Drivers of Infectious Diseases: Connections Matter

Clinician Outreach and Communication Activity (COCA) Call
May 12, 2016
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Objectives

At the conclusion of this session, the participant will be able to:

- Identify key drivers of zoonotic infectious disease emergence
- Describe approaches to identifying risk factors for zoonotic diseases
- Describe the difference between disease occurrence mapping and correlation-based disease risk mapping
Today’s Presenter

William B. Karesh, DVM
Executive Vice President, Health & Policy
EcoHealth Alliance
Drivers of Infectious Disease: Connections Matter

William B. Karesh, DVM

Executive Vice President for Health and Policy, EcoHealth Alliance
President, OIE Working Group on Wildlife
Co-Chair, Wildlife Health Specialist Group, International Union for the Conservation of Nature

Local conservation. Global health. The findings and conclusions in this presentation are those of the author(s) and do not necessarily represent the views of the Centers for Disease Control and Prevention.
Zoonoses

Zoonotic disease organisms include those that are endemic in human populations or enzootic in animal populations with frequent cross-species transmission to people...

...with endemic and enzootic zoonoses causing about a billion cases of illness in people and millions of deaths every year.”

Karesh, et al., The Lancet, Dec 1, 2012
Temporal patterns in EID events

- EID events have increased over time, correcting for reporter bias (GLM$_{P,JID}$ F = 86.4, p < 0.001, d.f.=57)
- ~5 new EIDs each year
- ~3 new Zoonoses each year
- **Zoonotic EIDs from wildlife** reach highest proportion in recent decade

Jones et al. 2008
Spatial patterns in EID events

Jones et al. 2008
Relative risk of a new zoonotic EID

<table>
<thead>
<tr>
<th>factors</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>
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<td>...</td>
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</tbody>
</table>
“The emergence of zoonoses, both recent and historical, can be considered as a logical consequence of pathogen ecology and evolution, as microbes exploit new niches and adapt to new hosts...

Although underlying ecological principles that shape how these pathogens survive and change have remained similar, people have changed the environment in which these principles operate.”

Karesh, et al., The Lancet, Dec 1, 2012
Pasture Data

Source: Ramankutty and Foley, Department of Geography, McGill University

Description: Global historical pasture dataset, available at an annual timescale from 1700 to 2007 and at 0.5 degree resolution.

Proportion of land devoted to pasture, 1900 vs 2000
Original v. New Hotspots Model

Original hotspots model (100km)  
New hotspots model v2.0 (100km)  
Includes anthropogenic activities
Drivers of Disease Emergence in Humans

- Land-use change
- Agricultural industry change
- Int’l travel and commerce
- Medical industry change
- War and famine
- Climate and weather
- Human demography & behavior
- Other
- Breakdown of public health
- Bushmeat
- Food industry change

E. Loh et al. 2015. Vector-borne and Zoonotic Diseases 15(7)
Country-Level Drivers of Disease Emergence

- Land use changes: 26%
- Agricultural intensification: 18%
- Human susceptibility to infection: 13%
- Antimicrobial agent use: 13%
- Food industry changes: 7%
- War and famine: 4%
- Bushmeat: 2%
- Other: 2%

[Map showing distribution of disease emergence across the world]
Actionable information to target surveillance and prevention

Land use change n= 39

Agricultural industry change n=27

Medical industry change n=11
Global Distribution of relative risk of EID events

a) Zoonotic pathogens from wildlife
b) Zoonotic pathogens from domestic animals
c) Drug resistance pathogens
d) Vector-borne pathogens

Jones et al. Nature 2008
Drivers of Foodborne EID events

- Food industry changes
- Human susceptibility
- International travel
- Antimicrobial resistance
- Human demography
- Agricultural intensification
- War and famine
- Medical industry changes
- Climate and Weather
- Breakdown public health
- Other
- Land use change

Foodborne EID events 1940-2004 (n=100)

A Day in a Food Market
1,000,000,000 Kgs / Year (Central Africa)
BioGeography of Human Infectious Diseases

Based on similarity analysis of zoonotic human infectious disease assemblages at country level.
Global vulnerability index

- Calculating index
  - $E_i = \text{Jones et al. hotspots}$
  - $C_{ij} = \text{Est. Number of passengers}$
  - $H_i = \text{Healthcare spending per capita}$
    - $i = \text{source of risk}$
    - $j = \text{destination of risk}$
    - $\phi_j = \sum_{all\,i} \frac{C_{ij} \cdot E_i}{H_i}$

- We then interpolate risk out from airport locations globally
- Using Inverse Distance Weighted interpolation
EID risk per airport

Hosseini et al. (in review)
Our prediction of which countries were at risk for Ebola spread
July 31st 2014

Red = earliest arrival; Green = last arrival. Grey = countries that can’t be reached in 2 legs or less.

There are 10 countries that can be arrived at via direct flights, and 95 that can be reached by flights of two legs or less.
EcoHealth Alliance HP3 Database

2755 unique mammal-virus associations

768 mammal species
  • 374 genera, 80 families, 15 orders

590 ICTV unique viruses found in mammals
  • 382 RNA; 208 DNA viruses
  • 258 of all these viruses have been detected in humans (44%)
  • 93 exclusively human.
  • 165 (64%) of human viruses are ‘zoonotic’

Olival et al. In Review: NATURE
Observed viral richness varies little by Order, but proportion of zoonotic viruses does.
Phylogenetic Distance to Humans Significant Predictor of the Number of Shared Viruses

Olival et al. In Prep
Climate Change and Emerging Diseases

Future Climate Change Scenario for the distribution of Nipah virus. Year 2050, optimistic scenario (B2). Red areas show new potential areas for virus spread.
Background on Leptospirosis

- Leptospirosis is a widespread zoonotic disease
  - Can affect a wide variety of domestic animals and wildlife, as well as humans
- Caused by *Leptospira*, an anaerobic spirochete
IDEXX Data Overview

Extent of MAT and PCR Testing Coverage for Leptospirosis across the Contiguous United States

Legend
- Test(s) Submitted
- No Tests Submitted

Source: IDEXX Laboratories
MAT Results

Number of Positive MAT Tests per County

Legend
Number Positive
- 0
- 1 - 5
- 6 - 10
- 11 - 20
- 21 - 100
- 101 - 670
- No Data

Source: IDEXX Laboratories
Spatial Clusters: Percent of Tests Positive

Clusters of Positive PCR Results: Proportion of Positive Results to Total Tests

Clusters of Positive MAT Results: Proportion of Positive Results to Total Tests
Dog Population Data

- Used county-level human population census data to estimate population of dogs per county
- Assuming that within each state, dogs are distributed within the state similar to humans

- Human population data from US Census
- State-level data for dogs from AVMA US Pet Demographics Sourcebook 2012
Spatial Clusters: Positive Tests per Estimated County Dog Population

Clusters of Positive PCR Results:
Positive Tests per Estimated Dogs

Clusters of Positive MAT Results:
Positive Tests per Estimated Dogs
Leptospirosis Vaccination

Number of Dogs Vaccinated per State 2010-2014

Four-Year Vaccination Numbers per Estimated Dog Population by State

Source: Zoetis Inc.
Possible Importance of Rainfall

Determine how other factors could affect transmission and support the ability to predict an outbreak
Climatic Variables

- Climate Data
  - Mean Precipitation
  - Mean Temperature
  - Bioclimatic Data
    - Represents annual trends, seasonality, and extreme factors (e.g., temperature in coldest month)
Income and Education Data

Distribution of Education Levels By County

Scatterplot of Income and Education

EcoHealth Alliance
Partial Dependence Plots: MAT Results

deciduous_forest_2011 (10.7%) 19_precip_coldest_quarter_average  shrub_scrub_2011 (6.1%)  developed_low_intensity_2011 (5.2%)

pasture_hay_2011 (4.9%)  temp_average (4.8%)  8_precip_warmest_quarter_average  woody_wetlands_2011 (4.1%)

precip_average (3.8%)  16_precip_wettest_quarter_average  median_income (3.2%)  mixed_forest_2011 (3.1%)
## Boosted Regression Tree Results

### PCR Model: Top 5 Predictors

<table>
<thead>
<tr>
<th>Variable</th>
<th>Relative Influence</th>
</tr>
</thead>
<tbody>
<tr>
<td>Evergreen Forest Cover</td>
<td>12.24919776</td>
</tr>
<tr>
<td>Shrub/Scrub Cover</td>
<td>9.887439268</td>
</tr>
<tr>
<td>Grassland/Herbaceous Cover</td>
<td>7.161191081</td>
</tr>
<tr>
<td>Developed Open Space Cover</td>
<td>6.195173737</td>
</tr>
<tr>
<td>Median Income</td>
<td>5.81007611</td>
</tr>
</tbody>
</table>

### MAT Model: Top 5 Predictors

<table>
<thead>
<tr>
<th>Variable</th>
<th>Relative Influence</th>
</tr>
</thead>
<tbody>
<tr>
<td>Deciduous Forest Cover</td>
<td>10.6624204</td>
</tr>
<tr>
<td>Average Precipitation in Coldest Quarter</td>
<td>8.622065784</td>
</tr>
<tr>
<td>Shrub/Scrub Cover</td>
<td>6.067515302</td>
</tr>
<tr>
<td>Developed Low Intensity Cover</td>
<td>5.785643682</td>
</tr>
<tr>
<td>Pasture/Hay Cover</td>
<td>4.897024777</td>
</tr>
</tbody>
</table>
Predictive Modeling Results by County

Inverse Logit Transformed Prediction by County: PCR

Inverse Logit Transformed Prediction by County: MAT
Summary of Final Results: MAT

Inverse Logit Transformed Prediction by County: MAT

Clusters of Positive MAT Tests Relative to the Estimated County Dog Population
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Local conservation.
Global health.
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  - “Click” the Q&A tab at the top left of the webinar tool bar
  - “Click” in the white space
  - “Type” your question
  - “Click” ask

- **On the Phone**
  - Press Star (*) 1 to enter the queue
  - State your name
  - Listen for the operator to call your name
  - State your organization and then ask your question
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Atlanta, Georgia
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