One Health surveillance for emerging infectious diseases

Pranav Pandit
BVSc & AH, MPVM, PhD
EpiCenter for Disease Dynamics,
One Health Institute, School of Veterinary Medicine,
University of California Davis

@PanditPranav
Pathways to emergence

Evolutionary trajectory

Stage 1: Wildlife reservoirs only
Stage 2: Primary Spillover
Stage 3: Short outbreaks
Stage 4: Prolonged outbreaks
Stage 5: Sustained human to human transmission

Animal ecology, population biology, biogeography, behavioural ecology, landscape ecology, agricultural sciences

Disease ecology, animal epidemiology, infectious disease dynamics, immunology, microbiology, veterinary medicine

Microbiology, disease ecology, vector ecology, epidemiology, spatial ecology, infectious disease dynamics

Human epidemiology, medical anthropology, vector ecology, social sciences, behavioural ecology, infectious disease dynamics

Microbiology, innate and adaptive immunology, cell biology of pathogen–host interactions, pathology, genetics, evolutionary biology

Plowright et al. 2017, Sokolow et al 2019

Johnson, Rushmore, Smiley Evans, Gardner, Pandit
Where to look for Flaviviruses in Wildlife?

Predicting regions with high diversity of wildlife hosts
Global distribution of *Flaviviruses*

- Mostly vector borne
  - Mosquitoes and Ticks
- Endemic in regions of the World: JEV, DENV
- Emerging in new regions: Zika, WNV
- Threat to vulnerable populations
  - New World Primates: Yellow fever
  - Yellow-billed Magpie: West Nile virus
Why we need to know wildlife hosts of Flaviviruses?

• Wildlife hosts promote viral evolution
• Potential zoonotic sources of recurring epidemics

• Difficult to detect positive species
  • Logistics of sampling species from remote habitats
  • Short shedding periods

• Can we predict unknown hosts by looking at known hosts?
Wildlife Hosts

140 mammal species (Out of 5536)
277 avian species (Out of 10424)

Mosquitoes
- Aedes aegypti: 7
- Culex pipiens: 6
- Culex annulirostris: 6
- Aedes albopictus: 5
- Culex tritaeniorhynchus: 5
- Culex perfuscus: 5
- Aedes vexans: 5
- Culex quinquefasciatus: 5
- Aedes africanus: 5

Ticks
- Dermacentor marginatus: 3
- Dermacentor silvarum: 3
- Hyalomma marginatum: 3
- Amblyomma variegatum: 2
- Rhipicephalus muhsamae: 2
- Ornithodoros capensis: 2
- Ixodes ricinus: 2
- Haemaphysalis longicornis: 2
- Haemaphysalis concinna: 2
- Haemagogus lucifer: 2
Distribution of Predicted Hosts

Yellow fever virus and Zika virus
Distribution of Predicted Hosts

Japanese encephalitis virus
Targeted surveillance of wildlife

<table>
<thead>
<tr>
<th>Viruses</th>
<th>Number of predicted hosts</th>
<th>Known hosts</th>
</tr>
</thead>
<tbody>
<tr>
<td>Yellow fever, Zika</td>
<td>112</td>
<td>14</td>
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<td>West Nile, St. Louis, Usutu</td>
<td>708</td>
<td>254</td>
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<td>Dengue</td>
<td>173</td>
<td>23</td>
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<tr>
<td>Japanese encephalitis</td>
<td>408</td>
<td>20</td>
</tr>
</tbody>
</table>
Wildlife surveillance for early detection of wildlife health events

Unusual wildlife events that increase pathogen release from wildlife hosts
Wildlife rehabilitation centers as wildlife health indicators

• Rehabilitation Centers assimilate large amounts of data
• Uniquely poised to advance knowledge of threats to wildlife health and populations

• Intelligent surveillance system is essential to:
  • Assimilate and process large amounts of data
  • Identify spatio-temporal trends in wildlife admissions
  • Provide real-time information on wildlife health events
Wildlife Morbidity and Mortality Event Alert System (WMMEAS)

- Runs parallel to the Wildlife Rehabilitation Database (WRMD)
- California wide: 30 participating centers participate data real-time
Wildlife Morbidity and Mortality Event Alert System (WMMEAS)

https://www.wmmeas.health/
Mallard: all cases

Accipitridae: all cases

Striped Skunk: Neurological cases
Outbreak investigation

Neurological cases in Rock Pigeon

- Monthly, biweekly, and weekly alerts
  - Neurological cases in *Columba livia*
Pigeon Paramyxovirus Type 1 (PPMV-1) outbreak in Columbids

- PPMV-1 Outbreak in 2017 in Columbids
- Detected in various Doves and Pigeons
- Pathogen of concern, can spillover to native wildlife
Early indication of health events

- Comparison with **strandings observed in independent surveillance system**.
- SARIMAX model
- WMMEAS (lag of first order) is significantly associated with the marine birds stranding observed in the BEACHCOMBERS data ($p > 0.001$).
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Zoonotic transmission risk of novel viruses

Evolutionary trajectory of novel viruses

Predicting the potential for zoonotic transmission and host associations for novel viruses

UC Davis Veterinary Medicine

One Health Institute

USAID PREDICT
Risk-based Surveillance of Wildlife

- Influenza viruses
- Coronaviruses
- Paramyxoviruses
- Filoviruses
- Flaviviruses
Network Based Approach for understanding zoonotic risk

• For data driven quantification of zoonotic risk and to prioritize viruses for further in-vivo characterization

  • Grange et al (2021) presented an opinion-based ranking of novel viruses.

• Host-virus networks behave similar to social networks and missing links can help understand zoonotic potential of viruses.
Quantifying zoonotic risk

Developed prioritization score:
- Number of predicted human links (support) and
- Average probability of links formed due to sharing human as host

Prioritization scores for known zoonotic and non-zoonotic viruses.
Key ecological insights in ecology of novel viruses

- Novel viruses are more host specific than previously recognized viruses
  - Longer tails of $G_{\text{predicted}}$ compared to $G_C$
  - Lower centrality measures for novel viruses compared to recognized viruses

- Novel coronaviruses predicted to infect a greater number of species novel viruses from other families.
  - Significantly higher predicted network centralities

- Prioritization score:
  - Data driven metric to quantify zoonotic risk for novel viruses.
  - Requires the data on hosts and virus families
Key animal-human interfaces for zoonotic transmission

Understanding human exposure
Key Animal-Human Interfaces

Dr. Pranav Pandit
BVSc & AH, MPVM, PhD
@PanditPranav