



Surveillance for Future Threats

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Preventing, Detecting, Responding to and
Recovering from Future Threats (WS304)

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LEANING INTO THE PANDEMIC ERA



Emergence of Pandemic Threats

Evolution of mutation-prone RNA viruses in wildlife hosts

Transmission between animal species

Globalized human-to-human transmission

Majority of newly emerged infectious disease have wildlife origins



Human Coronaviruses

Virus – date of first discovery, most common disease manifestation, suspected source(s)

1. 229E – 1968, causes mild disease



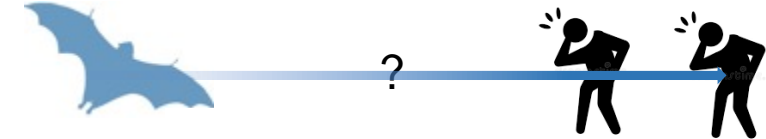
2. OC43 – 1967, causes mild disease



3. SARS-CoV – 2002, causes severe respiratory disease



4. NL63 – 2004, causes mild disease, occasionally croup



5. HKU1 – 2005, causes mild disease



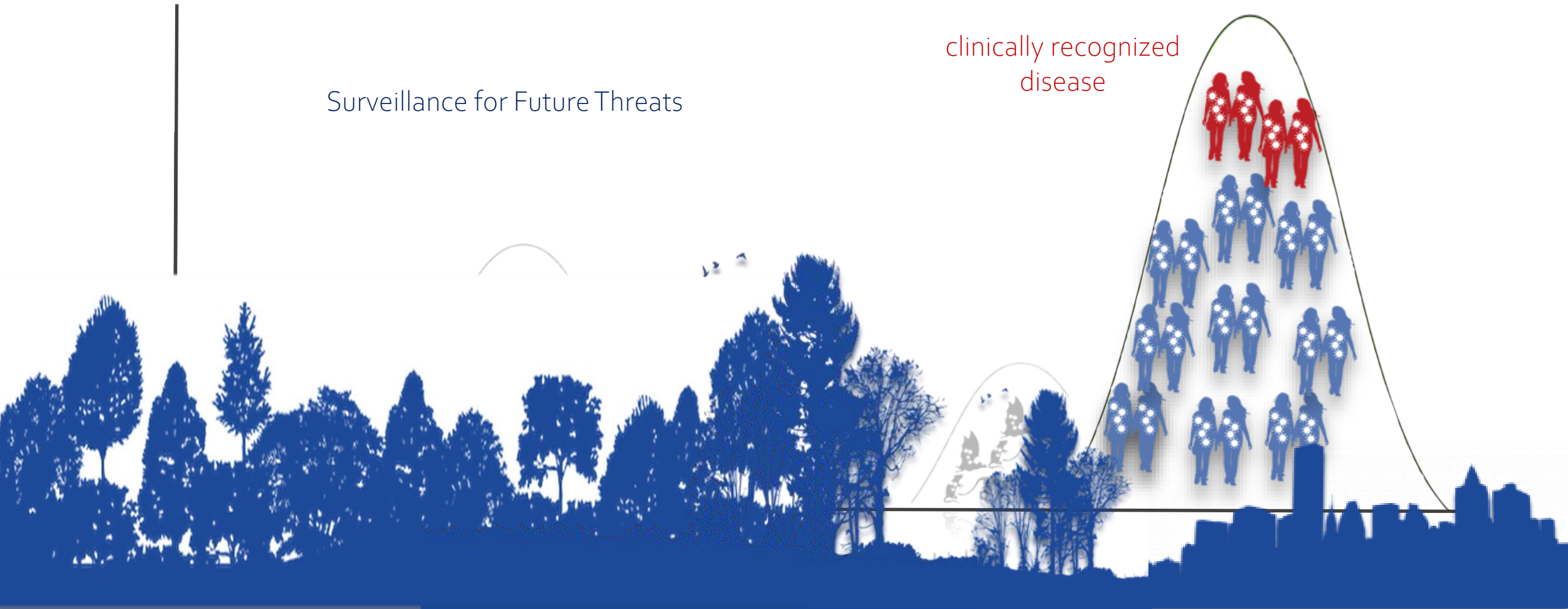
6. MERS-CoV – 2012, causes severe disease



7. SARS-CoV-2 – 2019, causes severe disease (COVID-19)



Emergence of a Pandemic Threat



Accelerated Global Change

- Agricultural development, industrialization, urbanization
- Globalization and movement at the international scale
- Substantial net gains in human well-being and economic development
- Degradation of ecosystem services
 - Increased nonlinear or abrupt changes in ecological processes
 - Diminished regulatory processes
 - Increasingly frequent emerging infectious diseases

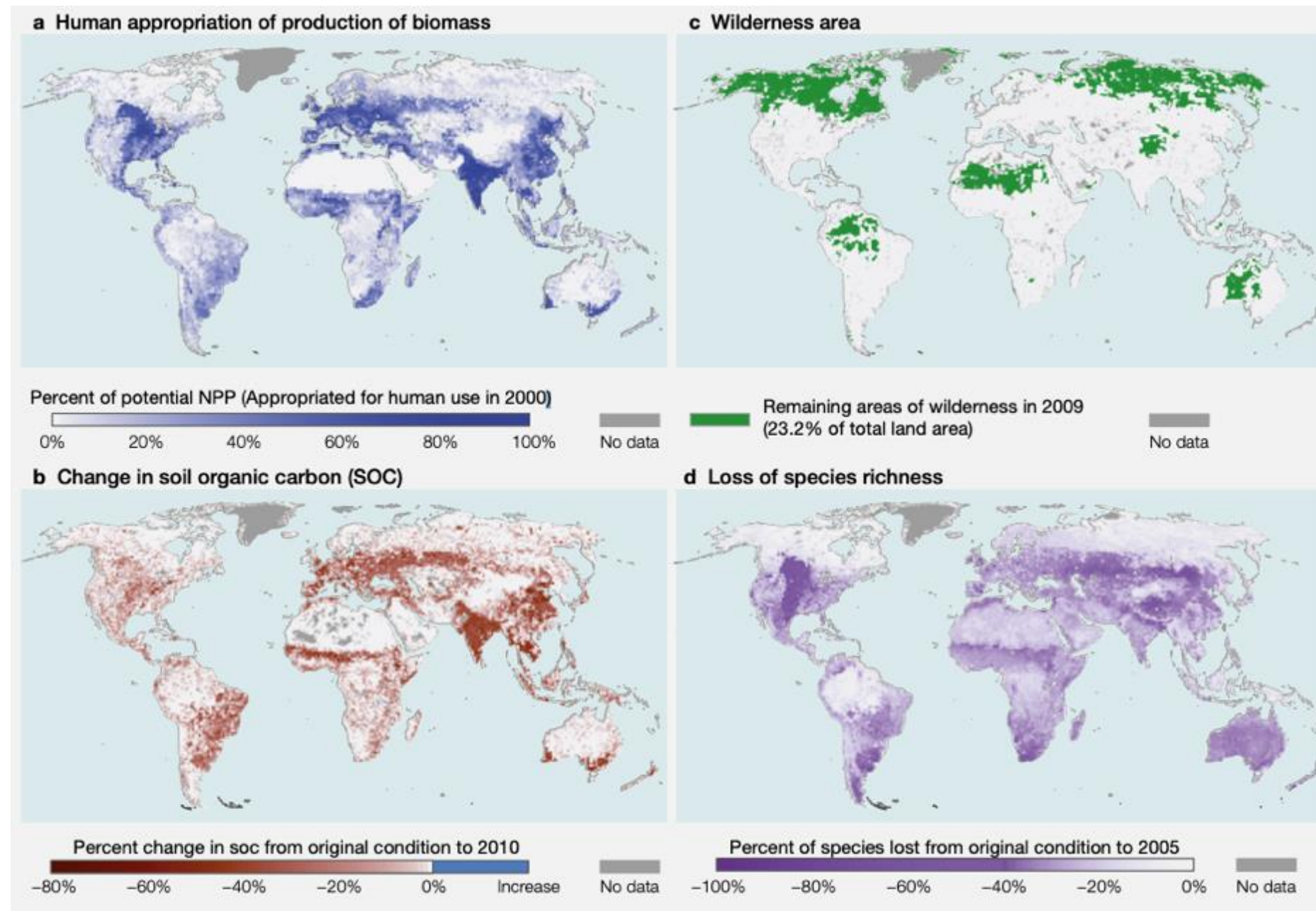


Assessment Report on Land Degradation and Restoration (2018)

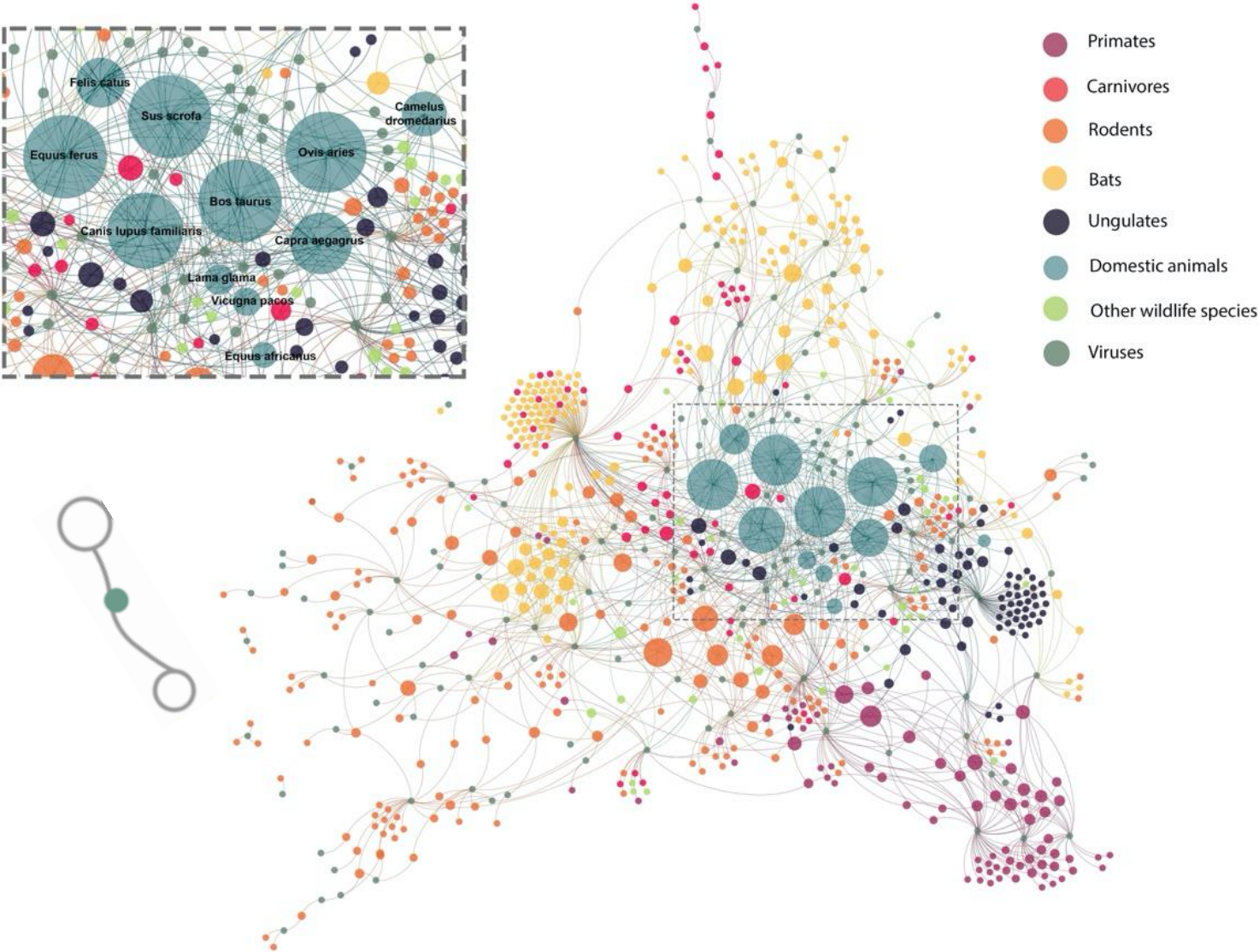
Human activity has drastically
changed the planet

Cultivated systems cover over
1/3rd of earth's surface

Less than 1/4 of land surface
considered “wilderness”
(ecological and evolutionary
processes operating with
minimal human disturbance)



Amplification in Livestock Production

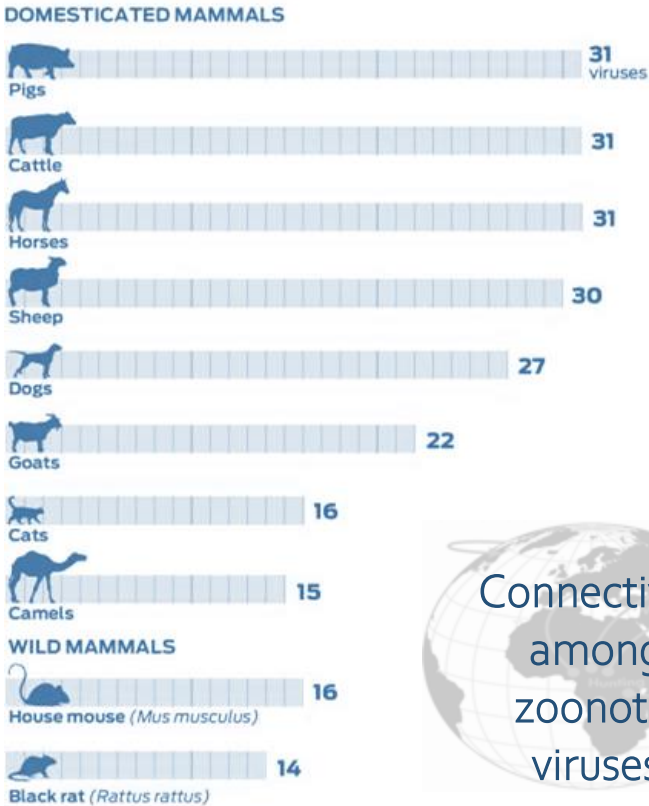


Global shifts in mammalian population trends reveal key predictors of virus spillover risk

Christine K. Johnson¹, Peta L. Hitchens², Pranav S. Pandit¹, Julie Rushmore¹, Tierra Smiley Evans¹, Cristin C. W. Young¹ and Megan M. Doyle¹

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Species with Most Zoonotic Viruses



Zoonotic Viruses found in Mammalian Species

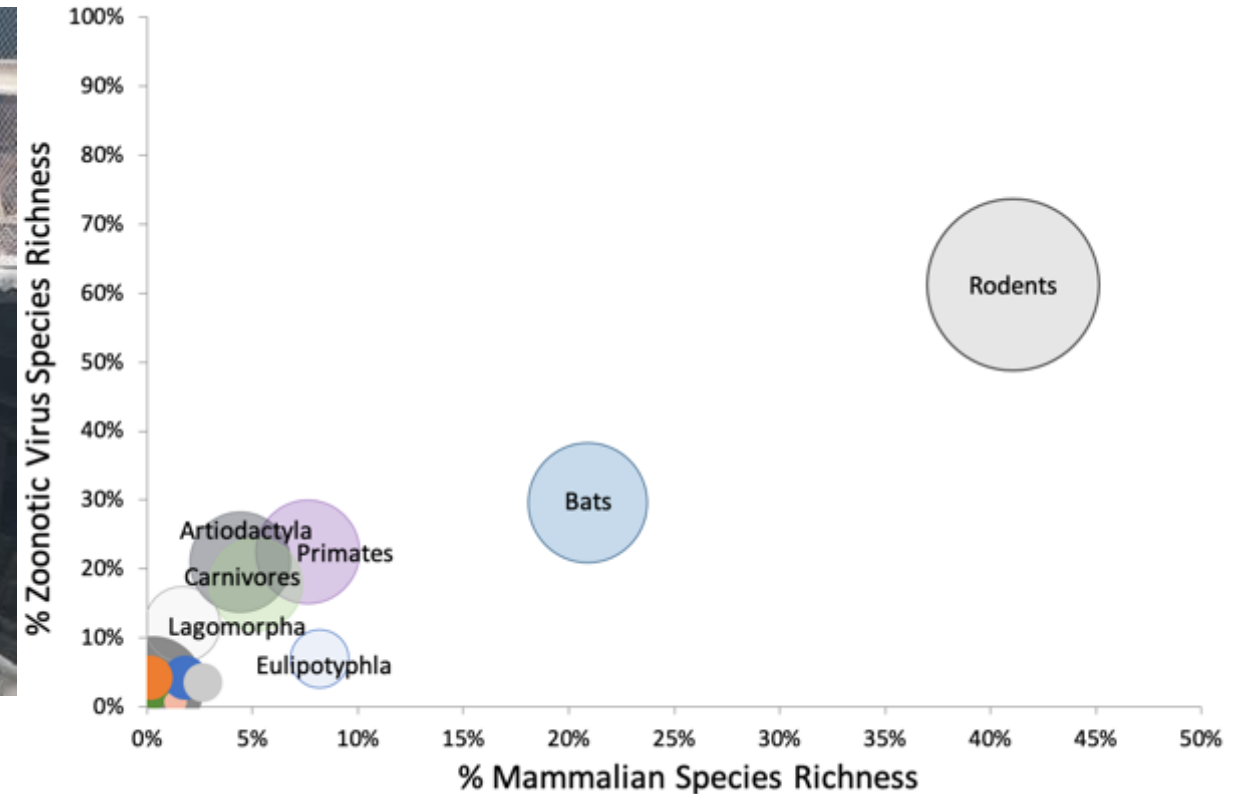
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by species for domesticated animals and humans



by taxonomic order for wildlife

Informing Surveillance for Virus Spillover

variables	IRR ^b	95% confidence interval	p-value
number of pubmed publications by species (log)	1.281	(1.26, 1.30)	<0.001
conservation status ^c			
least concern increasing	1.528	(1.19, 1.95)	0.001
least concern decreasing	0.750	(0.60, 0.94)	0.011
near threatened decreasing	0.347	(0.23, 0.52)	<0.001
vulnerable threatened status	0.169	(0.09, 0.30)	<0.001
endangered threatened status	0.138	(0.07, 0.25)	<0.001
critically endangered threatened status	0.076	(0.03, 0.16)	<0.001
IUCN Criteria for Threatened Status ^d			
population size reduction by direct observation (A1, A2, A4(a))	2.601	(1.62, 4.21)	<0.001
decline in area of occupancy or habitat quality (A1–A4(c))	1.840	(1.02, 3.31)	0.042
population size reduction based on levels of exploitation (A1–A4(d))	2.28	(1.36, 3.83)	0.002
small extent of occurrence (B1)	0.192	(0.07, 0.54)	0.002
Taxonomic Order ^e			
Primates	1.363	(1.13, 1.64)	0.001
Chiroptera	2.112	(1.80, 2.47)	<0.001
Diprotodontia	0.274	(0.12, 0.61)	0.001
Eulipotyphla	0.192	(0.10, 0.36)	<0.001
Domesticated Species	8.051	(5.89, 11.01)	<0.001

Most **common wildlife species**, especially that are increasing in numbers, have shared more viruses with people

Model predicting the number of zoonotic viruses in a species



Informing Surveillance for Virus Spillover

Global shifts in mammalian population trends reveal key predictors of virus spillover risk

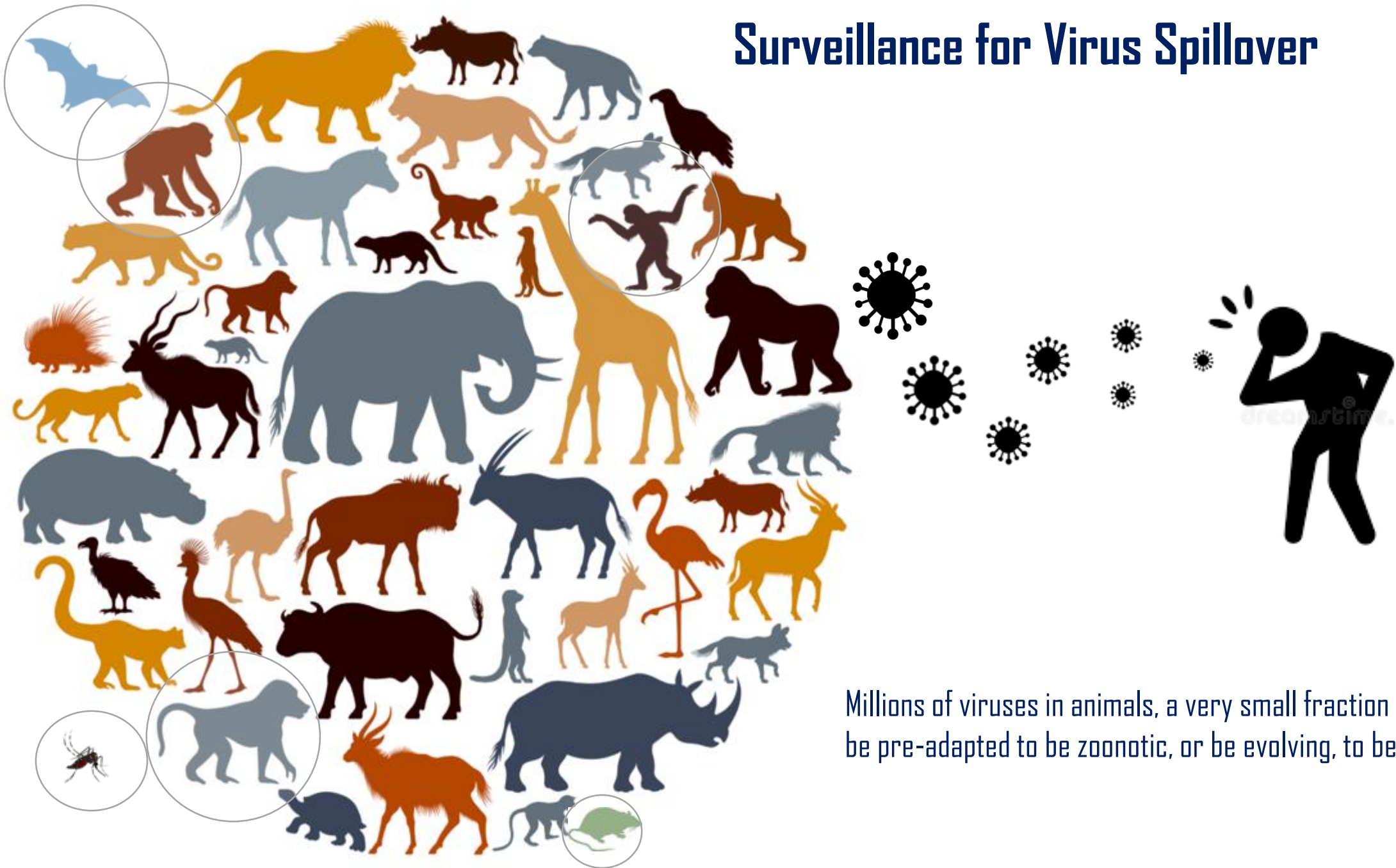
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- Species in global decline because of habitat loss and exploitation shared more viruses with people
- **Declines in habitat for wild** due to deforestation, development, and conversion to cropland - increase disease distribution and animal-human interactions
- **Exploitation of wildlife** through and the live wild animal trade - the perfect epidemiologic setting for spillover

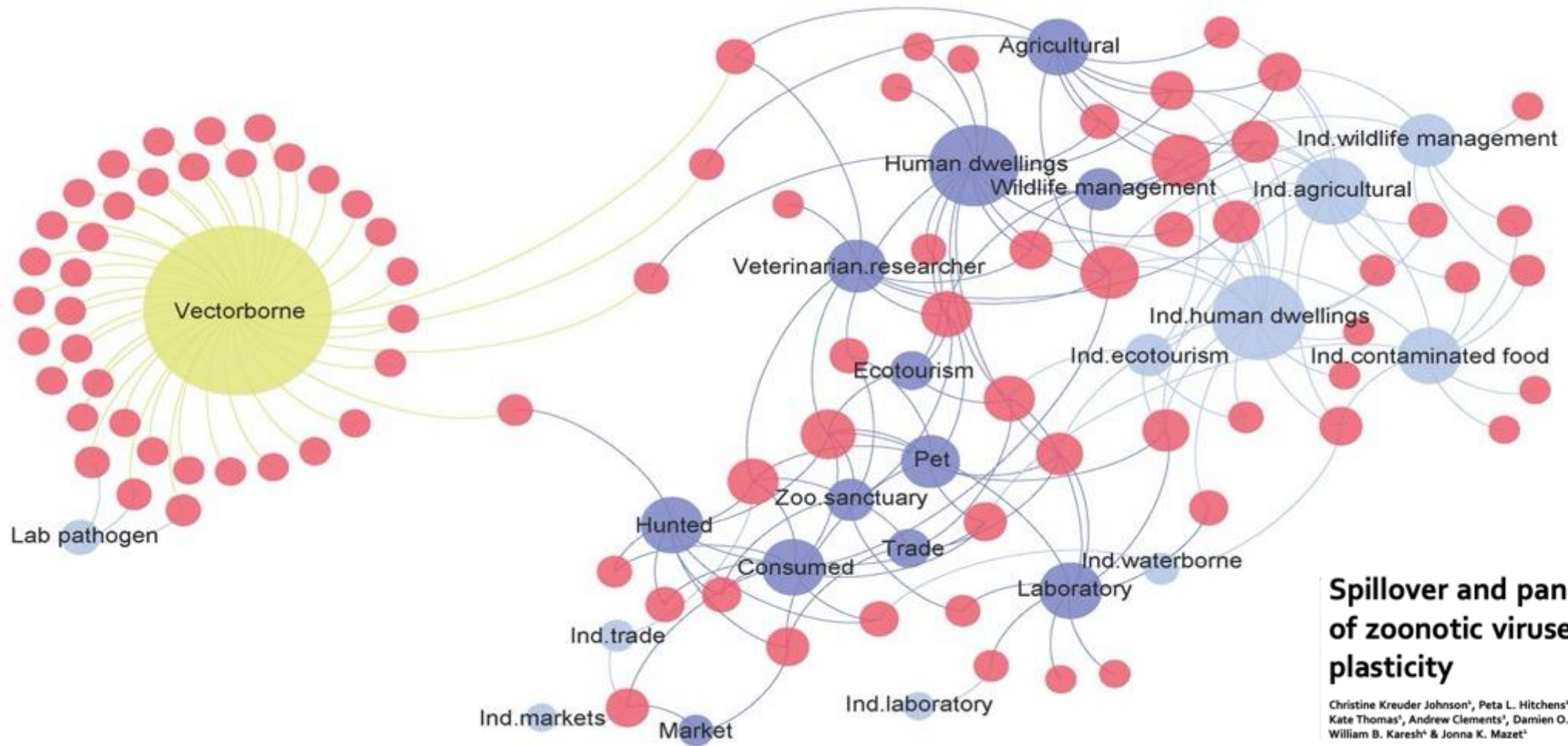


Surveillance for Virus Spillover



Millions of viruses in animals, a very small fraction of which, could be pre-adapted to be zoonotic, or be evolving, to be zoonotic

Fault Lines for Zoonotic Spillover



High-Risk Interfaces with direct and indirect contact with wildlife

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

One Health Surveillance Strategy

for viruses with pandemic potential (disease x)

Improved detection capabilities,
linking healthcare access with laboratory innovations

Acute febrile surveillance at health care facilities



Improved diagnostics for early
detection of threats



One Health Surveillance Strategy

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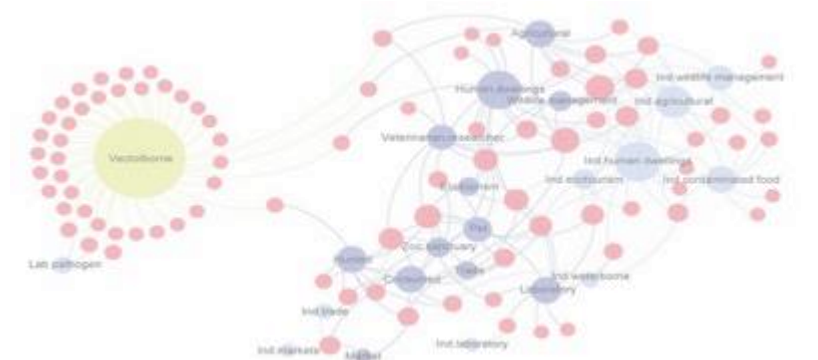
Strengthened capacity for One Health in practice

Longitudinal cohort studies in high-risk communities, and livelihoods to detect rare and emerging threats



Concurrent surveillance in people, wildlife, and vectors

Longitudinal cohort studies in high-risk animals to detect rare and emerging threats



People in contact with animals

Wildlife impacted by landscape change





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Surveillance on the frontiers of disease emergence





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Collaborative Disease Surveillance Workforce





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International Disease Detection Workforce





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One Health Surveillance
for viruses with pandemic potential

Community Leadership,
Government Engagement,
Transformative Change

Readiness in between outbreaks by active
ongoing surveillance





An investment in our future
