Big Data for Global Health: Shifting to prevention paradigm for emerging infectious diseases

Jonna Mazet
One Health Institute
School of Veterinary Medicine
University of California, Davis
U.S.A.
The Challenge

Pre-empt or combat, at their source, the first stage of emergence of zoonotic diseases that pose a significant threat to public & animal health (potentially pandemic infections)
PREDICT

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

Source: Karesh et al. 2012. The Lancet & WHO
One Health in Action

Source: Karesh et al. 2012. The Lancet & WHO
PREDICT Strategy

An iterative and adaptive process

• Modeling to help focus surveillance
• Targeting key interfaces & species
• Pathogen diagnostics and discovery
  • Molecular identification
  • Both known and unknown agents
• Informatics & Reporting
Scientific Strategy: Interface Risk

Identify human activities with frequent and direct contact with animals facilitating transmission of zoonotic viruses

Adapted from Kreuder Johnson et al. Nature Scientific Reports, 2015
Bat Guano Farms

Vietnam, Cambodia & Thailand
Targeted, Risk-based Surveillance

High Risk Interfaces
Specific situations enabling contact between wild animal hosts and people

Large-scale Ecological Drivers
Wildlife biodiversity
Human population density
Land use change
Agricultural industry change

Pathogen

Zoonotic disease emergence in humans

Host

Environment
MAJOR GLOBAL ACHIEVEMENTS
Safely Sampled More than 56,000 Animals
PREDICT-1 Viral Detection Success

Overall 984 known and new viruses:

- 812 novel and 147 known in animals
- 3 novel and 31 known in human pilot studies

<table>
<thead>
<tr>
<th></th>
<th>Bats</th>
<th>Nonhuman Primates</th>
<th>Rodents and Shrews</th>
<th>Humans</th>
<th>Other taxa**</th>
<th>TOTAL</th>
</tr>
</thead>
<tbody>
<tr>
<td>Novel</td>
<td>431</td>
<td>234</td>
<td>143</td>
<td>3</td>
<td>9</td>
<td>820</td>
</tr>
<tr>
<td>Known</td>
<td>80</td>
<td>55</td>
<td>15</td>
<td>31</td>
<td>1</td>
<td>182</td>
</tr>
<tr>
<td>Total</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>1002*</td>
</tr>
</tbody>
</table>
## Viruses Detected in 28 Viral Families

<table>
<thead>
<tr>
<th>Viral family</th>
<th>Novel Bat</th>
<th>Known Bat</th>
<th>Novel Primate</th>
<th>Known Primate</th>
<th>Novel Rodent/Shrew</th>
<th>Known Rodent/Shrew</th>
<th>Novel Human</th>
<th>Known Human</th>
</tr>
</thead>
<tbody>
<tr>
<td>Adenovirus</td>
<td>53</td>
<td>3</td>
<td>6</td>
<td>4</td>
<td>32</td>
<td>1</td>
<td>1</td>
<td>3</td>
</tr>
<tr>
<td>Astrovirus</td>
<td>153</td>
<td>33</td>
<td>19</td>
<td>3</td>
<td>31</td>
<td>1</td>
<td>0</td>
<td>1</td>
</tr>
<tr>
<td>Coronavirus</td>
<td>61</td>
<td>30</td>
<td>3</td>
<td>0</td>
<td>6</td>
<td>0</td>
<td>0</td>
<td>2</td>
</tr>
<tr>
<td>Dependovirus</td>
<td>0</td>
<td>0</td>
<td>11</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>Flavivirus</td>
<td>3</td>
<td>0</td>
<td>0</td>
<td>1</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>Hantavirus</td>
<td>3</td>
<td>1</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>2</td>
<td>0</td>
<td>1</td>
</tr>
<tr>
<td>Herpesvirus</td>
<td>46</td>
<td>0</td>
<td>48</td>
<td>25</td>
<td>43</td>
<td>6</td>
<td>0</td>
<td>5</td>
</tr>
<tr>
<td>Orbivirus</td>
<td>1</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>Paramyxovirus</td>
<td>63</td>
<td>7</td>
<td>0</td>
<td>2</td>
<td>11</td>
<td>2</td>
<td>0</td>
<td>3</td>
</tr>
<tr>
<td>Polyomavirus</td>
<td>27</td>
<td>1</td>
<td>4</td>
<td>3</td>
<td>8</td>
<td>0</td>
<td>0</td>
<td>1</td>
</tr>
<tr>
<td>Arenavirus</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>7</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>Rhabdovirus</td>
<td>19</td>
<td>0</td>
<td>2</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>Seadornavirus</td>
<td>1</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>Bocavirus</td>
<td>0</td>
<td>2</td>
<td>1</td>
<td>3</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>Enterovirus</td>
<td>0</td>
<td>0</td>
<td>5</td>
<td>4</td>
<td>2</td>
<td>0</td>
<td>0</td>
<td>5</td>
</tr>
<tr>
<td>Retrovirus</td>
<td>0</td>
<td>0</td>
<td>4</td>
<td>7</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>1</td>
</tr>
<tr>
<td>Alphavirus</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>1</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>Poxvirus</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>1</td>
<td>1</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>Influenza</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>1</td>
<td>0</td>
<td>0</td>
<td>5</td>
</tr>
<tr>
<td>Mononegavirales</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>Papillomavirus</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>Picobirnavirus</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>120</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>Picornavirus</td>
<td>0</td>
<td>0</td>
<td>4</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>Picornavirales</td>
<td>0</td>
<td>0</td>
<td>4</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>Phlebovirus</td>
<td>1</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>Rotavirus</td>
<td>0</td>
<td>0</td>
<td>1</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
</tbody>
</table>
Novel beta CoV from bat guano

Thailand bat CoV

MERS-CoV, Saudi Arabia

Wacharapluesadee et al.  
Emerging Infectious Diseases, 2013
Informing on Surveillance

Viral Discovery Curves:
Number of samples for testing to discover all new viruses

Anthony et al. *mBio*, 2013
<table>
<thead>
<tr>
<th>Variable</th>
<th>Relative Influence (%)</th>
<th>Std. Dev.</th>
</tr>
</thead>
<tbody>
<tr>
<td>population</td>
<td>27.99</td>
<td>2.99</td>
</tr>
<tr>
<td>mammal diversity</td>
<td>19.84</td>
<td>3.30</td>
</tr>
<tr>
<td>change: pop</td>
<td>13.54</td>
<td>1.54</td>
</tr>
<tr>
<td>change: pasture</td>
<td>11.71</td>
<td>1.30</td>
</tr>
<tr>
<td>urban extent</td>
<td>9.77</td>
<td>1.62</td>
</tr>
</tbody>
</table>

**Predicted Relative Risk of Zoonotic EID Events**

The map shows the predicted relative risk of zoonotic EID events across the world, with the relative influence and standard deviation indicated for various variables:

- **Population**: 27.99% relative influence with a standard deviation of 2.99.
- **Mammal Diversity**: 19.84% relative influence with a standard deviation of 3.30.
- **Change in Population**: 13.54% relative influence with a standard deviation of 1.54.
- **Change in pasture**: 11.71% relative influence with a standard deviation of 1.30.
- **Urban Extent**: 9.77% relative influence with a standard deviation of 1.62.
Information Flow & Ministerial Engagement
With Governments: Making Data Available to the Public

A new Adenovirus, PREDICT_AdV-8, was found in 1 Indian flying fox (Pteropus giganteus). The samples were collected in Feb 2008.

There is no evidence at this time to suggest this virus poses a threat to human health.

Click here to access this virus in Genbank
Scientific Strategy: Virus Risk

Expanded characterization of viruses with epidemic and unknown pandemic potential combined with risk assessment

\[
\text{Virus-independent traits} + \text{Virus-specific traits} = \text{Spillover risk}
\]

\[
\text{Pandemic risk}
\]
Triangulating with EPT Partners

- Use reporting infrastructure established by our EPT partners
- Prioritize field sites with EPT partners
- Share best practices and protocols for fieldwork, data collection and laboratory testing
- Collect data using common data collection templates
Scientific Strategy: Ecological Risk

- Identify large-scale transboundary ecological processes underlying human activities at high-risk interfaces
- Characterize pathways for disease emergence
- Evaluate behaviors and potentially palatable changes to activities to mitigate risk
What Do We Know?
Drivers for Disease Emergence are Intensifying

Rapidly increasing human population
Drivers for Disease Emergence are Intensifying

Emerging Threats Program

Global Health Security and Development
Drivers for Disease Emergence are Intensifying

Emerging Threats Program

- Rapidly increasing human population
- Increasing domestic animal production
- Increasing crop production
- Increasing natural resource extraction

Expanding Settlements + Increasing domestic animal production + Increasing crop production + Increasing natural resource extraction = Increasing animal-human contact and spillover rate

All Drive Habitat Change

Global Health Security and Development
Small proportion of viruses capable of infecting humans

Potential zoonotic virus diversity

Viral host diversity

Spillover into humans

Few hosts harbor zoonotic viruses
Towards a proactive paradigm for early disease detection and response

One Health approach to understanding the dynamics of zoonotic virus evolution, spillover from animals to people, amplification, and spread to inform prevention and control