



During this outbreak, the Kentucky Department of Fish and Wildlife Resources (KDFWR) mounted a detailed surveillance effort to delineate the area affected, to determine the EHDV and/or BTV serotypes responsible for mortality, to determine the species affected, to acquire preliminary information on possible *Culicoides* vectors, and to assess potential impacts on the white-tailed deer population. These efforts were supported at SCWDS by diagnostic testing and *Culicoides* identification.

From July-September 2017, KDFWR received 1,812 reports representing 4,625 cases of sick (20%) and dead (80%) deer. Over 90% of the cases originated from eastern Kentucky counties in the Appalachian Plateau. Typical of previous HD outbreaks, most of the affected deer (57%) were found near water. Tissue samples from 59 deer suspected to have HD were submitted to SCWDS for virus detection: EHDV-2 was isolated from 38 samples and was detected in another nine samples by reverse transcriptase polymerase chain reaction (RT-PCR). No viruses were isolated from eight samples collected from dead elk within the outbreak area. SCWDS sent CDC black light traps to KDFWR and collaborators at the University of Kentucky to support *Culicoides* collections during August and September 2017; insect sorting and *Culicoides* identification are ongoing at SCWDS.

Estimates of HD-related mortality and potential population impacts are extremely rare and difficult to determine. Such estimates require the collection of follow-up data to identify infection rates, detailed population analysis utilizing pre- and post-outbreak data, and in some cases, the quick thinking of wildlife professionals to recognize unique opportunities. Follow-up data collection and population/harvest analyses currently are underway. Serologic testing of hunter-killed deer demonstrated that infection rates were consistent with the distribution of clinical reports with  $\geq 50\%$  of samples collected in the outbreak area testing positive for antibodies to EHDV. A low antibody prevalence ( $< 1\%$ ) was detected in areas adjacent to the outbreak area.

Personnel from KDFWR identified an interesting opportunity to better understand the impacts of HD on the affected white-tailed deer population. As part of a study unrelated to HD, KDFWR biologists had 69 does in the outbreak area equipped with radio telemetry collars, of which 59 had detectable

frequencies. From April 2017 through the HD outbreak, 25/59 (42%) of these does died. Although mortality from April to the time of HD detection could not be estimated, this 42% mortality rate was excessive compared to the approximately 89% annual survival rate observed prior to April 2017.

Although many recovered carcasses were in an advanced state of decomposition, consisting only of bones, SCWDS attempted to detect EHDV by RT-PCR from samples collected from 12 recovered carcasses. Extremely small pieces of remnant marrow were extracted from long bones and EHDV nucleic acid was detected in seven of these samples. Based on these data, KDFWR estimated that the EHDV mortality rate in this study population during the outbreak likely was between 25 and 42%.

Population assessments related to the 2017 HD outbreak in Kentucky are continuing, and the information gained to date has greatly advanced our understanding of HD epidemiology and potential population impacts. We have reported previously that the epidemiology of HD in North America appears to be changing: new serotypes are establishing in the United States, reports of HD in northern latitudes are increasing, and outbreaks are more severe. The 25-42% estimated mortality rate observed in Kentucky and the additional HD reports and diagnostic samples provided by other state agencies affected by this regional outbreak certainly support an increase in HD frequency, range, and potential population impacts. This outbreak investigation continues a long history of collaborative efforts between SCWDS and our supporting state wildlife agencies in order to better understand wildlife diseases and exemplifies the value of a strong cooperative approach. (Prepared by David Stallknecht, Mark Ruder, Iga Stasiak [KDFWR], and Gabe Jenkins [KDFWR])

## Exotic Tick in New Jersey

On November 9, 2017, the USDA-APHIS National Veterinary Services Laboratories (NVSL) confirmed the identification of an exotic tick, *Haemaphysalis longicornis*, collected in large numbers from a domestic sheep in Hunterdon County, New Jersey. No other farm animals were present on the property and the ticks recovered from the ewe initially were identified by the Hunterdon County Health Department and

Rutgers University. This species, also known as the longhorned tick, bush tick, scrub tick, or cattle tick, had not been found previously on the United States mainland, except on material and/or animals at ports of entry. The timing and route of the introduction remain unknown. The detection of *H. longicornis* in the United States has potentially far-reaching implications for several reasons: 1) it is a known invasive species in other parts of the world, 2) it has a wide potential host range due to its non-specific host preference and its three-host life cycle, and 3) it is a known vector of multiple pathogens of concern to wildlife, livestock, and human health. Therefore, it is important to determine if *H. longicornis* has become established in the area.

In November and December 2017, SCWDS conducted initial surveys in collaboration with the New Jersey Division of Fish and Wildlife (NJDFW) and USDA-APHIS Wildlife Services (APHIS-WS) to determine if the ticks were infesting local wildlife. During this period, 57 white-tailed deer, two raccoons, and one opossum were examined, yielding nearly 1,400 ticks. All ticks that were collected represented two common native species, *Ixodes scapularis* and *Dermacentor albipictus*; *H. longicornis* was not found.

*Haemaphysalis longicornis* is an ixodid tick native to northeast Asia, but it has been established for more than a century in Australia and New Zealand (likely due to cattle shipments), as well as other western Pacific Rim Islands. This species generally is restricted to temperate regions. However, some populations (Russia, China, Japan) are capable of surviving harsh winters by diapausing (suspending development) during the nymphal stage, while other populations in different parts of its current range (Australia, New Zealand) are limited by cold temperatures. The tick also is sensitive to low humidity, particularly in the nymphal stage, and thrives in tall grass habitats with higher soil moisture and regular precipitation. Some populations of *H. longicornis*, particularly in introduced parts of its range, are parthenogenetic, thereby capable of asexual reproduction. These populations are made up predominantly of female ticks. Based on these aspects of *H. longicornis* biology, the source population of an introduced tick likely would play a large role in its ability to survive a New Jersey winter and reproduce.

*Haemaphysalis longicornis* is a three-host tick, meaning each major life stage—larva, nymph, and

adult—requires a blood meal from a different individual to complete its life cycle and reproduce. Additionally, *H. longicornis* has a broad host range and is known to feed on a variety of domestic and wild animals, as well as people. For instance, although cattle are a primary host, this species will feed on sheep, goats, pigs, horses, cervids, canids, felids, other large, meso-, and small mammals, and a variety of birds (particularly ground-dwelling). In general, larval and nymphal life stages are more likely to be found on smaller hosts, while adults are more likely to be found on larger hosts, such as livestock. Severe infestations on livestock may result in anemia, weight loss, reduced milk production, and severe scratching of the skin, which can have a significant impact on livestock health and production.

Another important consideration for *H. longicornis* is the possibility of pathogen transmission. It is a confirmed or likely vector of numerous pathogens across its native and introduced range including several *Theileria* species of importance to animal health (e.g., *T. equi*, *T. sergenti*, *T. buffeli*, *T. luwenshuni*, and *T. orientalis*), the latter of which recently has been increasing its range and severity in cattle populations across Australia. In its native range, *H. longicornis* also transmits several *Babesia* species of importance to human, dog, cattle, sheep, goat, and possibly horse health. Other zoonotic pathogens possibly transmitted by *H. longicornis* include *Anaplasma* spp., *Ehrlichia* spp., *Bartonella* spp., *Borrelia* spp., and *Rickettsia japonica*. Several viruses important to human health that have been linked to *H. longicornis* include Powassan virus in Russia, Huaiyangshan virus in China, and an emerging phlebovirus that causes severe fever with thrombocytopenia syndrome in China.

SCWDS continues to assist USDA-APHIS-Veterinary Services in determining if *H. longicornis* has become established in wildlife near the index case. Multiple surveys will need to be performed in various seasons to determine if *H. longicornis* has become established in New Jersey: Surveys, in collaboration with NJDFW and APHIS-WS, are planned for the spring and summer of 2018 to coincide with the periods when previously diapausing nymphs would become active and seek a blood meal (spring), and newly molted adults would seek a blood meal before laying eggs (summer). These surveys will allow SCWDS to determine if *H. longicornis* has overwintered in the New Jersey area and become established in

wildlife populations. Surveys will be expanded to include a greater diversity of wildlife, including small mammals, mesomammals, and birds through live trapping and mist netting. More information on detection of this exotic tick in New Jersey can be found in Rainey et al, J of Medical Entomology, 2018. (Prepared by Stacey Vigil, Mark Ruder, and Michael Yabsley)

## **CWD in the Wild, February 2018**

Since our last update in April 2016, chronic wasting disease (CWD) has continued to be found in free-ranging cervids in endemic states as well as in two new states. We'll start there and then follow up with new information from selected states that had found CWD in wild cervids in the past.

Montana and Mississippi became the 22<sup>nd</sup> and 23<sup>rd</sup> states to detect CWD in free-ranging deer in November 2017 and February 2018, respectively. Montana's first case was found in Carbon County, which runs along its border with Wyoming, and three additional wild animals subsequently tested positive. In early December, Montana Fish, Wildlife and Parks announced detection of CWD in a wild deer in Liberty County, which borders Alberta. Wyoming and Alberta have endemic CWD in their wild cervid populations. A special hunt held in response to the Carbon County detections ended February 15, 2018, but complete testing results are not yet available on the 216 mule deer and 123 white-tailed deer that were harvested. As of March 6, 2018, a total of eight mule deer and two white-tailed deer in Carbon County and one mule deer in Liberty County have tested positive for CWD in Montana.

On February 9, 2018, the Mississippi Department of Wildlife, Fisheries, and Parks (MDWFP) was notified that a white-tailed deer in Issaquena County had tested positive for CWD. The deer had been observed to appear thin and disoriented a few days prior to death and its death was observed by a hunter. The MDWFP implemented its CWD Response Plan, which established management zones of 5-, 10-, and 25-miles around the positive animal, and supplemental feeding of wildlife was prohibited in six counties. The MDWFP hosted a public meeting in Jackson on February 22, and conducted a special collection of 60 wild deer in the 5-mile

management zone on February 23-24, 2018. Test results are pending.

The first animal detected with CWD in Arkansas was a wild elk killed by a hunter in late 2015 in Newton County. Since April 2016, the number of counties in Arkansas where CWD has been found in wild deer or elk has expanded from five to ten, with three added after testing animals from the 2017 hunting season. The number of positive animals detected also has increased from 93 to 371. Most of the CWD-positive animals (nine elk and 245 whitetails) were detected in Newton County.

The Iowa Department of Natural Resources announced in early February that a white-tailed deer killed in December 2017 in Wayne County had tested positive for CWD. Wayne County is in south-central Iowa adjacent to northern Missouri. This is the first positive wild deer in Iowa outside of the northeastern counties of Allamakee and Clayton counties. Testing in those two counties during the 2017 hunting season has yielded seven more positive deer so far with additional results pending.

Michigan first found CWD in 2015 in a wild white-tailed doe in East Lansing in Ingham County, and a total of five positive animals had been detected through April 2016. As of February 21, 2018, CWD has been confirmed or is suspected in 57 wild deer in the state. Deer Management Unit (DMU) 333 consists of contiguous portions of five counties (Clinton, Eaton, Ingham, Ionia, and Shiawassee) and was established after CWD detection in a wild deer in 2015, has nine CWD-suspect or positive deer of 12,935 tested. A single suspect or positive deer was detected among 4,535 deer tested in DMU 419, which consists of the remaining land outside DMU 333 but within the 5-county zone. In Montcalm County, 36 of 4,085 deer tested are CWD-suspect or -positive as are 11 of 580 deer tested in adjacent Kent County. A total of 30,500 wild deer have been tested in Michigan since May 2015.

The Missouri Department of Conservation conducted mandatory CWD testing of hunter-harvested deer in counties within the state's CWD management zones during first weekends of the 2016 and 2017 firearms seasons. In 2016, about 19,200 samples were collected in management

zones and another 3,200 were collected statewide. In 2017, the corresponding numbers were 20,705 and 2,751. To date, CWD has been found in 58 wild whitetails. Most of the positive animals (35/58) came from Adair and Macon counties in the northern CWD management zone established after Missouri's first detection in wild deer there in 2011. However, low numbers of positive animals have been found in several scattered counties remote from the northern management zone. In April 2016, we reported on a single positive buck in Cole County in 2014, and another buck in Franklin County in 2015. There have been no additional detections in Cole County, but six more positive deer were found in 2016 and 2017 in Franklin County. In 2016, CWD was found for the first time in one deer in Jefferson County and in two deer in St. Clair County. In 2017, another positive deer was found in St. Clair County, and CWD was found for the first time in wild deer in Cedar (1), Polk (1), and Sainte Genevieve (3) counties.

In early February 2018, the Nebraska Game and Parks Commission (NGPC) announced that surveillance during the 2017 season resulted in detection of CWD in 203 deer of 1,807 tested in its Northwest and Southwest districts. New counties added were Chase, Dundy, Franklin, Frontier, and Hayes. The NGPC has tested nearly 51,000 deer since 1997 and has found 499 positive animals in 40 counties.

The Pennsylvania Game Commission (PGC) offered free CWD testing for hunters harvesting deer in the state's two remaining Disease Management Areas (DMA) during the 2017-2018 seasons, and more than 1,500 deer heads were dropped off at collection sites. Staff from PGC also collected more than 3,000 other samples within the DMAs, and overall, more than 8,000 samples were collected statewide. Results from most of the samples are pending; however 51 deer have tested positive for CWD. Forty-eight positive deer came from DMA 2 in south-central Pennsylvania, the only DMA in which CWD had been detected in wild deer through 2016, but three samples came from DMA 3, which was established in 2014 in northwestern Pennsylvania following detection of CWD in a captive deer in Jefferson County. The 2017-18 numbers so far are higher than those from 2016-17 when 25 of more than 5,700 deer tested positive in DMA 2.

In Texas, CWD was confirmed in a free-ranging white-tailed deer for the first time in January 2017 in Medina County. The first wild mule deer with CWD in Texas was found in 2012 in the Hueco Mountains in far West Texas, and 12 additional positive mule deer have been found in this area since then. Four wild cervids (three mule deer and one elk) also have been found in the northwestern Panhandle of Texas.

In Wisconsin, CWD recently was found for the first time in wild white-tailed deer in Milwaukee County on the eastern border with Lake Michigan and in Lincoln County in the North Woods, making them the 22<sup>nd</sup> and 23<sup>rd</sup> counties with CWD in wild deer in the state. As required by state law, a ban on baiting and feeding was implemented in Lincoln County as well as in adjacent Langlade County because it lies within 10 miles of the positive deer. In 2017, Wisconsin found 593 positive whitetails of 9,731 deer tested, and the prevalence continued to rise in all age classes and genders in southwestern Wisconsin. In the core endemic region in north-central Iowa County, the prevalence in adult bucks increased from 22 to 50% from 2011-2016 and from 10 to 30% in adult does over the same period. Wisconsin has found 4,176 positive deer from more than 209,700 tested since 1999.

Preliminary results recently were reported from the first year of a five-year study in southwestern Wisconsin investigating differences in the survival of wild deer with or without CWD. Investigators found that deer that tested positive for CWD when captured, tested, radio-collared, and released were three times more likely to die than deer that tested negative. Positive deer died as a direct result of CWD, or indirectly via predation, hunting, or vehicular accidents due to being less aware of their surroundings, less responsive to stimuli, and less physically coordinated. The study will continue for another four years and provide more complete information on deer mortality in southern Wisconsin.

Moving overseas to Norway, it recently was reported that the last group of wild reindeer in the affected area of the Nordfjella district had been killed in an effort to contain or possibly eradicate CWD. The goal was to dispatch all wild reindeer in this zone before May 1 and the area now will be searched for any surviving animals. A total of 17

positive reindeer have been found in this zone since CWD first was detected in 2016. The plan is to reestablish a healthy local reindeer population after a fallow period. (Prepared by John Fischer)

## CWD in DC

The following information regarding bills that have been introduced in the United States House of Representatives and the U.S. Senate comes from the Winter/Spring 2018 issue of *The AFWA Strategist*, an update for the members and partners of the Association of Fish and Wildlife Agencies (AFWA).

“On November 21, 2017, Representatives Kind and Sensenbrenner (both of WI) introduced H.R. 4454, the Chronic Wasting Disease (CWD) Management Act of 2017, to support State and tribal efforts to address CWD among deer, elk, and moose populations, and to support applied research on CWD. The bill provides state departments of wildlife and agriculture and Tribes with \$35 million annually, to develop and implement management strategies, \$10 million per year for applied research grants on CWD, and requires the DOI and USDA land management agencies to work cooperatively with States on CWD research and response plans. On December 19, 2017, Senator Tester (D-MT) introduced a similar bill (S. 2252), which provides \$25 million per year for applied research grants and limits the overhead rate on such grants to 15%.”

## Oral Papillomatosis in a Coyote

A private landowner in Ritchie County, West Virginia, observed a female coyote feeding on a deer carcass in November. The landowner shot the coyote and upon closer inspection saw numerous nodules in the coyote’s mouth. The coyote was obtained by the West Virginia Division of Natural Resources and submitted to SCWDS for necropsy and diagnostic testing.

Gross examination revealed numerous raised nodules with a cobblestone texture covering the hard and soft palates, lips, and tongue and extending into the esophagus (Figure 1). Additional findings included small numbers of lice in the hair coat (likely *Trichodectes canis*), partially digested meat and fur in the stomach, and a few tapeworms in the intestines (likely *Taenia* sp.). Histological evaluation of the nodules from the oral cavity and esophagus revealed proliferations of

epithelial cells with large viral inclusion bodies consistent with those caused by papillomaviruses.

A sample of one of the nodules was tested at SCWDS for papillomavirus DNA using polymerase chain reaction. After confirming the presence of a papillomavirus, the sample was submitted for genetic sequencing and the specific virus was determined to be *Lambdapapillomavirus-2*.

Oral papillomatosis caused by *Lambdapapillomavirus-2* has been reported in domestic dogs, coyotes, and wolves in North America, and genetic studies of these viruses suggest they likely are transmitted between these three canid species. Lesions caused by these viruses usually are seen in young or immunosuppressed individuals, typically are self-limiting, and do not result in severe debilitation of the animal. However, large papillomas may affect the ability to consume food. In domestic dogs, the lesions associated with *Lambdapapillomavirus-2* can progress to squamous cell carcinomas, but this finding has not been reported in wild canids.



Figure 1.

Oral papillomatosis is unlikely to have significant population impacts in wild canids, and there is no evidence of transmission to humans. However, the detection of this virus and the lesions that it causes emphasize the importance of studying pathogen interactions between wild and domestic animals. (Prepared by Kevin Niedringhaus)

## Brucella Vaccine Prize Winners

Researchers at the University of Georgia's College of Veterinary Medicine (UGA CVM) recently were awarded a Phase 1 prize of

\$100,000 for their proposal in the *Brucella* Vaccine Prize competition sponsored by AgResults and managed by the Global Alliance in Livestock Veterinary Medicine (GALVmed). AgResults is a multilateral initiative between the governments of Australia, Canada, the United Kingdom, the United States, and the Bill & Melinda Gates Foundation to incentivize and reward high-impact agricultural innovations that promote global food security, health, and nutrition and provide benefits to farmers. GALVmed, through its partners, makes livestock vaccines, medicines, and diagnostics available to smallholder livestock and poultry farmers in developing countries in Africa and Asia. The four successful UGA CVM investigators involved with this project include Danny Mead with SCWDS and the Department of Population Health. The UGA team plans to develop a new vaccine platform to deliver *Brucella* antigens that provide complete, long-lasting, and cross-species immunity against pathogenic *Brucella* bacteria.

Brucellosis is a widespread zoonotic disease that causes economic losses in the food animal production sector as well as a significant public health burden. The responsible genus, *Brucella*, is a homogenous group of ten species with *B. melitensis* (sheep, goat), *B. abortus* (cattle), and *B. suis* (swine) causing most cases of human disease. In domestic animals, the organisms cause abortions, stillbirths, weak offspring, infertility, reduced milk production, and weight loss.

*Brucella* bacteria usually are transmitted to humans via direct contact with infected animals and materials, or indirectly by ingestion of raw milk and fresh cheese or inhalation of aerosolized bacteria from infected livestock. Human infections cause a protracted and debilitating systemic disease known as “undulant fever” or “Mediterranean fever.” Acutely, it presents with non-descript signs and symptoms including fever, chills, malaise, headaches, hepatomegaly and splenomegaly. Untreated chronic infections may be characterized by recurrent fever, arthritis, swollen testicles, chronic fatigue, depression, neurological signs, and swollen liver and spleen.

*Brucella* bacteria can invade and replicate within host cells, which promotes dissemination to deep tissues (liver, spleen) where the organisms can reside in a latent state, form chronic lesions, and be difficult to reach with antibiotics. Brucellosis is

difficult to diagnose and requires prolonged antibiotic therapy; relapse rates are high.

No human vaccines are available, and licensed veterinary vaccines have significant shortcomings including incomplete protection against abortion, interference with diagnostic tests, and pathogenicity to humans. Additionally, pathogenic *Brucella* species are classified as select agents by the Federal Select Agent Program and are considered a serious national biosecurity threat. For these reasons, the availability of safe and effective countermeasures to protect humans and animals against brucellosis is a critical, unmet need and a high priority of international health organizations.

The *Brucella* Vaccine Prize competition is a world-wide contest to develop a vaccine for ovine and caprine brucellosis caused by *B. melitensis*. The competition is a five-year initiative with three phases: In Phase 1 (application phase) applications are reviewed and \$100,000 prizes are awarded to the institutions of submitters of the best ten proposals. In Phase 2 (solving phase) the ten Phase 1 prize recipients develop and validate their vaccine platforms. The first four projects that meet Minimum Viable Product (MVP) requirements that include a safe and efficacious *B. melitensis* vaccine that is affordable to smallholder farmers and has a long shelf life will be awarded a \$1,000,000 prize. In the final phase, the four Phase 2 prize recipients (solvers) will continue to develop and validate their platforms. The first solver to register a vaccine that meets MVP requirements will be awarded a \$20,000,000 Grand Prize for manufacturing and marketing. An additional \$5,000,000 prize is available if a solver meets Best in Class requirements, including protection against *B. melitensis* and *B. abortus* as well as a therapeutic effect on animals already infected, within one year of the Grand Prize award.

Other Phase 1 winners came from institutions in Argentina, China, France, South Africa, Spain, the United Kingdom, and two universities in the United States. We congratulate Danny and his colleagues and wish them all the best in the coming competition. More information on the Brucellosis Vaccine Prize can be found at <https://brucellosisvaccine.org>. (Prepared by Danny Mead and John Fischer)

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