



SCWDS BRIEFS

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

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Eds. M. Ruder and B. Kurimo-Beechuk

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White-tailed deer, Deb Carter

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Wildlife health updates

Wild pig parasite surveys

Wild pigs are an invasive species in the US known to harbor various pathogens that can be transmitted to humans, livestock, and wildlife. Despite extensive control efforts, their populations have grown due to factors like rapid reproduction rates, broad habitat use, and introductions/movements for sport hunting. Previous surveys, **including a nationwide effort from 2006 to 2010**, demonstrated that wild pigs in the US are reservoirs for *Trichinella* spp. and *Toxoplasma gondii*, two zoonotic parasites with significant implications for human and animal health. In fact, toxoplasmosis, caused by *T. gondii*, is considered to be a leading cause of death attributed to foodborne illness in the US and it is one of five neglected parasitic infections in the US that the **Centers for Disease Control and Prevention (CDC)** is targeting for public health action. *Toxoplasma gondii* infects warm-blooded animals, including humans. Wild pigs contribute to the transmission cycle by ingesting *T. gondii* tissue cysts from vertebrate hosts or oocysts from contaminated environments. *Trichinella* spp. are nematodes transmitted through consumption of infected meat, and human cases are often associated with eating undercooked wild game. Wild pigs are a primary source of transmission of species like *T. spiralis*

and *T. pseudospiralis*.

A collaborative project between SCWDS and the **USDA National Feral Swine Damage Management Program** was **recently published** in *Veterinary Parasitology* that investigated exposure of pigs to *T. gondii* and *Trichinella* spp. The project used wild pig serum samples collected by USDA from across the US between 2014 and 2020. Serum was tested for antibodies to *Trichinella* spp. and *T. gondii*, yielding contemporary data on prevalence and spatial distribution of antibodies in wild pigs (indicating previous exposure to these parasites). Specifically, the results of this study showed that the prevalence of *Trichinella* spp. and *T. gondii* antibodies in wild pig populations varies across different regions of the US. The overall *Trichinella* spp. antibody prevalence was 12.4% (927/7467), with seroprevalence highest in the Northeast (19.1% (9/47)) and the Midwest (18.4% (98/532)), and lower in the South (13.4% (763/5694)) and the West (4.8% (57/1194)). Significant differences were found between age classes and sexes, with lower seroprevalence observed in juveniles and males. Further, *Trichinella* spp. antibodies were detected in several states where previous surveillance had not been conducted (**figure, next page**).

Regarding *T. gondii*, the overall seroprevalence was higher than *Trichinella* spp. at 40.8% (2444/5984).

Summary timeline of HPIAV in the US

The introduction of A/goose/Guangdong/1/1996 lineage highly pathogenic clade 2.3.4.4b H5N1 influenza A virus (HPIAV) in North America in late 2021 has caused widespread mortality in wild and domestic birds, and it continues to spillover and infect novel species.



CDC, Centers for Disease Control and Prevention; USDA APHIS, United States Department of Agriculture Animal and Plant Health Inspection Service

First detection of HPIAV in **wild birds** within the continental USA begins with a hunter-harvested American wigeon in Colleton County, South Carolina. The virus rapidly spread throughout the US with additional introductions on both east and west coasts. To date, there are **> 9,500 detections of HPIAV in wild birds in 49 states.**

Wisconsin, Minnesota, Michigan, Iowa, New York, and Alaska see the first **mammal HPIAV detections in red foxes, bobcats, and Virginia opossums.** Detections primarily occur in terrestrial carnivores, which likely contract the virus via ingestion of infected prey species and carrion. Currently, the virus has been detected in more than 20 species of mammals.

A **dairy cattle worker in Texas** is infected with HPIAV. The CDC performs next generation sequencing of the virus genome collected in samples from this worker. HPIAV H5N1 clade 2.3.4.4b is identified and is closely related to viruses found in Texas dairy cattle. Analysis of the viral genome reveals the HA gene found in the human sample is closely related to the HA gene found in wild birds and domestic poultry infected with H5N1 clade 2.3.4.4b. **APHIS issues a federal order** requiring testing prior to interstate movement of lactating dairy cattle and mandatory reporting of positive test results in livestock.

January
2022

February
2022

May
2022

March
2024

April
2024

May
2024

Commercial meat turkeys in Indiana and commercial broiler chickens in Kentucky mark the start of HPIAV detections in **domestic poultry** across the USA. Currently, **> 99,000,000 domestic poultry across 48 states** have been affected by HPIAV. Sporadic outbreaks continue to occur.

Reports of illness primarily in older **dairy cattle** begin to occur throughout Kansas, New Mexico, and Texas during this month. HPIAV is confirmed in dairy herds in Kansas, Texas, and Michigan. At the time of writing, there are H5N1 virus detections in **>155 dairy herds across 13 states:** Kansas, Idaho, Iowa, Michigan, New Mexico, North Carolina, Ohio, South Dakota, Colorado, Wyoming, Texas, and Minnesota.

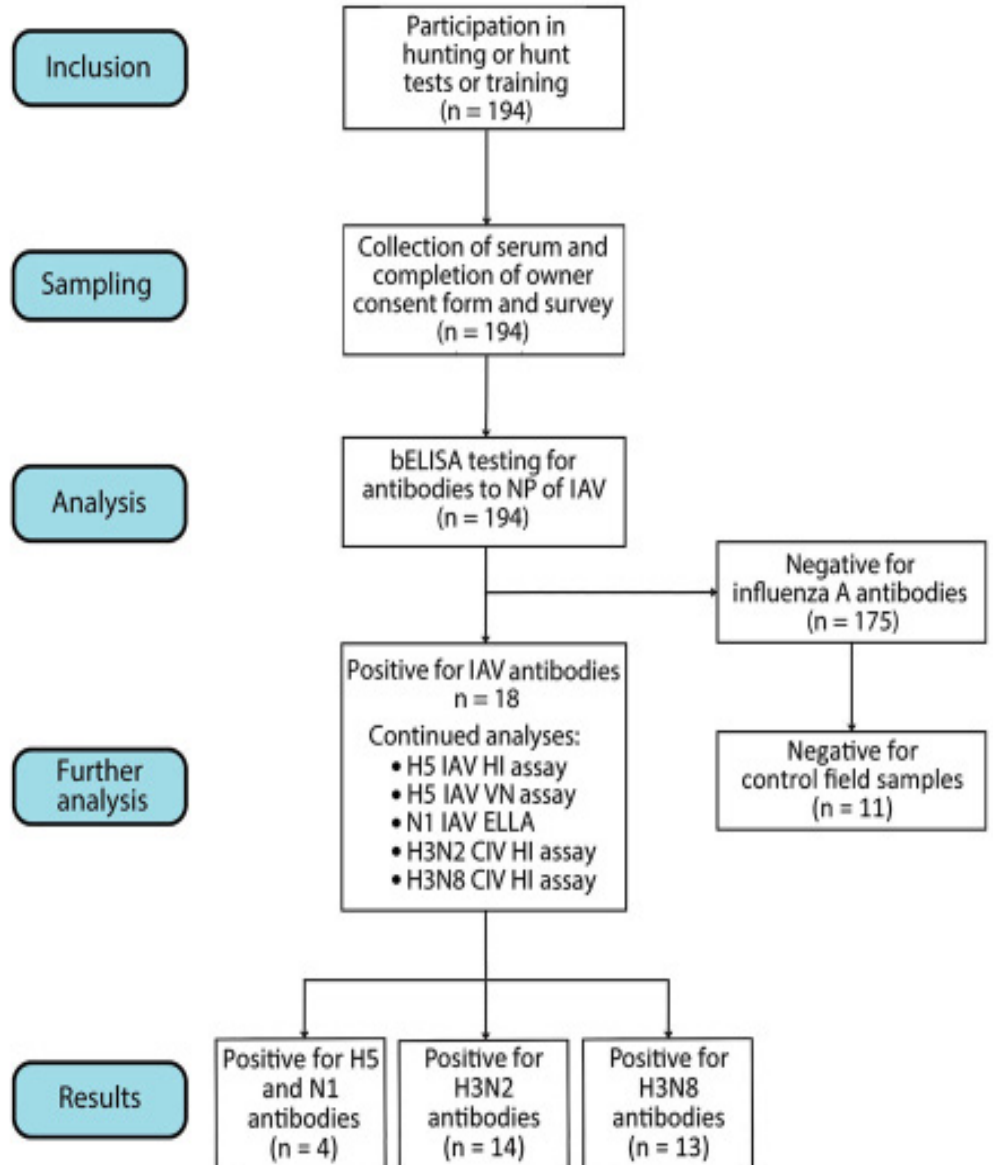
Two cases of HPIAV are reported in dairy cattle workers in Michigan. Analysis of samples collected from the first case reveals the genome of A/Michigan/90/2024 is very similar to sequences found in infected cows. The second case in Michigan reports respiratory symptoms, a deviation from previous cases. Direct cow-to-human transmission is suspected as a route of infection. USDA confirms **HPIAV in alpacas** from an Idaho farm. HPIAV H5N1 is found in **wastewater samples in 9 Texas cities.** **CDC unveils an influenza A wastewater dashboard**, which tracks influenza A virus at wastewater sites. Monitoring efforts reveal increased IAV RNA concentrations at **59 wastewater treatment plants** throughout the US. USDA announces **financial assistance** for HPIAV- affected herds.

This is a rapidly evolving situation: to view the most up to date detections of HPIAV, please visit the **USDA APHIS website**. For a summary of the current H5N1 situation and to view public health recommendations, please visit the **CDC website**.

HPIAV survey in bird dogs

As detections of H5N1 HPIAV continue in wild mammals, the risk of spread to domestic animals is of increased interest. To better understand the risk H5N1 HPIAV posed to retrieving dogs who actively come into contact with potentially infected birds, a collaborative team of researchers from **Pennsylvania State University, Cornell University, Washington Department of Fish and Wildlife, SCWDS**, and others, **recently published** the results of a serosurvey of hunting dogs from Washington state. Following the waterfowl hunting season (October 2022 – January 2023), 194 dogs who engaged in bird hunting or training exercises were sampled, and their owners given a survey for details on the dogs’ retrieving activities, canine influenza virus (CIV) vaccination status, and clinical history. Sera were screened using a commercially available blocking ELISA to detect antibodies to IAV and those that were IAV antibody positive were further tested for antibodies to H5 and N1. Antibodies to IAV were detected in 18/194 (9%) dogs tested;

four of those 18 were seropositive for both H5 and N1 antibodies (**above figure**), and each had reportedly hunted waterfowl in areas with H5N1 HPIAV detections in wild ducks. Fortunately, none of the antibody positive individuals displayed clinical signs of HPIAV infection. This, coupled with low seroprevalence in hunting dogs surveyed here indicates that H5N1 HPIAV strains that emerged in North America in 2022 were likely poorly adapted to dogs. Given the important interface between domestic dogs and humans, the continued surveillance of companion animals, especially those in contact with wildlife, is warranted.



HPIAV persistence in waterbodies

While the development of a tool to detect influenza RNA in wastewater has shown some promise, its efficacy is still unclear. It is clear however, that IAV can remain infective in natural waterbodies for extended periods of time, and they can be shed into the environment through wild birds. A **study recently published** by researchers at SCWDS and **USGS** builds on laboratory and field research that have shown low pathogenicity (LP) IAV persists longest at cold temperatures, and can remain infectious for up to 200 days at 17°C. In September 2020, surface water was collected from four waterbodies in northwestern Minnesota, filtered, then physically and chemically characterized. Paired cloacal and oropharyngeal (CL/OP) swabs were then collected from live-captured mallard ducks (*Anas platyrhynchos*) into distilled water, which was then used to inoculate replicate tubes from each natural waterbody. Samples collected at time point 1 (T1) were returned to the lab where they were tested for IAV, and replicate tubes for each sample were placed at the field sites in steel drums. Retrieval of the samples deployed in the environment occurred at ecologically relevant periods of the year: October 2020 (ice formation), April 2021 (ice out), and June 2021 (summer), and were returned to the lab for viral testing. LP IAV was isolated from 65/266 (24%) samples collected at T1, and the most commonly identified subtypes were H3N8 and H4N6, common duck subtypes; H4N8, H4N9, H6N1, and H7N3 were also detected. Over the course of the experiment, H3N8, H4N6, and H4N8 IAVs remained infectious over the wintering period or for at least 202 days under semi-ambient conditions in northwestern Minnesota waterbodies. The ability of IAVs to remain infectious in the environment, especially over seasons, may play a role in subsequent transmission to wild bird hosts. The results of this study help further delineate our understanding of IAV persistence in natural settings.



Prepared by Jake Shurba, Dave Stallknecht, Becky Poulson, and Betsy Kurimo-Beechuk

Bovine TB in Michigan deer

Bovine tuberculosis (bTB) is endemic in wild white-tailed deer (WTD) in part of the northeastern portion of Michigan's Lower Peninsula (LP) and the **SCWDS BRIEFS** has provided updates on this unique situation since it was recognized in 1994. Here we report on recent developments involving detection of infected deer a considerable distance from the endemic area, human bTB infections associated with deer, and a field study evaluating the effectiveness of delivering tuberculosis vaccines to wild deer.



Domestic cow, B. Kurimo-Beechuk

Bovine tuberculosis is a transmissible, zoonotic disease caused by *Mycobacterium bovis* infection in humans, wildlife, and domestic animals. In 1994, the **Michigan Department of Natural Resources (MDNR)** identified severe pulmonary tuberculosis due to *M. bovis* infection in a single deer in the northeastern LP. Follow up surveillance in 1995 detected additional cases in the area and suggested that the *M. bovis* had become established in a wild WTD population for the first time. Previous detections of bTB in wild WTD, including one in the same area of Michigan in 1975, were regarded as isolated spillover cases from cattle with no epidemiological significance to free-ranging wildlife or domestic livestock. Additional investigations in the 1990s in Michigan identified high population densities and unnatural congregation of wild deer at baiting and supplemental feeding sites as facilitators

of disease transmission and major contributors to the establishment of a wildlife reservoir of bTB.

It is hard to believe that it has been 30 years since this unusual situation emerged and it serves as an excellent example of the great difficulty of managing established disease in free-ranging wildlife. In that time, active and passive surveillance has detected 1,024 cases of bTB in wild deer. Management of bTB in wild deer has focused largely on reducing population density and prohibiting or restricting baiting and feeding, and some successes have been achieved. However, the disease persists in wild deer at a low prevalence in the endemic area and eradication does not appear possible under the current management strategies.

Bovine tuberculosis was eradicated from cattle in Michigan in 1979 as part of the **National Tuberculosis Eradication Program**. However, the presence of bTB in the wild deer reservoir has taken a heavy toll on the state's cattle industry since the first detection of an infected herd in 1998. Bovine TB has been found in 83 cattle and bison herds. Statewide bTB accredited-free status was lost resulting in split-state status with an Accredited Free Zone comprising 95% of the state and a Modified Accredited Zone (MAZ) encompassing a four-county area where bTB is endemic in wild deer. All cattle and bison herds in the MAZ are under movement restrictions and bTB testing protocols that are much more stringent than for herds in the Accredited Free Zone.

In February 2024, the **MDNR announced detection of bTB in a wild deer** in Benzie County on the Lake Michigan coast remote from the MAZ. As required by the Memorandum of Understanding the **Michigan Department of Agriculture & Rural Development (MDARD)** has with MDNR and USDA, a testing area for cattle must be designated around the location of a bTB-positive wild deer outside of the MAZ in order to maintain

bTB in Michigan deer

Michigan's split-state bTB status. All cattle and bison herds within this area must then be tested to ensure they have not contracted the disease. Consequently, MDARD has proposed an order that requires bTB testing within specific portions of Benzie and adjacent Manistee counties by December 31, 2024. In March 2024, **four cases of human infection** with *M. bovis* associated with Michigan's wild deer were reported, bringing the total to seven affected humans since 2002. These four cases occurred between 2019 and 2022 and included cutaneous disease, two severe pulmonary infections, and human-to-human transmission. *M. bovis* was cultured from three of the cases and results of molecular testing indicated the isolates were closely related to the *M. bovis* strains circulating in Michigan deer and cattle. All of the patients improved with treatment.

A review of all seven reported cases revealed direct contact with deer in five patients. Inoculation with *M. bovis* in the two cutaneous cases occurred when patients accidentally cut their hands while field dressing or doing taxidermy work on deer from the endemic area. Transmission modes in the five pulmonary cases are less clear. Some may be due to inhalation of *M. bovis* while field dressing deer. One patient had hand fed deer and cared for a sick fawn while another had no reported contact with deer. Transmission of *M. bovis* from this latter patient to his girlfriend is suspected in the single case of human-to-human transmission. Interestingly, three of the disseminated pulmonary cases occurred in immunocompromised individuals.

A **field trial** to evaluate the efficacy of tuberculosis vaccine delivery to wild deer began in February 2024 in Alpena County in Michigan's LP where bTB is endemic in deer. The study is a collaborative effort between MDNR, **Michigan State University (MSU)**, and the U.S. **Department of Agriculture's Animal and Plant Health Inspection Service-Wildlife Services (WS)**. Vaccinating wild deer rather than cattle could be an additional tool

for bTB management because vaccinating cattle will result in false positive tuberculin test results: vaccinated cattle cannot be distinguished from diseased cattle via the test most commonly used.



The vaccine is an attenuated strain of *M. bovis* known as bacillus Calmette-Guerin (BCG). Previous, controlled studies have shown that BCG vaccine reduces disease severity in several species, including WTD, which is hypothesized to reduce disease transmission. In the current field trial, vaccine delivery units (VDUs) containing BCG vaccine were placed in crop fields frequented by deer. The VDUs consist of cubes of shredded alfalfa and molasses that house an edible sphere, encapsulating the liquid vaccine. Trail cameras and personnel from WS and MSU monitored the baited sites. After two days, unconsumed VDUs were removed from the environment. Wildlife Services personnel lethally removed a subset of deer from the study sites and analysis of samples is ongoing. The ultimate goal of this and related studies is to determine the practicality and viability of oral BCG vaccination of wild deer for bTB management. **Click here** for additional information on bTb in Michigan.

Prepared by John Fischer



Diagnostic Case Highlight

Droopy ears in a white-tailed deer

In recent years, the SCWDS Research & Diagnostic Service has received multiple reports from member states about sightings of white-tailed deer with ears of abnormal conformation (i.e., droopy). One or both ears may be affected. These reports often originate from game camera sightings or hunter-harvested animals. Droopy ears may be associated with a variety of causes such as chronic wasting disease or hemorrhagic disease, making it crucial to note behavior and physical signs.

In November 2022, SCWDS received a “droopy ear” case. A 5.5-year, male white-tailed deer was hunter-harvested in Rapides Parish, LA. Immediately after harvest, the hunter noted the buck’s abnormal ears, and notified the Louisiana Department of Wildlife and Fisheries (LDWF) who submitted the head and a photo to SCWDS for evaluation (image, below).

Gross examination revealed bilateral, chronic external ear (pinnae) lesions. Both ears were firm, of abnormal shape, and deviated downwards and backwards. Further, ear margins were irregularly folded and thickened,



with occasional scabbing. Internal surfaces of both ears were coated with dark brown to black, crumbly and granular material (consistent with dried blood and inflammatory debris). Low numbers of *Ixodes scapularis* (deer tick) adults were firmly attached near

the opening of the ear canal. The outermost (vertical) ear canals contained a small to moderate amount of orange-brown and slightly dry, waxy debris (image, next page). The right ear canal also contained scant, pasty to wet, yellow exudate (pus). The left ear had a rectangular, partial-thickness defect on the inner surface. The underlying soft tissues were less firm, slightly wet, friable (i.e., easily torn), and discolored brown. Microscopic evaluation of the

Droopy ears in a white-tailed deer



Image of the droopy ear with opened ear canal and skin reflected over the side of the head. Note waxy debris accumulation in the canal, SCWDS.

a heavy burden of ticks or other ectoparasites, damage to blood vessels, congenital (since birth) defects, trauma, or other causes of direct damage to the ear or its blood supply. Secondary infections from opportunistic bacteria may arise in deer with ear disease. Factors such as prolonged skin moisture and breaches in the outer skin layer (epidermis) may facilitate infections. *Pseudomonas aeruginosa*, the bacterium isolated from the affected ears in this case, has been implicated in a variety of ear infections in dogs and humans. In humans with weakened immune systems, severe and debilitating ear disease can result from infection. If this deer was similarly weakened, it may have been predisposed to bacterial infection. A previous SCWDS case of a deer with abnormal ears had abscesses in soft tissues around the ear; and thus, bacterial infection may be an important contributing factor in some of these cases. Another potential cause, severe ectoparasitism, can cause similarly abnormal and drooping ears in domestic ruminants. In these species, the condition (called “gotch ear”) is associated with Gulf Coast tick (*Amblyomma maculatum*) infestation.

Overall, “droopy ears” in deer likely is not due to one single cause, but as with many conditions in wildlife, is likely multifactorial with multiple, concurrent or cumulative, predisposing and contributing factors. These include mechanical or structural damage to the ears, tissues around them, or nerves controlling them, and systemic disease causing the deer to hold its head and/or ears abnormally. Other field signs, such as lethargy, may help narrow the list of differential diagnoses.

Prepared by Tori Andreasen, Alisia Weyna, and Nicole Nemeth

tissues revealed degenerative changes in the ear pinna cartilage, including chronic inflammation, cell death (necrosis), and scarring (fibrosis). A swab of the middle ear yielded heavy growth of *Pseudomonas aeruginosa* and no growth of anaerobic bacteria or *Mycoplasma* sp.

These chronic inflammatory and degenerative changes, especially in the cartilage, led to the permanent ear deformity in this case. While a definitive cause of these changes was not apparent due to lesion chronicity, a number of causes could incite the development of chronic ear disease. Those include

Changing faces at SCWDS

The SCWDS family tree, with branches all over the world, continues to change and grow. Over the last year, we have had several new staff and students join the SCWDS team, as well as several departures. Since SCWDS is a research unit at a land grant university, training the next generation of wildlife health professionals is an important part of the SCWDS mission and our faculty and staff are passionate in helping fuel this effort. We are proud of our former employees and students who are now contributing to the broader wildlife conservation, agricultural, domestic animal, and public health communities. We look forward to watching their continued growth and expect great things.

Dr. Chloe Goodwin accepted a faculty position in the Department of Pathology here at the University of Georgia's College of Veterinary Medicine. Chloe started as an Assistant Professor in March 2024, and continues to work with SCWDS on her PhD research investigating aspects of lymphoproliferative disease virus in wild turkeys.

Dr. Alisia Weyna accepted a Clinical Instructor position in the Department of Pathobiological Sciences, University of Wisconsin School of Veterinary Medicine in Madison, Wisconsin. Alisia previously completed her anatomic pathology residency with the Department of Pathology and SCWDS, then served as SCWDS staff pathologist until January 2024. She continues to work with SCWDS on her PhD research investigating multiple diseases of deer.

Dr. Adam Edge was recently hired by Tennessee Wildlife Resources Agency as the Deer Program Coordinator. While at SCWDS, Adam served as a Post-Doctoral Research Associate studying wild turkey pathogens and their potential population-level effects.

Prepared by Betsy Kurimo-Beechuk and Mark Ruder





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Parting views from the Southeast



Wood storks, B. Kurimo-Beechuk