

# Proceedings of the Cervidae Health Research Initiative Science Symposium

March 28, 2017 // Gainesville, FL



**Cervidae Health  
Research Initiative**

[www.wec.ufl.edu/cheri](http://www.wec.ufl.edu/cheri)



**1st Annual**



**UF | IFAS**  
UNIVERSITY of FLORIDA

## CERVIDAE HEALTH RESEARCH INITIATIVE

Dear CHeRI supporters:

Thank you all for your enthusiasm and support of the CHeRI project. This adventure has been hugely rewarding to the team of investigators, their students and post-docs. Together, we have figured out new and important ways that ecologists, geographers, virologists, entomologists, geneticists, and veterinarians can collaborate to tackle tough questions surrounding vector-borne diseases like epizootic hemorrhagic disease and bluetongue. The result is that we have new ways to think about diseases that affect deer and that translates into new and better ways of managing disease on deer farms.

While the emphasis of today's symposium is about the science that goes into CHeRI, we are already planning workshops and field days that will focus on how we can use this new knowledge to help control midge populations, increase deer health, and reduce mortalities on farms. Stay tuned for upcoming events!

Thank you, always, for your support - *Sam*

Dr. Samantha Wisely  
Director, CHeRI



## Affiliate Scientists

**Dr. Jeffrey R. Abbott**, Department of Infectious Diseases and Pathology  
abbottj@ufl.edu

**Dr. Jason K. Blackburn**, Department of Geography  
jkblackburn@ufl.edu

**Dr. Nathan Burkett-Cadena**, Florida Medical Entomology Laboratory  
nburkettcadena@ufl.edu

**Dr. Juan Campos**, Department of Large Animal Clinical Sciences and Department of Wildlife Ecology and Conservation  
jmcampos@cccipy.org

**Dr. Salvador Gezan**, School of Forest Resources and Conservation  
sgezan@ufl.edu

**Dr. John Lednicky**, Department of Environmental & Global Health  
jlednicky@phhp.ufl.edu

**Dr. Katherine Saylor**, Department of Wildlife Ecology and Conservation  
saylerk@ufl.edu

**Dr. Nicole Stacy**, Department of Aquatic Animal Health and Department of Large Animal Clinical Sciences  
stacyn@ufl.edu

**Dr. Kuttichantran Subramaniam**, Department of Infectious Diseases and Pathology  
kuttichantran@ufl.edu

**Dr. Heather Walden**, Department of Infectious Diseases and Pathology  
hdstockdale@ufl.edu

**Dr. Thomas B. Waltzek**, Department of Infectious Diseases and Pathology  
tbwaltzek@ufl.edu

**Dr. Emma Weeks**, Department of Entomology and Nematology  
eniweeks@ufl.edu

**Dr. Jim Wellehan**, Department of Small Animal Clinical Sciences  
wellehanj@ufl.edu

**Cervidae Health Research Initiative**  
**1st Annual Science Symposium**  
28 March 2017  
Harn Museum of Art Auditorium, UF Campus  
3259 Hull Road, Gainesville, FL 32611

**8:30 – 9:00AM Breakfast**

**Session 1: Deer Health**

- 9:00 Cervidae Health Research Initiative: Mission and Strategic Plan  
*Samantha M. Wisely, Department of Wildlife Ecology and Conservation, University of Florida, Gainesville FL 32611*
- 9:10 Epidemiology of epizootic hemorrhagic disease virus in white-tailed deer in Florida, USA: Surviving year round exposure  
*Katherine Saylor, Department of Wildlife Ecology and Conservation, University of Florida, Gainesville FL 32611*
- 9:30 Pathogen analysis of Florida white-tailed deer  
*Kathryn Pothier, Department of Wildlife Ecology and Conservation, University of Florida, Gainesville FL 32611*
- 9:50 Clinical pathology of CHERI: What makes a healthy fawn?  
*Allison Cauvin, Department of Wildlife Ecology and Conservation, University of Florida, Gainesville FL 32611*

**10:10-10:40AM Coffee Break and Poster Session**

**Poster Session (Meet the Authors)**

Communication and collaboration of the Cervidae Health Research Initiative  
*Shannon Moore, Department of Wildlife Ecology and Conservation, University of Florida, Gainesville FL 32611*

Prevalence of *Theileria* in white-tailed deer in Florida  
*Karen Hood, Department of Wildlife Ecology and Conservation, University of Florida, Gainesville FL 32611*

Culicoides, pesticides, and deer health  
*Laura Harmon, Department of Entomology and Nematology, University of Florida, Gainesville FL 32611*

Utilizing genotyping data to increase understanding of white tailed deer genetics, pathogen transmission, and beyond!  
*S.A. Gezan, School of Forest Resources and Conservation, University of Florida, Gainesville FL 32611*

**Session 2: Diagnostics and Virus Discovery**

- 10:40 Capacity building: Establishing the CHERI cervid virus research laboratory  
*John Lednicky, Department of Environmental and Global Health, University of Florida, Gainesville FL 32603*
- 11:00 Bioinformatic Approaches to Viral Discovery in Florida Farmed Deer  
*Subramaniam K, Department of Infectious Diseases and Pathology, University of Florida, Gainesville FL 32608*
- 11:20 Phylogenomic Characterization of Novel Viruses in Florida Farmed Deer  
*Thomas Waltzek, Department of Infectious Diseases and Pathology, University of Florida, Gainesville FL 32608*

### **Session 3: Community Ecology of Deer Farms and Implications to Disease Transmission**

- 11:40 Spatial ecology of larval *Culicoides* biting midges on a Florida deer ranch  
*Erik Blosser, Florida Medical Entomology Laboratory, University of Florida, Vero Beach, FL 32962*
- 12:00 At the trough or in insect hotspots? Evaluating risky behaviors in captive cervids and bovids on a wildlife ranch in Florida  
*Jason K. Blackburn, Department of Geography, University of Florida, Gainesville, FL 32603*
- 12:20 Living la Vida T-LoCoH: Site fidelity amongst Florida wild and captive white-tailed deer during the EHDV transmission risk period  
*Emily Dinh, Department of Geography, University of Florida, Gainesville, FL 32603*

#### **12:40 – 2:00PM Lunch**

### **Session 4: Vector ecology and the science of integrated pest management**

- 2:00 Ecology of host-seeking *Culicoides* spp. biting midges at a big game preserve in Gadsden Co., FL  
*Bethany McGregor, Florida Medical Entomology Laboratory, University of Florida, Vero Beach, FL 32962*
- 2:20 Identification of host-derived attractants and repellents for improving *Culicoides* management on deer farms  
*ENI Weeks, Dept. of Entomology and Nematology, University of Florida, Gainesville FL 32611*
- 2:40 Effectiveness of D-TERRENCE in protecting penned deer from biting midges  
*Alfred Runkel IV, Florida Medical Entomology Laboratory, University of Florida, Vero Beach, FL 32962*

#### **3:00 – 3:20PM Coffee Break**

- 3:20 Larval development of *Culicoides sonorensis* (Diptera: Ceratopogonidae) in mud supplemented with manure of various farm animal species  
*Dinesh Erram, Florida Medical Entomology Laboratory, University of Florida, Vero Beach, FL 32962*
- 3:40 Comparison of the efficiency of different light types and carbon dioxide in conjunction with CDC miniature light traps for trapping no-see-ums (Genus: *Culicoides*)  
*Kristin E. Sloyer, Florida Medical Entomology Laboratory, University of Florida, Vero Beach, FL 32962*
- 4:00 Patterns of host use of *Culicoides* spp. in Florida: Implications for pathogen transmission and vector interventions  
*Nathan Burkett-Cadena, Florida Medical Entomology Laboratory, University of Florida, Vero Beach, FL 32962*
- 4:20 Concluding Remarks

## Abstracts

### **Cervidae Health Research Initiative: Mission and Strategic Plan**

**Samantha M. Wisely**

Department of Wildlife Ecology and Conservation, University of Florida, Gainesville FL 32611

The UF IFAS Cervidae Health Research Initiative (CHeRI) has a tripartite mission of education, research and extension revolving around sustainable deer farming in Florida. The Initiative began in 2014 in response to a statewide outbreak of epizootic hemorrhagic disease virus that cost the industry more than \$32 M. One of the unique aspects of CHeRI is the transdisciplinary approach to tackling the question of deer health and disease. Fourteen faculty from 4 colleges mentor post-docs, graduate students, veterinary students and undergraduates in STEM sciences that span the breadth of the life science disciplines and all share five common goals that are at the center of our strategic plans. 1) Engage the deer farm industry in Florida and create a network of cooperators, 2) develop best management practices for hemorrhagic disease including a vaccine, 3) increase the health and welfare of farmed deer in Florida, 4) create an integrated pest management plan for the vector of hemorrhagic disease, 5) create useful decision making tools for the deer farm industry. Our ultimate mission is to promote the economic prosperity of the > 400 deer farmers in Florida while promoting the health of native wildlife and the ecosystems in which they live.

### **Epidemiology of epizootic hemorrhagic disease virus in white-tailed deer in Florida, USA: Surviving year round exposure**

**Katherine A. Sayler<sup>1</sup>**, Erik Blosser<sup>2</sup>, Bethany McGregor<sup>2</sup>, Nathan Burkett-Cadena<sup>2</sup>, Carisa L. Boyce<sup>1</sup>, Julia Loeb<sup>3</sup>, Jason K. Blackburn<sup>4</sup>, John A. Lednicky<sup>3</sup>, Samantha M. Wisely<sup>1</sup>

<sup>1</sup>Department of Wildlife Ecology and Conservation, University of Florida, Gainesville FL 32611, <sup>2</sup>Florida Medical Entomology Laboratory, University of Florida, Vero Beach, FL 32962, <sup>3</sup>Department of Environmental and Global Health, University of Florida, Gainesville FL 32603, <sup>4</sup>Department of Geography, University of Florida, Gainesville, FL 32603

Hemorrhagic disease (HD) is a vector-borne disease of ruminants caused by two distinct but related viruses: epizootic hemorrhagic disease virus (EHDV) and bluetongue virus (BTV). In terms of losses, HD is the most important viral disease of white-tailed deer in North America. In recent years, HD outbreaks have become more frequent, and HD has become a more global problem. The reasons for this incursion are not well understood but some hypotheses for this phenomenon include the expanding range of biting midge vectors (*Culicoides* spp.), potentially resulting in overwintering of these viruses, or the emergence of more virulent strains of these viruses. To explore this problem in northwest Florida, we measured seroconversion to 3 endemic EHDV serotypes in a sentinel herd using well-established serological methods. We also monitored the herd using RT-qPCR in order to detect all known EHDV serotypes. At the time of death, necropsies were performed on all animals in the herd to determine if HD was the cause. Simultaneously, we trapped *Culicoides* using CDC miniature light traps and by aspiration directly off of white-tailed deer enclosed within a 500 acre preserve. From January to March of 2016, seroconversion to EHDV-1 and 6 occurred across the herd in all age groups of animals. The virus was transiently detected by molecular methods in hosts during this time period. In September to November of 2016, HD was responsible for the deaths of 5 adult deer in the herd and over a dozen yearling deaths. However, EHDV-2 was transiently detected in the blood of hosts without an overt clinical disease from September 2016 to January 2017. Compared to midge abundance and diversity in the previous season (July-December), few midge species were present in either January of 2016 or 2017. Transmission of these viruses appears to be year-round, even in the absence of documented, competent vectors. Furthermore, in the same cohort of animals, some survive infection while others do not. Besides prior exposure to the homologous virus serotype, preliminary analysis indicates that

undescribed factors contribute to variable disease outcomes. These findings are an important component to understanding the unique disease risks to farmed deer in Florida.

## **Pathogen analysis of Florida white-tailed deer**

**Kathryn Pothier**

Department of Wildlife Ecology and Conservation, University of Florida, Gainesville FL 32611

The state of Florida has approximately 400 deer farms and hunting preserves that provide both meat and hunting opportunities to residents and visitors alike. This viable industry generates about 12.8 million dollars in revenue each year in a combination of licensure and hunting. These farms and preserves have created 1700 jobs in rural counties, giving small towns a thriving industry. To keep this business viable, it is essential to understand and combat diseases that kill animals or decrease production. White tailed deer are susceptible to multiple bacterial and viral pathogens, which infect both adult and fawn at different times throughout the year. CHeRI is currently working to understand the prevalence of these pathogens in order to prevent future outbreaks of disease and mortality. CHeRI obtains organ, blood, fecal and nasal samples from deceased animals via necropsy. These samples are tested for an assortment of viral and bacterial pathogens, and infections are detected through microbiological and molecular techniques. In 2016, more than 80 animals were submitted for post mortem diagnostic testing through CHeRI. In the beginning of summer 2016, fawns were the most susceptible to infection. They were almost exclusively infected with bacterial pathogens from May through August. Additionally, most of these mortalities were caused by co-infections of multiple bacteria. The most common species found were *E.coli*, *Streptococci* and *Trueperella*. Later in the fall and early winter months, more viral pathogens were found, specifically Blue Tongue Virus and Hemorrhagic Disease Virus. Interestingly, the viral pathogens infected high numbers of both adults and young animals. Viral infections were commonly found in conjunction with a septic bacterial infection as well, suggesting that the combination of multiple pathogens leads to a higher level of mortality due to a highly compromised immune system. CHeRI continues to look for solutions to help lower the incidence of these infections. Thus far, we can conclude that because a number of these pathogens are capable of persisting in the environment, changes in husbandry practices have the potential to decrease the incidence of these co-infections.

## **The Clinical Pathology of CHeRI: What Makes a Healthy Fawn?**

**Allison Cauvin**<sup>1</sup>, Nicole Stacy<sup>2</sup>, Rebecca Shuman<sup>3</sup>, Katherine Saylor<sup>1</sup>

<sup>1</sup>Department of Wildlife Ecology and Conservation, University of Florida, Gainesville FL 32611, <sup>2</sup>University of Florida College of Veterinary Medicine, Gainesville, FL 32608, <sup>3</sup>Florida Fish and Wildlife Conservation Commission

The growth of the cervid farming industry has led to many questions as to what constitutes a healthy deer. Following an outbreak of hemorrhagic disease in Florida cervids in 2014, the need for disease recognition, rapid diagnosis, and an understanding of neonate health became even more critical to the industry. In order to characterize what hematological parameters are associated with a healthy whitetail neonate, we used complete blood cell counts, otherwise known as a CBC, to inexpensively and rapidly gain insight to the health status of white-tailed deer neonates. While results are often nonspecific, this is the easiest way to understand if the animal is healthy or exhibiting an inflammatory response related to a disease state. In this study we evaluated and characterized whitetail neonate blood films taken between 12 and 24 hours of birth, as well as hematologic parameters including HCT, WBC, and serum biochemistry results. The future aims of this project include using a generalized linear model to determine if hematological values are associated with maternal antibody levels and fawn survivorship. Results will establish a baseline of values for healthy animals, which will allow veterinarians to more easily determine illness in farmed deer.

## Capacity Building: Establishing the CHeRI Cervid Virus Research Laboratory

John Lednicky<sup>1</sup>, Julia Loeb<sup>1</sup>, Katherine Saylor<sup>2</sup>, Jeffrey Abbott<sup>3</sup>, Thomas Waltzek<sup>3</sup>, Samantha Wisely<sup>2</sup>

<sup>1</sup>Department of Environmental and Global Health, University of Florida, Gainesville FL 32603, <sup>2</sup>Department of Wildlife Ecology and Conservation, University of Florida, Gainesville FL 32611, <sup>3</sup>Department of Infectious Diseases and Pathology, University of Florida, Gainesville FL 32608

Florida has a humid and mild subtropical climate in the northern half of the state, and a tropical climate in the southern portion. Due its wide array of climate conditions and abundant rainfall, there are many types of ecosystems in Florida including hardwood forests, swamps, saltwater marshes, scrub, and sandhills. Taken together, Florida is unique in that it can support a wide variety of animals, including native deer species and various species of farmed deer. These animals are susceptible to known infectious diseases of cervids, and occasional widespread outbreaks have been documented. These include virus-borne infections. Viruses are known to mutate frequently, and this can affect their virulence. Many deer viruses are vector-borne, transmitted by mosquitoes, midges, or other arthropods. Of major concern are emerging viruses, for which Florida deer have no immunity. As part of the CHeRI initiative, an interdisciplinary cervid virus research laboratory has been established. A major impetus for this research is to develop capacity and infrastructure for the identification of contemporary viruses affecting Florida deer, with the goal of developing countermeasures to eliminate the viruses, and where applicable, their vectors. Initial focus has been towards the detection and characterization of the many *Blue tongue virus* (BTV) and *Epizootic hemorrhagic disease virus* (EHDV) variants in Florida. Early successes include the isolation of EHDV-1 and EHDV-2, with virus genomic sequencing underway. Another success has been the isolation and sequencing of *Cervid pox virus*. These studies indicate that the viruses have unique genetic sequences that spotlight them as Florida strains. Additional studies are underway to identify other viruses. The laboratory will soon also analyze the viruses transmitted by arthropod parasites of deer. As knowledge of the viral agents mount, efforts will extend towards the development of protective vaccines.

## Bioinformatic Approaches to Viral Discovery in Florida Farmed Deer

Kuttichantran Subramaniam<sup>1,4</sup>, Katherine A. Saylor<sup>2</sup>, Julia Loeb<sup>3,4</sup>, John Lednicky<sup>3,4</sup>, Samantha M. Wisely<sup>2</sup>, Thomas B. Waltzek<sup>1,4</sup>

<sup>1</sup>Department of Infectious Diseases and Pathology, University of Florida, Gainesville, FL 32608, <sup>2</sup>Department of Wildlife Ecology and Conservation, University of Florida, Gainesville, FL 32611, <sup>3</sup>Department of Environmental and Global Health, University of Florida, Gainesville, FL 32603, <sup>4</sup>Emerging Pathogens Institute, University of Florida, Gainesville, FL 32608

Historically, the detection of viruses has relied upon the observation of cytopathic effect following the inoculation of tissue homogenates on permissive cell lines. Amplification of viral nucleic acid by PCR followed by Sanger sequencing has proven to be another invaluable tool for the detection and characterization of novel viruses. However, recently developed viral enrichment strategies paired with high throughput next generation sequencing (NGS) technologies have revolutionized the discovery and genomic characterization of novel viruses. Virus discovery using NGS approaches provides several advantages over PCR and Sanger sequencing approaches including: providing an unbiased snapshot of the virome (i.e. all RNA and DNA viruses in a sample) and recovering full genomes given the sheer amount of sequence generated. In this presentation, NGS approaches developed by the Wildlife and Aquatic Veterinary Disease Laboratory and CHeRI partners used to discover and characterize novel viruses in Florida farmed cervid populations will be discussed including: 1) viral enrichment strategies that minimize the impact of host nucleic acids (e.g., filtration, ultracentrifugation, nuclease treatment, methylated DNA removal kits), 2) library construction (e.g., Nextera and TruSeq), and 3) approaches to improving the quality of NGS datasets (e.g., read quality and trimming in the FASTX-toolkit, removal of host reads using Kraken software), 4) *de novo* versus reference-assisted assemblies of NGS datasets (e.g., CLC genomics, Velvet, and SPAdes), and 5) development of curated viral databases and computational approaches to

rapidly screen assembled contigs for novel cervid viruses (e.g., white-tailed deer poxvirus, white-tailed deer *Rhabdovirus*, EHD-1 and 2).

## Phylogenomic Characterization of Novel Viruses in Florida Farmed Deer

Thomas B. Waltzek<sup>1,4</sup>, Katherine A. Sayler<sup>2</sup>, Julia Loeb<sup>3,4</sup>, John Lednicky<sup>3,4</sup>, Samantha M. Wisely<sup>2</sup>, Kuttichantran Subramaniam<sup>1,4</sup>

<sup>1</sup>Department of Infectious Diseases and Pathology, University of Florida, Gainesville, FL, <sup>2</sup>Department of Wildlife Ecology and Conservation, University of Florida, Gainesville, FL, <sup>3</sup>Department of Environmental and Global Health, College of Public Health and Health Professions, University of Florida, Gainesville, FL, <sup>4</sup>Emerging Pathogens Institute, University of Florida, Gainesville, FL

Infectious agents (e.g., bacteria, fungi and water molds, unicellular and metazoan parasites, and viruses) pose a significant threat to Florida deer. Viruses are perhaps the least studied and among the most important pathogens negatively impacting Florida deer production. To date, a variety of RNA and DNA viruses have been detected within wild and managed cervid populations including highly significant arboviruses such as bluetongue (BT) and epizootic hemorrhagic disease (EHD). As part of the CHERI, we conducted the first concerted deer viral discovery effort among participating Florida deer farmers. Although ongoing, we have sequenced and characterized: 1) a novel white-tailed deer gammaherpesvirus of concern but unknown significance, 2) deerpox virus from an outbreak in Florida, and 3) a dozen or more EHD serotypes (1 & 2) associated with epizootics. The EHD sequences provide important data on the serotypes currently circulating in Florida. A better understanding of the prevalence and distribution of EHD serotypes circulating in Florida wild and managed cervid populations is needed to facilitate the development of effective detection and mitigation strategies.

## Spatial ecology of larval *Culicoides* biting midges on a Florida deer ranch

Erik Blosser<sup>1</sup>, Bethany McGregor<sup>1</sup>, Nathan Burkett-Cadena<sup>1</sup>, Katherine Sayler<sup>2</sup>, Samantha Wisely<sup>2</sup>, Jason Blackburn<sup>3</sup>

<sup>1</sup>Florida Medical Entomology Laboratory, University of Florida, Vero Beach, FL 32962, <sup>2</sup>Department of Wildlife Ecology and Conservation, University of Florida 32611, <sup>3</sup>Department of Geography, University of Florida 32603

Biting midges (*Culicoides* spp.), a.k.a. no-see-ums, are vectors of viruses causing Epizootic Hemorrhagic Disease (EHD) and Bluetongue disease (BT), which affect deer and livestock. Our ability to reduce animal risk of these diseases is limited by lack of information on which *Culicoides* species are the primary vectors of these viruses throughout the state (nearly 50 *Culicoides* species occur in Florida), and the paucity of specific information on the development sites of these species. This information is critical for *Culicoides* control and will aid in the understanding of environmental factors, which lead to outbreaks of midge populations and the viruses they transmit. Studies of the spatial ecology of the larval habitats of *Culicoides* midges were undertaken on a north Florida deer ranch. Based on light trapping for adult midges, 4 species comprised 98% of the total catch during the summer and fall while two different species dominated the spring collections. Emergence trapping results indicated low-lying forested areas as the most important larval development sites for the 3 most common summer/fall *Culicoides* species on the ranch: *C. stellifer*, *C. haematopotus*, and *C. venustus*. Although all three species overlapped in larval habitat, each species also showed strong association with a particular habitat type suggesting some segregation of larval habitats. Supporting evidence for these spatial patterns comes from the spatial distributions of the adult gravid (egg-bearing) midges, which were greatest in low-lying forested habitat. A similar distribution was seen in midges parasitized with a nematode that causes all infected adults to behave like gravid females and seek oviposition sites. The conclusion of this study is that low-lying forested areas are the most productive *Culicoides* larval habitats for the most common species on the study ranch. This information is a necessary step in predicting spatial emergence patterns of *Culicoides* midges within the landscape and making informed decisions for the judicious use of pesticide for larval midge control.

## **At the trough or in insect hotspots? Evaluating risky behaviors in captive cervids and bovids on a wildlife ranch in Florida**

**Jason K. Blackburn**<sup>1</sup>, Katherine Saylor<sup>2</sup>, Erik Blosser<sup>3</sup>, Bethany McGregor<sup>3</sup>, Jeremy Orange<sup>1</sup>, Samantha Wisely<sup>2</sup>, Nathan Burkett-Cardena<sup>3</sup>

<sup>1</sup>Department of Geography, University of Florida, Gainesville, FL 32603, <sup>2</sup>Department of Wildlife Ecology and Conservation, University of Florida, Gainesville, FL 32611, <sup>3</sup>Florida Medical Entomology Lab, University of Florida, Vero Beach, FL 32962

In the absence of efficacious vaccines and appropriate distribution mechanisms, like oral vaccines for wildlife, disrupting the transmission chain between vectors and hosts remains viable for disease control. Understanding when and where vectors contact hosts is important for interrupting transmission. Epizootic hemorrhagic disease virus (EHD) is an orbivirus transmitted by *Culicoides* insects that infects wild and captive cervids (deer) in many countries, including the United States. In some years, outbreaks can have very high mortality rates in native and farmed deer populations. In farming operations, or ranches where deer are fed supplemental feed, deer behavior at feeders, such as long duration stays during periods of high *Culicoides* activity, may increase transmission likelihood. To understand possible white-tailed deer, *Odocoileus virginianus*, interactions with *Culicoides*, we performed two parallel studies. First, we collared 11 deer and 9 exotic species (elk, Pere David deer, Indian blackbuck, axis and fallow) with GPS devices on a 500-acre ranch in northwest Florida where EHD is prevalent. Animals were collared from May - October 2015 at the same time 20 *Culicoides* traps were run weekly to monitor insect density. We developed a new function within the T-LoCoH package in R to calculate animal visitation, duration of visit, and directional movement between supplemental feeders and relative to vector density. Results will be discussed relative to species commingling/competition at feeders and feeder usage in areas of high insect density, with comments on those midge populations most likely transmitting virus. The goal of these analyses is to determine how feeding times, feeder locations, and wildlife density may be modified to reduce vector-host interactions.

## **Living la Vida T-LoCoH: Site fidelity amongst Florida wild and captive white-tailed deer during the EHDV transmission risk period**

**Emily Dinh**<sup>1</sup>, Jeremy Orange<sup>1</sup>, Katherine Saylor<sup>2</sup>, Rebecca Shuman<sup>3</sup>, Andy Lyons<sup>1</sup>, Catherine G. Haase<sup>1</sup>, Samantha Wisely<sup>2</sup>, Jason K. Blackburn<sup>1</sup>

<sup>1</sup>Department of Geography, University of Florida, Gainesville, FL 32603, <sup>2</sup>Department of Wildlife Ecology and Conservation, University of Florida, Gainesville, FL 32611, <sup>3</sup>Florida Fish and Wildlife Conservation Commission

Farmed deer operations represent a growing industry across the US and globally. Health and disease represent a major cost to wildlife managers/operators, and there is a need to better understand disease risks in these populations. For diseases with vector-borne transmission, such as epizootic hemorrhagic disease virus (EHDV) and blue tongue virus (BTV), understanding deer interactions with areas highest likelihood of vector/host interaction may be important for identifying areas for intervention. While experiments are underway to study the efficacy of vaccines for penned deer, the industry also has a large hunting and preserve deer component, where animals free range, often with feed subsidies (e.g. protein), and are more difficult to capture or vaccinate. In these situations, disease management will likely involve vector control, landscape modification, or behavioral modification to reduce transmission potential. In this study, we apply site fidelity metrics to compare revisitation and duration of visit to specific areas within white-tailed deer, *Odocoileus virginianus*, home ranges from a large high-fenced preserve population and wild native deer from nearby state-owned properties. Preliminary data from 2016 sampling indicate that EHDV rates are higher in the captive population. Here we aim to determine behavior differences, such as high site fidelity to risky habitats, between these two populations. We apply a novel function developed from the T-LoCoH R package to compare movement patterns in these two groups of deer.

## **Ecology of host-seeking *Culicoides* spp. biting midges at a big game preserve in Gadsden Co., FL**

**Bethany McGregor**<sup>1</sup>, Tanise Stenn<sup>1</sup>, Alfred Runkel<sup>1</sup>, Nathan Burkett-Cadena<sup>1</sup>, Katherine Saylor<sup>2</sup>, Samantha Wisely<sup>2</sup>, Jason Blackburn<sup>3</sup>

<sup>1</sup>Florida Medical Entomology Laboratory, University of Florida, Vero Beach, FL 32962, <sup>2</sup>Department of Wildlife Ecology and Conservation, University of Florida, Gainesville FL 32611 <sup>3</sup>Department of Geography, University of Florida, Gainesville, FL 32603

*Culicoides* spp. biting midges (no-see-ums) are a diverse (>1,000 species) group of blood-feeding flies with several significant vectors of animal pathogens around the world. For many species, little is known about their ecology and therefore management decisions are impeded by this lack of knowledge. To provide detailed information on ecology of host-seeking female midges, field studies were conducted at a big game preserve in Gadsden County, FL. We first determined the patterns of host utilization of common *Culicoides* species using molecular methods to determine animals fed upon by each midge species. We found that different *Culicoides* species showed distinct preferences for different host species on the property (n=1,300). Based upon the findings that some *Culicoides* fed heavily upon canopy birds and mammals, we then conducted experiments to determine host seeking heights of *Culicoides* by trapping at two heights: ground level (1.37m) and tree canopy (4.5m). Using this data, we can investigate where most *Culicoides* are found in vertical space. Landowners can use the data for more targeted insect control practices. Our research indicates that, although *Culicoides* are found in abundance at both heights (n=4,769), significantly greater numbers of midges were found host seeking in the tree canopy. Because artificially high densities of game animals occur on the ranch, our final study was to investigate how midge abundance and host use compare between big game preserves and nearby public lands. Our results indicate that higher midge abundance was found on the preserve property compared with nearby public lands, and that species diversity varied between these sites (n=5,230). This could help us identify key differences in these two environments, which could inform potential mitigation efforts for landowners. Combined, these experiments provide valuable ecological information about these insects that can be used to guide best management practices and control efforts to mitigate the spread of vector-borne animal pathogens, such as epizootic hemorrhagic disease virus and bluetongue virus, and to identify potential vector species.

## **Identification of host-derived attractants and repellents for improving *Culicoides* management on deer farms.**

**E.N.I Weeks**

Department of Entomology and Nematology, University of Florida, Gainesville, FL 32611

*Culicoides* biting midges are annoying blood feeding insects that, more importantly, are vectors of epizootic hemorrhagic disease virus (EHDV) and bluetongue virus to deer and other ungulates in Florida. White tailed deer (*Odocoileus virginianus*) are the most susceptible wild ungulate to EHDV in North America. When a blood-feeding insect is searching for food it uses visual, thermal, and chemical cues, amongst others, to detect its preferred host for a blood meal. The main *Culicoides* vector of EHDV in Florida and its preferred hosts is not currently known, but research on this topic is in progress. Identification of the chemicals that are involved in host location and preference can provide tools and techniques to manipulate the behavior of a pest insect. For example, attractant chemicals can be used in traps for surveillance, monitoring success of control measures and mass trapping for population suppression. Repellents could be used to protect valuable animals or as part of a push-pull system. The aim of this study was to identify potential host location cues from white tailed deer. Host odor samples have been collected through swabbing with cotton gauze. These samples were extracted and analyzed by gas chromatography to determine the host odor composition. Future research will involve testing by behavioral bioassay to demonstrate the response of the midges to the extracts and electrophysiology to determine the chemicals within the extract that are detected by the insect. Chemicals then will be tested by behavioral bioassay to determine if they have attractant or repellent properties for potential use in integrated pest management (IPM) of *Culicoides* by deer farmers in Florida and throughout the US.

## Effectiveness of D-TERRENCE in protecting penned deer from biting midges

Alfred Runkel IV<sup>1</sup>, Katherine Saylor<sup>2</sup>, and Nathan Burkett-Cadena<sup>1</sup>

<sup>1</sup>Florida Medical Entomology Laboratory, University of Florida, Vero Beach, FL 32962, <sup>2</sup>Department of Wildlife Conservation and Ecology, University of Florida, Gainesville FL 32611

*Culicoides* biting midges (aka no-see-ums) are major pests on deer ranches in the Southeast and are also important vectors of Blue Tongue Virus (BTV) and Epizootic Hemorrhagic Disease Virus (EHDV), which can be fatal to white-tailed deer. Without an effective vaccine, limiting deer contact with vectors is an important method for reducing EHDV and BTV risk in captive herds. In the current study, we tested the effectiveness of D-TERRENCE (Y-Tex<sup>®</sup>) a polyethylene screen treated with 0.4% Deltamethrin, for reducing the number of midges in deer breeding pens at a captive ranch in Gadsden County, Florida. Two breeding pens, each with 8-12 does were used in the study. One pen was wrapped once with D-TERRENCE to a height of three feet while the other was left unwrapped (control). CDC blacklight traps were used to quantify *Culicoides* numbers inside and outside of treated and untreated pens. Traps were wrapped in wire fencing to keep the deer from interfering with collection. Insects were collected directly into 15 mL of 90% ethanol, then identified to species. Midges were collected two days per week during July and August 2016. Five species of *Culicoides*: *C. arboricola*, *C. debilipalpis*, *C. spinosus*, *C. stellifer*, and *C. venustus* were collected. *Culicoides stellifer* was most abundant species, accounting for about 98% of the total midges. In July, greater numbers of *C. stellifer* were collected from traps placed inside the wrapped pen (320 total; 80/trap night) compared to the unwrapped pen (134 total; 34.83/trap night). Numbers of midges collected in August were much lower than July, although more midges were again trapped inside wrapped pens (94 total, 15.67/trap night) than unwrapped pens (11 total, 3.25/trap night). In total comparison, 414 *C. stellifer* were collected in the wrapped pen and 145 were collected in the unwrapped pen, with an average of 20.7 and 11.15 respectively. Our results suggest that D-TERRENCE may not provide adequate protection against *Culicoides*. However, several factors could have affected the effectiveness D-TERRENCE in the current study. Pens were not double-wrapped and properly positioned with D-TERRENCE, as per the instructions provided by Y-Tex<sup>®</sup>.

## Larval development of *Culicoides sonorensis* (Diptera: Ceratopogonidae) in mud supplemented with manure of various farm animal species

Dinesh Erram<sup>1,2</sup> and Ludek Zurek<sup>1</sup>

<sup>1</sup>Department of Entomology, Kansas State University, Manhattan, KS 66506, <sup>2</sup>Florida Medical Entomology Laboratory, University of Florida, Vero Beach, FL 32962

Understanding factors that affect *Culicoides* larval development is critical in suppressing adult midge populations that transmit economically important pathogens to ruminants such as bluetongue virus and epizootic hemorrhagic disease virus. In this study, the development of *Culicoides sonorensis* Wirth and Jones was investigated in substrates composed of mud mixed with varying concentrations of animal manures, from eight different farm animal species (dairy cattle, beef cattle, sheep, goat, pig, horse, chicken, and white-tailed deer). First instar larvae (~100/treatment) were added to the substrates, and adult emergence and development times were monitored for 90 days. In substrates with dairy cattle manure, significantly more *C. sonorensis* adults emerged ( $\geq 76.7\%$ ) and development time was shorter ( $\leq 25.5$  days) from 25.0% manure substrate than from lower or higher manure concentrations ( $\leq 41.3\%$  emerged;  $\geq 31.2$  days). Comparatively, white-tailed deer and chicken manures poorly supported *C. sonorensis* development with low emergence rates (deer  $\leq 13.0\%$ ; chicken = 0%) and longer development time (deer  $\geq 29.0$  days). Mud enriched with manure of beef cattle, sheep, goat, pig, and horse generally supported *C. sonorensis* development, although adult emergence and development time varied widely between species. These results suggest that manure of several farm animal species can contribute to *C. sonorensis* development in the field. Therefore, the potential of animals other than cattle in sustaining local populations of *C. sonorensis* cannot be overlooked.

## **Comparison of the efficiency of different light types and carbon dioxide in conjunction with CDC miniature light traps for trapping no-see-ums (Genus: *Culicoides*)**

**Kristin E. Sloyer** and Nathan D. Burkett-Cadena

Florida Medical Entomology Laboratory, University of Florida, Vero Beach, FL 32962

Biting midges (a.k.a no-see-ums) of the genus *Culicoides* are vectors for many viruses, particularly Orbiviruses, such as Bluetongue virus (BTV) and Epizootic Hemorrhagic Disease (EHD) virus, which affect wild and captive ruminants, including whitetail deer. These diseases are of particular importance in Florida, as deer farmers have lost over \$32 million dollars to these diseases in 2012 alone. Determining which *Culicoides* species (of 46 species in Florida) is the major vector of these viruses relies, in part, on field evidence in the form of trapping adult biting midges and testing them for virus infection. It is therefore important to use trapping methods that capture the greatest diversity and abundance of biting midges at diverse locations. To test this, I evaluated CDC-miniature light traps with both blacklight LED-arrays, and incandescent bulbs, with and without carbon dioxide, at 3 deer farms throughout the state, in order to determine which combination of these parameters attract the greatest diversity and abundance of *Culicoides* species. The results indicate that traps with blacklight LED-arrays collected greater abundance and diversity of *Culicoides* species compared to incandescent bulbs. The presence of carbon dioxide significantly increased the abundance of *Culicoides* species caught in traps, but only marginally increases the richness of *Culicoides* species found. Due to the expense and difficulty in obtaining carbon dioxide for trapping purposes, its inclusion may or may not be warranted under different conditions. These findings provide robust sampling methodologies for *Culicoides* species by confirming the efficiency of a widely used trap, and by ruling out the necessity for carbon dioxide with respect to presence-absence surveillance.

## **Patterns of host use of *Culicoides* spp. in Florida: Implications for pathogen transmission and vector interventions**

**Nathan Burkett-Cadena**, Kristin Sloyer, Tanise Stenn, Carolina Acevedo, Anna Carels Thompson

Florida Medical Entomology Laboratory, Vero Beach, FL 32962

Contact between vector and host is the most important interaction in the transmission of vector-borne pathogens. In the absence of effective vaccines, limiting contact between vectors and hosts is perhaps the most effective means of protecting humans and animals from vector-borne diseases. However, this strategy relies upon a firm understanding of the vector and reservoir species involved in transmission of specific pathogens. In Florida, hemorrhagic diseases (caused by epizootic hemorrhagic disease virus and bluetongue virus) cause significant morbidity and mortality in farmed deer. These viruses are generally transmitted by species of *Culicoides*, known as biting midges or no-see-ums. *Culicoides* is a diverse group, however, and dozens of species with very diverse life histories can often be found at a single location. Therefore, determining which *Culicoides* species transmits hemorrhagic disease in a region can be challenging with strong implications for how resources are allocated towards interventions aimed at interrupting transmission. Determining which *Culicoides* spp. are biting deer, as well as potential reservoir hosts, is an important step in incriminating vector species and identifying the larval habitat of those vectors in order to suppress the vector population below thresholds that can sustain transmission. In the current study, *Culicoides* abundance and patterns of host use were investigated at seven deer ranches and one cattle ranch in Florida. Traps utilizing blacklight LED arrays were used to sample adult biting midges, and host use was determined by PCR assays targeting 16S rRNA and cytb genes of vertebrate hosts in blood-engorged female midges. Of fourteen *Culicoides* species collected, *Culicoides insignis* was found to be the most common species at five of eight ranches, and was found to feed on predominantly deer and cattle. Other hosts included blackbuck, elk, horse, red deer, wild boar and bushbuck. As these animals potentially serve as asymptomatic reservoirs for hemorrhagic diseases, identifying networks of contact between putative vectors and these animals, including deer, coupled with data on hemorrhagic disease infection between locations may provide insight into maintenance and spillover of these pathogens in Florida deer ranches.

## **Communication and collaboration of the Cervidae Health Research Initiative**

**Shannon Moore**, Samantha Wisely, Katherine Sayler

Department of Wildlife Ecology and Conservation, University of Florida, Gainesville FL 32611

Interdisciplinary science, education, and outreach are central to the Cervidae Health Research Initiative mission. In order to best serve deer farmers and learn about the diseases impacting both captive and wild deer, 12 labs from 8 departments at the University of Florida collaborate to learn from a wide variety of disciplines. The CHERI Hotline (352-562-DEER) allows Florida deer farmers to submit blood and tissue samples from moribund deer for free diagnostics. Multiple diagnostic tests are used to determine the role of hemorrhagic disease, or HD, in each case. When deer farmers submit multiple tissue samples from a case, up to 30 different specimens are generated for different analyses. These specimens are sent to 3 additional laboratories at UF for virology, histopathology and microbiology. Results are then collated and a comprehensive report is sent to the submitting deer farmer. All results are confidential. The results help scientists understand the role of HD, and other disease processes, as causes of death in Florida farmed deer. The cooperation between the Cervidae Health Research Initiative and the public allows both parties to benefit, and to cooperatively improve the health of captive cervids. Additional education and outreach information regarding pathogens being found in moribund deer and other relevant information about cervids is shared on CHERI's social media platforms, including Facebook and Twitter, as well as on the CHERI website.

## **Prevalence of *Theileria* in White Tailed Deer in Florida**

**Karen Hood**, Katherine Sayler, Allison Cauvin

Department of Wildlife Ecology and Conservation, University of Florida, Gainesville FL 32611

*Theileria* spp. are protozoan hemoparasites, which undergo multiple stages in their life cycle to pass from host to tick vector to another host and so on. *Theileria* spp. cause theileriosis, which results in a range of symptoms from asymptomatic infection to death in naïve individuals. We surveyed for *Theileria* spp. in ruminants on deer ranches and in native, local white-tailed deer populations in order to understand prevalence and species composition of the organisms. Deer blood samples on ranches were collected from live deer by jugular venipuncture during routine handling and from deer on surrounding public lands. We assayed for protozoan DNA using conventional PCR, targeting the V4 hypervariable region of the 18s rRNA gene. Visualization of PCR products by gel electrophoresis revealed that 35/64 (54.7%) of adult individuals sampled on the ranch were infected with *T. cervi*. We found differences in prevalence based on host sex. Female deer had a higher prevalence than males; 26/38 (68.4%) female deer tested positive whereas only 9/26 (34.6%) male deer were PCR positive for *Theileria* spp DNA. Future work will identify the variation in genotypes of *Theileria* spp. in native and farmed individuals. Our study aids in the tracking of transmission of protozoa in cervids in Florida, which will ultimately preserve the health of herds.

## ***Culicoides*, pesticides, and deer health**

**L. E. Harmon**<sup>1</sup>, E. N. I. Weeks<sup>1</sup>, K. Sayler<sup>2</sup>, K. Sloyer<sup>1</sup>

<sup>1</sup>Dept. of Entomology and Nematology, University of Florida, Gainesville, FL 32611, <sup>2</sup>Department of Wildlife Ecology and Conservation, University of Florida, Gainesville FL 32611

*Culicoides* is a genus of biting midges that blood feed on a number of vertebrates, including human beings and domesticated animals. This blood feeding behavior makes them a potential vector of a number of pathogens worldwide, including African horse sickness virus (AHSV), bluetongue virus (BTV), and epizootic hemorrhagic disease virus (EHDV). In Florida, the most important diseases transmitted to deer by *Culicoides* are BTV and EHDV. To reduce the risk of these diseases being transmitted, deer farmers use pesticides, especially pyrethroids,

to manage *Culicoides* populations. The impacts these low-mammalian toxicity pesticides may have on deer health are not well understood. The aim of this study will be to first gauge deer farmer's perceptions about pesticide use, and determine the type of pesticide and frequency of use on their farms. This will be done through a survey delivered via email, over the phone, and/or in person. The second objective will be to evaluate the effect of known pesticide exposure on deer health using serum samples. These samples will be collected from wild and farmed deer populations, with residual pesticide levels expected to be higher in captive populations. The samples will be tested for pesticide presence and for markers of potential impacts on deer health, such as oxidative stress. The third objective of this study will be to measure pesticide efficacy on *Culicoides* to assess which pesticide has the potential to work best in managing populations. Pesticides to be tested will be determined through review of the literature, and from the survey. This study will benefit the deer farming industry by providing a better understanding of the impacts and efficacy of the currently used and available pesticides for *Culicoides* management.

### **Utilizing genotyping data to increase understanding of white tailed deer genetics, pathogen transmission, and beyond!**

**S.A. Gezan<sup>1</sup>, E.N.I Weeks<sup>2</sup>, J. Vann<sup>2</sup>, K. Sayler<sup>3</sup>**

<sup>1</sup> School of Forest Resources and Conservation, University of Florida, Gainesville FL 32603, <sup>2</sup> Entomology and Nematology Department, University of Florida, Gainesville FL 32608, <sup>3</sup> Wildlife Ecology and Conservation, University of Florida, Gainesville FL 32611

White-tailed deer are farmed in Florida and throughout much of the United States. There are currently over 300 deer breeding facilities in Florida alone. Most deer farmers incur substantial costs to submit samples to get access to genotyping data to obtain the pedigree for valuable breeding animals. In addition, they also are provided with microsatellites, which are typically underutilized by the farmers. The aim of this study is to use both the pedigree and microsatellite data to increase our understanding of white tailed deer genetics, particularly with regards to northern versus southern genotypes, and how this relates to susceptibility to transmitted viruses and disease resistance. Future research will focus on relating this data to other on-going studies. One example would be determining the relationship of deer genetics on deer odors and how this is related to host location and pathogen transmission by *Culicoides* biting midges. Understanding genetics can help to define appropriate breeding strategies and management plans to increase animal health and welfare on deer farms.



## **CERVIDAE HEALTH RESEARCH INITIATIVE**

### **5 year Strategic Plan for CHeRI**

**Samantha M. Wisely, Director  
Cervidae Health Research Initiative  
UF Institute of Food and Agricultural Sciences  
11 December 2016**

#### ***Executive Summary***

Deer farming is one of the fastest growing industries in rural North America. It generates \$3 billion for the US economy and employs tens of thousands of people. In addition to improving local economies, deer farms have the potential to improve habitat for other wildlife species. The Florida deer farm industry is the third largest in the nation and is vibrant and growing. Florida has approximately 400 deer farms that breed trophy deer and/or provide hunting opportunities to resident and non-resident hunters (Anderson et al. 2007).

In response to Florida stakeholders, the Florida Senate in FY 2014 provided a continuing academic appropriation to UF IFAS to form the Cervidae Health Research Initiative (CHeRI). CHeRI seeks to promote interdisciplinary science, education, and outreach that increases the health and production of captive cervids in a sustainable manner and promotes the health of native wildlife and the ecosystems in which they live. The cervid farming industry has identified hemorrhagic disease (HD) as a top priority for research and technical assistance from CHeRI. HD includes epizootic hemorrhagic disease virus (EHDV) and bluetongue virus (BTV), which is the most important viral disease of native and captive-farmed North American deer and elk. In response to this request for assistance, we have developed a multi-pronged approach to reduce mortality and increase production in deer.

Goals for the next 5 years:

- Engage the deer farm industry in Florida and create a network of cooperators
- Develop best management practices (BMP) for hemorrhagic disease (HD), including determination of disease drivers for acute HD, and development of an efficacious vaccine
- Identify and develop BMP for other infectious diseases in fawn and adult deer
- Create an integrated pest management plan for *Culicoides spp.*, the vectors of HD
- Create useful decision-making tools for the deer-farm industry

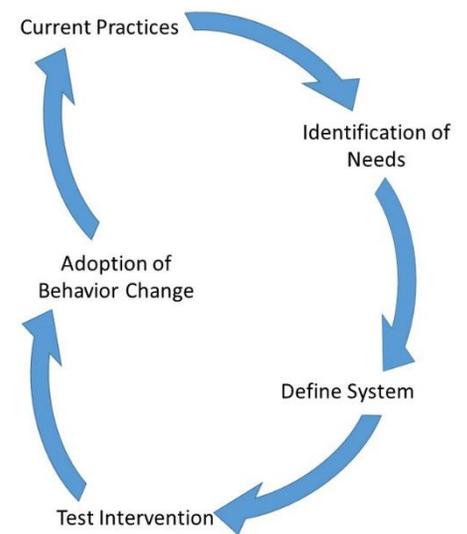
## Engaging producers in CHeRI

All aspects of CHeRI rely on our ability to connect with deer farmers. As researchers and extension specialists involved in CHeRI, we work directly with deer farmers to better understand the specific needs and practices of the industry. One of our first goals was to hire a faculty member that is the extension specialist for this industry. That goal has been realized and with the addition of Dr. Juan Campos in 2017, we will continue this dialogue and begin to take quantitative assessment of needs and practices. From its inception, CHeRI research has been driven by our ability to listen to producers to understand their needs and practices. We have attended trade shows and made dozens of field visits. In coming months, with the addition of Dr. Campos, we will ramp up our fact finding missions to include workshops, focus group studies, and surveys with a goal of engaging stakeholders and assessing their needs.

Engagement of stakeholders is also imperative in downstream aspects of research. Our success thus far has and will continue to depend on collaborations with deer farmers to collect data that helps solve problems. Access to animals on deer farms allows us to address questions of health and disease that is not possible in free-ranging wildlife. It also allows us to work with farmers to assess and fine tune best management practices that will help farmers increase production by reducing disease transmission and improving treatment regimes.

Finding and implementing solutions will require additional collaboration with the deer farm industry. Ultimately our goal is provide useful technologies and decision-making tools for best management practices. It is therefore imperative that as we produce products, we continue to build trust and credibility within the industry. As we begin to make research discoveries that support our goals, we will work with farmers to implement new technologies and design the best platforms for decision-making tools. Making science usable and relevant requires listening and involving the producers in solutions in an iterative fashion similar to adaptive management (Figure 1).

Figure 1. Iterative process that defines the CHeRI research agenda



## A Focus on Epizootic Hemorrhagic Disease

Key to the success of any farm is the production and maintenance of healthy deer. As reported by the industry, the biggest hurdle to maintaining healthy deer in Florida is epizootic hemorrhagic disease virus (EHDV).

This disease is caused by a virus carried by biting midges (no-see-ums, *Culicoides* spp.) and is prevalent throughout Florida. Captive deer often become sick and die within a few days of the onset of symptoms. Native, free-ranging deer become infected as well, but their population numbers are not threatened by the disease. For this reason, Florida Fish and Wildlife Commission does not actively manage for the disease.

For deer farmers, who manage small numbers of deer, even the loss of a few deer to EHDV can have a large economic impact. In 2012, deer farmers were hit particularly hard by EHDV and many suffered large economic losses (estimated to be approximately \$30M statewide). For deer farming to remain a viable industry, solutions to mitigate the devastating effects of EHDV must be found.

Captive deer farmers have partnered with researchers from University of Florida Institute of Food and Agricultural Sciences to better understand EHDV and to find solutions for deer farmers. EHDV is a complex and poorly understood disease, which makes quick solutions impossible. Confounding factors include: a) the presence of multiple co-circulating viral strains in Florida, b) the *Culicoides* spp. that transmit the virus to deer have not

been determined, c) multiple cervid species are affected, d) a complex epidemiological picture of the disease including acute, subclinical and chronic forms.

Research is needed to help deer farmers better manage their deer farms and reduce disease outbreaks. Long-term research needs include:

- Development of best management practices to reduce farmed deer mortality from EHDV
- Development of an EHDV outbreak model that predicts in advance when and where EHDV outbreaks will occur, so that deer farmers can prepare and prevent outbreaks
- Develop an efficacious vaccine for EHDV in deer

A major focus of the deer industry nationwide is to better understand the epidemiology of EHDV so that we can break or reduce the cycle of transmission. CHeRI was in fact born from the EHDV outbreak that devastated the industry statewide in 2012. Using the needs-based research model (Figure 1), we have identified the practices and needs of the industry, and the basic research that works towards a solution in combatting EHDV (Table 1).

### ***A Focus on Reducing Mortality***

In 2016, we initiated a dead deer hotline whereby farmers could report a dead animal and submit it for necropsy. In its first year, 15 farms participated and 246 animals were submitted. Necropsies revealed that while many animals did indeed die from EHD, many animals were misdiagnosed from clinical symptoms only. In fact, many deer died from severe bronchopneumonia whose clinical symptoms only superficially resembled EHD. In the coming months and years, our extension specialists and researchers will work with deer farmers to identify common causes of death and develop best management practices including diagnosis, treatment, and prevention to increase survival of adults and production of fawns. From 2016, we have developed an initial list of disease syndromes and pathogens that need to be evaluated more carefully in coming years (Table 2).

### ***Working Toward Decision-Making Tools for EHD Management***

Commodity production increasingly relies on decision-making tools for best management practices. Pesticide application, nutrient application, harvest timing and breeding can all be made more efficient and therefore cost effective if decisions are made based on the best available information about the production system. The best tools are those that are based on industry needs. We will use our iterative process of research design and stakeholder participation to develop decision-making tools that aid Florida deer farmers to increase production and quality of animals. Potential tools include:

- Pesticide application and deer vaccination calendar based on vector and/or virus emergence
- Risk calculator that shows locations of high risk of EHD emergence
- Encyclopedia of common deer farm diseases
- Stocking calculator that allows users to input the cervid species they want to farm and the acreage of their pens/preserves.

### ***References***

Anderson, D.P., Frosch, B.J., Outlaw, J.L. 2007. Economic impact of the United States cervid farming industry. Agricultural and Food Policy Center, The Texas A&M University System. APFC Research Report 07-4.

Table 1. Deer Farm Practice and/or the Needs identified by CHeRI to combat EHDV. The third column identifies the research that CHeRI funds to address those needs and the fourth column identifies the benefit to deer farmers.

| <b>Practice</b>  | <b>Need</b>  | <b>Research Needed</b>   | <b>Outcome and Application</b>   |
|--|--|--|--|
| <b>EHD Vaccination/Treatment</b>   | Efficacy Studies of all available vaccines         | Field trial Newport Vaccine (completed)  | Reduce use of ineffective vaccine. Farm specific field trials likely needed to establish buy-in  |
|  |  | Identification of and collaboration with other vaccine producers   | Assess the state of knowledge for vaccine development and production   |
|  |  | Challenge studies with naïve animals using novel subunit vaccines  | Test promising vaccines to hasten their production and marketing   |
|  | Understand HD epidemiology                         | Longitudinal studies of individual and population serology in white-tailed deer; longitudinal studies of EHDV genetics | Development of transmission and epidemiological models that will aid in predicting risk at the farm, regional, and national scale. Will aid in development of vaccine schedule and composition from year to year |
| <b>Permethrin spraying is used statewide without guidance on effective application</b> | Efficient, cost effective application of pesticide | Test efficacy of new pesticide products  | #Field trial of permethrin wrapped fences (partially complete)<br>#Communicate findings with stakeholders  |
|  |  | Vector ecology studies (underway)  | Essential to emergence modeling  |
|  |  | Development of vector emergence model that allows farmers to focus timing and location of pesticide application        | Essential to integrated pest management and recommendations for pesticide application  |
|  |  | Development of attractants   | Can aid in reducing host-vector interaction  |
|  |  | Integrated pest management   | Management of substrates, pesticide use, attractant use  |
|  |  | Vector competency studies  | By defining which Culicoides are competent vectors we can focus our ecological studies   |
|  |  |  |  |
| <b>Comingle exotics</b>  | Identification of reservoir hosts                  | Identify which species are refractory and which are reservoirs.  | Make recommendations about which cervids may increase the risk of EHDV to white-tailed deer  |
|  |  | Develop SIR model of host species composition  |  |
| <b>High density penned animals</b>   | Best stocking density                              | Prevalence of pathogen/exposure  | Recommendations of BMP on stocking density for farmed cervids  |

|  |  |  |   |
|--|--|--|---|
|  |  | may be different in populations of different density                                   |   |
|  |  | Develop SIR model of different host densities  |   |
| <b>Improper diagnosis of EHD</b>             | Better, cheaper, faster diagnostics  | Develop UF diagnostic pipeline to identify HD and non-HD causes of death and morbidity | Free, reliable diagnostic services for the deer farm industry are now available to Florida deer farmers |
| <b>Inconsistent vaccination year to year</b> | Understand regional risk of EHD each year                                    |  | Development of effective vaccines that are delivered to animals in a consistent and therapeutic way.    |
|  | Formulate regional vaccines based on predictive modeling of dominant strains | Risk models of EHD emergence   |   |

Table 2. Causes of mortality other than EHDV, the research need, and application to the deer farmer

| <b>Pathogen or disease syndrome identified in Florida-farmed deer</b> | <b>Research Needed</b>   | <b>Application to deer farmer</b>  |
|---|--|--|
| <b>Sepsis/enteritis</b>   | Novel diagnostics that consider the entire microbiota and coinfections   | Better diagnostics will help veterinarians and deer farmers treat deer with appropriate therapies  |
| <b>Co-infections associated with EHDV</b>                             | Many animals are infected with EHDV but are asymptomatic. Need to understand what makes EHDV pathogenic at the host and pathogen level | Treating the co-infection may increase survival and reduce mortality   |
| <i>Trueperella pyrogenes</i>  | Surveillance to understand the true cost of this pathogen  | Develop an appreciation for symptoms, treatment and BMP that reduce trueperella infection.   |
| <b>Cervidpox virus</b>  | Surveillance to understand the true cost of this pathogen  | This pathogen was found in moribund fawns for the first time on a farm in Florida. Increased familiarity with symptoms and appropriate treatment regimes will reduce mortality |

# Notes

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