Biodiversity Loss and Emerging Infectious Disease

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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

- Pathogen
- Host
- Environment
Something NEW under the sun
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

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

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

- **Pristine forest** (high diversity) - Primate and Vector Community Structure
- **Urban landscape** (low diversity)

- Increasing Risk of Emergence
- High host and virus diversity, more risk of emergence
- Less host and virus diversity, less risk of emergence

- But greater risk of transmission
A Role for Biodiversity in Lowering Disease Risk

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

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

Each virus has unique characteristics

Pathogen  
Host  
Environment
Predicting wildlife reservoirs and global vulnerability to zoonotic Flaviviruses

P. Pandit¹, M. Doyle¹ K. Smart², C. Young¹, G. Drape², C.K. Johnson¹
Similarities across Flaviviruses: Commonalties of Host Traits

Predicting wildlife reservoirs and global vulnerability to zoonotic Flaviviruses

P. Pandit, M. Doyle, K. Smart, C. Young, G. Drape, C.K. Johnson
Similarities across Flaviviruses: Co-occurrence of Potential Hosts

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)

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

- 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

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**Number of zoonotic viruses among threatened species**

**IUCN RED LIST CRITERIA TO EVALUATE FOR THREATENED CATEGORY**

**Population size reduction**

- A1. Population reduction observed, estimated, inferred, or suspected in the past where causes of the reduction are clearly reversible AND understood AND have ceased.
- A2. Population reduction observed, estimated, inferred, or suspected in the past where the causes of reduction may not have ceased OR may not be understood OR may not be reversible.
- A3. Population reduction projected, inferred or suspected to be met in the future.
- A4. An observed, estimated, inferred, projected or suspected population reduction where the time period must include both the past and the future, and where the causes of reduction may not have OR may not be understood OR may not be reversible.

**Geographic range**

- B1. Limited extent of occurrence
- B2. Limited area of occupancy

**Species that declined because of exploitation and habitat loss shared more viruses with people**

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Human Activities Implicated in Spillover Events

Direct and indirect contact with wildlife

Bunyaviridae, Flaviviridae, Togaviridae, Arenaviridae, Rhabdoviridae, Poxviridae, Filoviridae, Paramyxoviridae, Retroviridae, Orthomyxoviridae, Picornaviridae, Reoviridae, Bornaviridae, Coronaviridae, Hepeviridae, Herpesviridae
Relationship between Biodiversity and Emerging Infectious Disease

High host diversity, more animal-human interactions at the edge, greater risk of emergence
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
Most people are unaware of the wild animals living amongst us
Adaptive evolution in urban ecosystems

Colin M. Donihue, Max R. Lambert

Novel species interactions, at high density
Need for surveillance and monitoring in increasingly human-dominated landscapes
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
Emerging Pandemic Threats Program

Strengthening capacity for tackling emerging disease threats

Partnersing with 30 countries
2014-2019
Triangulation - Identify viruses shared among species at high-risk animal-human interfaces

Coordinated One Health Surveillance

Concurrent sampling of wildlife, livestock, and people
One Health Surveillance – in partnership with communities
Clinics in rural high-risk areas

Referral hospitals

One Health Surveillance – in partnership with hospitals

Enrolling patients meeting clinical case definitions
Acute febrile illness
• Severe acute respiratory disease
• Acute encephalitis
• Hemorrhagic fevers

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

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

- Local partner and stakeholder engagement
- Implementing partnerships with clinics and hospitals
- Training in surveillance protocols
- Design of animal and human data collection tools for P2
- IACUC revision
- IRB development
- Engagement of national and international partners in prioritization of surveillance sites
- Community engagement
- IRB approvals for human subjects research
- Community engagement
- Community engagement
- Community engagement
One Health Surveillance

as of June 2018
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
Sampling and Testing Effort

PREDICT 2009-2014
466,055 tests
180 known viruses
820 new viruses
Benefits and risks from bats
Reducing risk and contact with bats
Behavior change towards interventions

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


Living Safely with Bats
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.

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

Virus with High Host Plasticity
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
Government Engagement, Policy Change
Community Engagement, Behavior Change
Data Sharing

https://www.healthmap.org/predict/
Vigilant Surveillance Essential to Timely Response, Timely Response Essential to Vigilant Surveillance

– Larry Madoff
Thank you, PREDICT CONSORTIUM