EFFECTS OF DIVERSITY, TOPOGRAPHY, AND INTERANNUAL CLIMATE VARIABILITY ON PATHOGEN SPILLOVER

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Emerging Infectious Diseases (EIDs)

New in a population, or known but rapidly increasing

EIDs - Pathogen Spillover

“when disease epidemics are driven by transmission from an alternate reservoir host population” – Power & Mitchell (2004)


Cobb et al. 2010
EIDs - Pathogen Spillover

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Global Land and Ocean Temperature Anomalies, February
Disease Triangle

Pathogen

Susceptible Host(s)

Favorable Environment
Sudden Oak Death (SOD)

*Phytophthora ramorum* (oomycete) - water mold

Diagram showing the intersection of SOD affecting trees and shrubs in California forests.
Pathogen Spillover (SOD)

Asymmetry in host competency for pathogen transmission & reproduction
Research Question

How does environmental variation influence pathogen spillover?
Analytical Framework - SEM

Structural Equation Model
Relate observation to theory
Examine direct & indirect effects

Microclimate

Defines hypotheses
(independence claims)

Landscape

Disease

Community
Data - Spillover
Data - Spillover

~200 disease monitoring plots, 10 years

Ecology

Microclimate
Data Processing

Gaps in record
Data Processing

Gaps in record
Data Processing

Filled microclimate

Tonini et al. 2016. Spatio-temporal reconstruction of missing forest microclimate measurements
https://github.com/f-tonini/Microclimate-Sonoma
Data - Spillover

#SODsquad2016
Analytical Framework - SEM

Structural Equation Model
- Relate observation to theory
- Examine direct & indirect effects

Defines hypotheses (independence claims)
Path Model – Piecewise Modeling

Test independence claims using the C-statistic (Shipley 2000, 2004, 2009)

Mixed-effects models

Defines hypotheses (independence claims)
Path Model – Spillover

Topographic Wetness Index

Bay Laurel Density

Shannon's Diversity

Avg. Wet-Hours 14-22C

Symptomatic Leaf Count

Dry-Season Hours >25C

Disease Prevalence

Standardized path coefficients

0.04ns

0.06

-0.24

0.08

0.03

0.20

0.20

0.49

0.62

0.20 – 0.49

0 – 0.19

≥ 0.50

Negative

Positive

0.04ns

0.06

-0.24

0.08

0.03

0.20

0.20

0.49

0.62

0.20 – 0.49

0 – 0.19

≥ 0.50

Negative

Positive
Net Effects on Pathogen Spillover

Diversity: -0.58
Landscape (TWI): +0.19
Wet-days temperature: +0.21
Dry-season temperature: -0.05

Questions...?
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Spillover to dead end hosts (mortality) may increase reservoir host abundance
Path Model – Spillover

Unstandardized path coefficients

Topographic Wetness Index

Bay Laurel Density

Shannon’s Diversity

Avg. Wet-Hours 14-22C

Symptomatic Leaf Count

Dry-Season Hours >25C

Disease Prevalence

--- Negative

--- Positive

Path Model

Spillover

0.37 ns

0.51

0.01

0.19

0.07

0.21

0.29

0.37

0.11

1.69

124.21
EIDs - Pathogen Spillover

“when disease epidemics are driven by transmission from an alternate reservoir host population” – Power & Mitchell (2004)

Two Major Pathways of Spillover

1. the rate of intraspecific transmission in non-reservoir hosts may be too low to support epidemic or endemic disease. In this case, sustained transmission from a reservoir population is necessary to maintain disease in the non-reservoir population

2. there may be potential for sufficient intraspecific transmission to support a pathogen epidemic, but the pathogen is absent from the population when exposed to transmission from a reservoir.
Pathogen Spillover & Coexistence

Overstory Species Abundance

<table>
<thead>
<tr>
<th>Species</th>
<th>2005</th>
<th>2014</th>
</tr>
</thead>
<tbody>
<tr>
<td>arme</td>
<td>306</td>
<td>265</td>
</tr>
<tr>
<td>psme</td>
<td>329</td>
<td>325</td>
</tr>
<tr>
<td>quag</td>
<td>659</td>
<td>652</td>
</tr>
<tr>
<td>quch</td>
<td>100</td>
<td>109</td>
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<td>368</td>
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<td>quke</td>
<td>277</td>
<td>194</td>
</tr>
<tr>
<td>umca</td>
<td>8</td>
<td>112</td>
</tr>
</tbody>
</table>

Species: arme, psme, quag, quch, quga, quke, umca

Abundance: 0-1500
## Assessing Model Fit – Basis Set

<table>
<thead>
<tr>
<th>Variable 1</th>
<th>Variable 2</th>
<th>Conditioning Set</th>
</tr>
</thead>
<tbody>
<tr>
<td>disease prevalence</td>
<td>topographic index</td>
<td>diversity, symptomatic leaf count, hours &gt; 25°C</td>
</tr>
<tr>
<td>bay laurel density</td>
<td>diversity</td>
<td>topographic index</td>
</tr>
<tr>
<td>hours &gt; 25°C</td>
<td>diversity</td>
<td>bay laurel density, topographic index</td>
</tr>
<tr>
<td>disease prevalence</td>
<td>bay laurel density</td>
<td>topographic index, symptomatic leaf count, hours &gt; 25°C, diversity</td>
</tr>
</tbody>
</table>

$$C = -2 \sum_{i=1}^{k} \ln(P_i)$$
Assessing Model Fit – Model Pieces

\[
m1 <- \text{lm}(\text{Diversity} \sim \text{log(Topographic Index)})
\]

\[
m2 <- \text{lmer}(\text{log(Bay Density)} \sim \text{log(Topographic Index)} + (1 | \text{sample_year}) + (1 | \text{plotid}))
\]

\[
m3 <- \text{lmer}(\text{log(Symptomatic Leaf Count)} \sim \text{log(Bay Density)} + \text{Diversity} + \text{log(Topographic Index)} + \text{# of hours > 25 C} + (1 | \text{sample_year}) + (1 | \text{plotid}))
\]

\[
m4 <- \text{lmer}(\text{# of hours > 25 C} \sim \text{log(Bay Density)} + \text{Diversity} + (1 | \text{sample_year}) + (1 | \text{plotid}))
\]

\[
m5 <- \text{glmer}(\text{Disease Prevalence} \sim \text{log(Symptomatic Leaf Count} \text{+ log(# of hours >25 C)} + \text{log(Bay Density)} + \text{Diversity} + (1 | \text{sample_year}) + (1 | \text{plotid}), \text{family} = \text{binomial(link = "logit")})
\]
Pathogen Hotspots