Update: Modeling transmission of bovine tuberculosis in Uruguay using dynamic cattle movement networks - A potential model for the US

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Bovine TB in Minnesota, 2005-2009

• Identified in cow at slaughter plant
  – 12 infected beef cattle herds
  – 27 free-ranging deer

• Source and transmission
  – All but 2 herds connected through known cattle movements
  – M. bovis in positive cattle and deer linked to isolates from cattle in SW US and Mexico
Bovine TB surveillance

• Limitations
  – Slaughter surveillance only: 5 year delay in detection of infected herds (Fischer, 2005)
  – Impossible to perform cost-effective TB testing in all herds

• How to target surveillance?
  – Focus on the strata of the population more likely to have a case of disease as a consequence of their risk profile
  – Cattle movements
    • 90% of purchased cattle in index herd in 2005 MN BTB outbreak originated in other states (Shaw, 2008)
    • Number of cattle introductions and origin of trace-in cattle are known risk factors for Bovine TB (APHIS, 2009)
How evaluate cattle movement data as risk for disease transmission?

- Social Network Analysis uses **graph theory** and the **social science** of interactions
- A network of contacts is represented by a graph with **“nodes”** (individuals) connected by **“edges”** (contacts or movements)
- Model the **contact structure** of population based on **behavior** of individuals
Uruguay

• Complete, electronic-based animal traceability system for cattle.

• Since 2011, all cattle uniquely identified with electronic ear tag ID.

• Every cattle movement recorded by date, number animals by type, origin, destination.

• Since 2005, cattle movement database complete and electronically available.
Study objectives

1) Identify Bovine TB risk factors including herd-specific factors and between-herd interactions.

2) Develop simulation model of spread of Bovine TB within and between cattle herds.


Network of M. bovis-infected farms and their immediate connections in Uruguay
# Risk factors for Bovine TB in Uruguayan dairy herds

(C. Picasso, MS thesis, University of MN)

<table>
<thead>
<tr>
<th>Variable</th>
<th>Category (N)</th>
<th>OR</th>
<th>95% CI</th>
<th>P-value</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Herd size</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>(# cattle)</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>&lt;116 (76)</td>
<td>1.00</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>116-360 (73)</td>
<td>5.79</td>
<td>1.58-21.21</td>
<td>0.008</td>
<td></td>
</tr>
<tr>
<td>&gt;360 (79)</td>
<td>14.38</td>
<td>4.06-50.90</td>
<td>&lt;0.001</td>
<td></td>
</tr>
<tr>
<td><strong>Incoming steers</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>No (198)</td>
<td>1.00</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Yes (30)</td>
<td>2.88</td>
<td>1.12-7.37</td>
<td>0.027</td>
<td></td>
</tr>
<tr>
<td><strong>Total incoming cattle</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>(# cattle moved)</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>≤1 (79)</td>
<td>1.00</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>1-≤44 (71)</td>
<td>0.77</td>
<td>0.29-2.06</td>
<td>0.608</td>
<td></td>
</tr>
<tr>
<td>&gt;44 (78)</td>
<td>1.90</td>
<td>0.81-4.44</td>
<td>0.138</td>
<td></td>
</tr>
</tbody>
</table>

No significant two-way interactions
Modeling infectious diseases

• Why use dynamic epidemiologic models?
  – Represent “simplified” dynamics of system
  – Understand variability of epidemic outcomes due to stochasticity
  – Help determine plausibility of epidemiologic explanations and predict impact of changes to the system

• How develop simulation model?
  – Within-farm transmission dynamics captured by age-structured stochastic SORI model with a 1-mo. time step
  – Between-farm transmission
    • Local spatial spread modeled using a transmission kernel with exponential decay
    • Cattle movement modeled using a dynamic contact network
Cost-effectiveness of surveillance strategies for bovine TB in Uruguay
VanderWaal et al.

<table>
<thead>
<tr>
<th>Scenario</th>
<th>Type</th>
<th>Size criteria</th>
<th>Movement criteria</th>
<th>Description of farms tested annually</th>
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</thead>
<tbody>
<tr>
<td>Baseline</td>
<td>Dairy</td>
<td>---</td>
<td>---</td>
<td>All dairies</td>
</tr>
<tr>
<td>A</td>
<td>Dairy</td>
<td>&gt;360 &amp; &gt;44</td>
<td></td>
<td>High risk by size AND movements</td>
</tr>
<tr>
<td>B</td>
<td>Dairy</td>
<td>&gt;115 &amp; &gt;1</td>
<td></td>
<td>Med/High risk by size AND movements</td>
</tr>
<tr>
<td>C</td>
<td>Dairy</td>
<td>&gt;360 OR &gt;44</td>
<td></td>
<td>High risk by size OR movements</td>
</tr>
<tr>
<td>D</td>
<td>Dairy</td>
<td>&gt;115 OR &gt;1</td>
<td></td>
<td>Med/High risk by size OR movements</td>
</tr>
<tr>
<td>E</td>
<td>Dairy</td>
<td>&gt;360</td>
<td></td>
<td>High risk by size</td>
</tr>
<tr>
<td>F</td>
<td>Dairy</td>
<td>&gt;115</td>
<td></td>
<td>Med/High risk by size</td>
</tr>
<tr>
<td>G</td>
<td>All</td>
<td>Top 10th percentile</td>
<td></td>
<td>High risk by movement</td>
</tr>
<tr>
<td>H</td>
<td>Dairy</td>
<td>---</td>
<td>---</td>
<td>Improved slaughter surveillance (10%)</td>
</tr>
<tr>
<td>I (annual)</td>
<td>Dairy</td>
<td>&gt;115 OR &gt;1</td>
<td></td>
<td>Scenario D + all dairies every other year</td>
</tr>
<tr>
<td>I (biennial)</td>
<td>Dairy</td>
<td>---</td>
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<td></td>
</tr>
</tbody>
</table>
Scenarios D, H, and I resulted in similar epidemic sizes as baseline strategy.

Scenario D (targeting moderate to high risk farms by herd size and movements) required ~40% fewer farms to be sampled.
Next steps

- Adapt Uruguay model for US context
- Use Uruguay model to test assumptions necessary for US adaptation
  - Uncertainty about movements
United States - Limited Cattle Movement Data

- Simulated farm movements
  - FLAPS: farm location and farm size
  - USDA county level cattle movement data
  - NAHMS dairy and beef cow-calf survey data
- Simulate bovine TB spread with simulated cattle movement
  - Evaluate strategies for bovine TB surveillance
United States – County Level Movement

- Simulated county-level network from Lindström et al., 2013

County-level out movements from Minnesota

County-level in movements to Minnesota
Conclusions

• From location with movement data available (Uruguay)
  – Cattle movements key risk factor for disease spread
  – Relaxing surveillance on low-risk farms would reduce testing effort with no apparent increase in number of infected farms

• From location without movement data available (US)
  – Work currently ongoing
Acknowledgments

A Perez, KL VanderWaal, C Picasso, S Kao, M Craft, J Alvarez, EA Enns. University of Minnesota
F Fernandez, Ministerio de Ganadería, Agricultura y Pesca, Uruguay
A Gil, Facultad de Veterinaria, Universidad de la República, Uruguay

Funding: USDA NIFA AFRI Foundational Program