



VIRGINIA TECH™

EASTWOOD LAB



NEVBD

NORTHEAST REGIONAL CENTER FOR  
EXCELLENCE IN VECTOR-BORNE DISEASES



VECTOR-BORNE DISEASE  
ECOLOGY LAB

“Vector-borne disease ecology investigations in the Eastern USA and further afield”

Virginia Mosquito Control Association  
January 2022

*Dr Gillian Eastwood*  
*Virginia Tech University*  
*geastwood@vt.edu*

# Outline

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EASTWOOD LAB



- Who are we?
- One Health Approach
- Overseas projects
- Mosquito-focused projects
- Tick-borne Pathogens

## Postdoc



Dr. Alex Cumbie

## Graduate Students



**Lindsey Faw**  
PhD Student

The potential public health risks associated with lineage III LACV.



**Ahmed Garba**  
MS Student

Prevalence of tick-borne viruses in Virginia

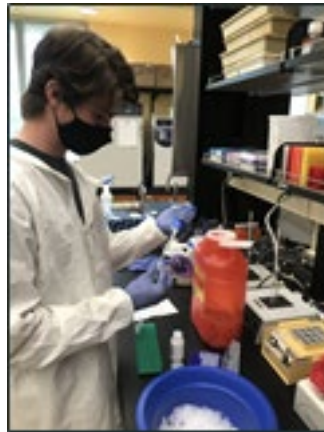
## Undergraduate Students



Melanie Turner



Lucas Raymond



Peter Schiff



Rebecca Trimble



**Based at VT since 2018**  
**Department of Entomology**

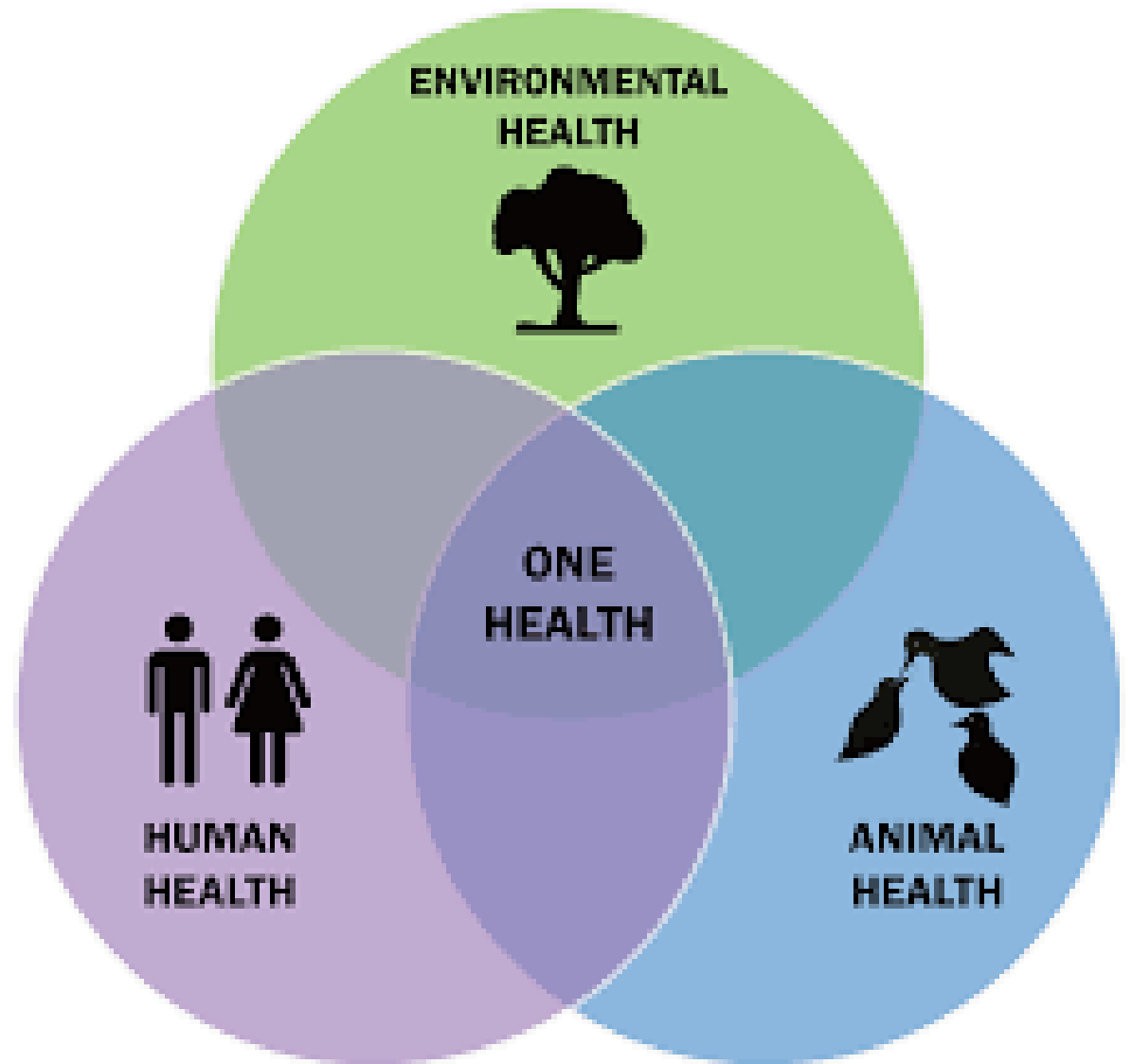
## **Focus: Vector-borne Disease Ecology**

Understanding *enzootic* transmission and the emergence potential of disease pathogens with a One Health lens

# ONE-HEALTH

- HUMANS
- LIVESTOCK
- WILDLIFE
- DOMESTIC ANIMALS
- ARTHROPODS
- ENVIRONMENT

*It is all interrelated!*



# VECTOR-BORNE DISEASE TRANSMISSION CYCLES

- **VECTORS** include *ticks*, *mosquitoes*, *tsetse flies*, culicoides midges, sandflies, kissing bugs, fleas, flies
- **Etiological AGENT** can be *viral*, bacterial, protozoan or filarial worm
- **Vertebrate HOSTS**
  - e.g: WNV (birds~mosquitoes)
  - Lyme disease *Borrelia* (white-footed mice~*Ixodes* ticks)
  - Trypanosomiasis (cattle/tsetse flies)

Arthropod-borne (arbo-) viruses

# Understanding Enzootic Spread and Spillover:

Urbanization

Declining population immunity to infection

Deforestation

Population movement

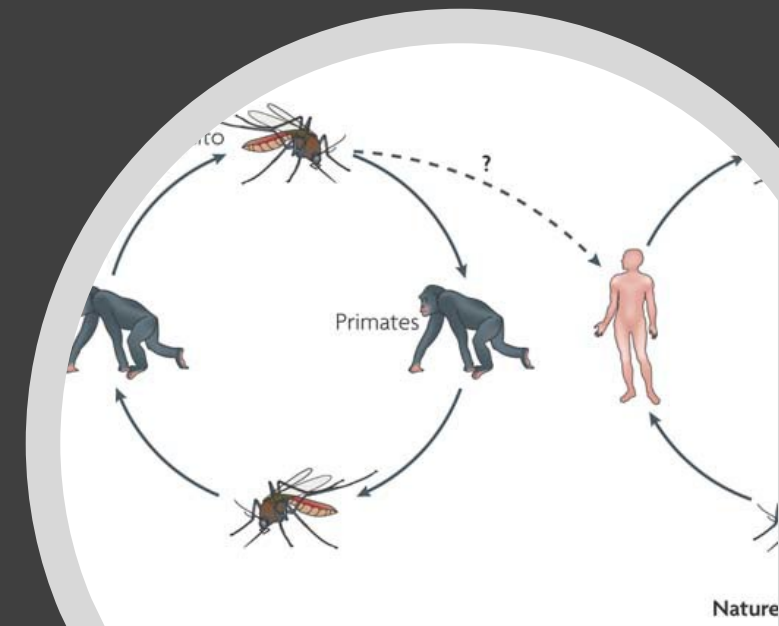
Encroachment on wildlife habitat

Climate change

Pathogen evolution

Invasive species

Insight for wildlife disease & spill-back



# Land-use change

## 3.2. Distinguishing farming, ranching, and land speculation

We manually interpreted all 4582 of the 2015 aerial photographs to test our hypothesis that illegal cattle ranching, rather than farming, is driving forest loss in the three sample areas of our study. It is important to reiterate that we not able to quantify narco-cattle ranching, just illegal cattle ranching.

percentage of suspected ranching (20.83 %), which is a category we argue captures land speculation associated with cattle ranching activities. Our qualitative research reveals that even when deforestation is not directly financed by drug money, narco-cattle ranching fuels land speculation in the park. Our interviewees describe opportunists with access to capital and equipment that engage in land speculation by illegally occupying large tracts of land, clearing the forest or natural

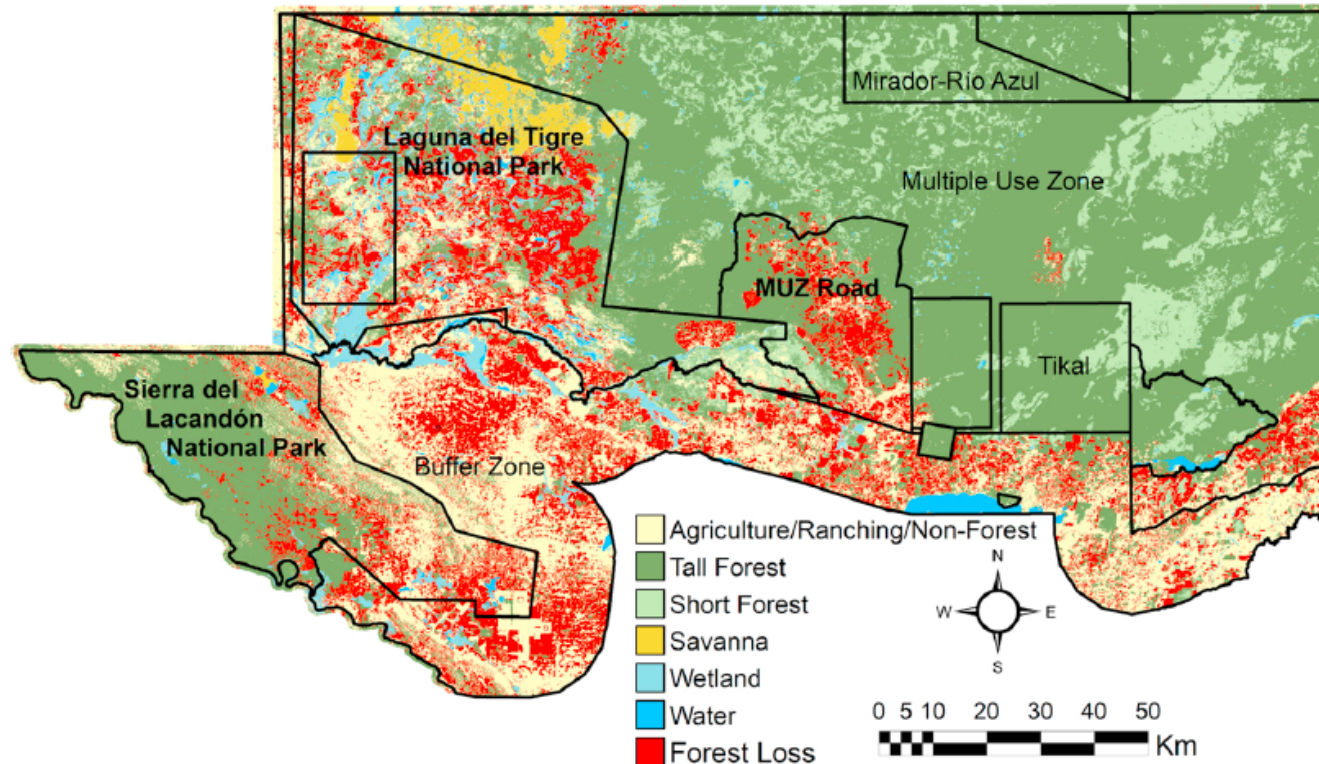


Fig. 4. Land Cover and Land Use Change: 2000 – 2015.



# 'Like Poking a Beehive': The Worrisome Link Between Deforestation And Disease

June 22, 2020 · 5:00 AM ET



NATHAN ROTT



The closer humans are to animals, the greater the opportunity for zoonotic spillover, where a pathogen jumps from animal to human.

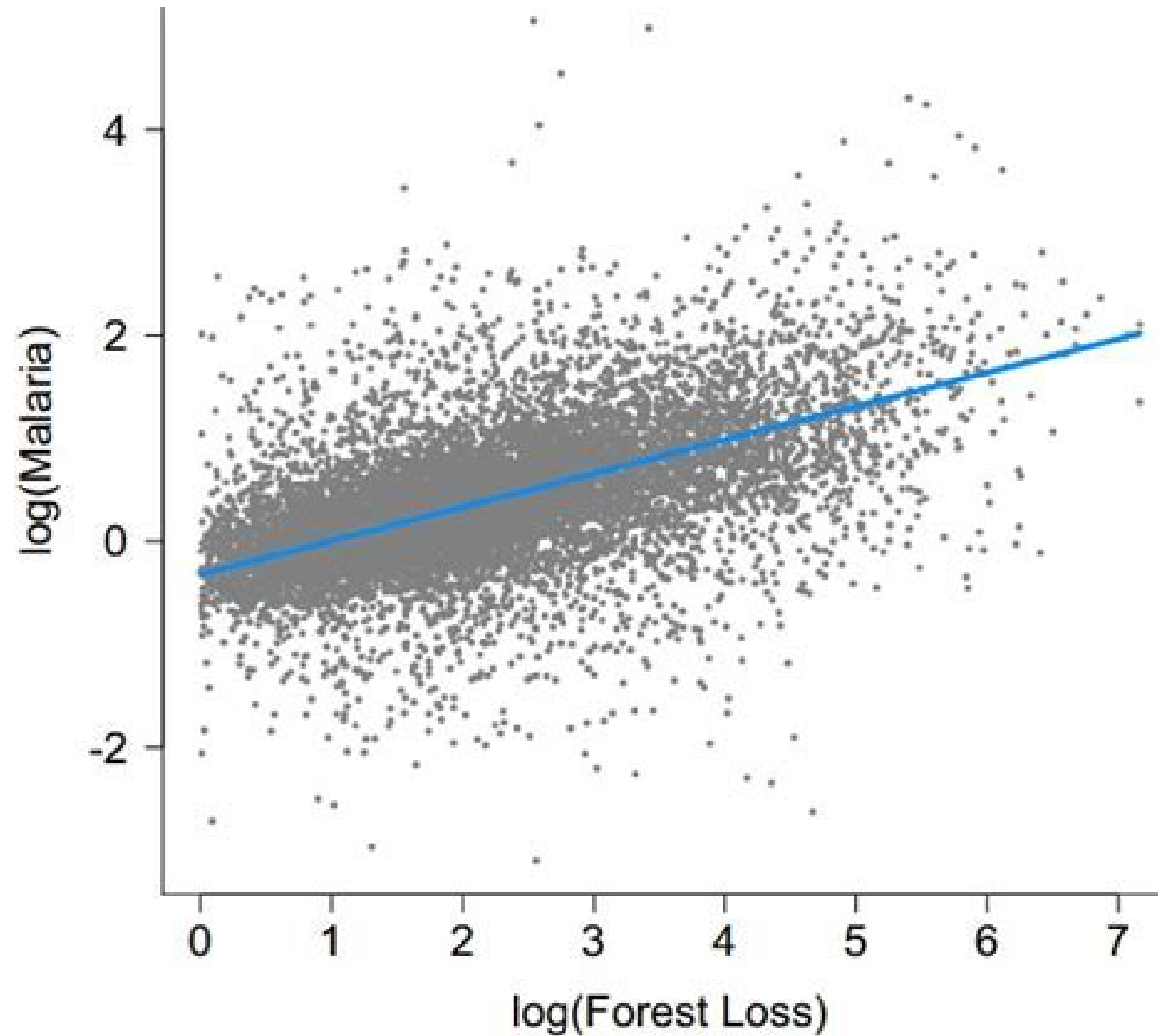


**Degraded soils mean tropical forests may never fully recover from logging**

December 17, 2019

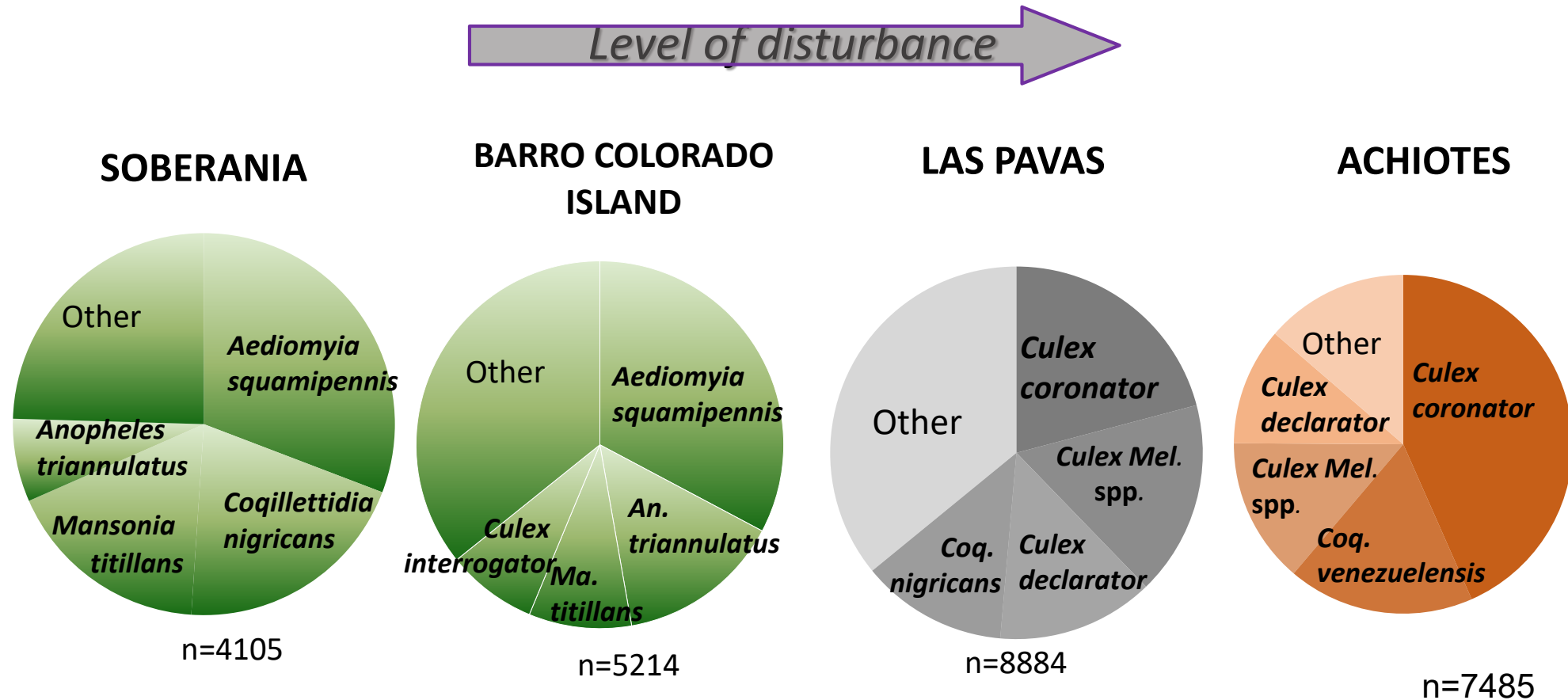
*"When you disturb a forest, it actually upsets the **balance** of nature, the balance between pathogens & people"*

# Tropical deforestation & increased risk of malaria




# Mosquito Species Composition across a forest degradation gradient

- Key species predominate at each habitat



## Disturbance and mosquito diversity in the lowland tropical rainforest of central Panama

Jose R. Loaiza<sup>1,2,3</sup>, Larissa C. Dutari<sup>1</sup>, Jose R. Rovira<sup>1,2</sup>, Oris I. Sanjur<sup>2</sup>, Gabriel Z. Laporta <sup>4,5</sup>, James Pecor<sup>6</sup>, Desmond H. Foley<sup>6</sup>, Gillian Eastwood<sup>7</sup>, Laura D. Kramer<sup>7</sup>, Meghan Radtke<sup>8</sup> & Montira Pongsiri<sup>8</sup>

The Intermediate Disturbance Hypothesis (IDH) is well-known in ecology providing an explanation for the role of disturbance in the coexistence of climax and colonist species. Here, we used the IDH as a framework to describe the role of forest disturbance in shaping the mosquito community structure, and to identify the ecological processes that increase the emergence of vector-borne disease. Mosquitoes were collected in central Panama at immature stages along linear transects in colonising, mixed and climax forest habitats, representing different levels of disturbance. Species were identified taxonomically and classified into functional categories (i.e., colonist, climax, disturbance-generalist, and rare). Using the Huisman-Olff-Fresco multi-model selection approach, IDH testing was done. We did not detect a unimodal relationship between species diversity and forest disturbance expected under the IDH; instead diversity peaked in old-growth forests. Habitat complexity and constraints are two mechanisms proposed to explain this alternative postulate. Moreover, colonist mosquito species were more likely to be involved in or capable of pathogen transmission than climax species. Vector species occurrence decreased notably in undisturbed forest settings. Old-growth forest conservation in tropical rainforests is therefore a highly-recommended solution for preventing new outbreaks of arboviral and parasitic diseases in anthropic environments.



# Vector-borne disease ecology in the Eastern USA



- Mosquitoes

- Ticks



# Phenology of Container-Breeding Mosquitoes in Southwest Virginia



Melanie Turner<sup>1</sup>, Lindsey Faw<sup>2</sup>, Gillian Eastwood<sup>2</sup>  
<sup>1</sup>Virginia Tech, Department of Biological Sciences, Blacksburg, VA. <sup>2</sup>Virginia Tech, Department of Entomology, Blacksburg, VA



Melanie Turner

## Abstract

Phenology of living organisms is an important area of study that focuses on the natural events that occur seasonally throughout plant and animal populations. Understanding the phenology of mosquitoes can help us to determine when certain vector-borne diseases may be a greater risk according to trends in local mosquito populations. By looking at the time of year that container breeding mosquitoes are depositing their eggs, we can determine vector seasonality in the New River Valley region. Mosquito eggs were collected weekly across the Montgomery County area from June through October 2021 using oviposition cups lined with seed germination paper. We expect to see three specific mosquito species, *Aedes albopictus*, *Aedes triseriatus*, and *Aedes japonicus*, all container-breeding mosquitoes. We have been rearing the mosquito eggs into adults, then identifying them as one of the three specified species. So far, we have 2,266 *Ae. triseriatus* adults, 60 *Ae. albopictus* adults, and 0 *Ae. japonicus* adults. We will continue to flood egg mosquito papers tracking the dates we collected them. With 80 papers flooded so far, we still have 390 papers left to flood.

## Background

- Phenology is the study of natural events that occur seasonally throughout plant and animal populations.<sup>5</sup>
- Temperature and precipitation are two of the main influencing factors that alter phenology.<sup>5</sup>
- Phenology can help us gain a better understanding of the spread of various mosquito-borne diseases.<sup>3</sup>

## Introduction

- Focus was on three specific container-breeding VA mosquito species:
  - Aedes triseriatus* (figure 1)
  - Aedes albopictus* (figure 3)
  - Aedes japonicus* (figure 2)
- Phenology of local mosquito species can help us determine when certain vector-borne diseases might be a greater risk in specific mosquito populations.
- Ae. japonicus* are an invasive species that are known to be competent vectors of many arboviruses like chikungunya, dengue, eastern equine encephalitis, and West Nile under laboratory conditions.<sup>1</sup>
- Ae. albopictus* have high phenotypic plasticity, making them a top invasive species throughout the world, as well as being known vectors of dengue and chikungunya virus.<sup>2</sup>
- Ae. triseriatus* is the native vector of La Crosse virus. This vector-borne disease typically occurs between July and September in the United States.<sup>4</sup>

Research Question: What time of year are container-breeding mosquitos actively laying eggs?



Figure 1: *Ae. triseriatus* Photo credit: Ohio Department of Health  
 Figure 2: *Ae. japonicus* Photo credit: Wikipedia  
 Figure 3: *Ae. albopictus* Photo credit: James Gethings, USDCP

## Acknowledgements

- I would like to thank Alex Cumble for her help in the field and for taking photographs for the project.
- I would also like to thank the VT landowners that gave us permission to use their properties for our research.

## Materials and Methods

- Collection of mosquito eggs:**
- Mosquito oviposition cups (figure 9) were set up at multiple locations across the Blacksburg, VA area (figure 7).
  - Egg papers were collected weekly and stored in the incubator at 25°C and 80% humidity for embryonation.
  - Egg papers were collected from the end of June through the beginning of October.
- Rearing of mosquito eggs:**
- Liver-yeast powder (3:2) was used for larval food when flooding papers.
  - Egg papers were each flooded twice.
  - Pupae were separated from larvae and placed in emergence containers (figure 8).
  - Adults were collected from emergence containers then chilled for morphological I.D. under the microscope (figure 4 & 10).
  - Egg papers (n=470), thus far 80 have been flooded between 6/28/21 and 7/26/21



Figure 4: I.D. of adult mosquitoes  
 Figure 5: Containers with mosquito larvae  
 Figure 6: Emergence containers and adult cages

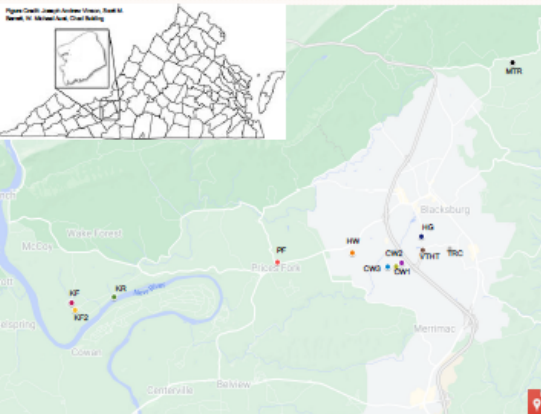


Figure 7: Map of field sites



Figure 8: Close up of emergence container  
 Figure 9: Oviposition cup  
 Figure 10: Counting of adult mosquitoes

## Results (to date)

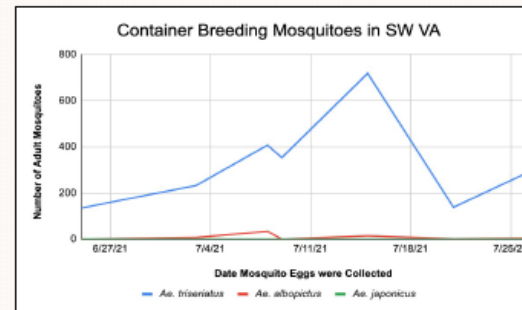


Figure 11: Phenology graph of container-breeding mosquitoes  
 Collected a total of 470 mosquito papers from 6/27/21 – 10/8/21.  
 Eighty egg papers have been flooded.  
 We have reared 2,326 adult F1 mosquitos.  
 So far, we have 2,266 adult *Ae. triseriatus*, 60 adult *Ae. albopictus*, and 0 adult *Ae. japonicus*.

Send PDFs

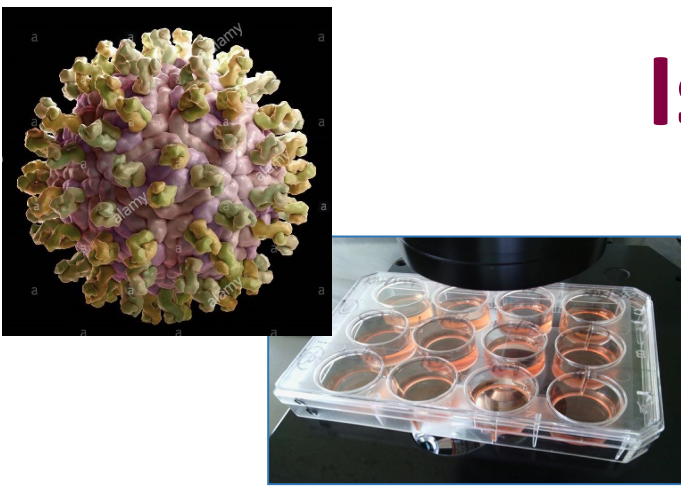
## Discussion/Future Direction

- We are currently still in the process of flooding mosquito papers, with about 390 papers left to flood.
- As we continue to flood more papers, we expect to see more *Ae. albopictus* and *Ae. japonicus* adults and will evaluate seasonal patterns in these local mosquito vectors.

## References

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# Isolated LACV (lineage III) in 2018 from Connecticut mosquitoes



*Journal of Medical Entomology*, 57(2), 2020, 534–541  
doi: 10.1093/jme/tjz200  
Advance Access Publication Date: 25 December 2019  
Research

Vector-Borne Diseases, Surveillance, Prevention

## Evaluation of Novel Trapping Lures for Monitoring Exotic and Native Container-Inhabiting *Aedes* spp. (Diptera: Culicidae) Mosquitoes

Gillian Eastwood,<sup>1,3,\*</sup> Andrew K. Donnellycolt,<sup>1</sup> John J. Shepard,<sup>1</sup> Michael J. Misencik,<sup>1</sup> Robert Bedoukian,<sup>2</sup> Lacey Cole,<sup>2</sup> Philip M. Armstrong,<sup>1</sup> and Theodore G. Andreadis<sup>1</sup>

<sup>1</sup>Center for Vector Biology & Zoonotic Diseases, The Connecticut Agricultural Experiment Station, 123 Huntington St, New Haven, CT 06511, <sup>2</sup>Bedoukian Research, Inc., 6 Commerce Drive, Danbury, CT 06819, and <sup>3</sup>Corresponding author, e-mail: [geastwood@vt.edu](mailto:geastwood@vt.edu)

Subject Editor: Lawrence Hribar

Received 26 July 2019; Editorial decision 9 October 2019

### Abstract

Surveillance for diurnal container-inhabiting mosquitoes such as *Aedes albopictus* (Skuse), *Aedes japonicus japonicus* (Theobald), and *Aedes triseriatus* (Say) have routinely relied on the deployment of multiple trap types, including CO<sub>2</sub>-baited light traps, gravid traps, oviposition traps, and BG-Sentinel. These trap configurations have met with varying degrees of effectiveness and in many instances likely under-sample these key mosquito vectors. Most recently, the BG-Sentinel trap used in conjunction with the human-scent lure has been largely accepted as the gold-standard for monitoring *Ae. albopictus*. However, its ability to attract other container-inhabiting *Aedes* species has not been fully evaluated. During 2018, we tested new scent lures, TrapTech Lure-A and Lure-H (Bedoukian Research, Inc.), using BG-Sentinel traps with CO<sub>2</sub> in two regions of Connecticut, Stamford and Hamden, against the BG-Lure. Pooled mosquitoes were additionally screened for arbovirus infection. A total of 47,734 mosquitoes representing 8 genera and 32 species were captured during the study, with the Stamford site deriving on average three times as many mosquitoes per trap, adjusting for sampling effort. Lure-A and Lure-H outperformed the BG-Lure in terms of total numbers, diversity evenness, and the proportion of both *Ae. j. japonicus* and *Ae. triseriatus*. There were no significant differences among lures in capturing *Ae. albopictus*, and in terms of species richness. **Fifty-seven isolates of virus (West Nile, Jamestown Canyon, and La Crosse viruses) were obtained during the study**, with no significant difference between trap-lure. We highlight both novel lures as effective attractants for use in mosquito surveillance— which

RESEARCH

Open Access

## Local persistence of novel regional variants of La Crosse virus in the Northeast USA



Gillian Eastwood<sup>1,2\*</sup>, John J. Shepard<sup>1</sup>, Michael J. Misencik<sup>1</sup>, Theodore G. Andreadis<sup>1</sup> and Philip M. Armstrong<sup>1</sup>

### Abstract

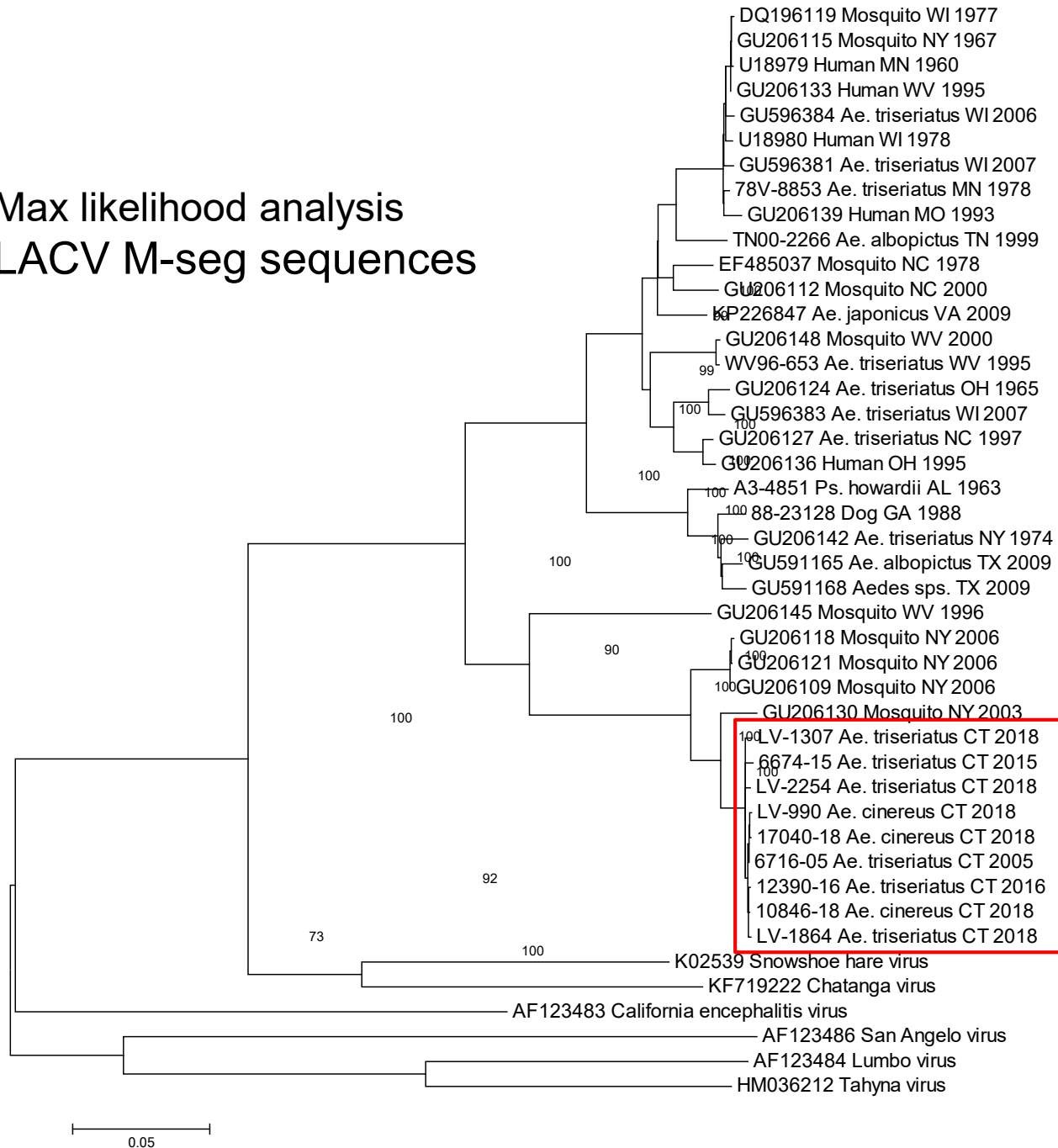
**Background:** La Crosse virus (LACV) (genus *Orthobunyavirus*, family *Peribunyaviridae*) is a mosquito-borne virus that causes pediatric encephalitis and accounts for 50–150 human cases annually in the USA. Human cases occur primarily in the Midwest and Appalachian regions whereas documented human cases occur very rarely in the northeastern USA.

**Methods:** Following detection of a LACV isolate from a field-collected mosquito in Connecticut during 2005, we evaluated the prevalence of LACV infection in local mosquito populations and genetically characterized virus isolates to determine whether the virus is maintained focally in this region.

**Results:** During 2018, we detected LACV in multiple species of mosquitoes, including those not previously associated with the virus. We also evaluated the phylogenetic relationship of LACV strains isolated from 2005–2018 in Connecticut and found that they formed a genetically homogeneous clade that was most similar to strains from New York State.

**Conclusion:** Our analysis argues for local isolation and long-term persistence of a genetically distinct lineage of LACV within this region. We highlight the need to determine more about the phenotypic behavior of these isolates, and whether this virus lineage poses a threat to public health.

Max likelihood analysis  
LACV M-seg sequences



Intensive mosquito trapping  
at LACV foci indicates  
**local persistence of  
lineage III strains in NE USA**

**An entomological risk exists  
What is the human risk?**





# Third lineage of La Crosse virus (Northeast USA)

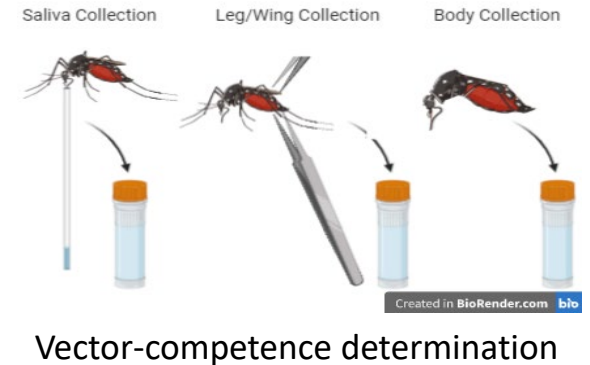
Is there an underlying public health risk?

## Entomological Risk



LACV-infection in mosquitoes:

- multiple species
- several areas
- multi-years)



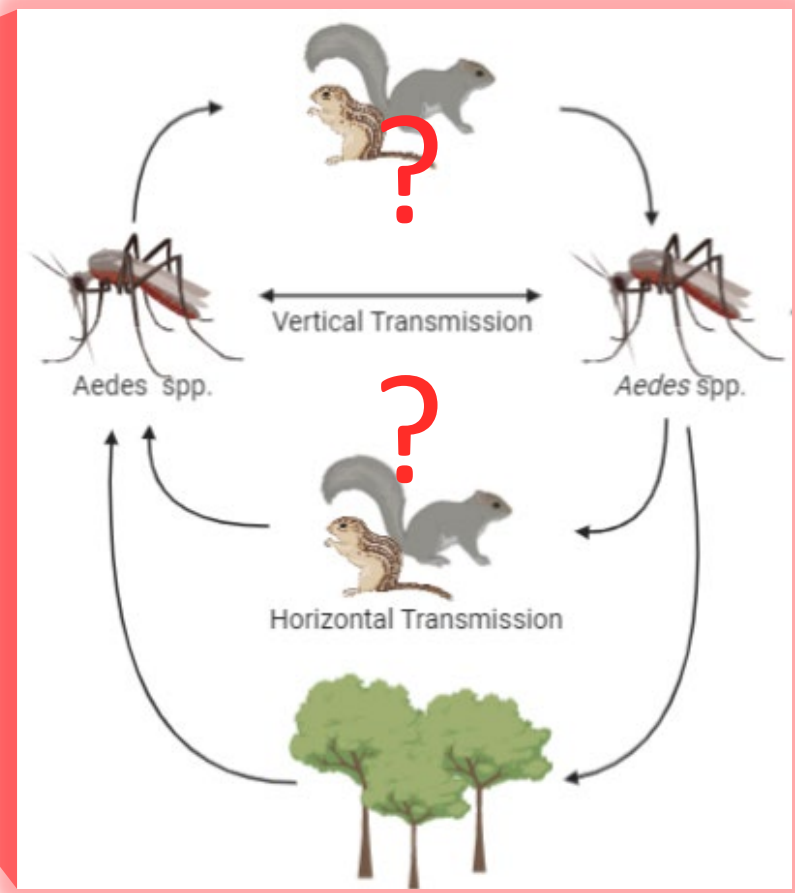
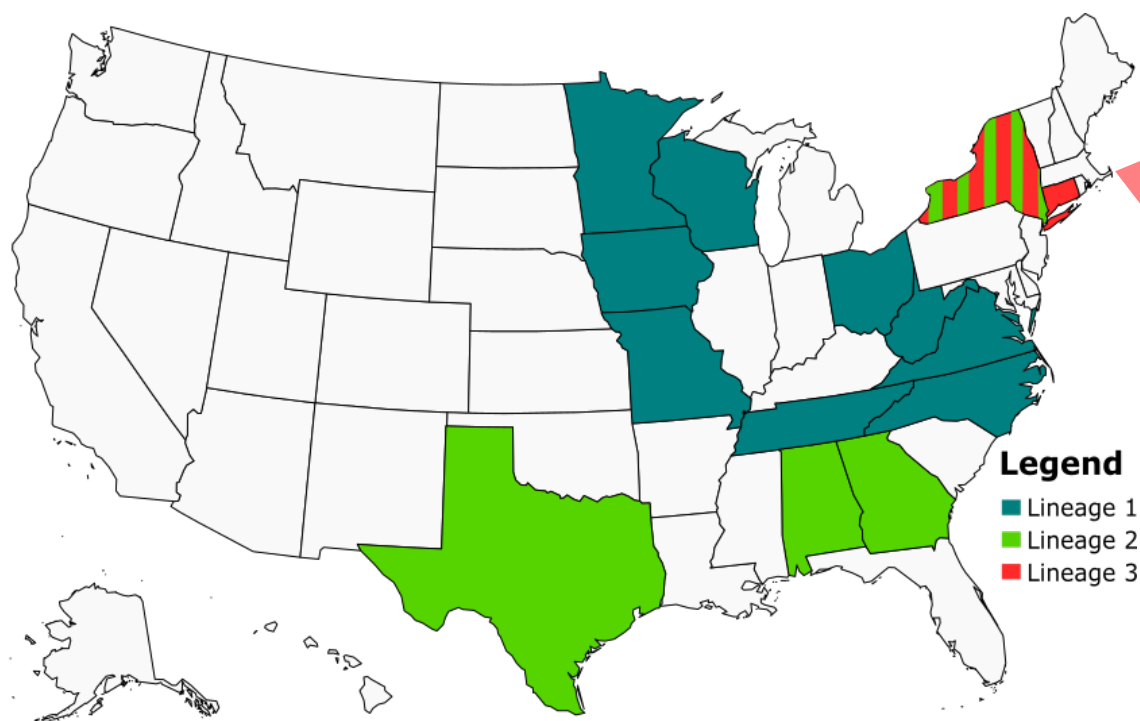
## Why have we not seen clinical cases?

- Under/mis-diagnosis?
- How does LACV III persist?  
Horizontal vs. Vertical transmission only ?
- Pathogenicity or virulence of LACV III strains?  
(compared to other lineages)



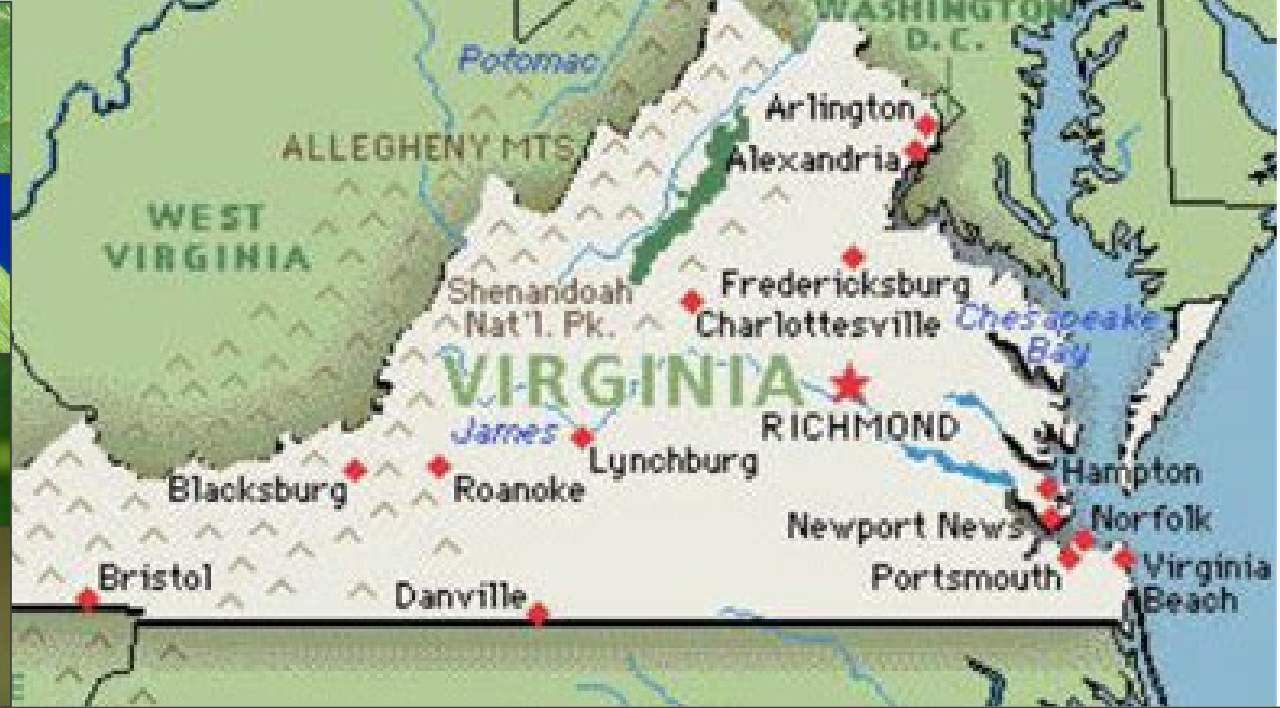
LINDSEY FAW

# Characterization of La Crosse Virus lineage III strains ~ Pathogenicity & Vectorial Competence in potential vector mosquitoes





Amanda  
Whitlow  
(Masters)



# A tick focus

Tick Species Diversity  
& Pathogen Prevalence  
in SW Virginia





# Tick sampling

- 8 counties in Virginia

  - 1 **pasture** site,

  - 1 **urban** site,

  - 1 **forest** site

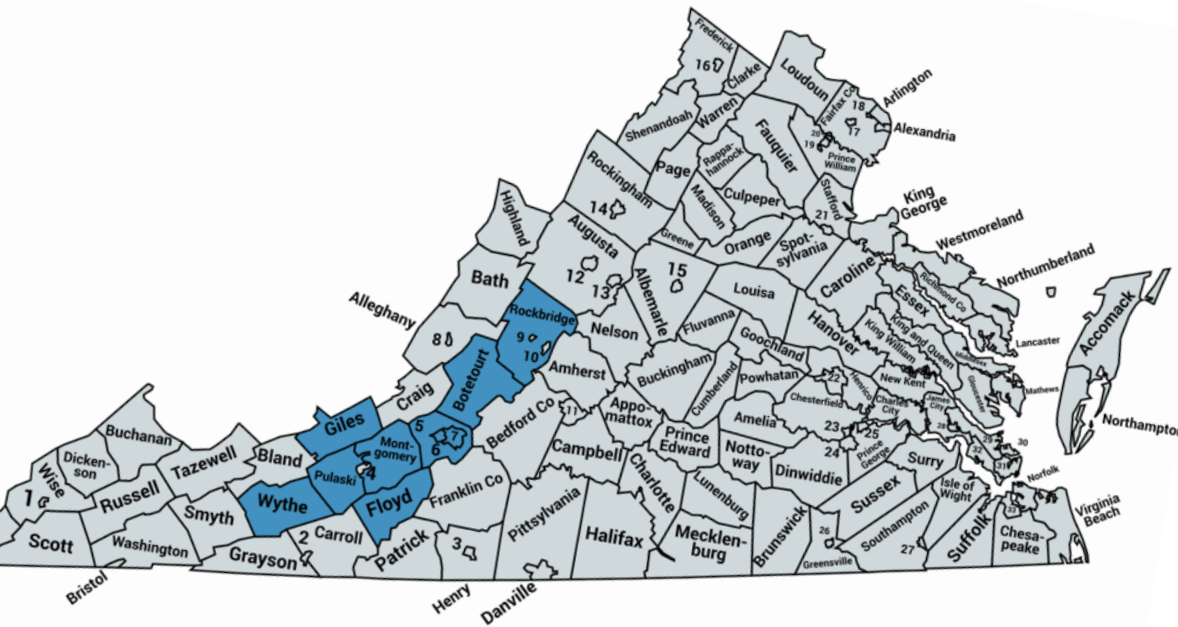
=24 total sites

- Each site dragged for 30 mins ~every 2 wks

  - Temp, humidity, & time recorded

- Trail cameras → Vertebrate presence

- Pathogen screening → qPCR/RT-PCR



# Objective 1: Determine tick species diversity across habitat

**N=7508** ticks collected ~ June 2019-Nov 2020

- **5782** *Haemaphysalis longicornis*
- **768** *Amblyomma americanum*
- **703** *Ixodes scapularis*
- **140** *Haemaphysalis leporipolustris*
- **97** *Dermacentor variabilis*
- **6** *Ixodes brunneus*
- **6** *Ixodes dentatus*
- **3** *Dermacentor albipictus*
- **2** *Ixodes cookei*
- **1** *Ixodes minor*

## Objective 2: Determine tick-borne pathogen prevalence in SW Virginia



***Ixodes scapularis*** (Whitlow & Schiff)

*Borrelia* spp., *Babesia microti*,  
*Anaplasma phagocytophilum*,  
Powassan virus

***Amblyomma americanum*** (Whitlow)

*Ehrlichia* spp.,  
Heartland virus, Bourbon virus

***Haemaphysalis longicornis*** (Trimble & Cumbie)

*Theileria orientalis*,  
Heartland virus, Bourbon virus

Pathogen spillover  
into the Asian  
longhorned tick,  
*Haemaphysalis  
longicornis* in  
Virginia

EASTWOOD LAB



Rebecca Trimble

Undergraduate researcher

Eastwood Disease Ecology Lab

Department of Biochemistry, Virginia Tech

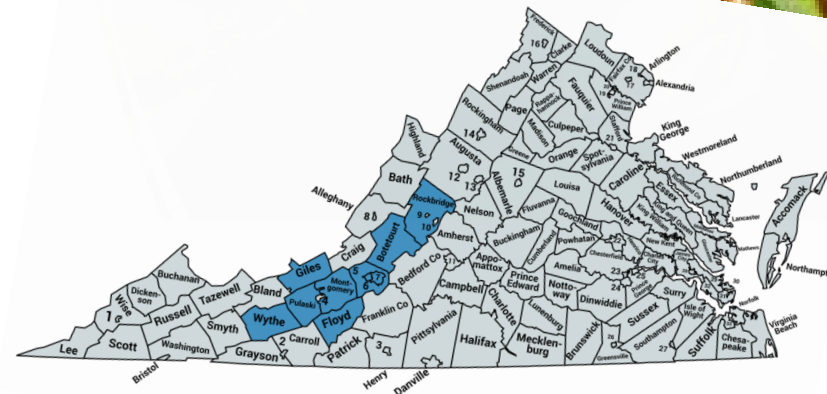
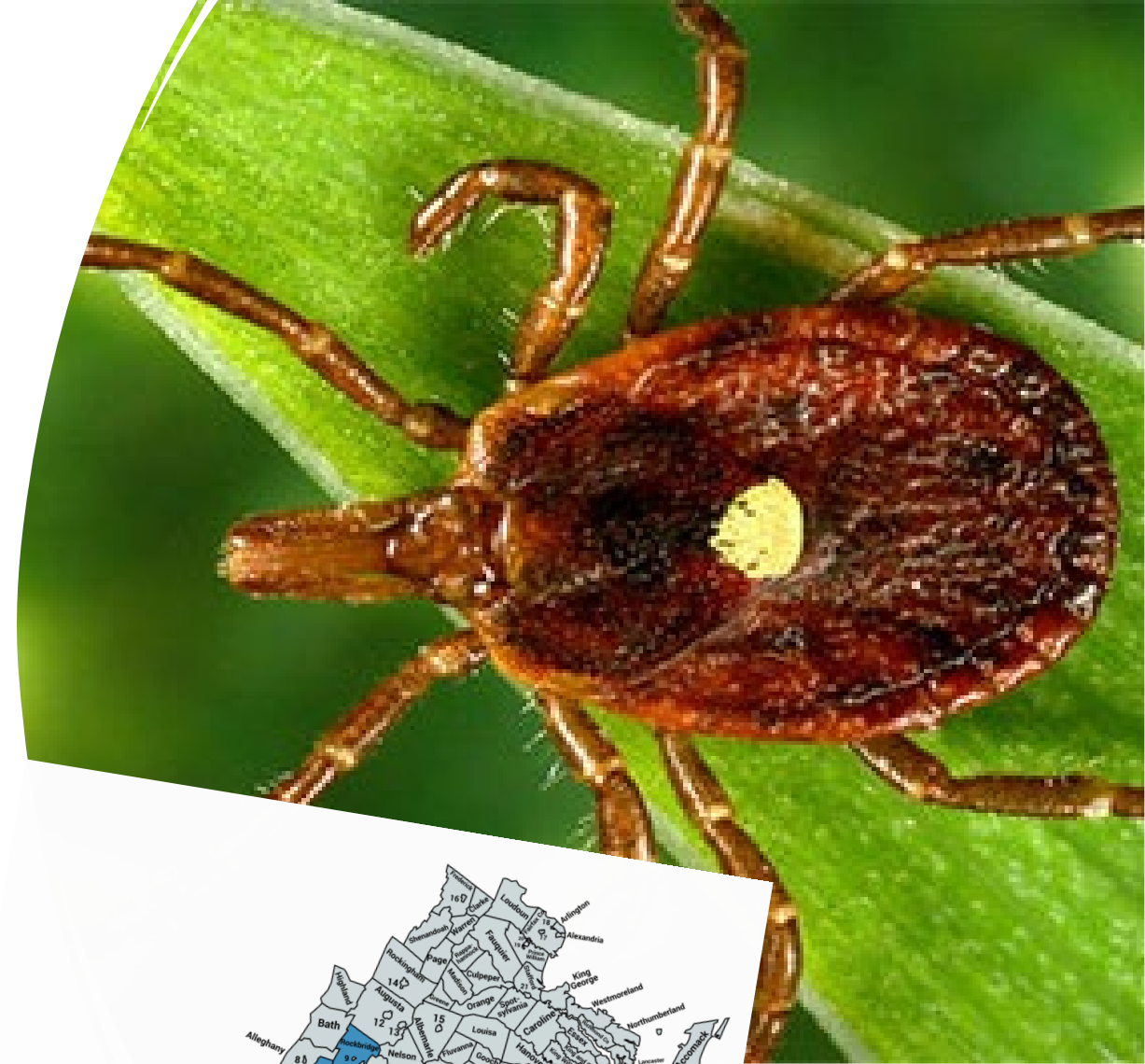


# *Amblyomma americanum*

All initial pools **negative**  
for presence of:

*Ehrlichia* spp.,  
*Heartland Virus*,  
*Bourbon Virus*

Further screening of ticks in 2022  
(New & Fall 2021 collections)



Whitlow *et al* (in press) JoVE



# Surveillance of Pathogens in Blacklegged Ticks from Southwest Virginia



Peter Schiff<sup>1</sup>, Alexandra Cumbie<sup>2</sup>, Gillian Eastwood<sup>2</sup>  
<sup>1</sup>Department of Biology, Virginia Tech, Blacksburg, Virginia  
<sup>2</sup>Department of Entomology, Virginia Tech, Blacksburg Virginia



Peter Schiff

## Abstract

Southwest Virginia is a suggested hotspot for tick-borne pathogens, specifically those carried by the blacklegged tick (*Ixodes scapularis*). In this study we surveyed blacklegged ticks from three counties in Southwest Virginia in 2021 (Floyd, Wythe, and Montgomery), and screened them for various pathogens including *Borrelia burgdorferi*, *Borrelia miyamotoi*, *Babesia microti*, *Anaplasma phagocytophilum*, and Powassan virus. Ticks were collected via traditional flagging techniques and were stored at -80°C prior to morphological identification and nucleic acid extraction. DNA and RNA were extracted from ticks pooled by site and life stage and were tested for the aforementioned pathogens using real-time PCR assays. All counties contained positive results for all pathogens except for *Babesia microti*. Two of the three counties showed evidence of Powassan virus. High rates of *Anaplasma phagocytophilum* were detected in each of the counties, however, further sequencing is needed to identify if it is the deer or human variant. Further expansion on this study should include the addition of more counties and additional tick pools to test in each county, along with Sanger sequencing for confirmation of pathogens. Such studies are useful indicators of tick-borne pathogen prevalence for public health in the region.

## Background and Introduction

- *Ixodes scapularis*, the blacklegged tick
  - Vector of multiple pathogens, including the causative agents of Lyme disease, anaplasmosis, babesiosis, and Powassan virus infection<sup>1</sup>
  - Frequently found in forested and edge habitats<sup>2</sup>
  - Prominent tick species collected in Southwest Virginia
- Based on passive surveillance data, Southwest Virginia is considered a hot spot for Lyme disease and potentially other pathogens including *B. miyamotoi*, *Ba. microti*, *A. phagocytophilum*, and Powassan virus.<sup>4</sup>



Active surveillance of local tick populations is needed to continue monitoring tick-borne pathogen prevalence and incidence

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7. Courtney, F.W., Kostelick, L.M., Dzibon, N.S., and Manning, R.F., 2004. Multiplex real-time PCR for detection of *Anaplasma phagocytophilum* and *Borrelia burgdorferi*. *Journal of Clinical Microbiology*, 42(7), pp.2348-2349.

## Research Objective

To monitor the prevalence of tick-borne pathogens in the southwest region of Virginia, specifically surveying *I. scapularis* ticks.

## Methods

- Ticks were collected monthly from 14 sites in 3 counties in Southwest Virginia (Fig 1) from January 2021 – August 2021 using standard flagging techniques.
- Ticks were identified morphologically and stored at -80°C prior to extraction.
- DNA and RNA was extracted from the ticks using a QIAamp MinElute Virus Spin kit.<sup>5</sup>
- Pathogen testing was accomplished using multiplex real-time PCR assays.<sup>6,7</sup>
  - Duplex real-time PCR reaction for *B. burgdorferi* and *B. miyamotoi*
  - Duplex real-time PCR reaction for *A. phagocytophilum* and *Ba. microti*
  - Single-plex RT-PCR reaction for Powassan virus



Figure 1: Map of Virginia, highlighting the surveilled counties. We surveyed 8 sites in Montgomery, 3 sites in Floyd, and 3 sites in Wythe counties. The red dot indicates the Tabor Valley area of Montgomery county.

## Results Summary

- A total number of 13 larvae, 39 nymphs, and 308 adults *Ixodes scapularis* were tested as 15 pools, 75 pools, and 6 pools, respectively.
- 15 pools (n=99 ticks) were tested from Floyd with 87% positive pools for *B. burgdorferi*, 13% for *B. miyamotoi*, 33% for *A. phagocytophilum*, and 7% for Powassan virus (Fig 2)
- 75 pools (n=240 ticks) were tested from Montgomery with 64% positive pools for *B. burgdorferi*, 36% for *B. miyamotoi*, 27% for *A. phagocytophilum*, and 2% for Powassan virus (Fig 3)
- 6 pools (n=21 ticks) were tested from Wythe with 67% positive pools for *B. burgdorferi*, 67% for *B. miyamotoi*, and 17% for *A. phagocytophilum* (Fig 4)

## Results

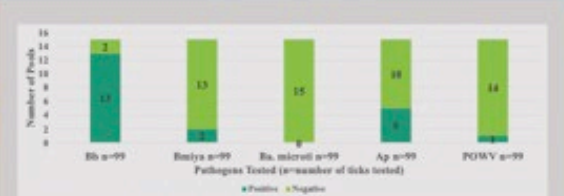


Figure 2: Real-Time PCR testing for pathogens in Floyd, Virginia.



Figure 3: Real-Time PCR testing for pathogens in Montgomery, Virginia.



Figure 4: Real-Time PCR testing for pathogens in Wythe, Virginia.

## Discussion & Future Directions

- All counties have *I. scapularis* populations harboring multiple pathogens of medical and veterinary concern in relatively high prevalences.
- High numbers of *B. burgdorferi* and *A. phagocytophilum*-positive pools from a specific area in Montgomery county called the Tabor Valley (indicated in Figure 1) is a public health concern we would like to explore further.
- Future Surveillance and Testing
  - Testing more ticks from other counties in SW Virginia
  - Pathogen confirmation of *A. phagocytophilum* and Powassan virus using Sanger sequencing

## Acknowledgements

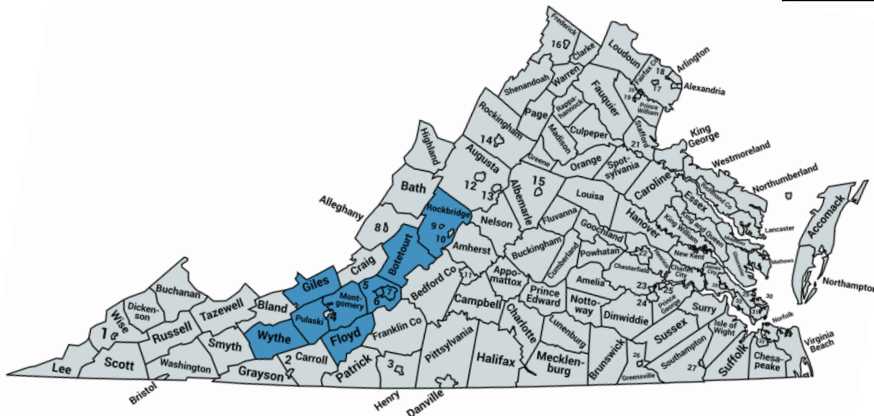
Special thanks to Lucas Raymond, Lindsey Fren, Rebecca Trimble, Mikayla Evans, and Ahmed Garba for their help in data collection. This work was supported in part by a Department of Defense Cancer Development Award (TR190061) awarded to Gillian Eastwood. Photo Credits: *Ixodes scapularis* photos by Graham Stovgoren and Dr. Marc Dolan.



# *Ixodes scapularis*

2019-2020 Pooled-infection rates

Pathogen	Max Likelihood Estimate
<i>Borrelia burgdorferi</i>	27.0% (20.7, 34.4)
<i>Borrelia miyamotoi</i>	7.1% (4.3, 11.4)
<i>Anaplasma phagocytophilum</i>	7.1% (4.3, 11.4)
<i>Powassan virus</i>	0.20% (0.04, 1.09)
<i>Babesia microti</i>	Not detected



Whitlow *et al* (in press) JoVE

## Key finding:

# POWV detected in counties of western VA

## First Evidence of Powassan Virus (Flaviviridae) in *Ixodes Scapularis* in Appalachian Virginia, USA

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**Abstract.** Here we report the first detection and confirmation of Powassan virus (POWV) (family: Flaviviridae) in *Ixodes scapularis* ticks collected from Appalachian Virginia. *Ixodes scapularis* ticks were collected from vegetation across field sites in eight counties of western Virginia from June 2019 to April 2021. From these collections, one nymph and one adult male *I. scapularis* were determined to be positive for POWV using real-time RT-PCR and Sanger sequencing. Both positive ticks were collected from Floyd county, VA, at residential sites; the nymph in June 2020 and the adult male in April 2021. The presence of POWV in Virginia in its natural tick vector is crucial knowledge in beginning to understand the movement and transmission of this pathogen into new geographical areas and the risk it poses to medical and veterinary health.

### INTRODUCTION

Powassan virus (POWV), transmitted by ixodid ticks, was first identified as a human pathogen in Powassan, Ontario, in 1958.<sup>1</sup> Since its first detection, POWV has been documented along the eastern seaboard on North America as far south as northern Virginia and as far north as Nova Scotia (Canada);

POWV to determine this pathogen's current status/prevalence in ticks in Virginia and its posed risk to residents who frequent tick habitat.

### MATERIAL AND METHODS

*Ixodes scapularis* ticks were collected from vegetation

Cumbie *et al* (in press) *AJTMH*





# THANK YOU! Questions?

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- Ahmed Garba
- Peter Schiff
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- Melanie Turner
- Lucas Raymond

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# The Influence of FOREST DEGRADATION on sylvatic mosquitoes in Panamá

Four ecologically-similar forest regions in Central Panama  
gradient of human modification ('degraded' to 'intact')



Gillian Eastwood, Wadsworth Center of the New York State Department of Health, United States

"The Effect of Land-Use on the Distribution and Enzootic Cycling of Mosquito-borne Viruses"



Overseas location  
Panama