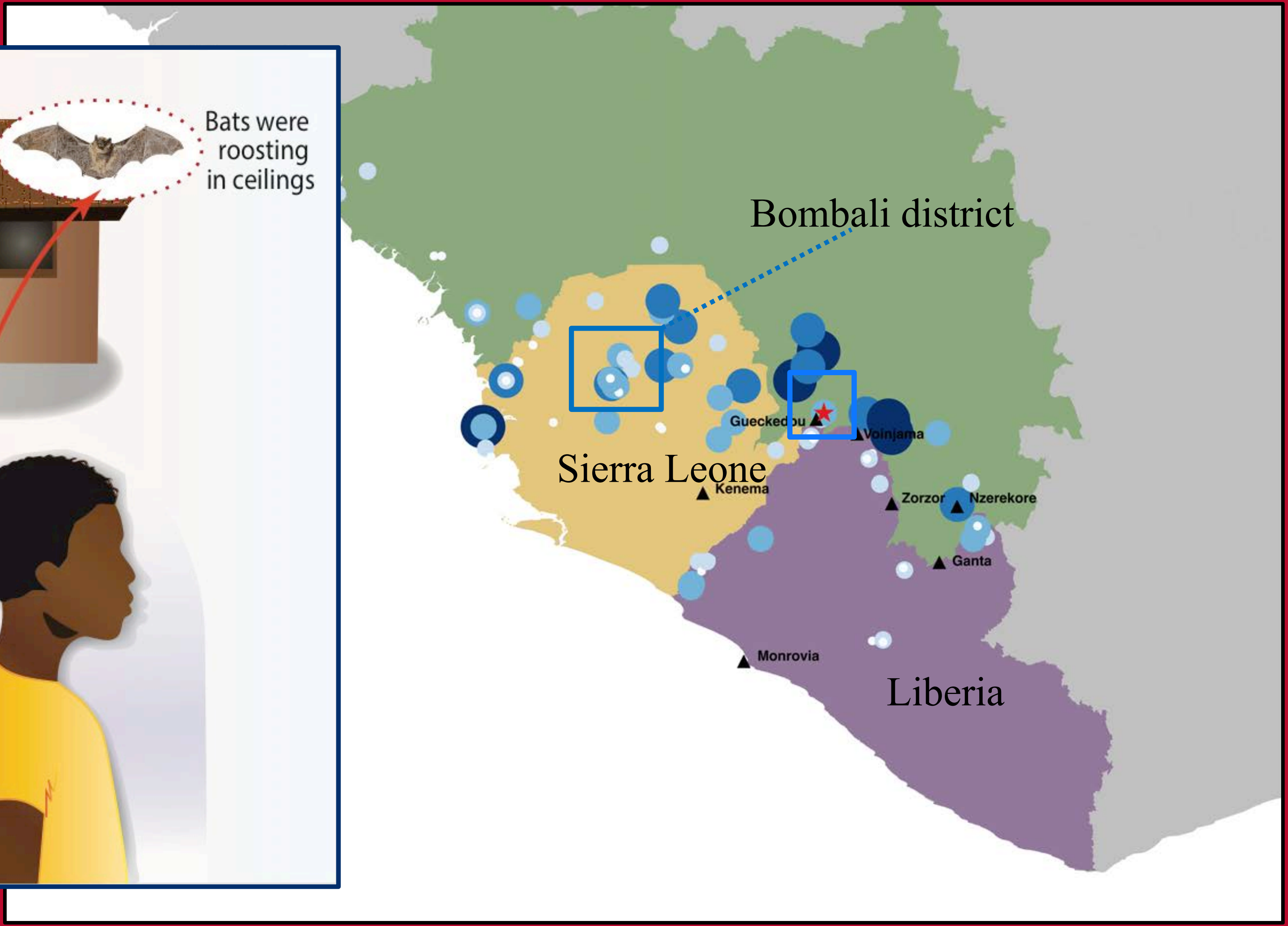


Coronaviruses – summary of major findings

- Bats are a major reservoir of CoVs
- Biogeography of CoVs is predictable based on host species
- Spike recombination is an important driver of host switching

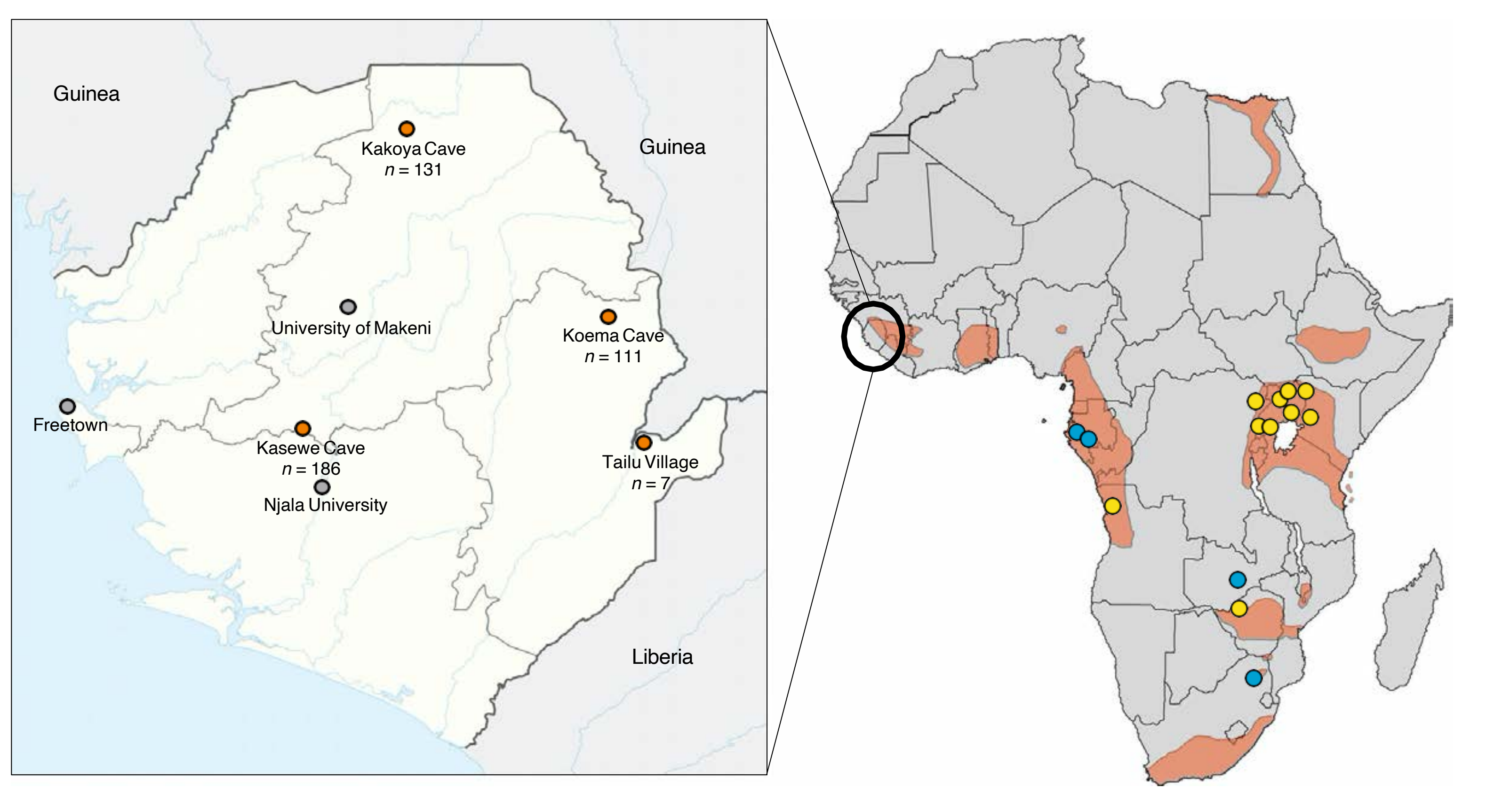
Filoviruses


Bombali Virus (BOMV) is a new ebolavirus found in bats
Bats were roosting in ceilings
provides an interface for potential transmission

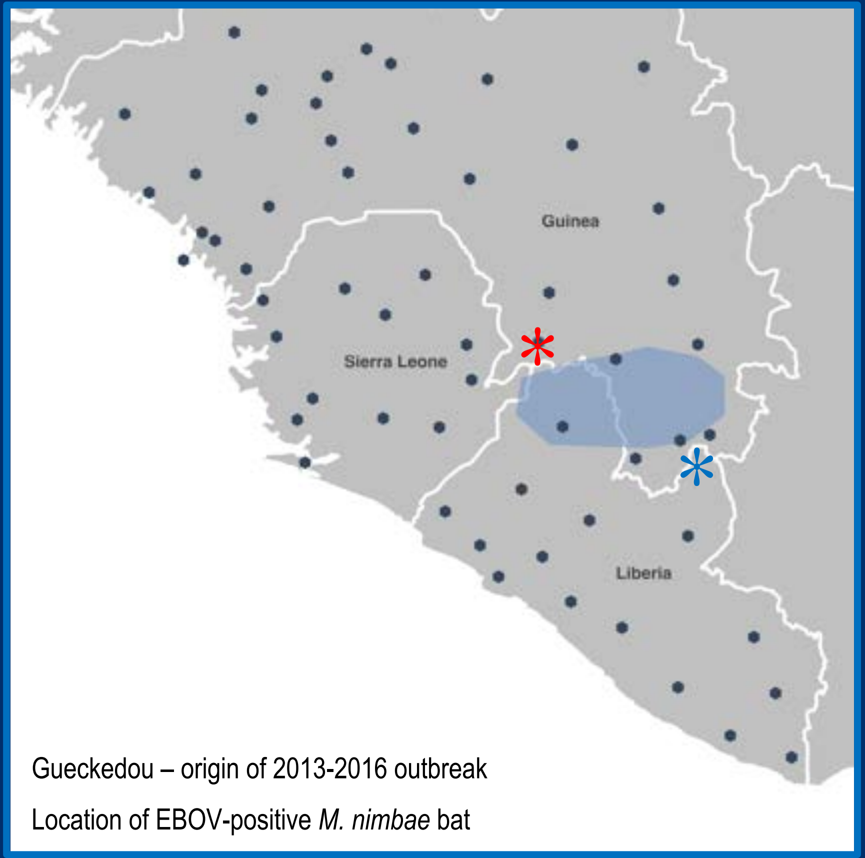

Bombali district
Sierra Leone
Liberia
Kenema
Monrovia
Voinjama
Zorzor
Nzerekore
Ganta

Marburg Virus in Sierra Leone

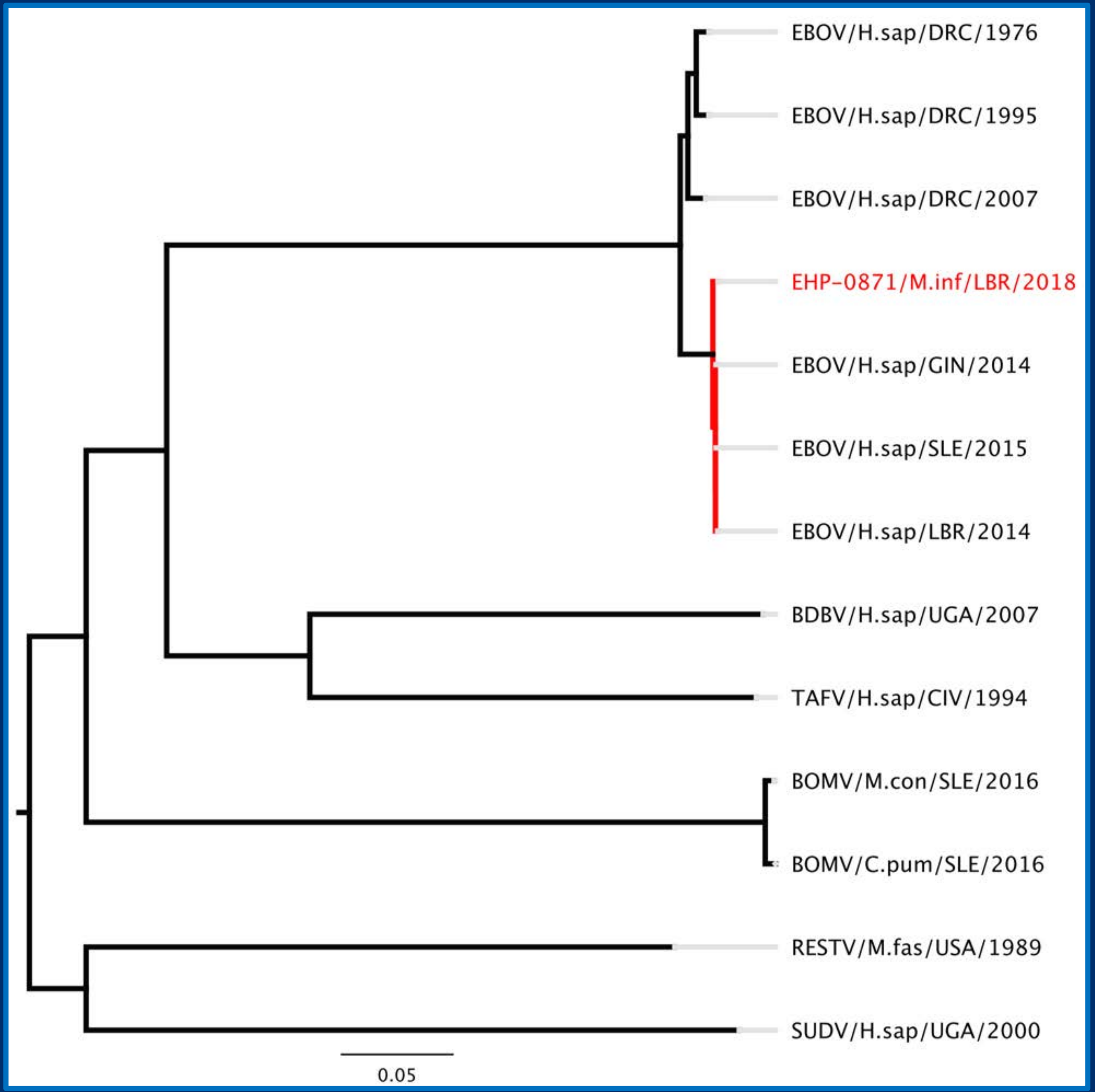
Rousettus aegyptiacus



M. nimbae

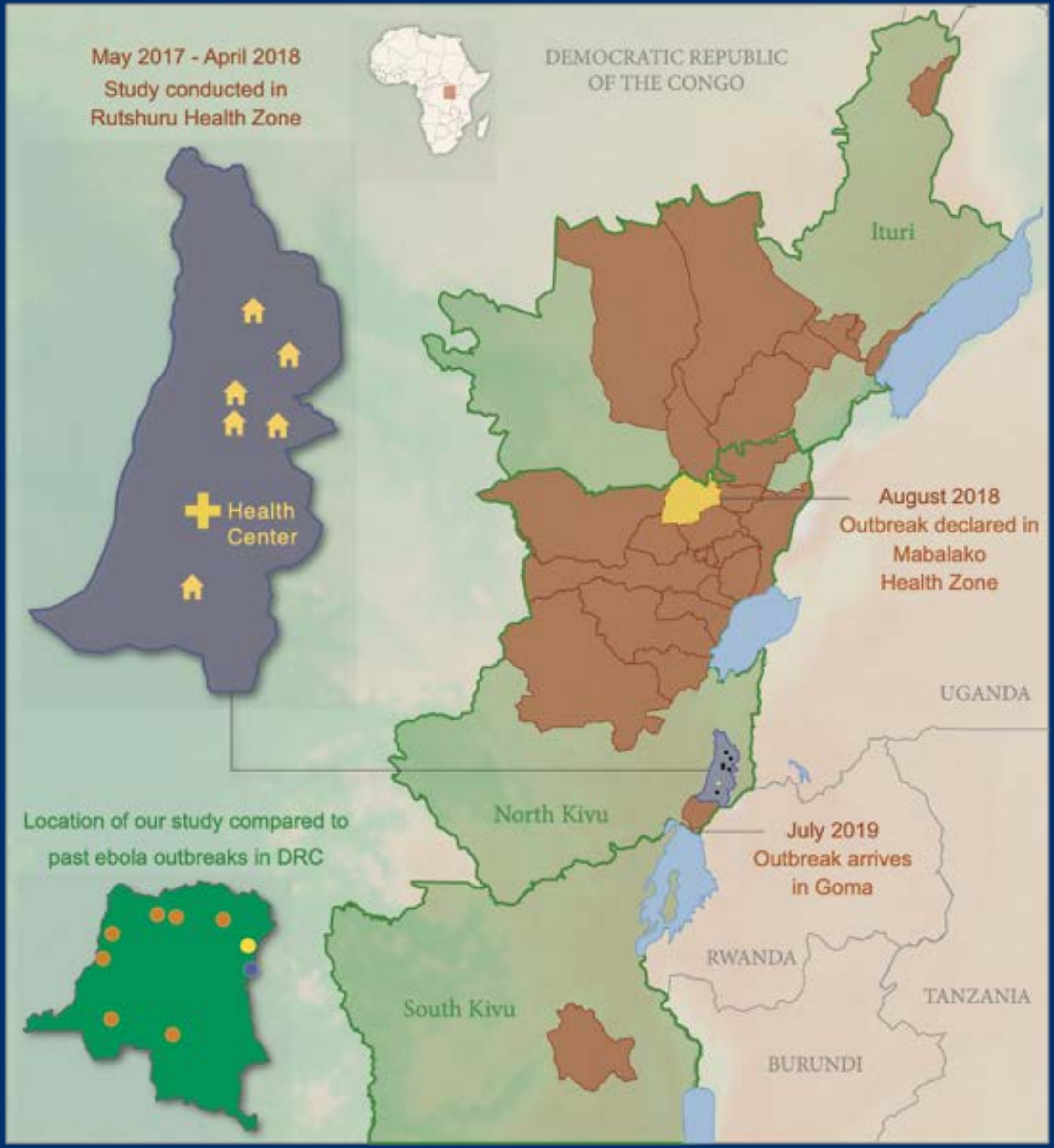


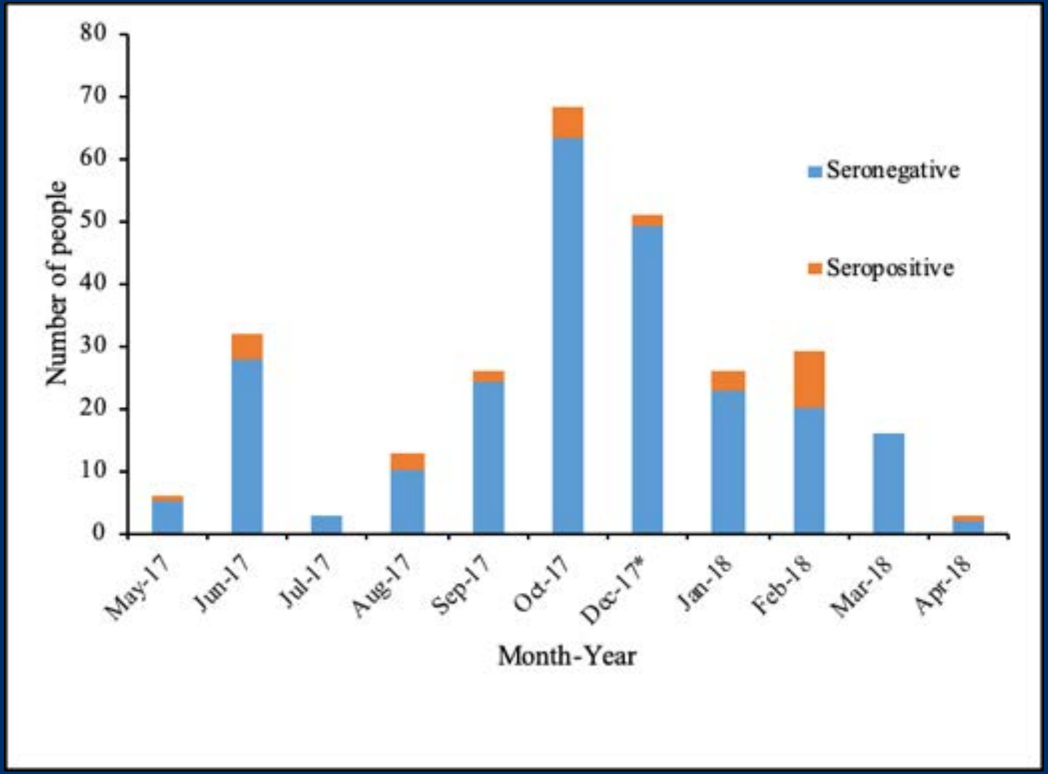
Guinea
Sierra Leone
Liberia
Gueckedou – origin of 2013-2016 outbreak
Location of EBOV-positive *M. nimbae* bat



EBOV/H.sap/DRC/1976
EBOV/H.sap/DRC/1995
EBOV/H.sap/DRC/2007
EHP-0871/M.inf/LBR/2018
EBOV/H.sap/GIN/2014
EBOV/H.sap/SLE/2015
EBOV/H.sap/LBR/2014
BDBV/H.sap/UGA/2007
TAFV/H.sap/CIV/1994
BOMV/M.con/SLE/2016
BOMV/C.pum/SLE/2016
RESTV/M.fas/USA/1989
SUDV/H.sap/UGA/2000
0.05

Ebolaviruses in Eastern DRC

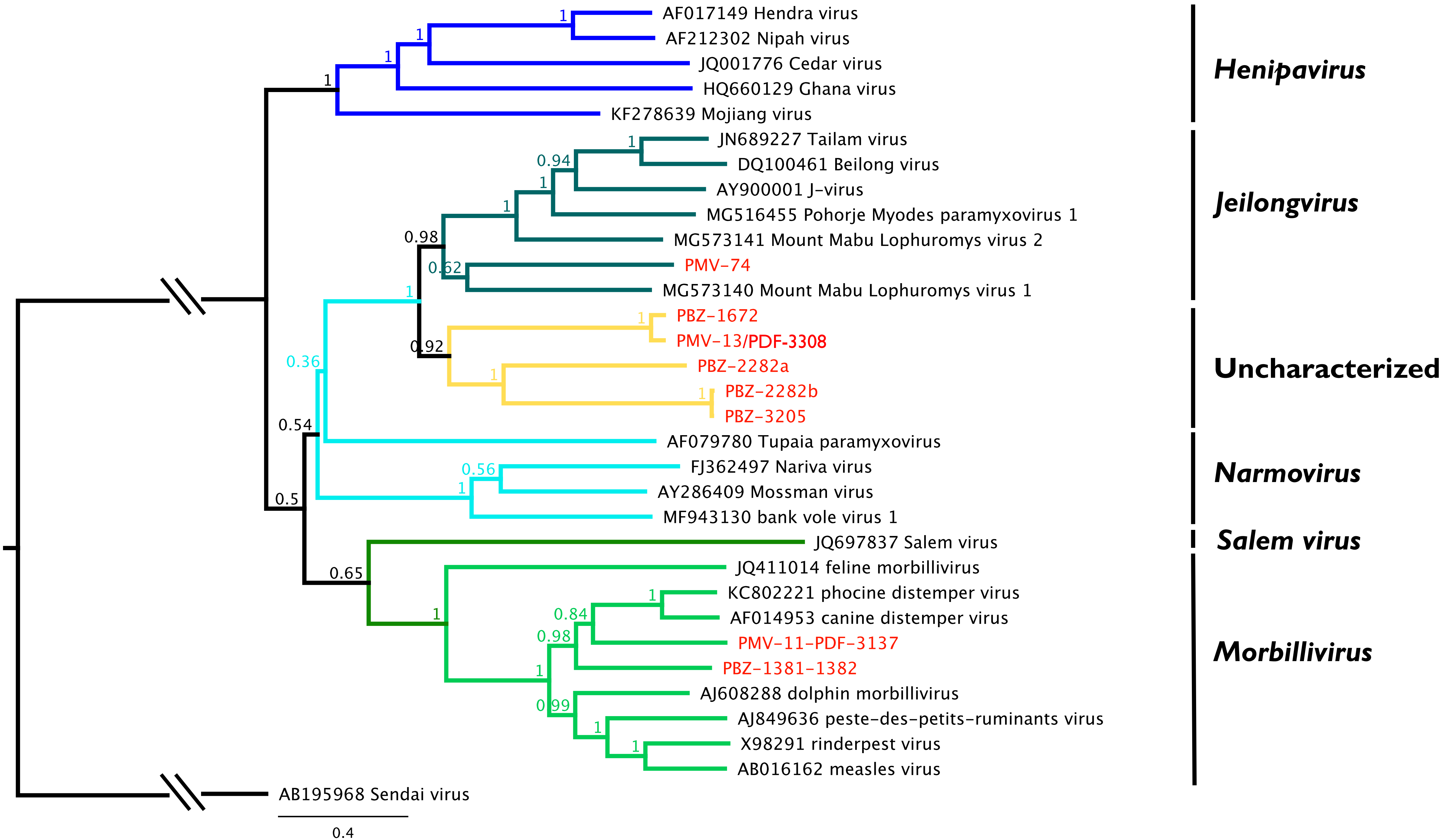


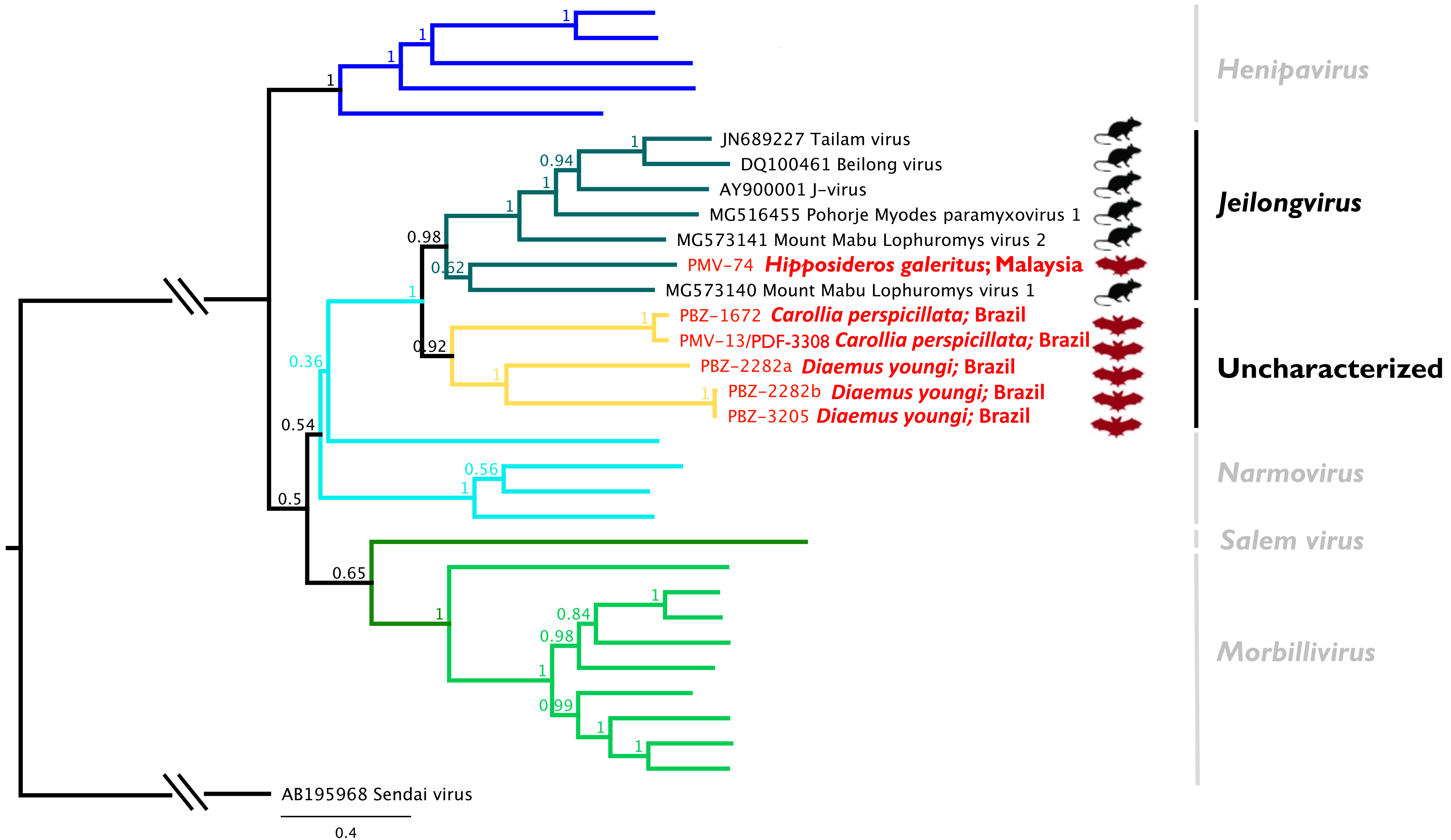


Filoviruses – summary of major findings

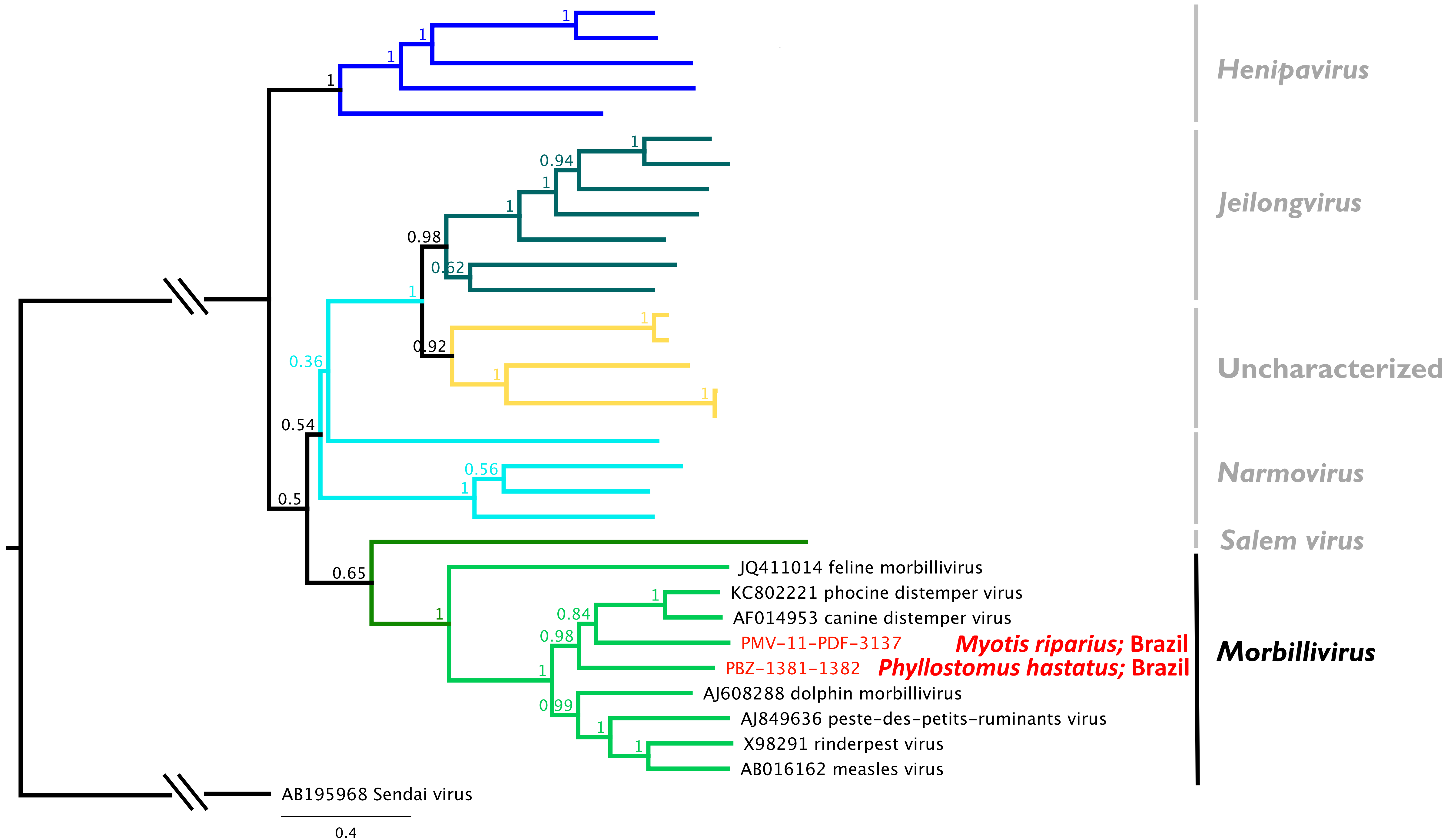
- Discovery of a novel ebolavirus in Sierra Leone
- Expansion of known range for Marburg virus
- Detection of Ebola virus in *M.nimbae* bat in Liberia

Paramyxoviruses


AF017149 Hendra virus
AF212302 Nipah virus
JQ001776 Cedar virus
HQ660129 Ghana virus
KF278639 Mojiang virus
JN689227 Tailam virus
DQ100461 Beilong virus
AY900001 J-virus
MG516455 Pohorje Myodes paramyxovirus 1
MG573141 Mount Mabu Lophuromys virus 2
PMV-74
MG573140 Mount Mabu Lophuromys virus 1
PBZ-1672
PMV-13/PDF-3308
PBZ-2282a
PBZ-2282b
PBZ-3205
AF079780 Tupaia paramyxovirus
FJ362497 Nariva virus
AY286409 Mossman virus
MF943130 bank vole virus 1
JQ697837 Salem virus
JQ411014 feline morbillivirus
KC802221 phocine distemper virus
AF014953 canine distemper virus
PMV-11-PDF-3137
PBZ-1381-1382
AJ608288 dolphin morbillivirus
AJ849636 peste-des-petits-ruminants virus
X98291 rinderpest virus
AB016162 measles virus
AB195968 Sendai virus
0.4
Henipavirus
Jeilongvirus
Uncharacterized
Narmovirus
Salem virus
Morbillivirus



JN689227 Tailam virus
DQ100461 Beilong virus
AY900001 J-virus
MG516455 Pohorje Myodes paramyxovirus 1
MG573141 Mount Mabu Lophuromys virus 2
PMV-74 *Hipposideros galeritus*; Malaysia
MG573140 Mount Mabu Lophuromys virus 1
PBZ-1672 *Carollia perspicillata*; Brazil
PMV-13/PDF-3308 *Carollia perspicillata*; Brazil
PBZ-2282a *Diaemus youngi*; Brazil
PBZ-2282b *Diaemus youngi*; Brazil
PBZ-3205 *Diaemus youngi*; Brazil
AB195968 Sendai virus
0.4
Henipavirus
Jeilongvirus
Uncharacterized
Narmovirus
Salem virus
Morbillivirus
1
1
1
1
0.94
1
1
0.98
0.62
1
1
0.92
1
1
0.36
0.54
0.56
1
0.5
0.65
1
1
0.84
0.98
1
0.99
1
1


Henipavirus
Jeilongvirus
Uncharacterized
Narmovirus
Salem virus
Morbillivirus
JQ411014 feline morbillivirus
KC802221 phocine distemper virus
AF014953 canine distemper virus
PMV-11-PDF-3137
Myotis riparius; Brazil
PBZ-1381-1382
Phyllostomus hastatus; Brazil
AJ608288 dolphin morbillivirus
AJ849636 peste-des-petits-ruminants virus
X98291 rinderpest virus
AB016162 measles virus
AB195968 Sendai virus
0.4

Paramyxoviruses – summary of major findings

- Expansion of known diversity (e.g., entirely new genera)
- Discovery of multiple bat morbilliviruses
- First rescue of any bat paramyxovirus directly from sequence

Laboratory Capacity and COVID-19 Response

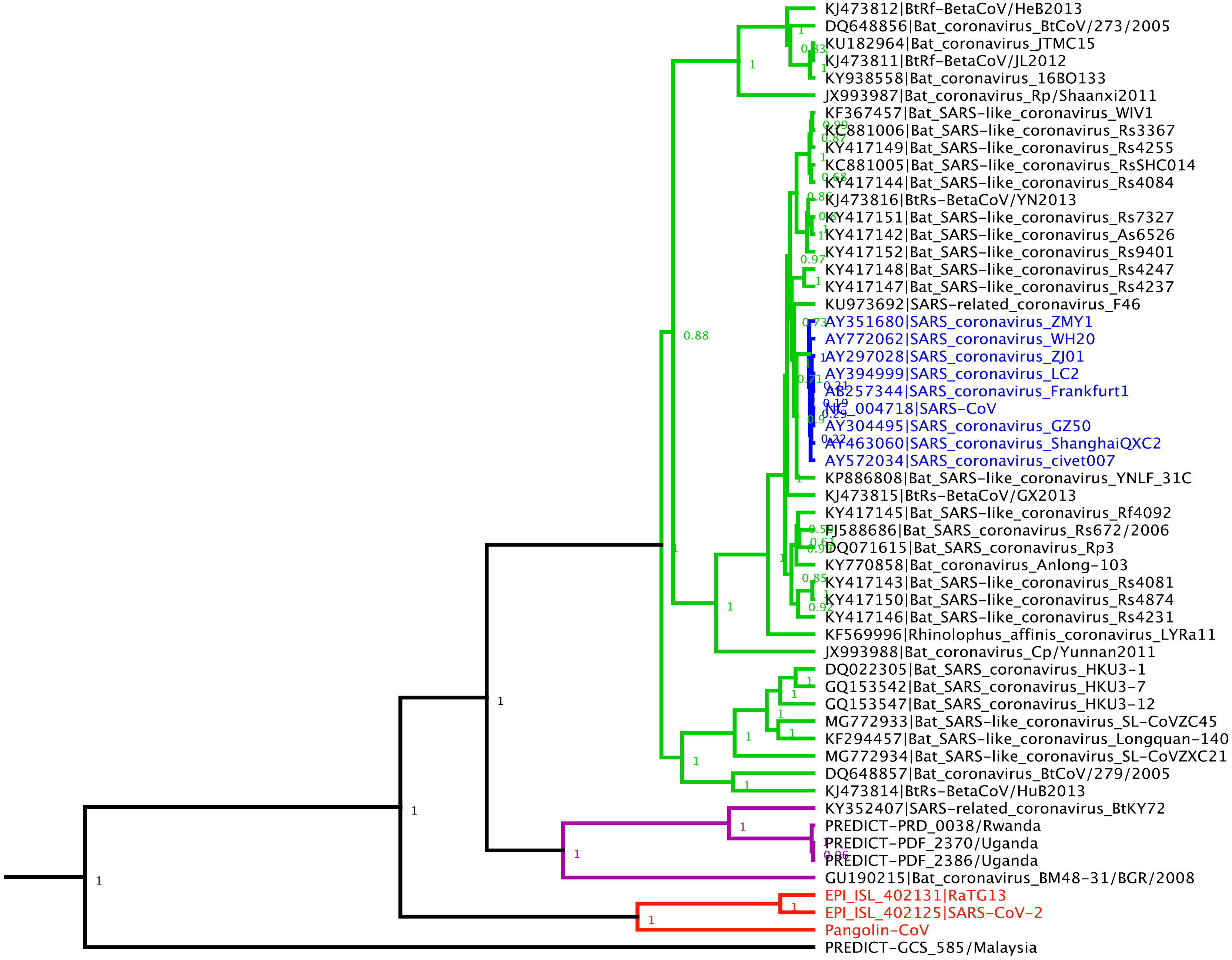
PREDICT improved testing capacity in 67 labs in 36 countries

Built a network of linkages between laboratories, countries and government ministries

Laboratories have additional tools and the ability to detect newly emerging viruses when assays or sequences do not yet exist

Importance of these skills was underscored following the emergence of SARS CoV-2 in China

Teams in Southeast Asia able to call on the PREDICT network to share experience using PREDICT assays to detect the new virus


KJ473812|BtRf-BetaCoV/HeB2013
DQ648856|Bat_coronavirus_BtCoV/273/2005
KU182964|Bat_coronavirus_JTMC15
KJ473811|BtRf-BetaCoV/JL2012
KY938558|Bat_coronavirus_16BO133
JX993987|Bat_coronavirus_Rp/Shaanxi2011
KF367457|Bat_SARS-like_coronavirus_WIV1
KC881006|Bat_SARS-like_coronavirus_Rs3367
KY417149|Bat_SARS-like_coronavirus_Rs4255
KC881005|Bat_SARS-like_coronavirus_RsSHC014
KY417144|Bat_SARS-like_coronavirus_Rs4084
KJ473816|BtRs-BetaCoV/YN2013
KY417151|Bat_SARS-like_coronavirus_Rs7327
KY417142|Bat_SARS-like_coronavirus_As6526
KY417152|Bat_SARS-like_coronavirus_Rs9401
KY417148|Bat_SARS-like_coronavirus_Rs4247
KY417147|Bat_SARS-like_coronavirus_Rs4237
KU973692|SARS-related_coronavirus_F46
AY351680|SARS_coronavirus_ZMY1
AY772062|SARS_coronavirus_WH20
AY297028|SARS_coronavirus_ZJ01
AY394999|SARS_coronavirus_LC2
AB257344|SARS_coronavirus_Frankfurt1
NC_004718|SARS-CoV
AY304495|SARS_coronavirus_GZ50
AY463060|SARS_coronavirus_ShanghaiQXC2
AY572034|SARS_coronavirus_civet007
KP886808|Bat_SARS-like_coronavirus_YNLF_31C
KJ473815|BtRs-BetaCoV/GX2013
KY417145|Bat_SARS-like_coronavirus_Rf4092
FJ588686|Bat_SARS_coronavirus_Rs672/2006
DQ071615|Bat_SARS_coronavirus_Rp3
KY770858|Bat_coronavirus_Anlong-103
KY417143|Bat_SARS-like_coronavirus_Rs4081
KY417150|Bat_SARS-like_coronavirus_Rs4874
KY417146|Bat_SARS-like_coronavirus_Rs4231
KF569996|Rhinolophus_affinis_coronavirus_LYRa11
JX993988|Bat_coronavirus_Cp/Yunnan2011
DQ022305|Bat_SARS_coronavirus_HKU3-1
GQ153542|Bat_SARS_coronavirus_HKU3-7
GQ153547|Bat_SARS_coronavirus_HKU3-12
MG772933|Bat_SARS-like_coronavirus_SL-CoVZC45
KF294457|Bat_SARS-like_coronavirus_Longquan-140
MG772934|Bat_SARS-like_coronavirus_SL-CoVZXC21
DQ648857|Bat_coronavirus_BtCoV/279/2005
KJ473814|BtRs-BetaCoV/HuB2013
KY352407|SARS-related_coronavirus_BtKY72
PREDICT-PRD_0038/Rwanda
PREDICT-PDF_2370/Uganda
PREDICT-PDF_2386/Uganda
GU190215|Bat_coronavirus_BM48-31/BGR/2008
EPI_ISL_402131|RaTG13
EPI_ISL_402125|SARS-CoV-2
Pangolin-CoV
PREDICT-GCS_585/Malaysia
0.88

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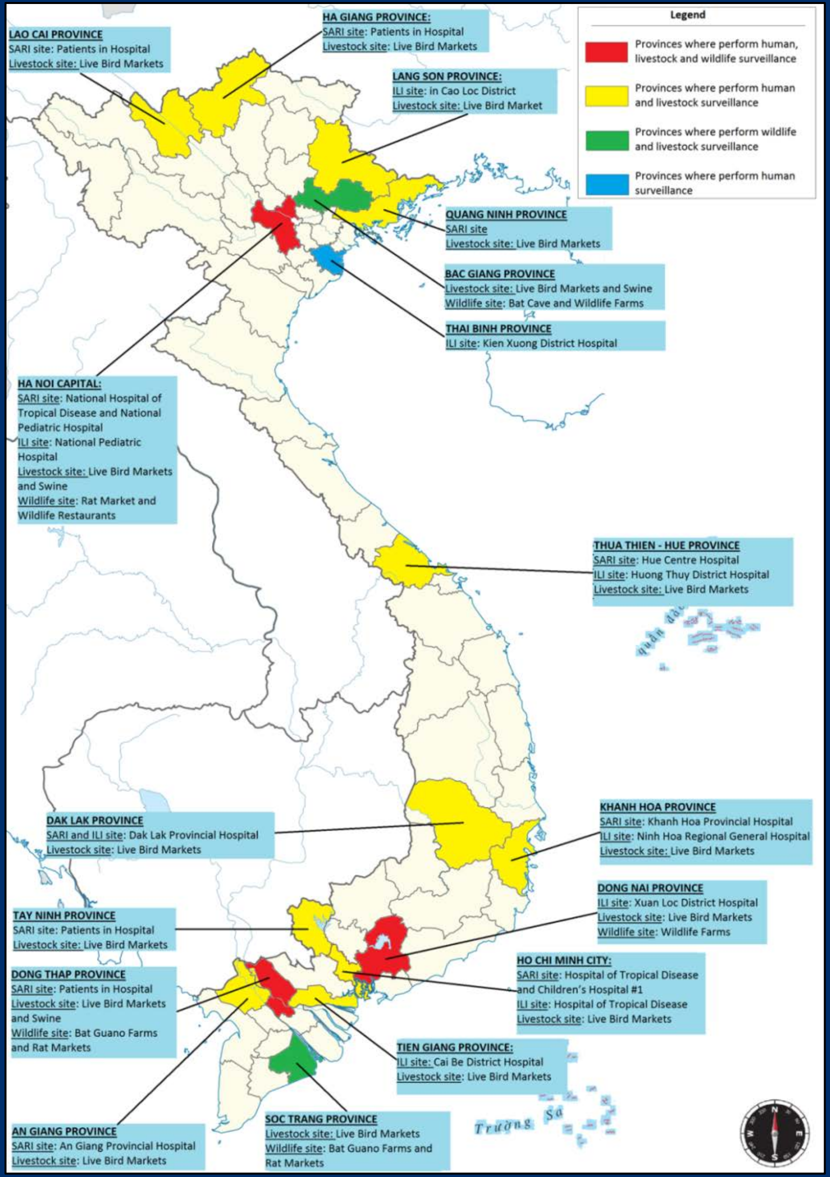
Coordinated Surveillance for Influenza and Viruses with Pandemic Potential – LISN (Longitudinal Influenza Surveillance Network) in Viet Nam

Amanda Fine, Wildlife Conservation Society

WCS



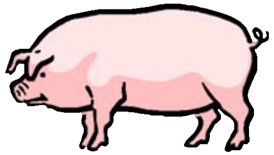
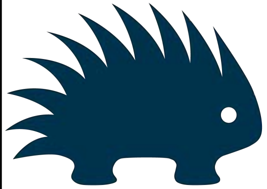
Mapping of human, livestock, and wildlife surveillance planned at 1st multi-sector LISN 'One Health' coordination workshop in Hanoi

Coordinated 'One Health' Surveillance for Influenza and Other Viruses with Pandemic Potential ("LISN")

The Vision:

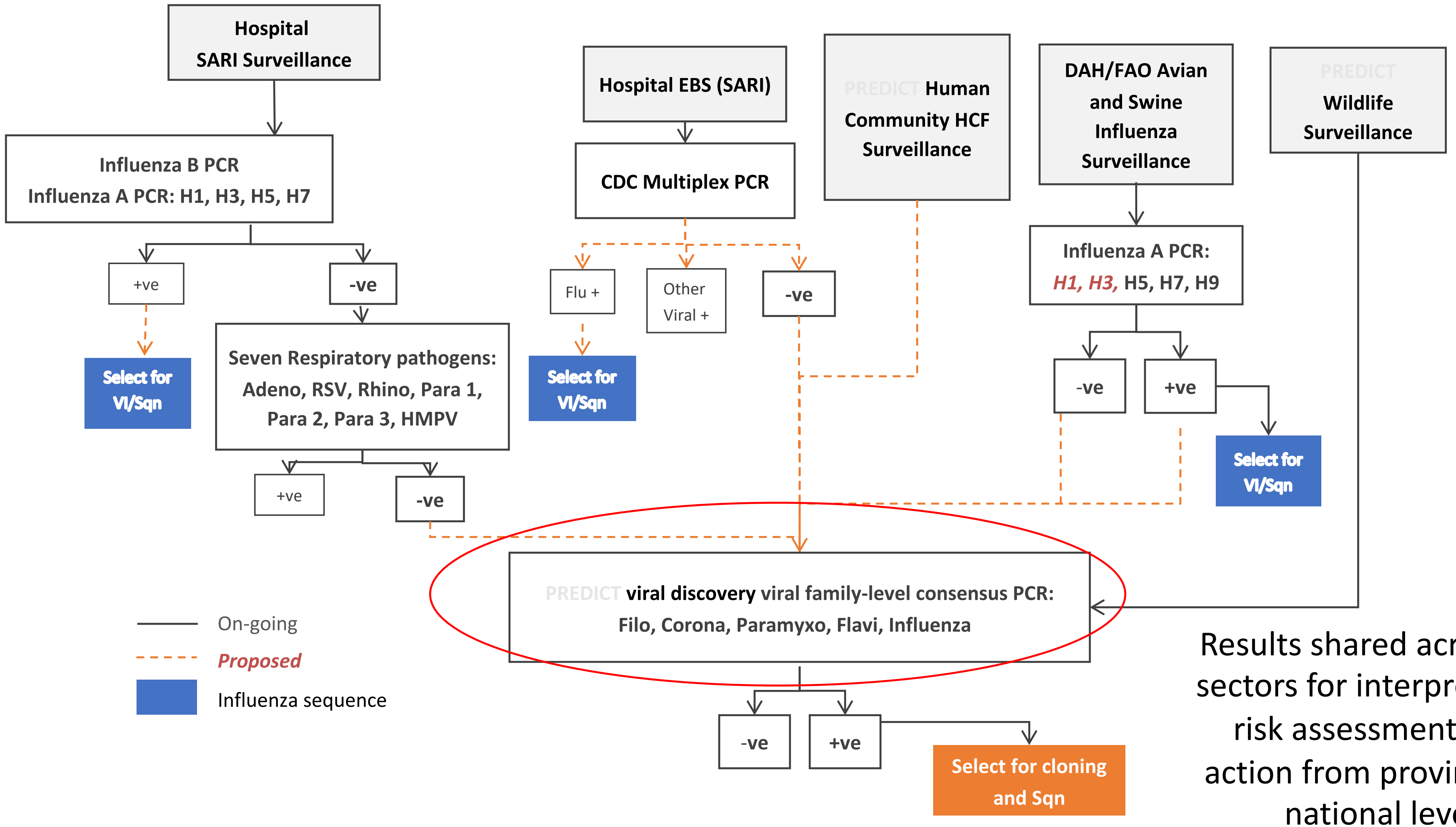
1. Alignment of the surveillance localities, sampling time and laboratory testing algorithm.
2. Monitor and characterize influenza viruses and other viruses with pandemic potential.
3. Regular information sharing, situation analysis, and risk assessment.
4. Coordination of PREDICT-2, FAO/DAH influenza surveillance in poultry and swine, WHO and US CDC SARI and ILI surveillance with GDPM/MoH.

Enhanced Existing Surveillance Systems in Viet Nam for Early Detection of Pandemic Threats

					
Human			**Poultry**	**Pig**	**Wildlife**
Hospital SARI/ILI	Hospital EBS	PREDICT Human Surveillance	DAH/FAO Influenza Surveillance	DAH/FAO Influenza Surveillance	PREDICT Wildlife Surveillance

Coordinated Surveillance "LISN" added
More capacity, more data sharing, more analysis, more knowledge for informed decision making

Coordinated Surveillance and Testing for Influenza and Potential Pandemic Pathogens



Results shared across the sectors for interpretation, risk assessment, and action from provincial to national level

Province (PPMC, Sub-DAH)	Region (NIHE, PI-HCM, RAHO2,6,7)	Country (GDPM, DAH, CITES)
• Quarterly coordination meeting between PPMC and S-DAH to review progress and trouble shoot	• Six monthly meeting to review virological and epidemiological data	• Annual meeting to review risk assessment results and identify potential intervention

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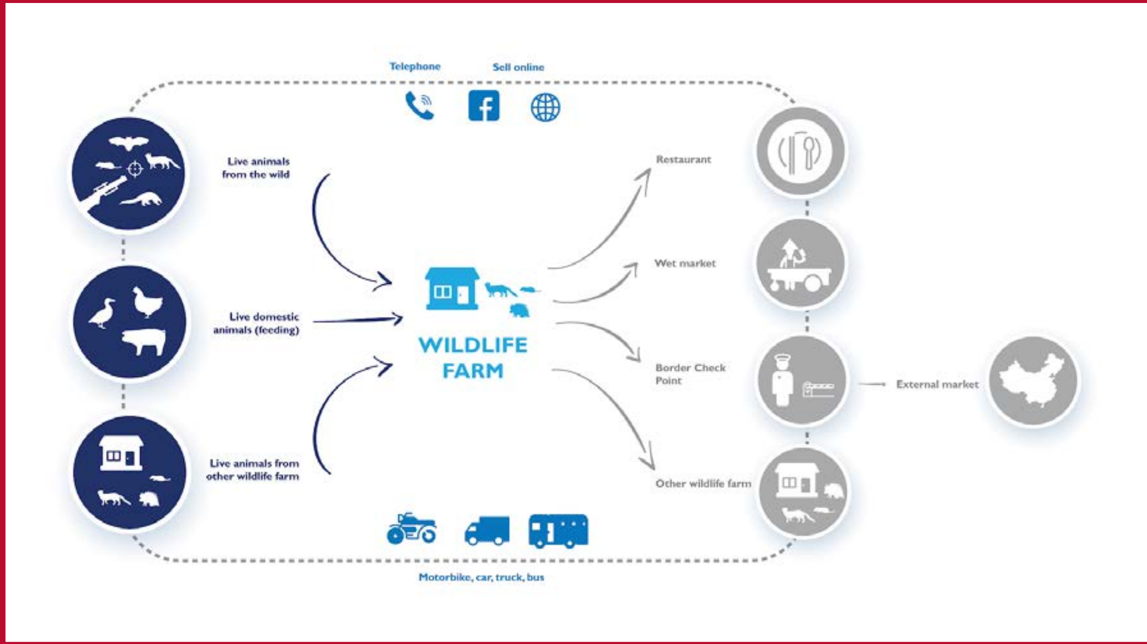
Coordinated 'One Health' Surveillance Results: The Wildlife Farm Interface

Dong Nai Province, Viet Nam



PREDICT Behavioral Risk Surveillance Research Reveals a Complex Wildlife Trade Chain

A masked palm civet on a wildlife farm in Viet Nam

Humans – Concurrent Surveillance Results at the Wildlife Farm Interface

Community Surveillance	Virus	No. of specimens
Influenzas	Influenza A	1
	Influenza B	1
Paramyxoviruses	Strain of Human Parainfluenzavirus 3	1

Hospital Surveillance	Virus	No. of specimens
Flaviviruses	Dengue virus serotype 1	5
	Dengue virus serotype 2	15
Influenzas	Influenza A	11
Paramyxoviruses	Measles virus	2
	strain of Mumps virus	1

Livestock – Concurrent Surveillance Results at the Wildlife Farm Interface

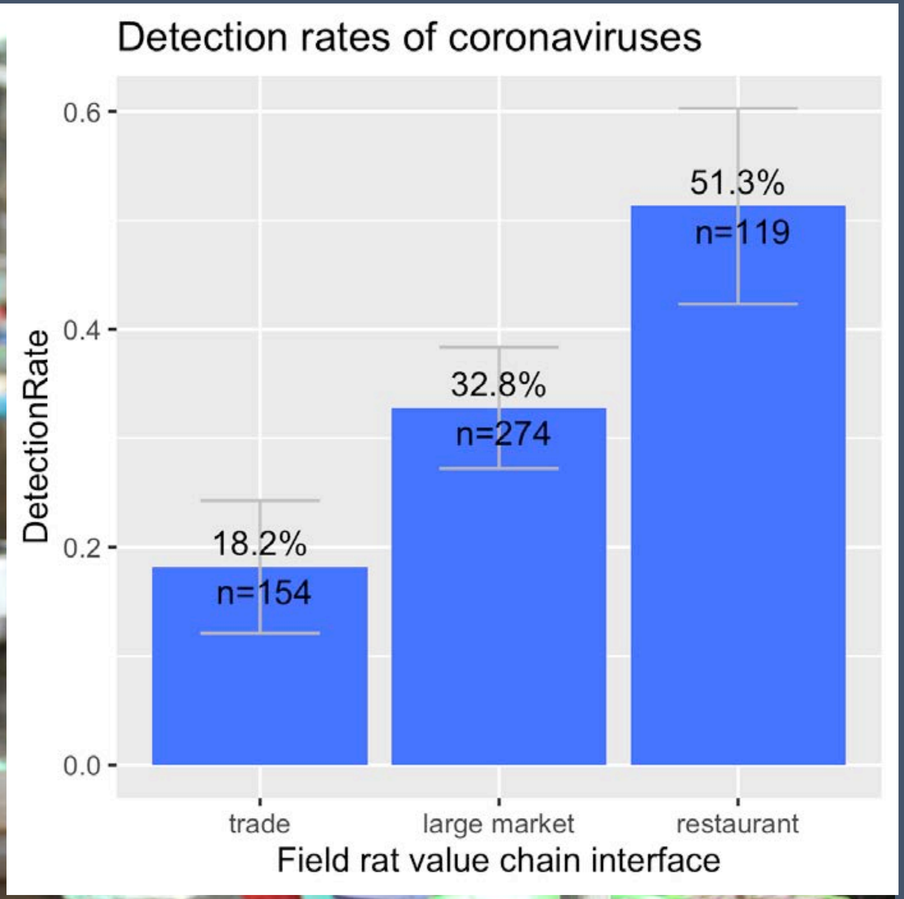
Swine Farm Surveillance	Virus	No. of specimens
Coronaviruses	Strain of Alphacoronavirus 1 (Transmissible gastroenteritis virus)	19
	Strain of Betacoronavirus 1 (Porcine hemagglutinating encephalomyelitis virus)	35
Paramyxoviruses	Strain of Porcine Parainfluenzavirus 1	2

FAO/DAH Poultry Surveillance

Wildlife – Concurrent Surveillance Results at the Wildlife Farm Interface

Species	Virus	No. of specimens
Hoary Bamboo Rat	Strain of Longquan Aa mouse coronavirus	1
Hoary Bamboo Rat	Strain of Murine coronavirus	21
Malayan Porcupine	Strain of Murine coronavirus	6
Black Giant Squirrel	Strain of Murine coronavirus	1

Detection of Corona Viruses along the rodent trade chain in the Mekong Delta



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Viral Detection in the Bat Guano Farming Interface in the Mekong Delta

- Strain of bat corona virus 512/2005
- Two novel corona viruses
  - PREDICT_CoV-17
  - PREDICT_CoV-35
- Four novel paramyxo viruses
  - PREDICT_PMV-13
  - PREDICT_PMV-63
  - PREDICT_PMV-66
  - PREDICT_PMV-67
- Four novel Rhabdoviruses
  - PREDICT_RbdV-21
  - PREDICT_RbdV-24
  - PREDICT_PbdV-27
  - PREDICT_RbdV-28

Viet Nam's experience with coordinated surveillance through PREDICT & LISN supported a rapid 'One Health' response to COVID-19


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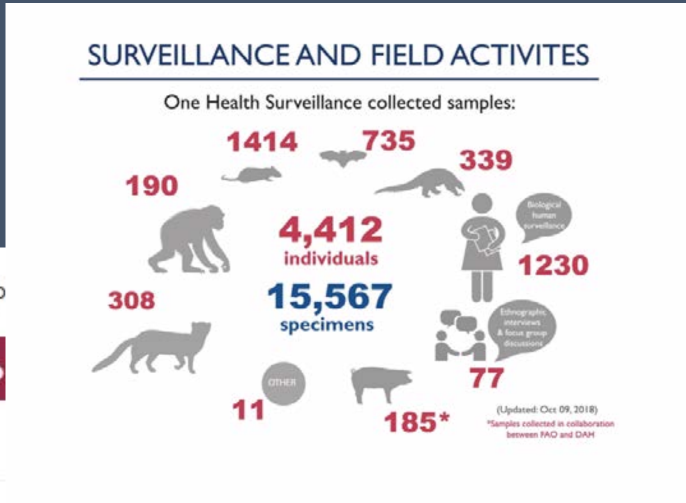
Vietnam urgently plans to respond to SARS-CoV-2 in animals

Phan Hậu
brakeautn@gmail.com

Like 271 Share

The Department of Animal Health (MARD) is urgently working to develop a plan to cope with the risk of SARS-CoV-2 virus causing Covid-19 infection in animals.

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Vietnam to ban wildlife trade following conservationists' demand

By Sen March 9, 2020 | 09:17 am GMT+7

Behavioral Risk & Community Engagement

Moving from evidence to interventions

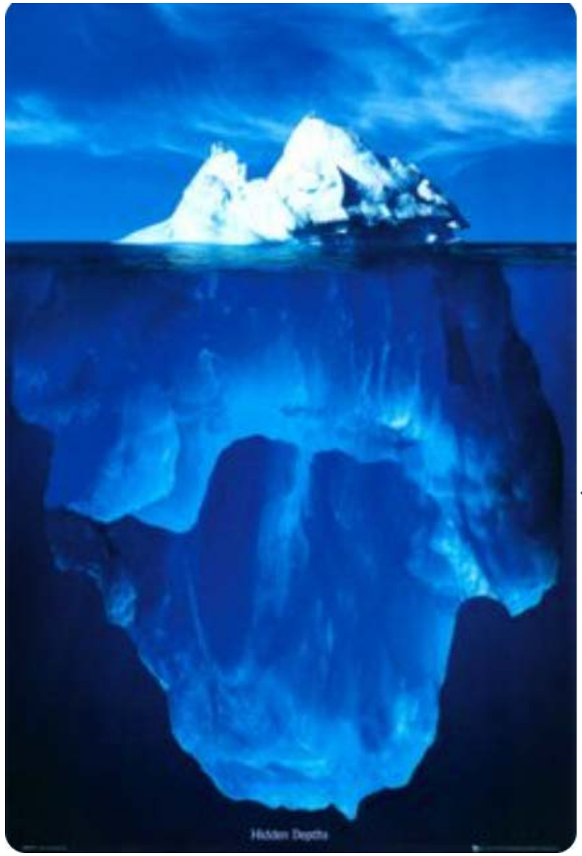
Beginning to dive deep into behavioral risk…

>20,000 EIDITH questionnaires for a broad, standardized view of behavioral risk…

>2,000 Qualitative interviews & focus groups for insight into hidden risks of behaviors:

- Which interfaces are most risky?
- Which behaviors are most likely to result in a spillover event?

Behavioral data, combined with PREDICT surveillance and virus, data allows for contextualized risk analyses



Working towards roadmaps of potential intervention strategies

Qualitative data looks more deeply at the dynamic, underlying behaviors and activities that drive zoonotic disease transmission

Cultural norms

Socio-economic drivers

Beliefs about animals

Animal care practices

Risk perceptions

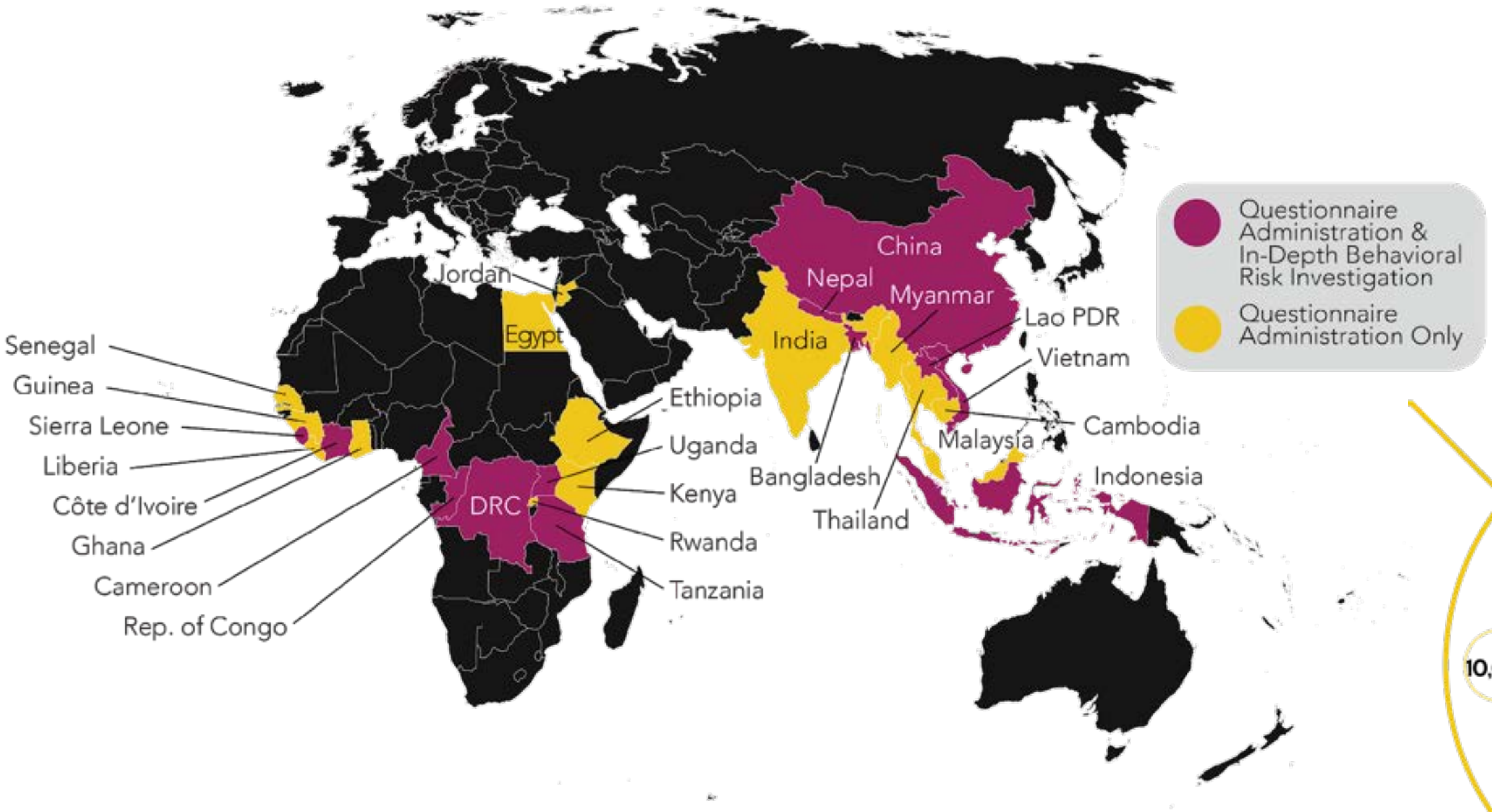
Identify behavioral and cultural practices promoting transmission of zoonotic viruses

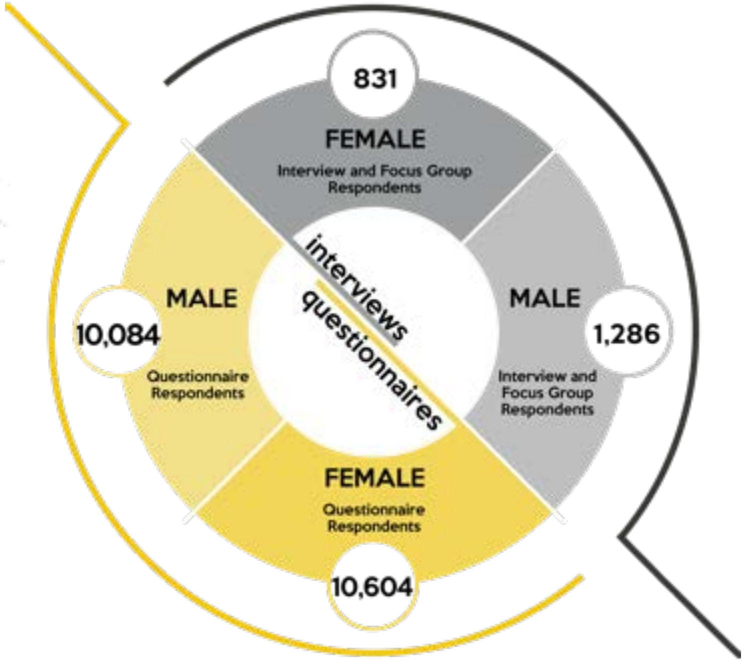
Qualitative data on perceptions of risk and illness: Interviews and Focus Groups

Quantitative data using streamlined behavioral risk surveys: EIDITH

Analyze data to identify behavioral risk and to inform intervention strategies

PREDICT Behavioral Risk Investigations





Country	Bat Guano Farming & Harvesting	Hunted Bats in the Value Chain	Bat-related Shared Food Resources	Bat-Community Interfaces	Bat-related Ecotourism	Market Value Chains
Bangladesh		•	•	•		
Cambodia	•		•	•		
Cameroon		•	•	•		•
China		•		•	•	•
Cote d'Ivoire			•	•		
DR Congo	•	•	•	•		•
Egypt						
Ethiopia				•		
Ghana		•	•	•		
Guinea			•	•		
India				•		
Indonesia		•				•
Jordan						
Kenya				•		
Lao PDR						•
Liberia				•		
Malaysia			•	•		
Myanmar	•		•	•		
Nepal		•		•		
ROC		•	•	•		•
Rwanda			•		•	
Senegal				•		
Sierra Leone		•	•	•		
Tanzania			•	•		
Thailand	•			•		
Uganda			•	•	•	
Vietnam	•					•

Key

= Qualitative and Quantitative

= Quantitative only

Examples of how qualitative findings were leveraged for behavior change intervention messaging

Targeted Behavior Change	Findings from PREDICT Behavioral Risk Work	Country
Reduce **killing** of bats	• Respondents from Luoding and Shantou expressed little concern about bats entering households, stating that bats are useful because they eat mosquitoes • While having bats nearby could lead to increased contact, the concept can be converted into positive messaging reinforcing why it is good to avoid killing them, in conjunction with recommended procedures for safe handling [resource: EIDITH protocols]	China
Reduce **contact** with bat secretions, organs, or body fluids of living or dead bats	• Bat excrement has been used as fertilizer • Raising awareness about excrement as a means for disease spread can reduce risk	DRC
Reduce **eating** of bats and thereby contact with secretions	• Several respondents believe eating bats cures night sweats and nocturia • Interventions can focus on enhancing knowledge to inform change in attitudes and practices regarding eating bats; they can be tailored to local beliefs revealed during interviews and discussed in conjunction with alternative therapies that are available locally	China
	• Many no longer eat bats because they follow the practices of their ancestors, who stopped eating bats (Inongo Nkoye custom) • Emphasizing following the practices of ancestors could be a means of preventing the consumption of bats	DRC
Increase **help seeking** behavior from a certified medical professional when scratched, bitten, or cut while butchering	• When bitten by bats, professional medical treatment may not be sought • Interventions could raise awareness that for more serious injuries (such as bites, scratches or if cut while butchering), certified medical professionals have medical treatments that traditional healers may not have access to; public health workers can also work more collaboratively with traditional healers	Indonesia

Behavioral Risk Communication Tools


Une seule santé

Le concept «une seule santé», une approche statégique pour réduire les risques des maladies infectieuses à l'interface Animal-Homme-Environnement.

www.onehealthinitiative.com

USAID PREDICT

Pour les consommateurs de viande de brousse:

Beaucoup d'entre vous ont dit avoir consommé de la viande crue ou insuffisamment cuite, mais cela peut être dangereux pour la santé.

Ne consomme que de la viande cuite.

Pour tout le monde:

Assurez-vous de jeter toutes vos ordures dans les poubelles. Ne jetez pas vos déchets dans la forêt et ne les laissez pas dans la rue.

Faire ses besoins dans les toilets appropriees.

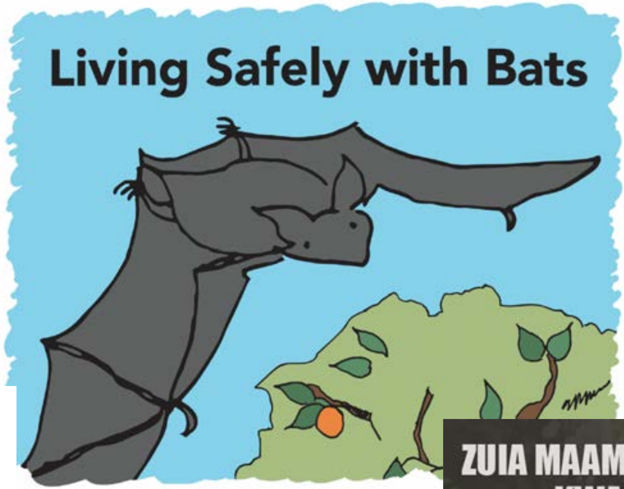
Évitez de vous soulager dans la forêt.

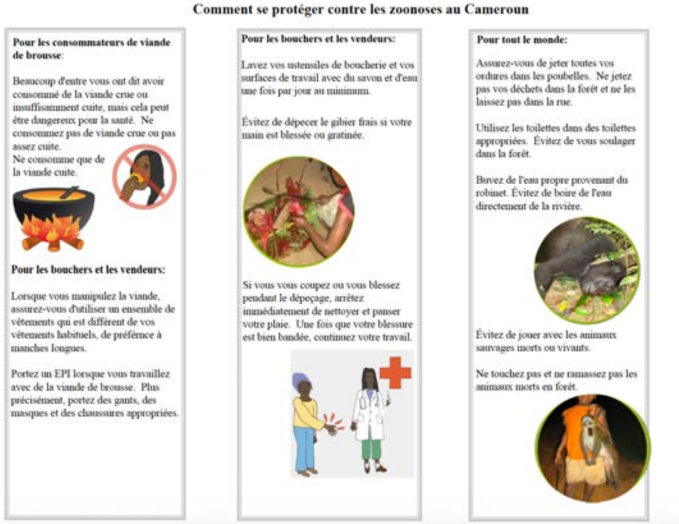
Buvez de l'eau propre provenant du robinet.

Évitez de boire de l'eau directement de la rivière.

Pour les enfants:

Évitez de jouer avec les animaux sauvages morts ou vivants.




Comment se protéger contre les zoonoses au Cameroun

Pour les consommateurs de viande de brousse:

Beaucoup d'entre vous ont dit avoir consommé de la viande crue ou insuffisamment cuite, mais cela peut être dangereux pour la santé. Ne consommez pas de viande crue ou pas assez cuite.
Ne consomme que de la viande cuite.

Pour les bouchers et les vendeurs:

Lorsque vous manipulez la viande, assurez-vous d'utiliser un ensemble de vêtements qui est différent de vos vêtements habituels, de préférnce à manches longues.

Portez un EPI lorsque vous travaillez avec de la viande de brousse. Plus précisément, portez des gants, des masques et des chaussures appropriées.

Pour les bouchers et les vendeurs:

Lavez vos ustensiles de boucherie et vos surfaces de travail avec du savon et d'eau une fois par jour au minimum.

Évitez de dépecer le gibier frais si votre main est blessée ou gratinée.

Si vous vous coupez ou vous blessez pendant le dépeçage, arrêtez immédiatement de nettoyer et panser votre plaie. Une fois que votre blessure est bien bandée, continuez votre travail.

Pour tout le monde:

Assurez-vous de jeter toutes vos ordures dans les poubelles. Ne jetez pas vos déchets dans la forêt et ne les laissez pas dans la rue.

Utilisez les toilettes dans des toilettes appropriées. Évitez de vous soulager dans la forêt.

Buvez de l'eau propre provenant du robinet. Évitez de boire de l'eau directement de la rivière.

Évitez de jouer avec les animaux sauvages morts ou vivants.

Ne touchez pas et ne ramassez pas les animaux morts en forêt.

12

TO DATE, THE NUMBER OF LANGUAGES INTO WHICH "LIVING SAFELY WITH BATS" HAS BEEN TRANSLATED

In **Sierra Leone**, the purpose of the bat book is explained

A discussion on living safely with bats in **Sierra Leone**

In **Guinea**, a conversation about one of the book's illustrations

In **Liberia**, the PREDICT team practices presenting the book

DRC

In 8 bushmeat markets in Kinshasa and in Inongo DRC, the PREDICT team conducted concurrent animal/human behavioral surveillance: while samples were taken from hunted wild animals, the behavioral team conducted interviews with the population living in contact with these animals, asking about animal exposure and behavioral risk factors and socio-economic drivers of subsistence hunting.

Based upon qualitative insights about the geographic origin of bushmeat coming into Kinshasa markets, we traced the animal value chain back to Mbandaka, the reported source of much non-human primate meat. Mbandaka is an Ebola outbreak site, so we used our interview data to generate hypotheses about Ebola exposure through bushmeat butchering, and did further sampling and serology of primates and bushmeat vendors to test this hypothesis.

A woman handles raw game in a DRC bushmeat market while a child looks on

A vendor sits in her stall in the Mbandaka bushmeat market

Our Legacy: PREDICT's Impact

Strengthening the Health Security Workforce

USAID
FROM THE AMERICAN PEOPLE

DEVELOPED the One Health Workforce by training more than 6,800 people in over 30 countries.

STRENGTHENED laboratory systems and zoonotic disease detection capabilities in over 60 labs around the world.

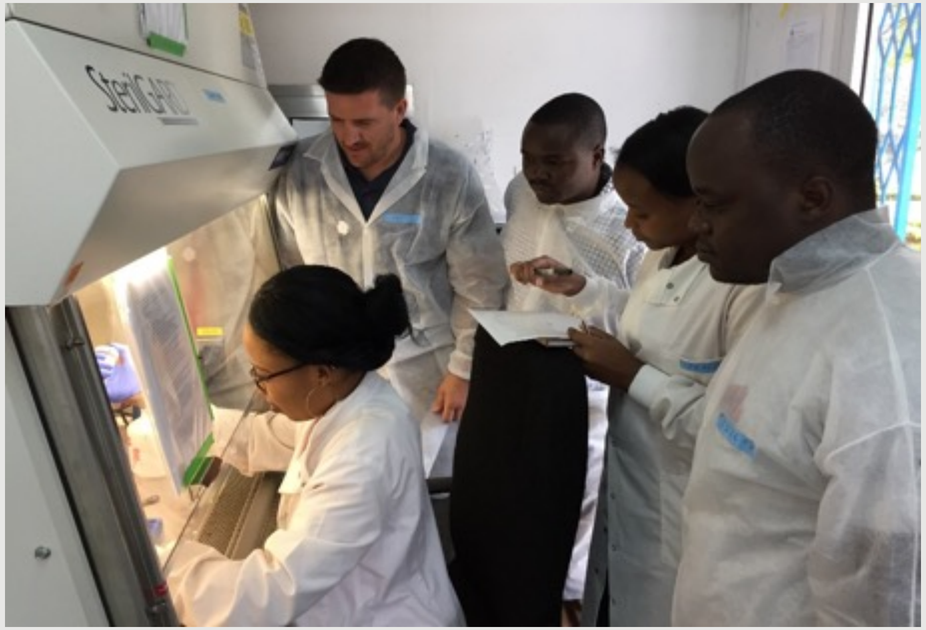
OPERATIONALIZED One Health surveillance and sampled over 164K animals and people, helping minimize the spillover of zoonotic disease threats from animals into human populations.

DETECTED over 1,100 unique viruses, including zoonotic diseases of public health concern such as Bombali ebolavirus, Zaire ebolavirus, Marburg virus, and MERS- and SARS-like coronaviruses.

PREDICT PARTNERS: USAID FROM THE AMERICAN PEOPLE, UC DAVIS VETERINARY MEDICINE One Health Institute, WCS, EcoHealth Alliance, METABIOTA™, Smithsonian Institution

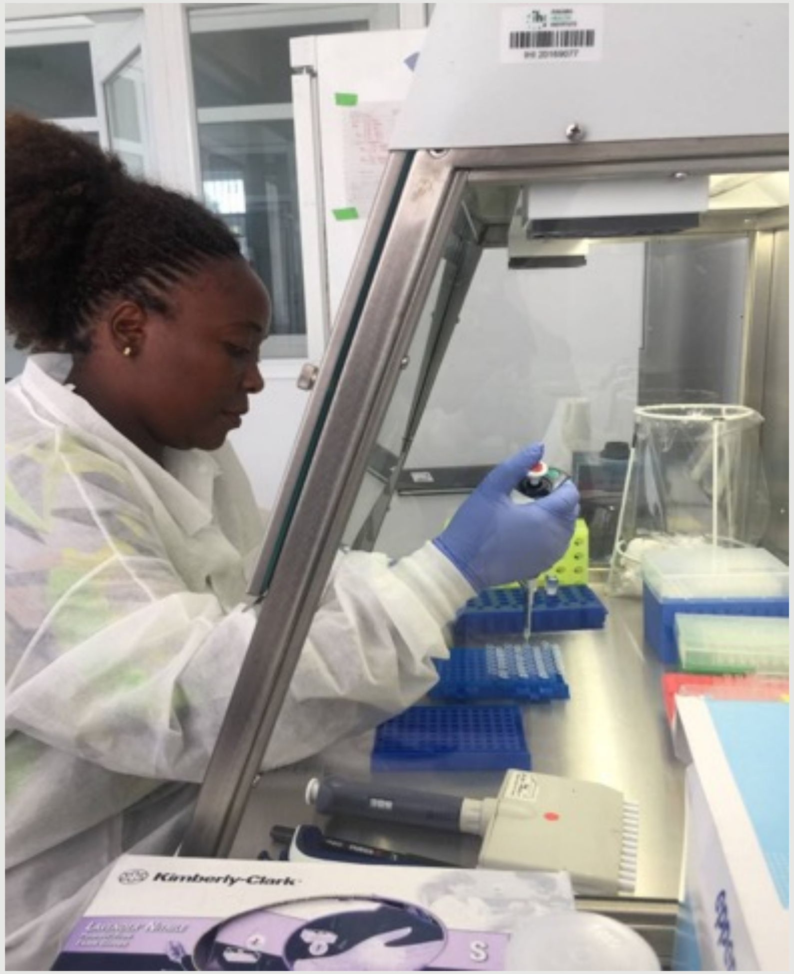
STRENGTHENING EMERGING THREATS SYSTEMS

Built capacity in both human and animal labs critical for strengthening national lab systems. Training of technicians occurred in university or partner labs



Senior Lab Scientist Brett Smith from UC Davis trains the PREDICT lab team in Tanzania on detection of viruses of pandemic potential.

Predict labs around the world have been called to action during the COVID-19 response for early identification of cases and ongoing technical assistance.



ON THE JOB TRAINING FOR FIELD, LAB, DATA TEAMS

In the field, PREDICT activities were implemented in collaboration with government health professionals (District Medical & Veterinary Officers, Livestock Field Officers, clinicians, and nurses) at the subnational levels.

The Predict-trained workforce is one of the best response resources available for COVID-19 and the next Disease X emergence. Our teams are helping improve capabilities where they are needed most.

PREDICT Training Guides

15 Publicly Available Training Modules for the One Health Workforce

Biosafety and Emergency Preparedness

One Health Surveillance & Field Sampling Guides

Behavioral Risk & Qualitative Research Guides

Demographics of Individuals Trained in PREDICT

2009-2019, n (%)

	PREDICT-1 Individuals n (%)	PREDICT-2 Individuals n (%)
Trainee Home Country		
Africa		**1975** (46)
Asia		**1387** (32)
Middle East		**43** (1)
North America		**97** (2)
Latin America		**-**
Unknown		**36** (1)
Gender		
Male		**2481** (57)
Female		**1858** (43)
Unknown		**1** (~0)
PREDICT affiliation		
Student		**716** (16)
Staff		**1125** (26)
Other-Community members, government officials, etc.		**2148** (49)
Total PREDICT Trainees	**2500** (100)	**4340** (100)

PREDICT's Workforce are the World's Leading Experts on Disease X

PREDICT Career Toolkit

Home | Toolkit Modules | Additional Resources

Career Toolkit

Curriculum Vitae/Resume

Take advantage of these resources and tools to develop and/or enhance your very own CV, also known as a resume in North America, Austrailia, and UK. Your developed and polished CV can be used for future fellowship, educational, or career endeavors!

PowerPoint

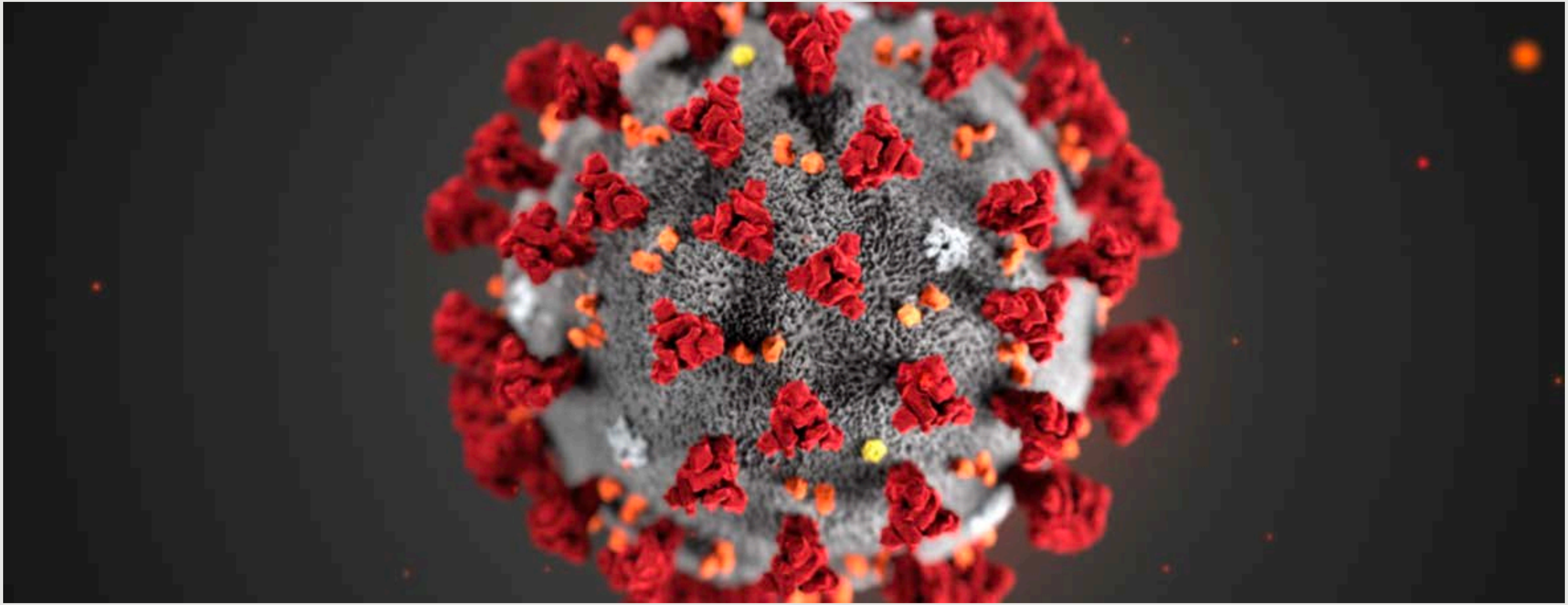
PowerPoint is a program used to create and display slides that can support your presentation. Take advantage of these resources and tools to develop an effective powerpoint presentation. Your developed and polished presentation can be used as support for your next presentation!

Public Speaking

Public speaking is skill used everyday, whether speaking at a team meeting or presenting to a large audience . Take advantage of these resources and tools to sharpen your public speaking skills and deliver crystal clear messages to your audiences. These can be used to enhance your next presentation!

The Future of Pandemic Preparedness

Readiness for responding to Disease X = COVID-19 (THIS TIME)



The Future of Pandemic Preparedness

Readiness for responding to Disease X = COVID-19 (THIS TIME)

Proof of Concept

- Feasibility assessment for finding viruses ahead of outbreaks
  - Determined emerging threats can be identified before spillover
  - Developed financial projections for forecasting
- Identified & trained a cadre of qualified professionals
- Protocols in place for detection in high-value geographic & species targets

- 60 laboratories in 30 of world's most vulnerable regions enabled
- Begun to catalogue the high-risk viruses & the metadata on transmission risk for mitigation, including for SARS-related CoVs
- Identified high-risk behaviors for surveillance & mitigation targeting
- Demonstrated the importance of multi-sectoral, One Health collaborations in emerging infectious disease control and prevention

USAID | PREDICT GLOBAL VIROME PROJECT UC DAVIS ABOUT LOGIN | REGISTER

RANKING COMPARISON RANK YOUR VIRUS DISCUSSION

SPILLOVER

VIRAL RISK RANKING

Developed by infectious disease scientists, SpillOver: Viral Risk Ranking is an interactive and adaptive platform for use by policy professionals, scientists and the general public to compare and explore the relative impacts of virus, host and environmental factors to evaluate the risk of zoonotic virus transmission.

LEARN MORE RANKING COMPARISON

USAID | PREDICT   GLOBAL VIROME PROJECT   UCDAVIS   ABOUT   LOGIN | REGISTER

DISCUSSION

Ranking Comparison

VIRUS

SEVERE ACUTE RESPIRATORY SYNDROME-RELATED CORONAVIRUS

NO.3 SPILLOVER RISK

355 RISK SCORE (OUT OF 400)

CONTRIBUTIONS OF RISK CATEGORIES: HOST, ENVIRONMENT, VIRUS

SEARCH BY: Virus Name

ORDER BY: Overall Rank

FILTER BY: Virus Genus; Virus Family; Country (China, Japan, Philippines); Human Virus?; Zoonotic Virus?; Host Species; Host Orders

POSITION	SCORE	SPECIES	GENUS	FAMILY
1	399	PREDICT - 123	Betacoronavirus	Coronaviridae
2	375	Zika virus	Flavivirus	Flaviviridae
3	355	Severe acute respiratory syndrome-related coronavirus	Betacoronavirus	Coronaviridae
4	325	PREDICT - 765	Rubulavirus	Rubulaviridae
5	300	Monkeypox virus	Orthopoxvirus	Poxviridae
6	295	Newcastle Disease Virus	Avulavirus	Paramyxoviridae
7	290	Apoi virus	Flavivirus	Flaviviridae

NO.3 SPILLOVER RISK OUT OF 651 VIRUSES

355 RISK SCORE (OUT OF 400)

SPECIES: **Severe acute respiratory syndrome-related coronavirus**

GENUS: **Betacoronavirus**

FAMILY: **Coronaviridae**

VIRUS

- Global Distribution: **Large, Regional**
- Human Virus: **Yes**
- Zoonotic Virus: **Yes**
- Human-Human Transmission: **Yes**

HOST

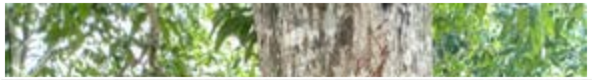
- Global Distribution: **Large, Regional**
- Plasticity: **12 species**, **8 orders**
- Contributors

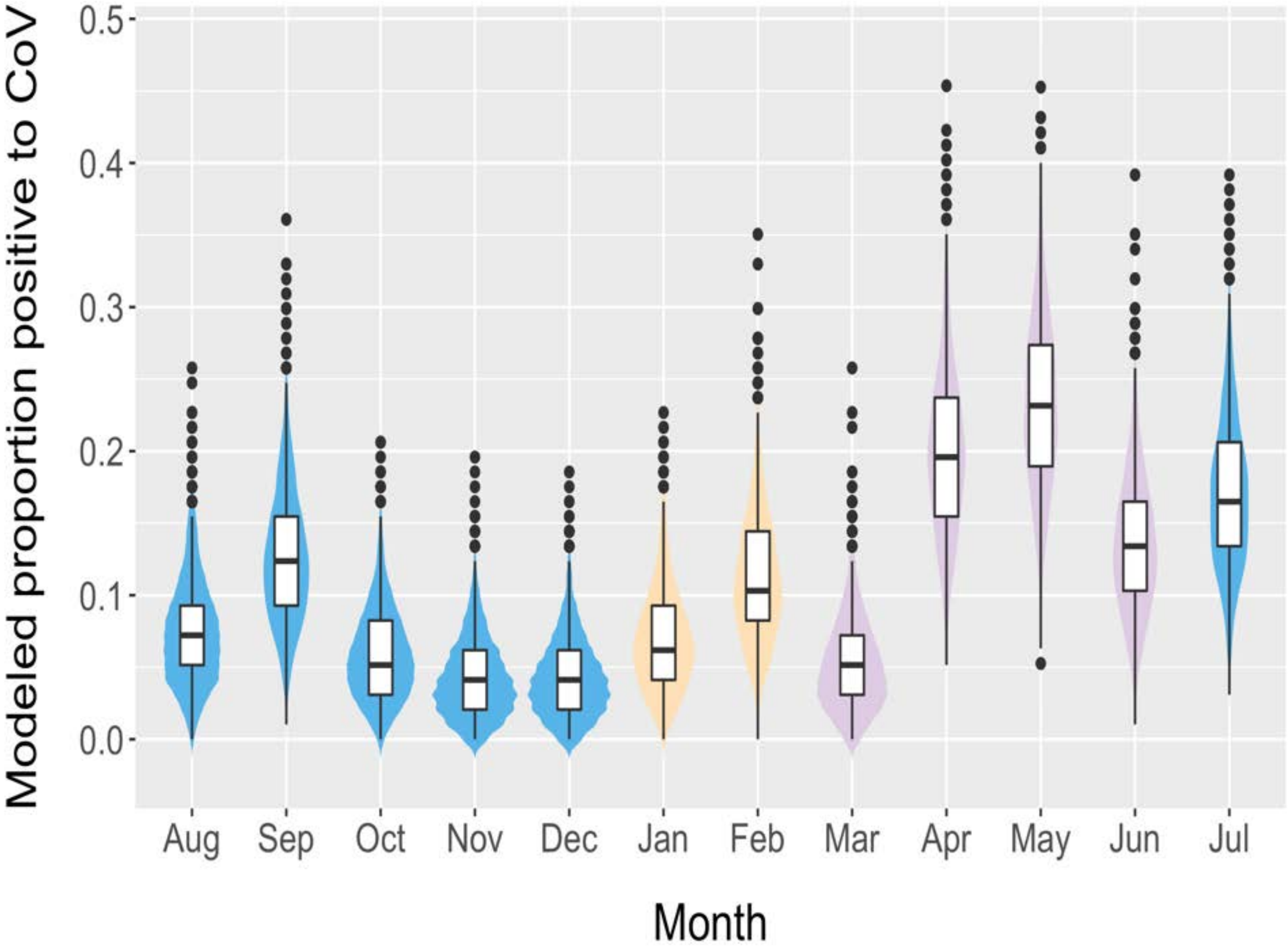
FULL DETAILS

Deve... e by
p... d

PREDICT-wide tools for community outreach & systems strengthening: "Living Safely with Bats" book

PREDICT-wide tools fo
systems strengthening





Modeled proportion positive to CoV
0.5
0.4
0.3
0.2
0.1
0.0
Aug
Sep
Oct
Nov
Dec
Jan
Feb
Mar
Apr
May
Jun
Jul
Month

Impact of Continuing Work & Identifying Targets for Spillover Prevention

Reducing Risk of & Preventing Impacts from Disease X

Impact of Continuing Work & Identifying Targets for Spillover Prevention

Reducing Risk of & Preventing Impacts from Disease X

- Better characterization of viral risks & **INSPIRING CALM** by providing data on:

  Geography **Hosts** **Risk interfaces**

  Ability to identify and control the transmission of viruses from animals to people at the source at the earliest possible stages of spillover

- Lowered risk for and impacts from future outbreaks
- Enable prevention measures, public health campaigns, differential diagnoses by clinicians & possibly even early development of prophylactics and treatments when warranted

Assisting Governments with Outbreaks

Successes and Impact

Specific guidelines for PREDICT Involvement

Key Questions:

- – Known etiology/cause?
- – Credible threat to human health?
- – Infectious cause?
- – Multi-species involvement (host-jumping)?
- – Evidence of animal origin?

USAID | PREDICT
FROM THE AMERICAN PEOPLE

PREDICT Outbreak Involvement Guidance

During infectious disease outbreaks, PREDICT is sometimes asked by the host government to provide assistance. All involvement in outbreak investigations and responses by PREDICT personnel, using USAID funds, will be considered on a case-by-case basis in consultation with USAID AOR. Said consultation will be made without delay by the PREDICT PI or her designated representative.

When requested to support an outbreak investigation or response, PREDICT personnel (usually Country Coordinator) should rapidly gather as much information about the situation as possible and report this information up the chain to his/her regional lead, who will contact the PREDICT PI or designated representative immediately.

In cases of disease of unknown origin, PREDICT will consider support for governments in response to outbreaks if the following criteria are met:

- Credible threat to human health likely from an infectious cause (based on symptoms) or evidence for multi-species involvement (i.e. host jumping) with associated animal morbidity and mortality
- Evidence of animal origin or involvement in disease dynamics (e.g. animal host is thought to be involved in transmission)

If assistance is offered in these circumstances, PREDICT personnel will endeavor to keep expectations regarding level of involvement and duration of response reasonable, including that assistance may be halted if a non-zoonotic disease cause is identified.

If the cause of disease is reasonably known and the disease is thought to be human-to-human or vector-borne transmitted, PREDICT will likely not actively participate in the investigation or response. However, if requested by the affected country's government for support or by another US government agency, PREDICT will consider providing assistance in consultation with USAID.

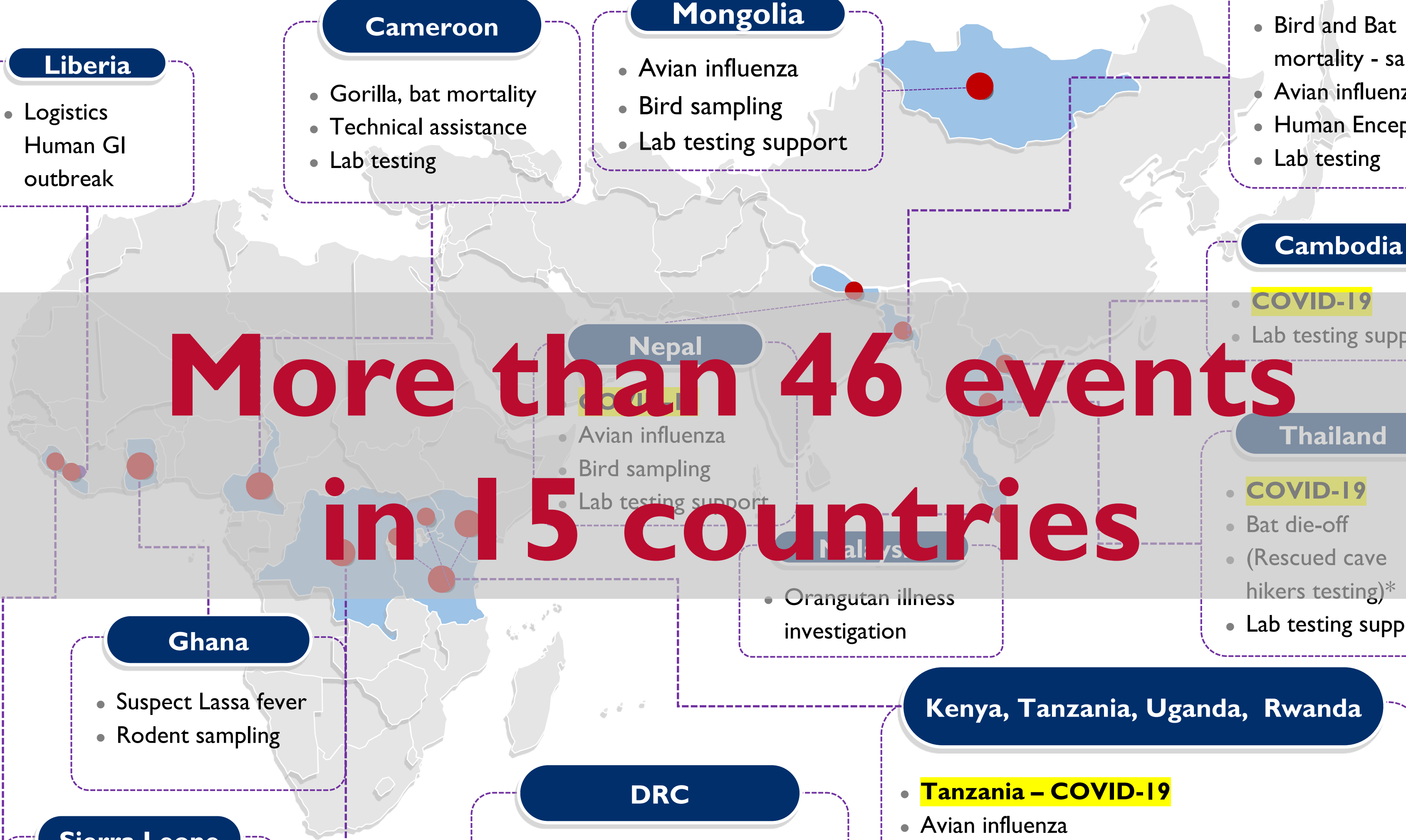
In the case of a zoonotic disease outbreak with a diagnosed cause, PREDICT involvement will be determined based on the following stated USAID priorities:

- An epidemic or pandemic is imminent
- Disease is caused by a zoonotic pathogen that is a priority for USAID Emerging Pandemic Threats Program (e.g. filovirus, influenza virus, coronavirus, or henipavirus), especially if there is evidence for multi-species involvement
- PREDICT involvement is reasonably likely to result in information that expands on what is known about a priority disease's transmission dynamics or distribution (geographic or host)
- There is a realistic doubt that the cause of the outbreak has been properly diagnosed, and PREDICT involvement can help to identify the actual cause

In any case, PREDICT's role in an outbreak investigation or response should be primarily advisory to the affected country's government. When requested, we aim to support in areas of technological or knowledge gaps. The expectation for the duration of PREDICT's involvement should never be open-ended, and there should be a defined plan for support based on prioritized needs, identified roles, and anticipated costs. In general, PREDICT's role should be primarily advisory with potential field support only in gap areas, such as identifying animal/environmental exposure risks, or by providing access to alternative laboratory approaches, when the cause of disease is unknown. Specific activities should be proposed and approved on an ongoing basis through the appropriate PREDICT and USAID chain.

USAID UC DAVIS VETERINARY MEDICINE WCS EcoHealth Alliance METABIOTA

PREDICT's Workforce in Action: Outbreak Assistance



Liberia
- Logistics
  Human GI outbreak

Cameroon
- Gorilla, bat mortality
- Technical assistance
- Lab testing

Mongolia
- Avian influenza
- Bird sampling
- Lab testing support

Bangladesh
- Bird and Bat mortality - sampling
- Avian influenza
- Human Encephalitis
- Lab testing

Cambodia
- COVID-19
- Lab testing support

Nepal
- Avian influenza
- Bird sampling
- Lab testing support

Thailand
- COVID-19
- Bat die-off
- (Rescued cave hikers testing)*
- Lab testing support

- Orangutan illness investigation

Ghana
- Suspect Lassa fever
- Rodent sampling

Sierra Leone
- Monkeypox (human)
- Rodent sampling – Lassa fever

DRC
- Suspect VHFs/Ebola (human)
- Avian influenza
- Lab testing

Kenya, Tanzania, Uganda, Rwanda
- **Tanzania – COVID-19**
- Avian influenza
- Yellow fever
- Technical information
- Partner communications
- Info only reports (RVF- Uganda)

More than 46 events in 15 countries

PREDICT Workforce Outbreak Assistance

<u>Capacity gains:</u>

- Technical information to government (Training modules)
  - safe sampling, specimen collection/transport, cold chain
- PPE or other equipment
  - N95, gloves, Tyvek suits, faceshields, cryotubes, boxes, cold chain (LN2), freezer packs
- Laboratory Testing Protocols
- Assist communication and coordination
  - MoH, MoAg, MoW, MoF, NGOs, WHO, FAO, MSF, etc…

Democratic Republic of Congo 2014
Ebola virus - Zaire

Nine suspected cases of Human Viral Hemorrhagic Fever and 2 deaths in the Bas-Uele Province was reported, and the laboratory at INRB confirmed Ebola virus (EBOV) in a subset of five patient specimens. PREDICT participated in GoDRC taskforce meetings and was requested by the INRB Director to utilize PREDICT protocol testing for secondary confirmation of EBOV. PREDICT continued to participate in National task force meetings and provide technical assistance until the cessation of the outbreak.

PREDICT's Workforce in Action – COVID19 Outbreak Assistance

- Technical information to governments (training modules)
  - Safe sampling, specimen collection/transport, cold chain
- PPE & other equipment
  - N95, gloves, Tyvek suits, faceshields, cryotubes, boxes, cold chain (LN2), freezer packs
- Laboratory testing protocols
- Assisting communication and coordination
  - MoH, MoAg, MoW, MoF, NGOs, WHO, FAO, MSF, etc…

Nepal, Thailand, Cambodia, Tanzania 2020 COVID-19 Pandemic

PREDICT testing platforms and outbreak response network used for initial rule-in/rule-out testing in several countries. Systematic investment and technical capacity building resulted in rapid first detections of COVID-19 cases.

The Power of PREDICT is the PEOPLE

- Throughout the PREDICT network of 30 countries teams have been supported to:
  - Understand what is needed for successful outbreak investigations
  - Understand the biosafety and biosecurity needs
  - Understand the critical importance of timelines, cold-chain, and rapid-action!
  - ***Constitute an important front-line in each country to support zoonotic disease investigations***

Policy and Partnerships for Health Security

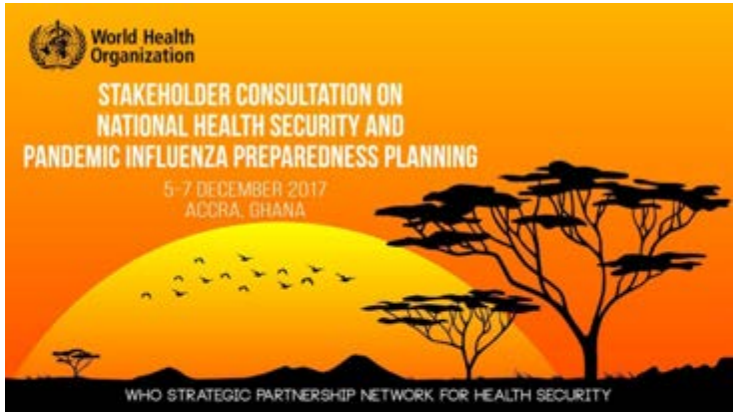
Evidence-based advocacy to prevent pandemics
at the national and global scale

Sharing Best Practices from Countries

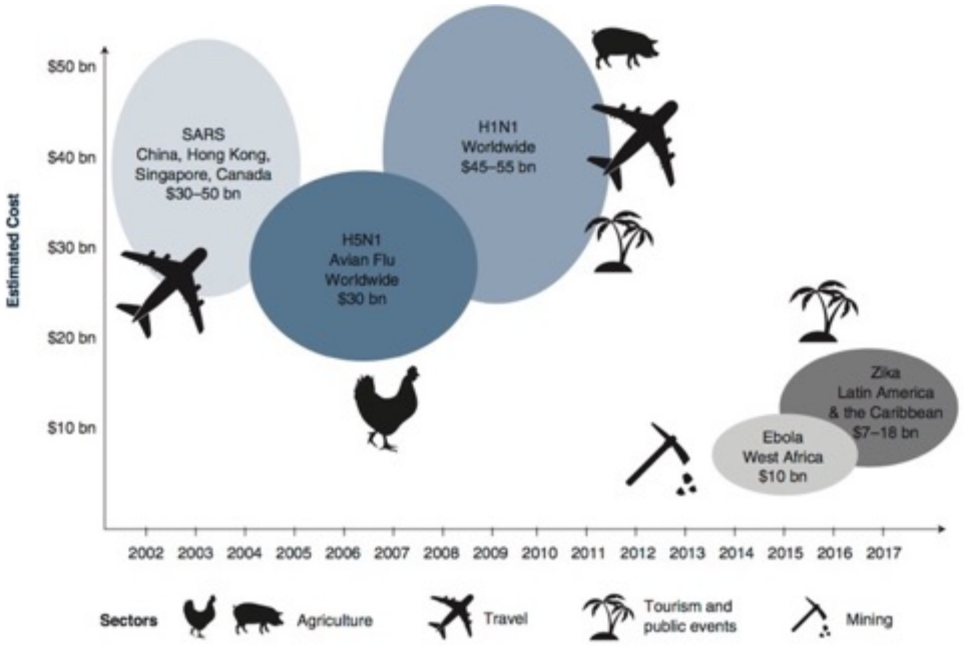
PMAC | PRINCE MAHIDOL AWARD CONFERENCE 2018

Global Health Security 2019
International Convention Centre
Sydney 18-20 June 2019

UN BIODIVERSITY CONFERENCE
Investing in biodiversity for people and planet
COP 14 - CP/MOP9 - NP/MOP3
Sharm El Sheikh, Egypt, 2018

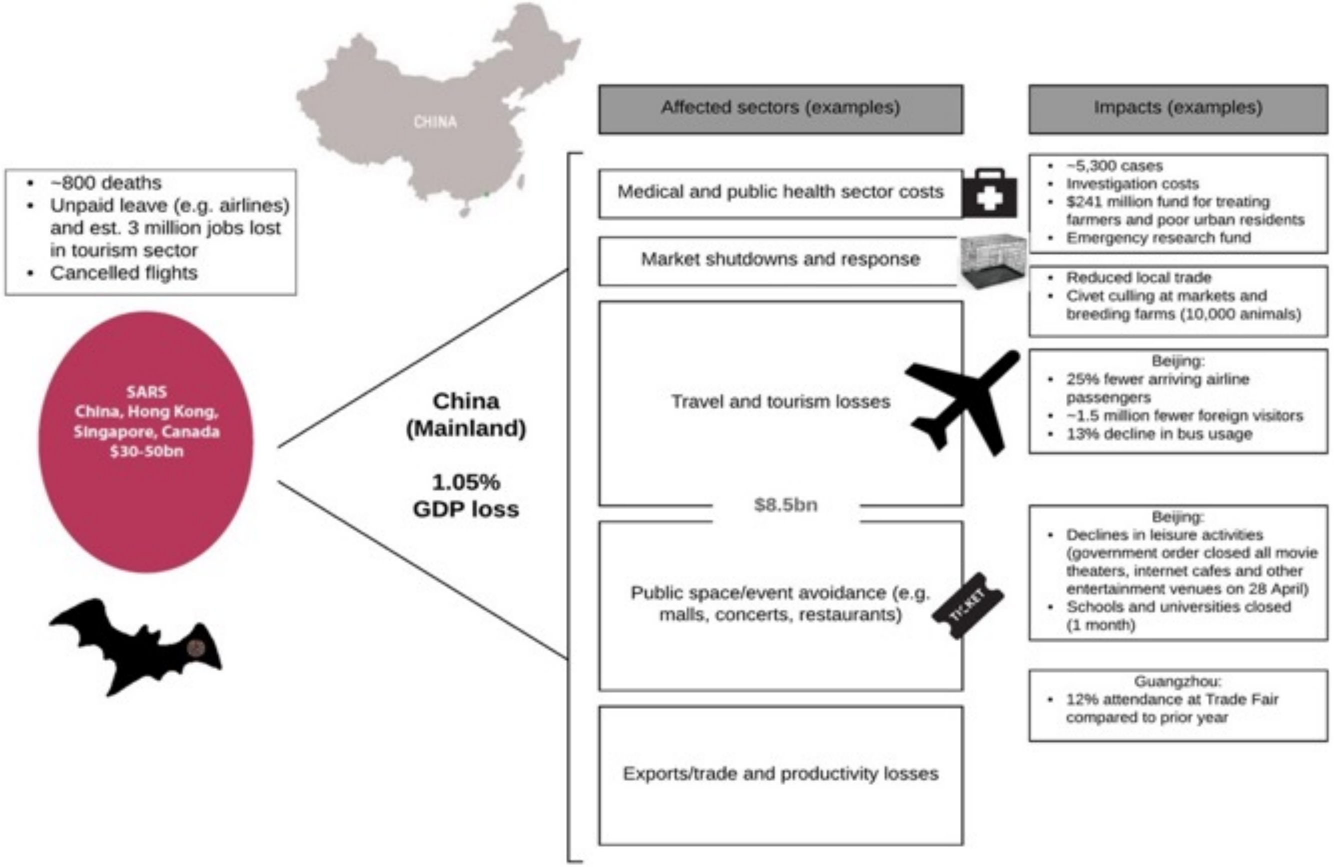


High Cost of Epidemics

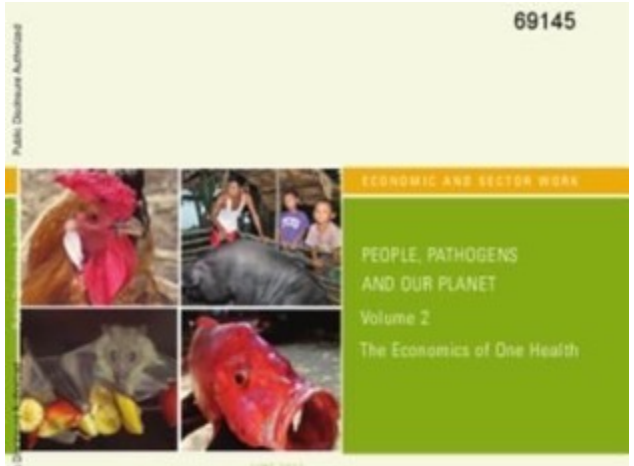


Figures are estimates and are presented as relative size. Based upon BioEra, World Bank, and UNDP data. Chart updated by EcoHealth Alliance.

Putting costs in tangible, local terms to inform budgeting for zoonotic disease prevention and control



One Health Economics




Trans R Soc Trop Med Hyg 2017; 00: 1–3
doi:10.1093/trstmh/trx039

COMMENTARY

One Health Economics to confront disease threats

Catherine Machalaba[a], Kristine M. Smith[a], Lina Awada[b], Kevin Berry[c], Franck Berthe[d], Timothy A. Bouley[d], Mieghan Bruce[e], Jose Cortiñas Abrahantes[f], Anas El Turabi[g], Yasha Feferholtz[a], Louise Flynn[h], Giulaume Fournié[i], Amanda Andre[a], Delia Grace[j], Olga Jonas[k], Tabitha Kimani[l], François Le Gall[d], Juan Jose Miranda[d], Marisa Peyre[m], Julio Pinto[n], Noam Ross[a], Simon R. Rüegg[o], Robert H. Salerno[h], Richard Seifman[p], Carlos Zambrana-Torrelio[a] and William B. Karesh[a,b,*]

[a]EcoHealth Alliance, New York 10001, USA; [b]World Organisation for Animal Health, Paris 75017, France; [c]Institute of Social and Economic Research, University of Alaska, Anchorage 99508, USA; [d]World Bank, Washington, D.C. 20433, USA; [e]University of Liverpool, Liverpool L69 3BX, UK; [f]European Food Safety Authority, Parma 43126, Italy; [g]Graduate School of Arts and Sciences, Harvard University, Cambridge 02138, USA; [h]DAI, Bethesda 20814, USA; [i]Royal Veterinary College, London NW1 0TU, UK; [j]International Livestock Research Institute, Nairobi 00100, Kenya; [k]Global Health Institute, Harvard University, Cambridge 02138, USA; [l]Emergency Centre for Transboundary Animal Diseases-Eastern Africa, Food and Agriculture Organization of the UN, Nairobi, Kenya; [m]CIRAD, Montpelier Cedex 5, France; [n]Animal Production and Health Division, Food and Agriculture Organization of the UN, Rome 00153, Italy; [o]Washington, D.C. 20433, USA; [o]Section of Epidemiology, Vetsuisse Faculty, University of Zurich, Zurich CH-8057, Switzerland; [p]Washington, D.C. 20433, USA

*Corresponding author: Present address: 460 West 34th Street, 1701, New York, NY 10001, USA; Tel: +1 212 380 4463; E-mail: Karesh@ecohealthalliance.org

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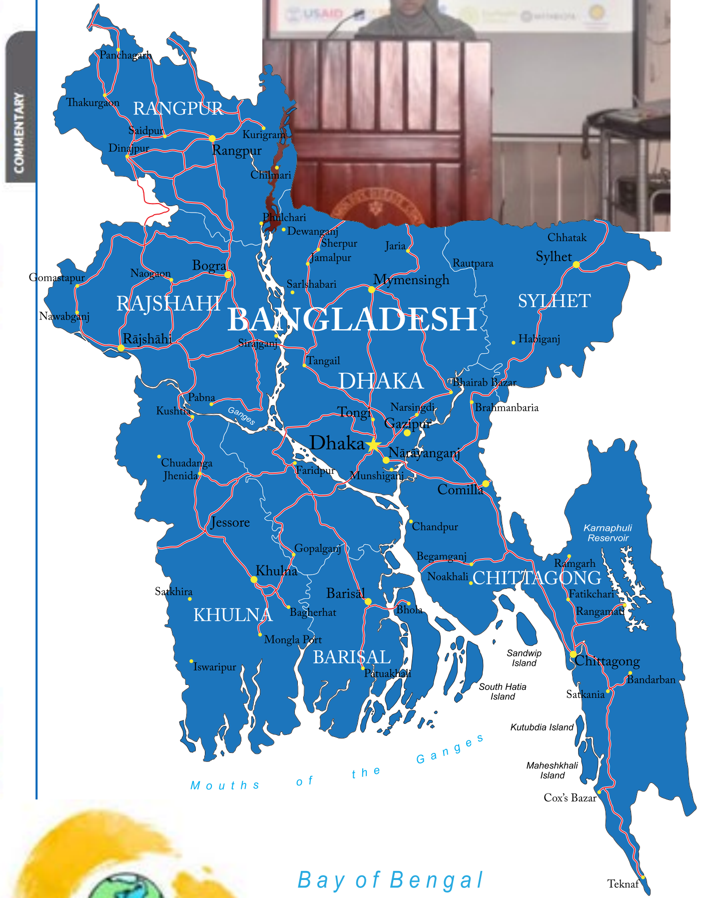
Global economic impacts of epidemics suggest high return on investment in prevention and One Health capacity. However, such investments remain limited, contributing to persistent endemic diseases and vulnerability to emerging ones. An interdisciplinary workshop explored methods for country-level analysis of added value of One Health approaches to disease control. Key recommendations include: 1. systems thinking to identify risks and mitigation options for decision-making under uncertainty; 2. multisectoral economic impact assessment to identify wider relevance and possible resource-sharing, and 3. consistent integration of environmental considerations. Economic analysis offers a congruent measure of value complementing diverse impact metrics among sectors and contexts.

Keywords: Economic, Environment, Epidemic, Multisectoral, One Health, Prevention

Recent outbreaks of emerging infectious disease resulted not only in high health impacts, but also substantial economic costs locally, regionally and globally. Most emerging diseases are zoonotic, and many are driven by agricultural intensification and changes in land use, demographics and behavior.[1,2] Human and animal health communities also continue to grapple with endemic diseases (e.g. rabies, brucellosis), with low- and middle-income countries disproportionally bearing the brunt of global burden of zoonoses (some estimate over 2 billion human cases and 2 million deaths per year).[3] Given the increasing factors facilitating disease emergence and spread, a One Health approach is needed to manage threats at the ground investments remain limited, relying on reactive and segregated resource-intensive disease response.

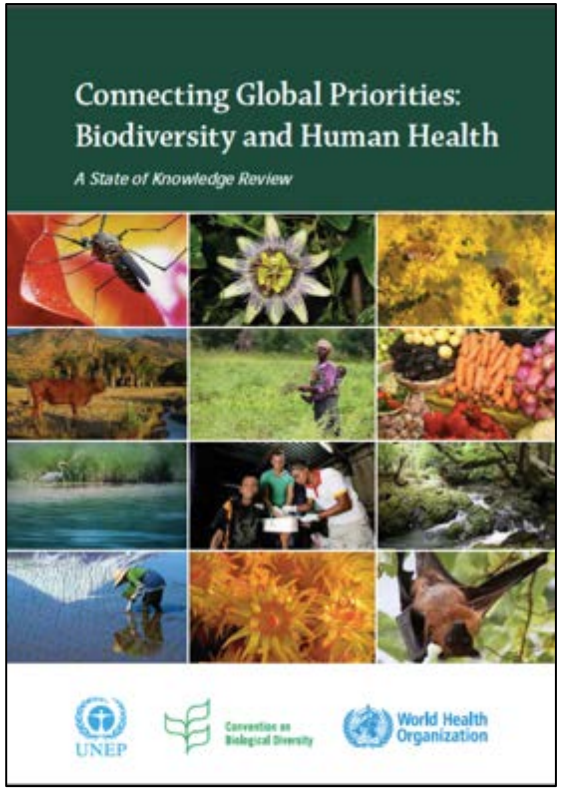
Thus, One Health approaches for early detection and rapid containment of outbreaks warrant economic examination. Global-based analyses suggest high return on investment in human and animal health systems in low- and middle-income countries to mitigate pandemic and epidemic risks, predicting US$1.8 billion to US$4.5 billion annual expenditure would yield a >US$30 billion to US$60 billion benefit per year in avoided cost.[4,5] Analysis of country-level impacts can provide tangible information for policy making, based on locally relevant and accurate data and aligned with local priorities and options. Since economic analysis of inte-

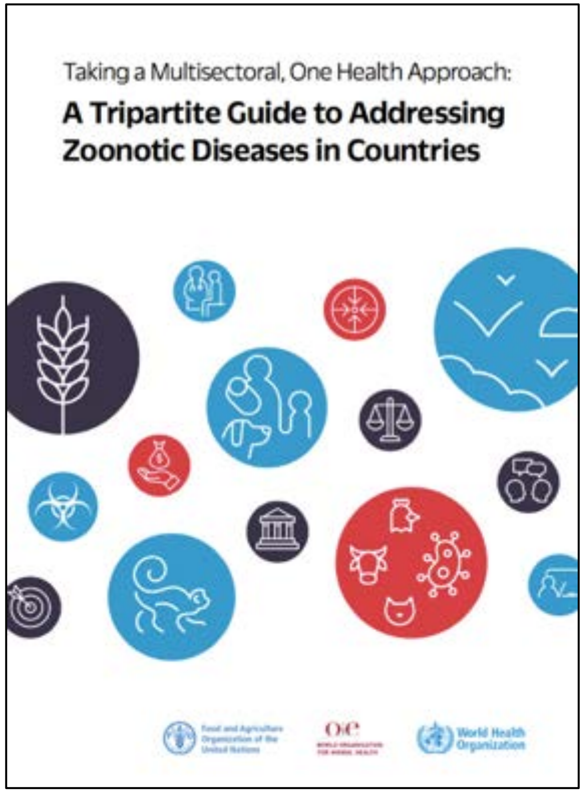


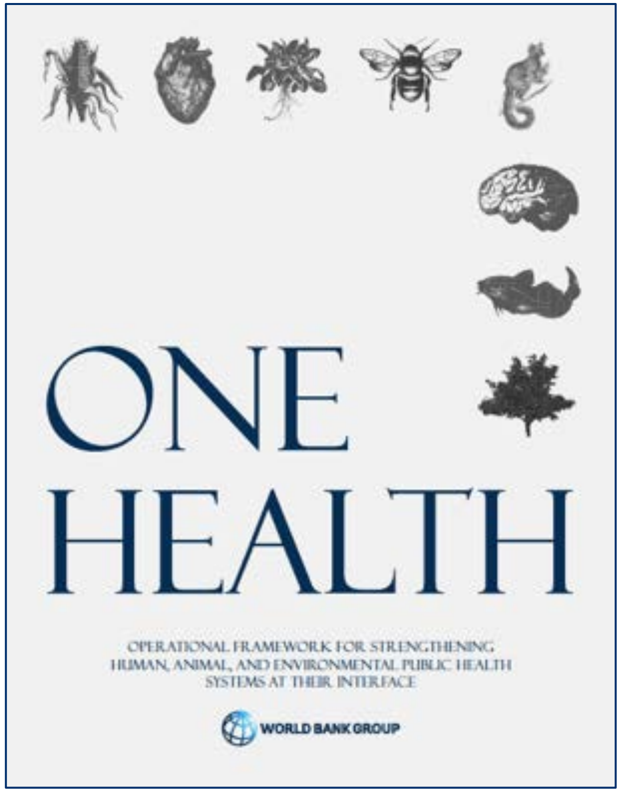
Multisectoral data collection to inform cost-effective disease prevention and control options

GHSA Sustainable Financing

Multisectoral Risk Reduction Guidance







Over 12,400 downloads from World Bank websites

UNISDR
United Nations Office for Disaster Risk Reduction

OIE

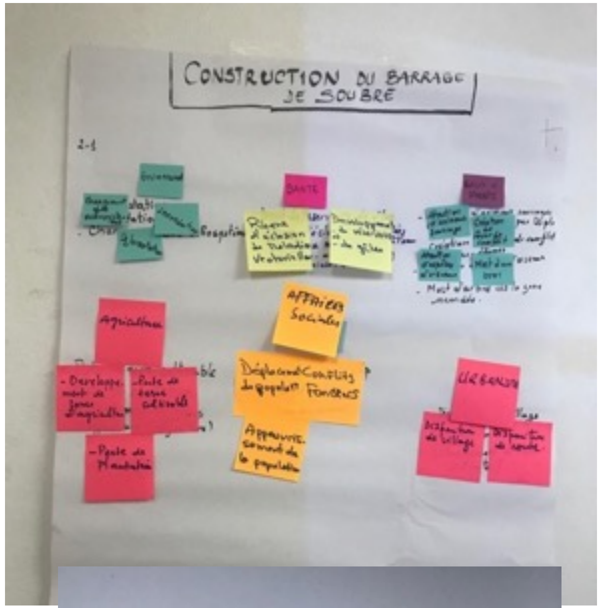
Food and Agriculture Organization of the United Nations

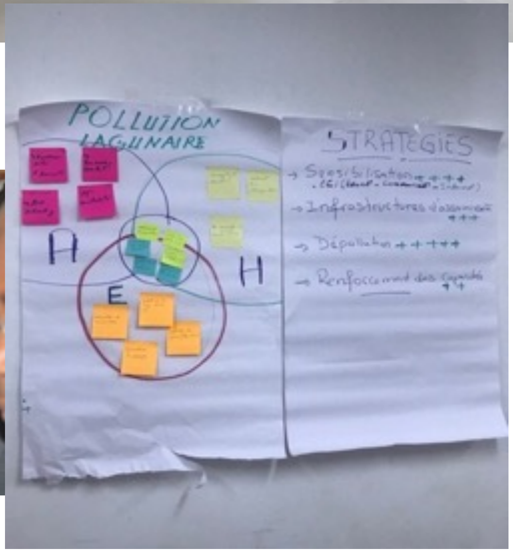
THE WORLD BANK
IBRD • IDA | WORLD BANK GROUP

World Health Organization

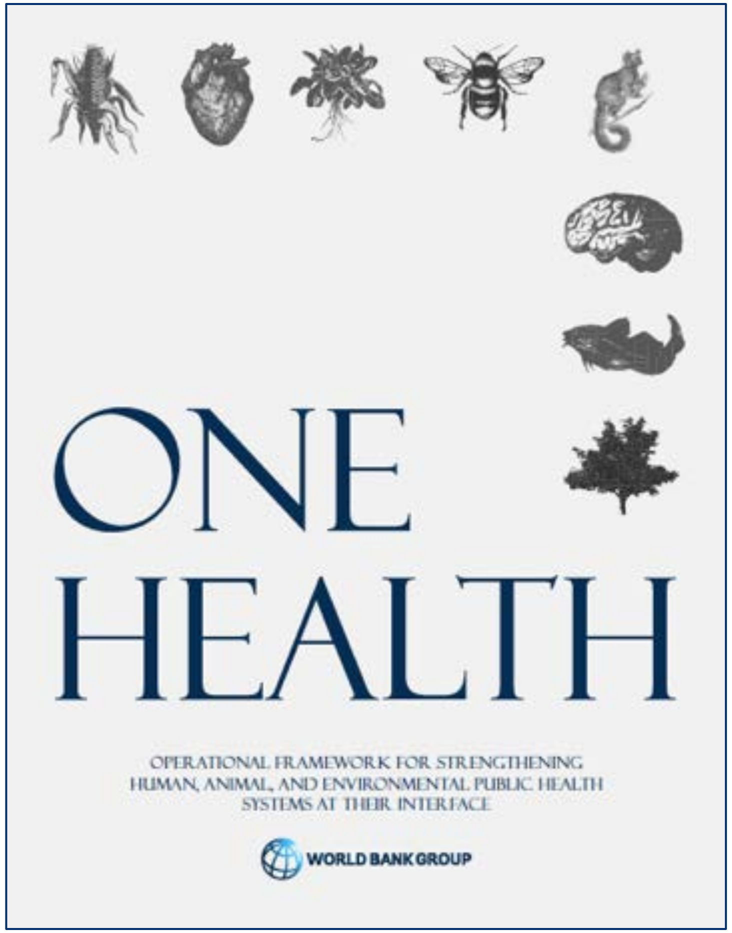
Convention on Biological Diversity

Making One Health Operational





Prevention Policies & Practices



	STAGE			
DOMAIN	PREVENT	DETECT	RESPOND	RECOVER
III. Communication and information	Access to information for risk assessment and mitigation: List of pathogens in country; list of known disease hosts and reservoirs in country; prior finding of exposure in country (e.g., antibodies to pathogen); risk forecasting e.g., weather data for climate-sensitive diseases	Chain of command for information reporting and verification Regional risk profile	Chain of command for information reporting and action Pre-identification of risk factors likely to facilitate spread; multi-sectoral awareness of relevant risk and response protocols	Multisectoral resilience planning and prioritization
	Contacts established between ministries Chain of command for information reporting		Ongoing coordination among authorities and between relevant ministries, affected sectors, logistical players (e.g., medical supply chain, treatment centers, vaccine producers, security), the media, and the public	After-action review and refinement of communication/information dissemination strategies
	Population-specific and sensitive messaging (e.g., gender or cultural)	Population-specific and sensitive messaging (e.g., gender or cultural)	Population-specific and sensitive messaging (e.g., gender or cultural)	Population-specific and sensitive messaging (e.g., gender or cultural)
IV. Technical infrastructure	National, regional, or international access to laboratory diagnostics (known and novel) Sentinel surveillance in animals (wild or domestic) or vectors and investigation Hazard identification and other relevant stages of risk analysis Risk mitigation (e.g., at points of entry)	National access to laboratory diagnostics (known pathogens and toxicology); confirmatory analysis at reference laboratory, if needed Disease prioritization Detection at point of entry	Risk management for disease control, including via contact tracing, awareness campaigns, etc. Medical treatment, where relevant Control at point of entry Containment to reduce potential for cross-border spread	Health systems strengthening (general) Risk mitigation measures, e.g., universal vaccination campaigns Climate-smart and other resilient health care infrastructure Risk assessment refinement (e.g., with new epidemiological analyses) Continued medical treatment provision, where relevant Biosafety (facility and personnel)
	Identification of vulnerable populations (heightened risk and/or	Identification of vulnerable populations	Identification of vulnerable populations	Identification of vulnerable populations

Moving from Pandemic Response toward Risk Reduction

2nd OIE Global Conference on Biological Threat Reduction
Enhancing Health and Security for All
OTTAWA, CANADA 31 Oct-2 Nov 2017

GHSAC
Global Health Security Agenda Consortium

BIPARTISAN COMMISSION ON BIODEFENSE

APHA
AMERICAN PUBLIC HEALTH ASSOCIATION
For science. For action. For health.

Disaster Management

Security & Defense

Public Health

Technical Expertise: In Emergencies and in Peacetime

2019 novel Coronavirus
Global research and innovation forum: towards a research roadmap

R&D Blueprint

SELECTED KNOWLEDGE GAPS

Some knowledge gaps merit being highlighted given their relevance to the goals that have been set forth.

1. Animal species of origin of the virus
2. Animal species involved in spill-over to humans: reservoir/ intermediate host
3. Modalities of transmission between animals and humans
4. Risk factors due to animal trade and consumption

1. Modes/duration of person-to-person transmission, role of different age groups
2. Importance of pre-/asymptomatic transmission
3. Surrogate markers for infectivity
4. Environmental stability of the virus and conditions associated with increased transmission
5. Virus compartments of replication, duration shedding
6. Risk factors due to animal trade and consumption

1. Spectrum of clinical disease
2. Groups at high risk of severe disease
3. Pathophysiology of severe disease
4. Clinical prognosis associated with viral loads and immunomarkers
5. Potential for antibody dependent enhancements to disease/infection
6. Adequate animal models that can mimic human disease characteristics

1. Optimal strategies for supportive care interventions
2. Role of host-targeted therapies
3. Safety and efficacy of candidate therapeutics and their combinations
4. Context for post-exposure prophylaxis trials conduct

1. Strength, duration of immunity, cellular immunity
2. Possibility of enhanced disease after vaccination
3. Animal models for prioritizing vaccines
4. Animal models for evaluating potential for vaccine-enhanced disease
5. Assays to evaluate immune response to vaccines
6. Design of late phase vaccine clinical trials

1. Risks factors for health care workers exposure
2. Approaches to support health care workers' health/ psychosocial needs
3. Perception/ compliance to infection prevention and control measures
4. Isolation, quarantine, optimal pathways to deliver care safely

1. How to address drivers of fear, anxieties, rumours, stigma
2. How to promote acceptance, uptake, adherence to public health measures and implement ethics, R&D innovations into education

1. Ethics questions around the inclusion of vulnerable populations in research
2. Best methods to involve and sensitize communities ... in research

World Health Organization

MEETING OF THE OIE *AD HOC* GROUP ON MERS-CoV

Paris, 22 –24 January 2019

Background

MERS-CoV is not an OIE listed disease. However OIE Member Countries would be obliged to report to the OIE a confirmed case of MERS-CoV in animals, as an "emerging disease" with public health impact in accordance with Article 1.1.4 of the OIE Terrestrial Animal Health Code. A detailed case definition for reporting positive MERS-CoV cases to OIE was published in May 2017 that would help the Member Countries to identify confirmed and suspected MERS-CoV cases in camels and, accordingly, report positive cases to the OIE.

http://www.oie.int/en/scientific-expertise/specific-information-and-recommendations/mers-cov/

World Organisation for Animal Health

Home > Scientific expertise > Specific information and recommendations > **Questions and Answers on the COVID-19**

Questions and Answers on the 2019 Coronavirus Disease (COVID-19)

- **What causes COVID-19?**

Coronaviruses (CoV) are a family of RNA (ribonucleic acid) viruses. They are called coronaviruses because the virus particle exhibits a characteristic 'corona' (crown) of spike proteins around its lipid envelope. CoV infections are common in animals and humans. Some strains of CoV are zoonotic, meaning they can be transmitted between animals and humans, but many strains are not zoonotic.

In humans, CoV can cause illness ranging from the common cold to more severe diseases such as Middle East Respiratory Syndrome (caused by MERS-CoV), and Severe Acute Respiratory Syndrome (caused by SARS-CoV). Detailed investigations have demonstrated that SARS-CoV was transmitted from civets to humans, and MERS-CoV from dromedary camels to humans.

In December 2019, human cases of pneumonia of unknown origin were reported in Wuhan City, Hubei Province of China (People's Rep. of). A new CoV was identified as the causative agent by Chinese Authorities. Since then, human cases, most of them with travel history to Wuhan or Hubei region, have been reported by several provinces in China (People's Rep. of) and by a number of other countries. For up to date information please consult the WHO website.

The CoV which causes COVID-19 has been designated as SARS-CoV-2 by the International Committee on Taxonomy of Viruses (ICTV); this is the scientific name. The virus may also be referred to as "the COVID-19 virus" or "the virus responsible for COVID-19". COVID19 refers to the disease caused by the virus.

- **Are animals responsible for COVID-19 in people?**

The predominant route of transmission of COVID-19 appears to be from human to human.

Current evidence suggests that the COVID-19 virus has an animal source. Ongoing investigations are important for identifying the animal source (including species involved) and establishing the potential role of an animal reservoir in this disease. Yet, to date, there is not enough scientific

Intergovernmental Policy Change

CITES: In Sickness and in Health?

Mass mortality events in wildlife associated with disease and multiple stressors appear to be increasing (Fey and others 2015), and a lack of rapid access to diagnostic analyses can hamper conservation responses. Timely diagnosis is a crucial factor for effective disease investigation and response in humans and agricultural species, but it is also critical for wildlife conservation in the face of mass mortality. Rapid and accurate diagnoses, especially for unusual agents or in unusual species, often require advanced laboratory techniques which are currently unavailable in many countries. Efficient international collaboration among field and laboratory staff can therefore be critical for effective conservation.

The Convention on International Trade in Endanger… Species of Wild Fauna and Flora (CITES) regulates mov… ment of species threatened with extinction. Under CITE… diagnostic specimens from listed species are effectiv… considered trade products, requiring permits for intern… tional movement. While due process is surely warranted … prevent overexploitation and ensure fair and equitable u… of genetic material, mechanisms are critically needed f…

…ment and processing may also present technical challenges. In any given setting, a gap in cold chain may compromise sample quality if proper storage facilities are not available in addition to delaying access to critical information that could inform control measures.

Solutions to facilitate international collaboration to control disease impacts on threatened and endangered species are critically needed. A recent CITES-OIE collaborative agreement (CITES-OIE 2015) may provide a framework for a new pathway for collaboration. Through a mechanism that could be agreed upon by CITES, international or regional reference laboratories officially linked to the World Organ-…

ECOHEALTH

CITES CoP 18

More reliable, efficient movement of emergency diagnostic specimens from wildlife for investigation of animal and public health disease threats

UNEP — CBD

Convention on Biological Diversity

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GENERAL

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Twenty-first meeting
Montreal, Canada, 11-14 December 2017
Agenda item 5

GUIDANCE ON INTEGRATING BIODIVERSITY CONSIDERATIONS INTO ONE HEALTH APPROACHES[1]

3. Integrated data collection, monitoring and surveillance

37. Promote integrated mechanisms of data collection, monitoring, review and surveillance, which are central to the effective implementation of One Health approaches, including the following:

(a) Strengthening national surveillance capacity for early warning, prevention and control of disease outbreaks by establishing coordinated active surveillance systems that facilitate systematic inputs and data exchange between public health, environment, wildlife and other sectors;

(b) Establishing data-sharing platforms between the field level and national levels, with a view to establishing a central surveillance mechanism to gather and disseminate data;

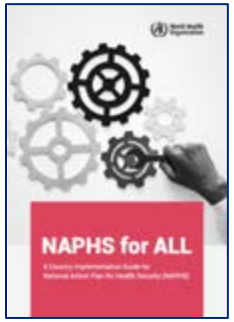
(c) Collecting and disseminating geospatial data of high-risk areas for disease transmission in biodiversity hotspots;

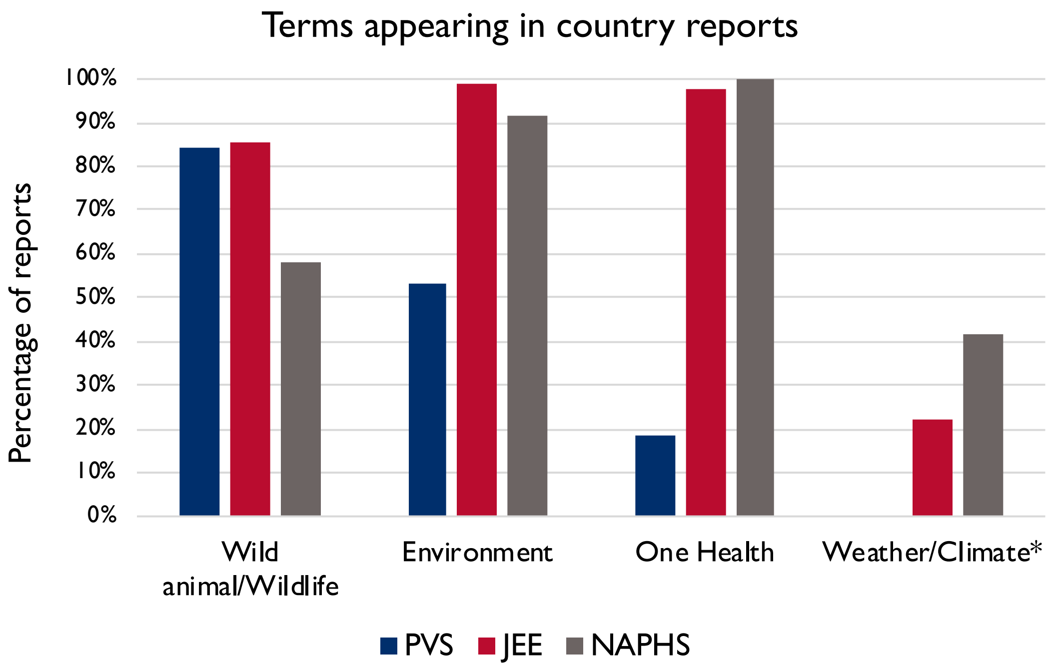
(d) Developing alternative scenarios that jointly predict effects on biodiversity, ecosystems and human health for the design of sustainable conservation strategies;

(e) Identifying and scaling up best practices in the sustainable management of ecosystems and health outcomes, sharing this knowledge via available tools and shared knowledge platforms in information technology, and supporting technological development and innovation to develop new data collection methods, such as citizen science; e-health platforms, etc.

Adoption of One Health approaches for integrated health and biodiversity risk assessments, sentinel surveillance, and cost-effective prevention strategies

Identifying Health Security Gaps





73% of countries reported gaps, mainly:

- Poor coordination (e.g. planning, response)
- Poor data integration from wildlife and/or environment sector
- Wildlife disease surveillance not operational
- Workforce shortages

Are One Health-relevant policies in place for health security?

- Do countries consider infectious disease risk in land use planning?
- Do they have a cross-ministerial effort to address zoonotic diseases?
- Do they share surveillance data across veterinary, wildlife, and public health professionals?

PREDICT

Ministries of Health, Agriculture & Environment and
Implementing University and NGO Partners in 35 Countries