



SCWDS BRIEFS

A Quarterly Newsletter
Southeastern Cooperative Wildlife Disease Study
College of Veterinary Medicine
The University of Georgia
Athens, Georgia 30602

Winter 2025

Volume 42

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Eds. M. Ruder and B. Kurimo-Beechuk

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Redhead & lesser scaup, B. Kurimo-Beechuk

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Cervid health updates

2024 HD summary

Hemorrhagic disease (HD) is one of the most important diseases of white-tailed deer in North America. During 2024, as in every year since the early 1990's, SCWDS conducted passive surveillance for EHDV (epizootic hemorrhagic disease virus) and BTV (bluetongue virus) in support of wild ruminant mortality investigations by state wildlife agencies. Annually, we receive submissions from throughout much of the U.S., and testing involves a combination of classical and molecular virologic methods. For all submissions, samples were screened for EHDV and BTV using real-time reverse transcription polymerase chain reaction (rRT-PCR) assays with virus isolation attempted on rRT-PCR-positive samples. For isolated EHDV and samples with sufficient viral genetic material, virus serotype was determined. For BTV serotyping, we collaborate with virologists at **USDA's National Veterinary Services Laboratories (NVSL)**. This passive surveillance approach is dependent upon tissue sample submissions by state wildlife agencies. Here, we present results of HD diagnostics performed at SCWDS during 2024. As there is no national surveillance program for HD in the U.S., the results of this long-term passive surveillance effort provide important information regarding annual HD activity in much of the U.S.

In the **Summer issue** of the **SCWDS BRIEFS**, we provided a sneak peek into the 2024 HD season. At that time, we anticipated that the season would be busy based on the timing and locations of detections

observed at the end of August. Our first detection (EHDV-2) for the main summer/fall transmission season was in a white-tailed deer that died in Indiana on June 27 – about a month before we typically have our first detection. Further, the bulk of confirmed HD outbreaks by the end of August were occurring in the Midwest, Mid-Atlantic, and Northeast; deer populations in this geographic region are prone to high-mortality outbreaks. Indeed, outbreaks in those areas continued to build the rest of the transmission season. In fact, the number of SCWDS sample submissions for HD testing during 2024 was among the highest ever received.

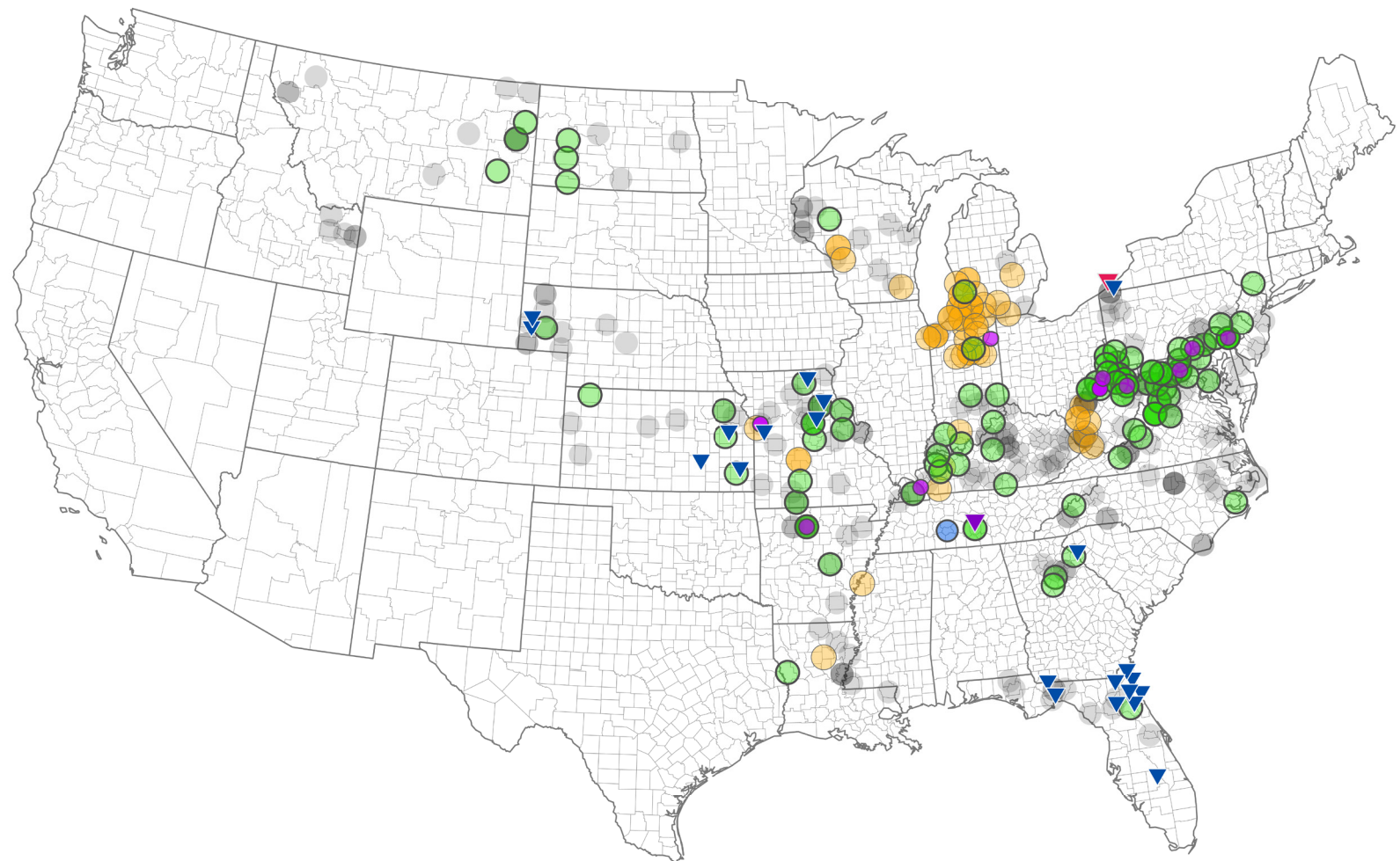
During calendar year 2024, 440 wild ruminant tissue samples from 24 states were received for HD diagnostics. Consistent with other years, white-tailed deer dominated these submissions (404 white-tailed deer, 17 elk, 11 mule deer, six moose, one pronghorn, and one bighorn sheep). After the first detection (EHDV-2) in late June, EHDV and BTV submissions and detections continued through December with the peak occurring in September, [barplot on page 4](#). This temporal pattern is consistent with our observations over the last 30 years. However, the high number of submissions combined with the sustained high proportion of positives encountered during October was atypical. Confirmed HD cases generally decline during October as colder temperatures reduce the *Culicoides* spp. activity that is at the heart of the transmission cycle. Typical of most vector-borne disease systems, patterns of HD are susceptible to variable weather and climatic conditions, and such potential influences are important areas of research.

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Outside of the main summer/fall transmission season, a small number of rRT-PCR detections were made during winter months in southern areas (Florida) where transmission seasons are extended, or in northern areas (Nebraska, West Virginia) that represent detections of viral RNA remaining after prior infection. The geographic distribution of submissions and detections is shown in the [map below](#).

Overall, 217 animals (214 white-tailed deer, two mule deer, and one bighorn sheep) tested positive for EHDV and/or BTV by rRT-PCR. Virus was isolated from 136 (63%) of these. EHDV was detected by rRT-PCR in 190 white-tailed deer from 21 states. All three EHDV serotypes established in the United States (EHDV-1, -2, -6) were detected. EHDV-2 was detected in 120 white-tailed deer from Arkansas, Florida, Georgia, Indiana, Kansas, Kentucky, Louisiana, Maryland, Michigan, Missouri, Montana, Nebraska, New York, North Carolina, North Dakota, Pennsylvania, Tennessee, Virginia, West Virginia, and Wisconsin; EHDV-6 in 56 white-tailed deer from Indiana, Kentucky, Louisiana, Michigan, Mississippi, Missouri, West Virginia and Wisconsin; and EHDV-1 from a single white-tailed deer in Tennessee. EHDV serotype could not be determined in 13 white-tailed deer. There were 32 BTV detections, including 30 white-tailed deer from Florida, Georgia, Kansas, Missouri, Nebraska,

2024 EHDV/BTV Disease Detections By SCWDS



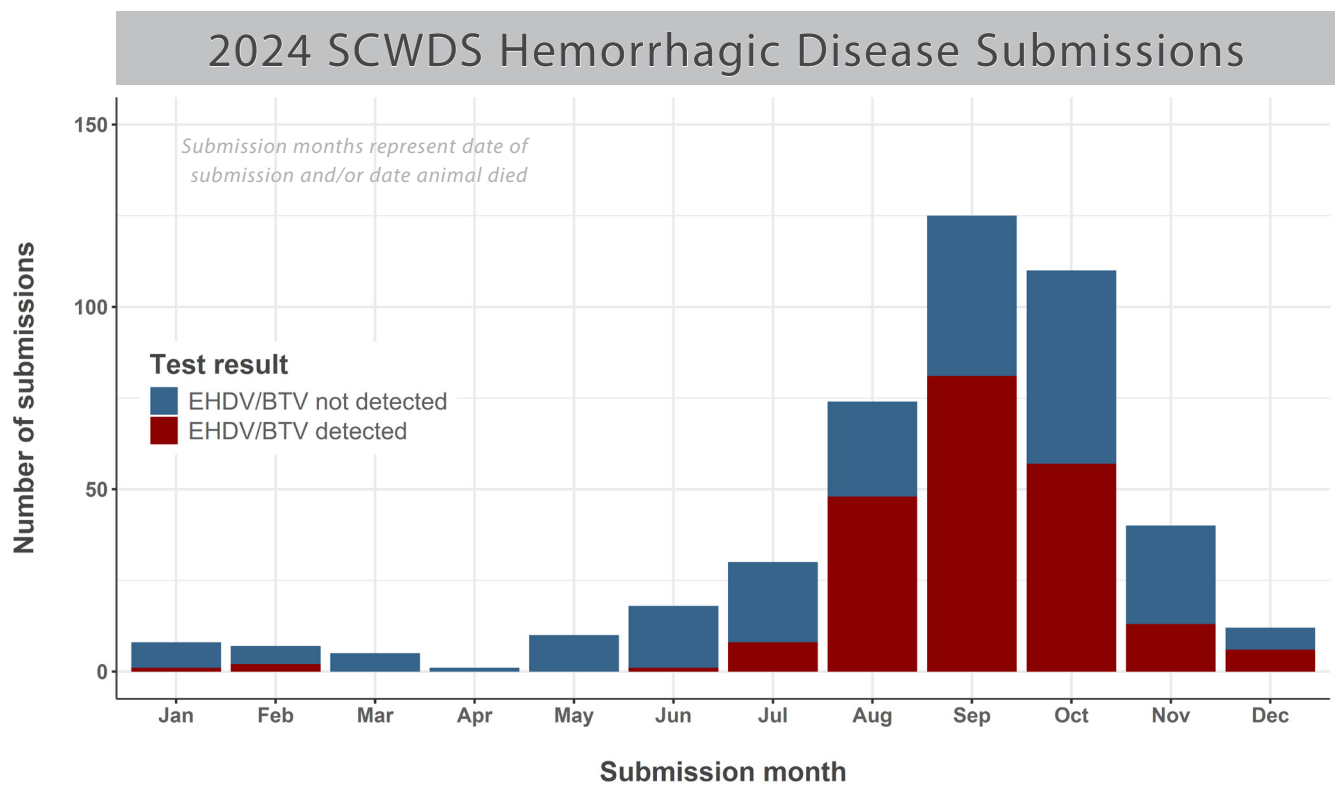
Virus(es) detected

- | | | | |
|---------|----------|----------|-------------------|
| ▼ BTV | ▼ BTV-13 | ● EHDV-1 | ● EHDV-6 |
| ▼ BTV-6 | ● EHDV | ● EHDV-2 | ● HD not detected |

Points represent detections by serotype and county; locations are approximate for visualization purposes.

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Pennsylvania, and Tennessee, as well as a mule deer and bighorn sheep from Nebraska. In collaboration with NVSL, genetic sequencing has identified BTV-6 in Tennessee and BTV-13 as the serotype associated with the bluetongue outbreak in northwest Pennsylvania. Further characterization of other BTV detections is pending. The locations of HD outbreaks and the viruses involved vary annually within the historical and expanding range of HD in the U.S. This variation is likely driven by interacting climatic and biologic factors that are not well defined at this time. The virologic data we generate through annual diagnostic testing provides important information that strengthens the morbidity/mortality annual reporting received through our long-term, annual National HD Questionnaire. This 43-year long-term data set can be utilized to better understand these interactions but also serves as a baseline to detect changes in disease distribution, intensity, and EHDV/BTV diversity. Based on samples submitted to SCWDS during 2024, there were prominent HD outbreaks that appear to have centered on parts of the Upper Midwest, Ohio River Valley, and Mid-Atlantic. EHDV-6 was the predominant virus involved in a large outbreak in northern Indiana, southern Michigan, and parts of Wisconsin;



this particular outbreak was notable due to the long duration. Initial detections in this region began in late June and were sustained through mid- to late-October, which may have been facilitated by favorable environmental conditions. Based on communication with Dr. Mike Tonkovich with **Ohio Department of Natural Resources**, confirmed HD activity in Ohio spanned diagonally across the state from the northwest to the southeast. A large number of detections, primarily EHDV-2, occurred in parts of West Virginia, Virginia, southern Pennsylvania, and Maryland. Similar to the upper Midwest, the duration of this outbreak continued into late October and November, well past historical expectations of outbreaks in this area. Aside from these larger foci of HD, there were scattered detections of EHDV and BTV throughout portions of the Great Plains and Southeast. Interestingly, in addition to EHD outbreaks in southern Pennsylvania, there was an outbreak of BTV-13 in white-tailed deer in Erie County, Pennsylvania. Despite multiple detections from this county, there were no other reports of sick or dead deer in adjacent counties, highlighting the sometimes highly localized nature of HD outbreaks. BTV-13 is an established serotype in the U.S. and has been known

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to circulate for many decades. BTV-6 was isolated from a deer in Tennessee for the first time, although this serotype is considered established in the U.S. The BTV detections in north Florida, Missouri, Kansas, and Nebraska have not yet been identified to serotype.

Results of the 2024 National HD Questionnaire are currently being compiled, which will help to better visualize the true geographic footprint of suspected and confirmed HD during 2024. The continued detection of EHDV and BTV in northern states demonstrates the continued expansion into the upper Midwest and Northeast. What once was an extremely uncommon occurrence is becoming frequent to the point of normalcy – highlighting the dynamic nature of HD. As always, we thank the many wildlife professionals who submitted tissue samples for diagnostic testing this past season. We also thank Dr. Mia Torchetti and others at NVSL for their continued collaboration with confirming and characterizing BTV isolates.

Prepared by Mark Ruder, Lyndon Sullivan-Brugger, Dave Stallknecht, Paul Oesterle, Betsy Kurimo-Beechuk, and Rebecca Poulson

NAS review of CWD

On December 20, 2024, the **National Academies of Sciences, Engineering, and Medicine (NAS)** Committee published the **Review of Transmission and Geographic Spread of Chronic Wasting Disease in U.S. Cervid Populations**. The report is titled **State of Knowledge Regarding Transmission, Spread, and Management of Chronic Wasting Disease in U.S. Captive and Free-Ranging Cervid Populations. America’s Conservation Enhancement Act**, which Congress passed in 2020, encouraged the Secretaries of the Interior and Agriculture to commission the NAS to produce “a special resource study to identify the predominant pathways and mechanisms of the transmission of CWD in free-ranging and captive populations in the U.S.”. The review was supported

by the **U.S. Geological Survey (USGS)**, **U.S. Fish and Wildlife Service (USFWS)**, and the **USDA - Animal and Plant Health and Inspection Service (APHIS)**.

In collaboration with APHIS and USFWS, the USGS requested NAS to convene a committee to draw conclusions about the state of knowledge regarding CWD. The ad hoc committee comprised eleven experts that were chaired by Dr. Lonnie King of **The Ohio State University** and formerly of APHIS. The Committee reviewed published and current research regarding infectious doses and concentrations, modes



of transmission, the means of geographic spread, the effectiveness of interventions to reduce transmission or spread, and the human societal implications of CWD. In particular, the committee was asked to identify areas of uncertainty regarding the current understanding of CWD and its management. The committee was not asked to provide recommendations for future actions but rather to provide conclusions based on current evidence to inform future decision-makers as they prioritize CWD research and develop management and mitigation strategies “with the understanding that the complete control or elimination of CWD at

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the national or local scales may not be within reach.” The committee reached the following conclusions:

Conclusion 1: Multiple drivers and epidemiological factors affect CWD transmission and infectivity. The precise roles, interrelationships, and relative importance of these factors are not fully understood and may differ for captive and free-ranging cervid populations.

Conclusion 2: As of this writing (August 2024), no cases of CWD transmission to humans have been diagnosed nor has natural transmission to non-cervid animal species been detected. (Note: A January 2025 **publication** reports detection of prions in feral swine from areas with CWD.)

Conclusion 3: The known geographic distribution of CWD is expanding. However, the distribution is incompletely understood and likely is underestimated. Inconsistent surveillance has compromised knowledge about changes in CWD distribution over time in the U.S.

Conclusion 4: Natural movement of infected cervids and other epidemiological factors are responsible for the local distribution of CWD. Human-mediated movement of infected cervids (i.e., transport of live, dead, captive, or free-ranging cervids) and infected cervid products for commerce, recreation, conservation, and other purposes increases the likelihood of CWD spread to new geographic areas in unpredictable ways.

Conclusion 5: Official USDA postmortem CWD diagnostic approaches are useful for disease surveillance in free-ranging and captive cervids. Newer, currently unapproved, detection approaches may have more wide-ranging applications, including live-animal testing and screening of cervid byproducts, environmental surfaces, and other relevant materials.

Conclusion 6: Well-founded epidemiological principles inform strategies for CWD prevention or control in both captive and free-ranging cervids, beginning with effective early ongoing surveillance followed by timely aggressive sustained local response upon CWD detection. Methods based on

those principles can reduce or prevent large increases in prevalence and slow the spread of CWD when properly applied.

Conclusion 7: Differing philosophies and approaches to CWD management adopted by agricultural and wildlife management authorities at different levels of government impact the effective control of CWD in the U.S.

Conclusion 8: Prevention is key to controlling the spread of CWD given that existing tools and technologies make eradication of CWD in captive or free-ranging cervid populations, once established, improbable.

Conclusion 9: Genetic selection, vaccines, environmental decontamination, and therapeutic options are being investigated as tools for CWD control but need further inquiry and review.

Conclusion 10: Human behaviors can influence the transmission, spread, and consequences of CWD. Interest groups hold diverse viewpoints regarding the seriousness of CWD and its spread, prevention, and control; their decisions may not always be informed or influenced by the best available science.

Conclusion 11: Existing data gaps make CWD-related economic measurements and analyses difficult to quantify. These deficiencies can result in a lack of appreciation of the full impact of the disease and in the inability to evaluate and compare the direct and indirect costs and benefits of various management strategies. Excerpts from the full report were used in this article.

Prepared by John Fischer

CWD in the Southeast

Chronic wasting disease (CWD) continues to be detected in new areas throughout the country, and unfortunately, a new state in the Southeast. **Georgia Department of Natural Resources**

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(GADNR) reported that CWD was confirmed in a hunter-harvested white-tailed deer from Lanier County, Georgia. The 2.5-year-old buck was harvested on private property in November 2024 and was tested for CWD as part of GADNR's routine surveillance program. The retropharyngeal lymph nodes were screened at the **University of Georgia Athens Veterinary Diagnostic Laboratory** before being confirmed by immunohistochemistry at the **National Veterinary Services Laboratory (NVSL)**. Upon receiving confirmation from NVSL, GADNR implemented their **CWD Response Plan**. More information about CWD and GADNR's response and management can be found [here](#). With this detection, the only member state agency of the **Southeastern Association of Fish and Wildlife Agencies (SEAFWA)** without a CWD detection is South Carolina. Territorial members of SEAFWA (U.S. Virgin Islands and Puerto Rico) also have not had CWD detections in white-tailed deer, which is an invasive species on these islands.

In addition, there have been several noteworthy CWD detections in captive cervids during 2024 in the Southeast, including first time detections in Kentucky and Louisiana, and a detection distant from the existing **CWD Containment Area in West Virginia**. The wildlife management agencies in these states are long-term members of SCWDS and all have detected CWD previously in free-ranging white-tailed deer. There have been other CWD detections in captive and free-ranging deer and elk in 2024 in new locations, but this update focuses on the three states mentioned.

CWD was detected in a captive white-tailed deer facility in Marion County, WV during mid-September 2024 in a 2.5-year-old doe. The doe was in a breeding facility that consisted of 25 deer and was one of several deer in the herd that apparently died of epizootic hemorrhagic disease (EHD). The EHD outbreak in 2024 affected deer in at least 25 WV counties, including Marion. This herd was enrolled in the **USDA CWD Herd Certification Program (USDA HCP)** and was certified as low risk for CWD

infection. After the CWD detection at this facility, the herd was depopulated and investigation is ongoing. Previously in 2021 and 2022, CWD was confirmed in captive white-tailed deer in Hampshire and Hardy Counties, respectively. Both of these facilities were located within the CWD Containment Area.

The first detection of CWD in WV was in a free-ranging deer from Hampshire County in 2005. More recently, WVDNR reported that CWD was detected in wild deer from Jefferson (2023) and Grant (2024) Counties representing the first new WV counties since 2018. Two of the positive Jefferson County deer were collected as part of a deer population reduction program implemented to preserve historic landscapes in **Harpers Ferry National Historical Park**, and this detection was the first in a National Park within WV. Previously, CWD detections had occurred only in Berkeley, Hardy, Hampshire, Mineral, and Morgan Counties. Two nearby national parks in Maryland, the **Antietam** and **Monocacy National Battlefields**, also reported CWD-positive deer for the first time in 2024.

On October 14, 2024, **The KY Department of Agriculture (KDA)** and the **KY Department of Fish & Wildlife Resources (KDFWR)** announced the detection of CWD in a 4.5-year-old doe in a breeder herd of 70 deer in Breckenridge County. This represents the first CWD detection in a captive cervid in KY. The herd was also enrolled in the USDA HCP and was certified as low risk for CWD infection. Captive cervids in KY are under the regulatory authority of KDA and KDFWR. In response to the detection, the **KDA State Veterinarian** placed the facility under quarantine, which restricted movement (live deer and/or deer products) into or out of the facility, and recent movement records were reviewed.

In addition to the quarantine of this facility, the detection of CWD activated the **KY CWD Response Plan**. Both KDA and KDFWR approved the KY CWD Response Plan in 2022, and referred to the plan as they addressed the new detection. The KDA established a 5-mile radius management zone and a 15-mile radius surveillance zone for nearby



Elk, M. Jorge

captive herds. All captive deer herds within these zones were placed under restricted movement until further notice from KDA.

The KDFWR has tested more than 40,000 free-ranging deer and elk statewide since 2002. The first case of CWD detected in the state was in a free-ranging deer in December 2023 in Ballard County. The agency encourages hunters to assist with monitoring efforts by dropping off heads of harvested deer for aging and CWD testing at self-serve CWD Sample Drop-Off sites. Hunters are not charged for this testing.

On November 7, 2024, CWD was confirmed in a 1.5-year-old buck in a breeding herd of 59 deer in Jefferson Davis Parish, LA. The herd participated in the USDA CWD HCP administered by the **LA Department of Agriculture & Forestry (LDAF)** and was also certified as low risk for CWD infection. The herd was placed under quarantine restricting movement (live deer and/or deer products) into or out of the facility, and a surveillance zone of 25-miles was established. Captive deer facilities within this zone are under movement restrictions until further notice from LDAF.

Review of the recent movement records from the Jefferson Davis herd and testing of animals that

left this herd prior to CWD detection resulted in three more positive deer in captive facilities in Concordia, St. Landry, and Tangipahoa Parishes. These facilities were not enrolled in the USDA HCP but did participate in the state's deer program. Sixty deer were present in the Concordia Parish herd but the number of animals in the other two herds is unknown. The three herds were also placed under quarantine. Furthermore, deer from these positive pens have been traced to permitted deer pens in 11 additional parishes throughout the state, although no additional positives had yet been identified.

The **LA Department of Wildlife & Fisheries (LADWF)** began conducting CWD surveillance of free-ranging deer statewide in 2002. The disease was first detected in the state in free-ranging white-tailed deer in January 2022 in Tensas Parish along the Mississippi border. A total of 27 CWD-positive wild deer have been detected through the 2024 - 2025 sampling season, all within this Parish. Information for this article was obtained from the websites of agriculture and/or wildlife agencies of the three states and **the USDA webpage on captive herd status**.

Prepared by John Fischer and Mark Ruder

Population immunity & HPIAV

Since the introduction of clade 2.3.4.4b highly pathogenic (HP H5N1) influenza A virus (IAV) into North America in 2021, SCWDS, in collaboration with many federal, state, private, and academic partners, has been involved in ongoing research and surveillance efforts to gain insight into epidemiologic patterns associated with these new viruses in waterfowl. Specifically, we have endeavored to understand the mechanisms that drive these observed epidemiologic patterns. Population immunity is one of these potential factors. However, understanding and measuring population immunity to IAV in waterfowl present unique challenges due to the complex antigenic nature of these viruses, the potential for partial protective responses, and limitations associated with sample collection, testing, and serologic data interpretation.

Along with HP H5N1, waterfowl can be infected with a diversity of low pathogenic (LP) influenza virus subtypes that are characterized by two antigenic viral proteins: hemagglutinin (HA) and neuraminidase (NA). In North America, there are 15 HA subtypes (H1-14, H16) and 9 NA subtypes (N1-9) that occur as LP IAV in wild birds: primarily waterfowl, shorebirds, and gulls. Research by SCWDS and others have documented that previous infections with LP IAV can result in protection or reduced viral shedding during subsequent LP IAV infection. These benefits can occur regardless of LP IAV subtypes involved, whether the same or different. Such pre-exposure can also increase the amount of virus needed for a subsequent infection. Previous infections with IAV can also provide complete or partial protection to ducks and geese subsequently infected with HP H5 viruses. Such protection, even if partial, can result in both reduced mortality and transmissibility and this could impact population susceptibility as well as drive HP H5N1 seasonal outbreaks.

In order to provide some estimate of the complex immunity landscape of waterfowl populations, we

have incorporated a suite of serologic tests that individually, and in concert, can provide insight into previous exposure to LP IAV as well as HP H5N1. Generally speaking, the suite of tests goes from general to more specific in order to gain increasingly detailed information. Serologic testing begins with a bELISA test for antibodies to the IAV nucleoprotein (NP). Since NP is conserved among all IAV subtypes, a positive result indicates previous infection with any IAV (LP or HP). To obtain more specific data, we then test NP antibody positive sera for antibodies to H5 using two antigens that represent a LP North American H5 and the HP H5N1 using two tests for each antigen (hemagglutination inhibition, HI; and virus microneutralization, VN). We also test NP positive sera for antibodies to N1 using an enzyme-linked lectin assay (ELLA). Combined, these results give us an indication of previous exposure to IAV, LP H5, HP H5, and N1. These data also identify birds that are seropositive for both H5 and N1 providing additional evidence of previous infection with HP H5N1. Collectively, these data provide an estimate of partial immunity to HP H5 that may provide some protection against infection with HP H5N1 (antibodies to LP IAV, but not H5 or N1) and more complete protection provided by existing immunity to both H5 and N1. The application of these serologic testing efforts related to understanding the epidemiology of HP H5N1 in North American waterfowl populations was recently reported in two studies (summarized below).

An open door: Field research often benefits from seizing opportunistic events, and during the winter of 2022, HP H5N1 was detected at a field site in Tennessee where ducks were being routinely tested for IAV. The project was a collaboration between **Tennessee Tech University, Tennessee Wildlife Resources Agency** and SCWDS. This was the first detection of HP H5N1 from the Mississippi flyway. During this same time, a telemetry study was being conducted which included numerous mallards that were later found to be infected with HP H5N1 at the time of release. Results from the telemetry **study**,



Blue-winged teal, B. Kurimo-Beechuk

which also involved researchers from the USGS, indicated that the HP H5N1 infections had little impact on the migration behavior of infected birds. These events further provided an opportunity to explore the IAV antibody status of this population prior to and during the introduction of HP H5N1, the short-term immune response in naturally infected mallards, and how existing immunity in this population could have benefited the survival of these HP H5N1 infected mallards. The **study** was recently published in the journal **Emerging Infectious Diseases**. Prior to the introduction of HP H5N1, the prevalence of antibodies to LP IAV in the birds tested was high (79%), but antibodies to H5 and N1 were very limited with only 17% of tested birds being seropositive for both antigens. These results suggest that these wintering mallards did have some partial protection against HP H5N1, and while this may have prevented morbidity and mortality (which was not observed in any of these birds), it did not prevent infection with HP H5N1. This partial protection may have contributed to the lack of observed effects on migration behavior of infected birds reported in the telemetry study.

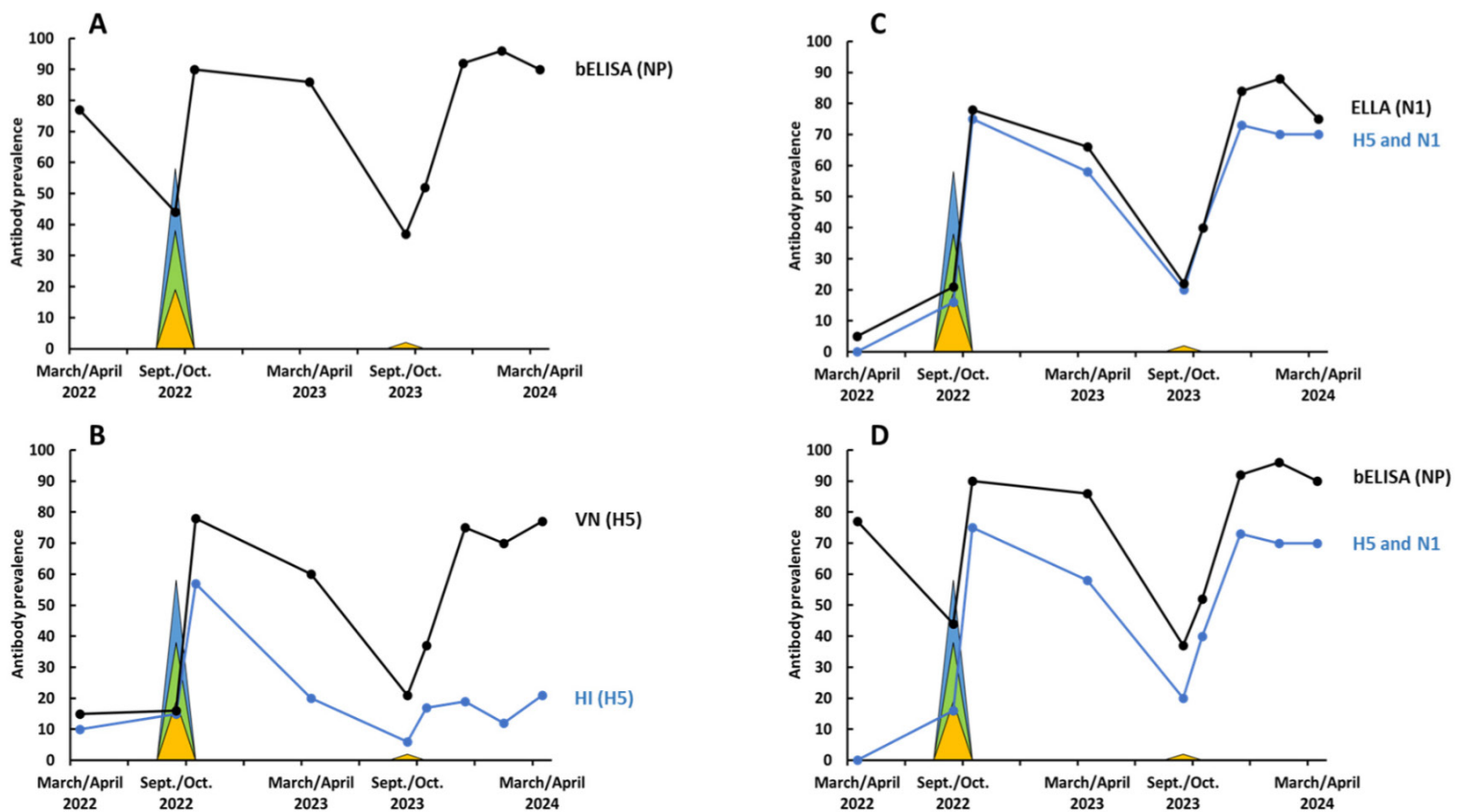
Within one week following detection of HP H5N1, the antibody profile changed drastically with 62% of birds testing positive for antibodies to both H5 and N1. This result not only provided evidence that we could successfully measure a short-term immune response in naturally infected mallards, but also demonstrated the high transmissibility of this virus. It is possible that this high transmissibility and low population immunity may have facilitated the rapid spread and successful introduction of HP H5N1 into North American waterfowl populations. If these results mirrored the situation in other waterfowl populations at the time of introduction, HP H5N1 essentially had an “open door” to exploit susceptible North American waterfowl populations.

Sitting ducks: Thanks to past and current support from the **Mississippi Flyway Council**, we have had the opportunity to annually monitor ducks (primarily blue-winged teal) in the northern (Minnesota) and southern (Louisiana/Texas) portions of the Mississippi flyway before, during, and after the introduction of HP H5N1 to North America. Testing includes both virus and antibody detection. This work is being

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conducted in collaboration with **Louisiana Department of Wildlife & Fisheries**, **Minnesota Department of Natural Resources**, and **U.S. Fish and Wildlife Service**. Results from spring 2022, immediately after HP H5N1 was introduced into the United States, through spring 2024 were **recently published** in the journal **Pathogens**. The objectives of this study were to determine: if the seasonal patterns of HP H5N1 in ducks follow the historic seasonal patterns of LP IAV; if the detection of antibodies to H5 and N1 are predictive of observed seasonal patterns; and if results observed with blue-winged teal can be applied to other duck species.

Despite widespread movement of HP H5N1 within North America during the spring and winter of 2022, this virus was not detected in 1,103 ducks sampled in Louisiana during January to April 2022. Most of the ducks (77%) had antibodies to IAV, which was similar to results from previous years. However, similar to the Tennessee study, only 15% and 5% tested positive for antibodies to H5 and N1, respectively. This indicates



Estimated prevalence of antibodies in blue-winged teal sampled from March 2022 to April 2024: (A) antibodies to nucleoprotein (NP), as detected with bELISA; (B) antibodies to H5, as detected by hemagglutination inhibition (HI) and virus neutralization (VN); (C) antibodies to N1, as detected by enzyme-linked lectin assay (ELLA) and the percentage of teal testing positive for antibodies to both H5 and N1; (D) the percentage of teal testing positive for antibodies to both H5 and N1 compared to those testing antibody-positive to all subtypes based on NP. Filled color areas represent the prevalence of HP H5N1 infection detected in blue-winged teal sampled in Minnesota (blue) and Louisiana/Texas (gold) and mallards sampled in Minnesota (green). Figure previously published in Stallknecht et al., *Pathogens*, 2024.

that although the population had some protective immunity to IAV, specific immunity to H5N1 was minimal. Things changed drastically during September 2022, when HP H5N1 was detected at a high prevalence in blue-winged teal sampled in Minnesota, Louisiana, and Texas. This was followed by a notable increase in the prevalence of birds testing positive for antibodies to both H5 and N1 from 37% in September to 75% and 58% in October and March/April 2023, respectively. We did not detect HP H5N1 in any ducks sampled in these later months. Despite not detecting HP H5N1 in Minnesota blue-winged teal during September



2023, the same antibody response to H5 and N1 was observed increasing from 20% in blue-winged teal sampled in Minnesota during September to 40% in birds sampled in October in Louisiana, to 70-73% of birds sampled from November 2023 to April 2024, [figure on the previous page](#). With the exception of Spring 2022, immediately after the first detected introduction of HP H5N1, the seasonal pattern of this virus has followed the historic pattern of LP IAV in the Mississippi flyway. This pattern is likely driven by low population immunity to IAV as a result of the annual recruitment of naïve hatch-year birds. In September sampling of blue-winged teal in Louisiana during 2022 and 2023, only 10% and 4% of hatch-year birds had antibodies to H5 and N1. Antibodies to NP also were low in this age cohort with only 38% and 23% having antibodies to NP. This implies that these birds were “sitting ducks” with limited protection against HP H5N1 infection. In both years, based on both virus isolation results and serology, this limited protection resulted in seasonal infection followed by increased antibody prevalence and limited infection during the winter and spring. The same seasonal and age-related patterns observed in blue-winged teal were seen with mallards and green-winged teal. Understanding seasonal patterns of HP H5N1 infections and predicting seasonal risks of infection based on something that we can measure (antibody profiles) has potential value in better defining periods of increased risk associated with wildlife mortality, spillover to mammals and other birds, risk of introduction to domestic poultry, and exposure

risks to hunters and wildlife professionals. These risks are not consistent throughout the year and such seasonal variation is important to managing them.

Although peak HP H5N1 infection in duck populations, like LP IAV, is primarily associated with fall migration, precise timing and location within this seasonal window are difficult to predict. During 2022 fall migration, a high prevalence of infection was observed during pre-migration and early migration in Minnesota. During 2023, peak infection may have occurred later, and we did not detect HP H5N1 in September sampled birds in Minnesota or during additional sampling in South Dakota and North Dakota. Additional sampling at these same sites also failed to detect HP H5N1 in September 2024 but the virus was detected through **USDA-National Wildlife Disease Program** surveillance efforts in October and November. This later emergence of HP H5N1 during fall migration is consistent with patterns observed in Europe. Differences in annual patterns within the fall migration period deserve additional study and may relate to many other factors affecting population structure (annual recruitment of hatch-year birds) or migration timing (weather, habitat conditions) that were not considered in this study.

Prepared by Dave Stallknecht and Becky Poulson



Diagnostic Case Highlight

Egg yolk coelomitis in an American robin

Egg yolk coelomitis is most commonly reported in domestic birds, such as chickens, which continuously lay eggs, and in captive parrot species. Rarely, it has been documented in wild birds. Over years of diagnostic evaluations at SCWDS, this condition has been an uncommon diagnosis in free-ranging avian species and is most often secondary to trauma or infection. Historically, cases have been most commonly documented in wild turkeys (Meleagris gallopavo), with individual reports in raptors, aquatic bird species, small game birds, and a woodpecker.

The carcass of an adult female American robin (*Turdus migratorius*) from Kenton County, Kentucky, was submitted for postmortem examination by the **Kentucky Department of Fish & Wildlife Resources (KDFWR)**. On October 9, 2023, the robin was admitted to a wildlife rehabilitation clinic, where it appeared to have leg paralysis and was lethargic with dull mentation. It was noted to be in poor nutritional condition with no obvious external injuries and died within an hour of arrival.



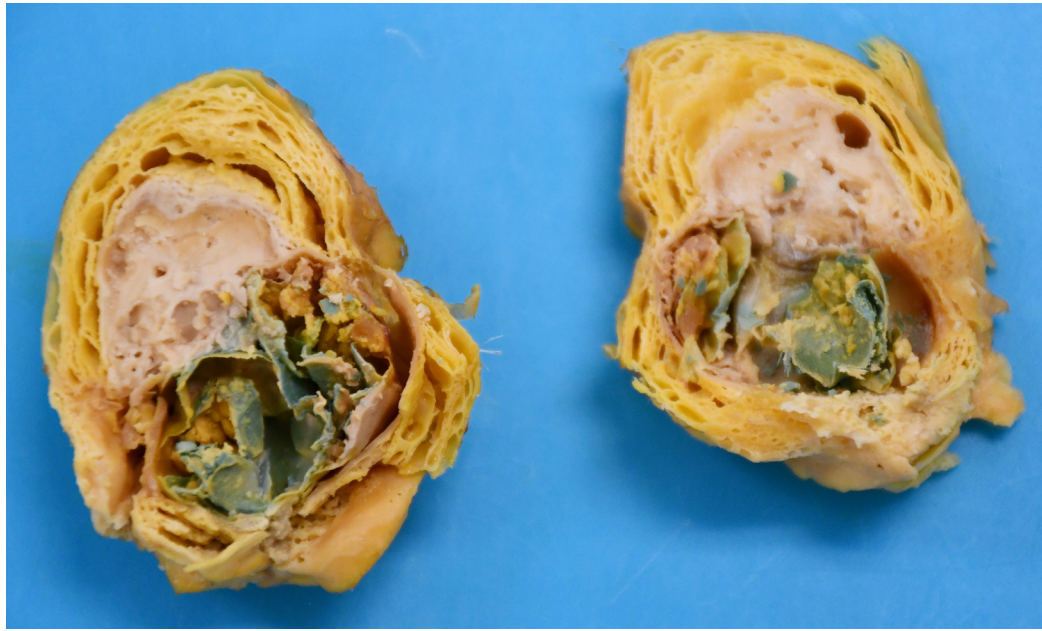
Gross examination at SCWDS revealed that the main body cavity (coelom) was distended by a large (6.0 x 4.5 x 3.0 cm), firm, yellow mass that weighed 30 g (33% of body weight). The mass occupied most of the coelom, while displacing internal organs from their normal position, [image on the left, this page](#). On cut surface, the mass consisted of a thin, yellow, multi-layered structure with a solid, tan, soft center surrounding fragments of hard, sharp-edged turquoise material consistent with eggshell fragments, [image on the next page](#). Additional findings included distended ureters with urinary tract filtrate (urates) and thickened, pale, yellow air sacs with roughened surfaces.

The gross presentation in this robin is consistent with egg yolk coelomitis (sometimes called peritonitis), marking the first recorded case of this condition in a passerine species at SCWDS. Egg yolk coelomitis is a common reproductive disease in domestic birds but is less frequently documented in wild birds, particularly passerines. This condition typically results from an inflammatory response during ovulation, when egg contents are released into the coelomic cavity. In domestic birds, acute or chronic coelomitis can develop secondary to trauma,

Egg yolk coelomitis in an American robin

infection, or other underlying conditions. Mild cases often resolve within 24–48 hours as the material is reabsorbed.

Most cases of severe egg yolk coelomitis in wild birds likely result in death. In rare instances clinical signs may be observed before death, such as in this case. Diagnosis is based on gross and microscopic examination. Histologically, the coelomic mass in this robin contained necrotic material (e.g., dead cells and cell debris) and colonies of gram-



negative bacteria, later identified as *Escherichia coli* (*E. coli*). The latter may have represented contamination from the gastrointestinal tract, such as from traumatic rupture; however, clear evidence of this at necropsy was lacking.

Common sequelae to egg yolk coelomitis include pneumonia, which can occur if egg material enters the air sacs, and body-wide bacterial infection (sepsis), which may result from bacterial colonization (usually *E. coli*) of the yolk. Additional sequelae include yolk clots (i.e., emboli), adhesions, and spread of infection to other organs (e.g., pancreas, spleen, liver, kidneys).

This condition is not important at the population level, but rather appears limited to individuals and is more common in certain species observed at SCWDS, such as wild turkeys. It represents a unique sequela to several inciting causes and is infrequently observed. In the present case of an American robin, potential causes of egg rupture include traumatic injury as the egg was passing through the oviduct. Alternatively, the egg may have been too large or misshapen, causing it to become lodged and eventually rupture. Other factors, such as an obstruction or underlying reproductive issues leading to retrograde movement, could also have disrupted its normal passage, leading to eventual rupture.

The mass created by the ruptured egg was compressing the spinal nerves, which likely resulted in the robin's inability to use its legs and forage effectively. The bird's poor nutritional condition was likely compounded by the mass inhibiting digestion and further limiting normal foraging behavior. Ultimately, death was likely due to a combination of malnutrition and bacterial sepsis.

SCWDS extends its gratitude to KDFWR for submitting this case, as well as to all our member states for their continued and vital contributions to the **SCWDS Research and Diagnostic Service**.

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SCWDS BRIEFS

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Parting views from the Southeast



Black-bellied whistling duck, B. Kurimo-Beechuk