Population impacts and patterns of hemorrhagic disease in white-tailed deer: understanding the role of an emergent disease

Sonja A. Christensen, William Porter and David Williams
Boone And Crockett Quantitative Wildlife Center
Department Of Fisheries And Wildlife
Michigan State University
Epizootic hemorrhagic disease
Vector-transmitted virus affecting deer species

Host (deer)

Midge + Virus
Epizootic hemorrhagic disease (EHD)

- The pathogen is the Orbivirus EHDV
- EHDV vector agent is a midge (*Culicoides* spp.)
- Midge activity corresponds with disease outbreaks in deer during late summer, near water
- Both EHD virus (EHDV) and Bluetongue virus (BTV) result in hemorrhagic disease (HD).
Disease outbreaks are localized, may kill a high percentage of infected deer, and are associated with water bodies (Gaydos et al. 2004, Davidson 2006)

The vector (*Culicoides spp.*) is tied closely to weather conditions and available water for life cycle completion (Mellor et al. 2000)
Multiple HD serotypes of BTV and EHDV are established in North America.
Exposed deer that survive can develop immunity.
Greater mortality in naïve deer populations.
Multiple HD serotypes of BTV and EHDV are established in North America.
Exposed deer that survive can develop immunity.
Greater mortality in naïve deer populations.
Hemorrhagic Disease In Deer

(Stallknecht et al. 2015)

- **HD reported 1980-2009**
- **New reports of HD 2010-2012**
High deer mortality in Michigan

- ~15,000 deer died of EHD in 2012
- Largest outbreak of EHD in Michigan history
- Reduced deer populations locally?
Hemorrhagic disease in deer

Why do we care?

- White-tailed deer are an important wildlife resource
- Emergent EHD may result in mass mortality of deer
- We don’t know what the disease is doing to deer populations and what the spatial extent of that impact might be
Can we detect localized differences in deer abundance associated with EHD mortality?

What is the spatial distribution of these impacts?

How long will it take for these populations to recover?
Objectives

1) Test whether we could detect a change in abundance of a deer population attributable to an EHD outbreak in 2012

2) Quantify the fine-scale spatial extent of EHD impacts associated with riparian habitats and corresponding disease risk for deer populations

3) Determine if populations increased over time in response to local population impacts from EHD.
Prediction for deer abundance in a forest-agriculture landscape
Prediction: greater deer density near forest and riparian habitat
Prediction: greater deer density near forest and riparian habitat
Increased EHD mortality near riparian habitat
Increased EHD mortality near Riparian habitat
Expected population recovery
Study areas:
EHD site & control site

- **Study Area 1: EHD Site**
  - Maple River corridor in central Michigan
  - Confirmed EHD activity in 2012

- **Study Area 2: Control site**
  - Cass River corridor in the thumb region
  - High deer density, similar landscape, no past EHD reports
Study design for road transects

- Transects = 15 miles
  - 1km from Riparian zone
  - 5km from Riparian zone
Study design for road transects

- Transects = 15 miles
- 1km from Riparian zone
- 5km from Riparian zone
Population abundance estimates for unmarked populations

Distance Sampling – An extension of plot sampling where not all animals in the covered region are detected. Estimates abundance and detection parameters.

(Buckland et al. 2001)
Population abundance estimates for unmarked populations

Distance Sampling – An extension of plot sampling where not all animals in the covered region are detected. Estimates abundance and detection parameters.

(Buckland et al. 2001)
Population abundance estimates for unmarked populations

- Consistent road-based surveys in 2 study areas for 5 years
- Surveys occurred between June and August, 2013-2017
- Evening distance sampling surveys without spotlights
Study design for road transects

Transects = 15 miles
- 1km from Riparian zone
- 5km from Riparian zone
Land-cover and disease impact: distance sampling design
Land-cover and disease impact: distance sampling design

Maple River Area (EHD Site)

MAPLE RIVER STUDY AREA SURVEY TRANSECTS

CONCLUSION
Land-cover and disease impact: distance sampling design

Maple River Area (EHD Site)

Cass River Area (Control Site)

Agriculture

Riparian

N

0 1.75 3.5 7 10.5 14 Kilometers

Maple River Study Area Survey Transects

Michigan Counties

N

0 1.75 3.5 7 10.5 14 Kilometers

Cass River Study Area Survey Transects

Michigan Counties
Population abundance estimates

- Evaluated variables for detection probability \( \hat{P}_a \) using program DISTANCE analysis for each year in each study area
  - Covariates: Group size, vegetation, behavior upon detection, observer, weather
- Stratum area = 1km buffer (~100 km\(^2\))
- Used AIC for model selection, evaluated qq-plots, \% CV, and Goodness of Fit for top models
Results: Population estimates by habitat
Maple River - Wetland Stratum Deer Density

Maple River - Agricultural Stratum Deer Density

Deer Density (Deer/km sq.)

Year
Predicted population impact
Expected population recovery
Take home messages

- Local-scale impact in deer abundance where disease outbreak occurred
- Deer abundance was lowest in wetland areas affected by EHD compared to nearby (~5km) agricultural areas
- Deer abundance is increasing post EHD outbreak where disease was severe
Thank you to our funders and collaborators

Funding support provided by the U.S. Fish and Wildlife Service through the Pittman-Robertson Wildlife Restoration Act Grant MI W-155-R
Deer are managed at a Deer Management Unit scale

Deer management units do not capture local changes in deer population from EHD
Summary

- Established WHAT happened after an EHD outbreak
  - Impacts on deer were severe and occurred near riparian areas
  - Populations recovered post-EHD outbreak
- Established WHY we are observing emergent but infrequent disease patterns
Questions?
Deer density by habitat in EHD site
Deer density by habitat in EHD site

- **Agricultural stratum**
  - 2013: 1.5
  - 2014: 3.0
  - 2015: 2.5
  - 2016: 2.0

- **Wetland stratum**
  - 2013: 0.5
  - 2014: 1.0
  - 2015: 1.5
  - 2016: 2.0

*Note: The data shows a significant increase in deer density in the Agricultural stratum from 2013 to 2016, with a peak in 2014.*
Deer density by habitat in control site

Agricultural stratum
- 2014: 2.0 Deer/sq. km²
- 2015: 4.0 Deer/sq. km²
- 2016: 3.0 Deer/sq. km²

Wetland stratum
- 2014: 4.0 Deer/sq. km²
- 2015: 5.0 Deer/sq. km²
- 2016: 5.0 Deer/sq. km²
Some assumptions
- Site-level abundance is a random variable
- Sites are independent of one another
- Equal detection probability among individuals within a spatial unit
- Effective sample area $\sim$ the sum area of $i$ units
- Survey unit size
Areas of research interest and desired impact:

- Emerging wildlife diseases & impacts on wildlife populations
- Spatial epidemiology of emerging wildlife disease
- OneHealth – Humans, Animals, Environment
Population abundance estimates: Distance sampling

- Assumptions:
  - Detection probability = 1 at the transect line
  - Distances are measured accurately
  - Objects are distributed independently from the transect line
  - Spatial inference is explicitly defined

(Buckland et al. 2001)
Fixed-wing aerial survey study design

- Line-transects, bisecting riparian habitat
- Double-count approach each day (2 counts/day)
- 3 replicate surveys conducted within a month, between February and March
- 2 years (2014 and 2016)
- Consistent time of day, observers, and snow/weather conditions
5 transects, 21 km in length
~5km apart
Bisecting riparian habitat
Application of two analytical methods

- Estimated deer abundance and detection probability using:
  - Distance sampling, Program DISTANCE analysis (Thomas et al. 2010)
  - An open N-mixture model across days using a Bayesian implementation with JAGS in program R (Kery and Schaub 2012)
- Survey area for estimation – truncated at 900m
Two study design and analytical frameworks

- N-mixture model – did a second count immediately after the first, for each transect; Collected GPS locations for each observation

- Distance sampling – collected distance data for each observation along line transects

Used distance intervals of 100m, 200m, 350m, 500m, and 800m
Sensitivity analysis:
Spatial unit size for N-mixture models

Varied unit size length by:
1km, 2km, 4km, 5km, 6km, 8km, and 10km
Sensitivity analysis:
Spatial unit size for N-mixture models

Varied unit size length by:
1km, 2km, 4km, 5km, 6km, 8km, and 10km
Sensitivity analysis: Spatial unit size for N-mixture models
Sensitivity analysis: Spatial unit size for N-mixture models

Detection probability (p)

<table>
<thead>
<tr>
<th>Spatial Unit Size</th>
<th>Detection Probability</th>
</tr>
</thead>
<tbody>
<tr>
<td>1km</td>
<td>0.25</td>
</tr>
<tr>
<td>2km</td>
<td>0.40</td>
</tr>
<tr>
<td>4km</td>
<td>0.45</td>
</tr>
<tr>
<td>5km</td>
<td>0.45</td>
</tr>
<tr>
<td>6km</td>
<td>0.45</td>
</tr>
<tr>
<td>8km</td>
<td>0.45</td>
</tr>
<tr>
<td>10km</td>
<td>0.50</td>
</tr>
<tr>
<td></td>
<td>Estimate</td>
</tr>
<tr>
<td>--------------------------</td>
<td>----------</td>
</tr>
<tr>
<td>(Intercept)</td>
<td>3.36E+00</td>
</tr>
<tr>
<td>Drought Severity</td>
<td>-1.57E-02</td>
</tr>
<tr>
<td>Latitude</td>
<td>-1.69E-01</td>
</tr>
<tr>
<td>Wetland</td>
<td>8.08E-01</td>
</tr>
<tr>
<td>Region 2</td>
<td>-4.63E-01</td>
</tr>
<tr>
<td>Region 3</td>
<td>6.61E-02</td>
</tr>
<tr>
<td>Region 4</td>
<td>-1.32E-01</td>
</tr>
<tr>
<td>TAuto</td>
<td>6.97E-01</td>
</tr>
<tr>
<td>Drought:Latitude</td>
<td>5.28E-04</td>
</tr>
<tr>
<td>Drought:Wetland</td>
<td>-6.05E-03</td>
</tr>
</tbody>
</table>
FIG. 2. Maps showing the known distribution of confirmed (C. sonorensis, C. insignis) and suspected (C. debilipalpis, C. stellifer) vectors of bluetongue virus (BTV) and/or epizootic hemorrhagic disease virus (EHDV) in the United States. These distributions are not based on uniform, coordinated entomological surveys but rather the coalescence of smaller unrelated studies, as compiled by Blanton and Wirth (1979). More recent Culicoides surveillance is needed to determine if the known distributions of certain Culicoides spp. have changed.
Full model:

\[ \text{logit}(P_{ij}) = \alpha + \beta_1 \times D_{ij} + \beta_2 \cdots \beta_5 \times \text{Region}_{ij} + \beta_6 W_i \\
+ \beta_7 L1_{ij} + \beta_8 L2_{ij} + \beta_9 D_{ij} \times L1_{ij} + \beta_{10} D_{ij} \times W_{ij} \\
+ \gamma T_{ij} + \alpha_j + \delta_i \]

Where, \( \alpha_j = N(0, \sigma^2_\alpha) \) and \( \delta_i = N(0, \sigma^2_\delta) \)

- GLMM Logit model
- Hemorrhagic Disease Mortality -> Response Variable
- Model selection using AICc
Participatory research: deer surveys by deer hunters

- Incorporated local hunters as volunteers for conducting surveys
- Road-based surveys were cost effective and relevant to the scale of EHD occurrence
Application of estimation method

- Offers a practical assessment of local deer abundance
- Allows for the inclusion of stakeholders in the scientific process and better information after a disease outbreak
- Informs long-term disease management and surveillance
Localized abundance and management-scale mismatch

For game species, harvest data is useful at large scales. Deer management units do not capture local changes in deer population abundance, and do not reflect local perceptions from stakeholders.
Can N-mixture models be meaningfully applied to a deer population with an aerial survey approach?
Results
Population abundance by habitat

EHD Site

Abundance

Stratum

2013
2014
2015
Assessing Severe Localized Mortality

**Targeted management efforts**
(reduction in local deer population)

**Disease related mortality**
(reduction in local deer population)
Localized mortality and scale

- Perceived deer population declines are concerning for the public and wildlife managers.
- Need for improved population assessment in a disease context.